Conflict between heterozygote advantage and hybrid incompatibility in haplodiploids (and sex chromosomes)

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Running title:
Heterosis *versus* hybrid breakdown

Abstract

In many diploid species the sex chromosomes play a special role in mediating reproductive isolation. In haplodiploids, where females are diploid and males haploid, the whole genome behaves similarly to the X/Z chromosomes of diploids. Therefore, haplodiploid systems can serve as a model for the role of sex chromosomes in speciation and hybridization. A previously described population of Finnish *Formica* wood ants displays genome-wide signs of ploidally and sexually antagonistic selection resulting from hybridization. Here, hybrid females have increased survivorship but hybrid males are inviable. To understand how the unusual hybrid population may be maintained, we developed a mathematical model with hybrid incompatibility, female heterozygote advantage, recombination, and assortative mating.

The rugged fitness landscape resulting from the co-occurrence of heterozygote advantage and hybrid incompatibility results in a sexual conflict in haplodiploids, which is caused by the ploidy difference. Thus, whereas heterozygote advantage always promotes long-term polymorphism in diploids, we find various outcomes in haplodiploids in which the population stabilizes either in favor of males, females, or via maximizing the number of introgressed individuals. We discuss these outcomes with respect to the potential long-term fate of the Finnish wood ant population, and provide approximations for the extension of the model to multiple incompatibilities. Moreover, we highlight the general implications of our results for speciation and hybridization in haplodiploids versus diploids, and how the described fitness relationships could contribute to the outstanding role of sex chromosomes as hotspots of sexual antagonism and genes involved in speciation.

Introduction

Haplodiploids are an emerging system for speciation genetics (Koevoets and Beukeboom, 2009; Kulmuni and Pamilo, 2014; Lohse and Ross, 2015; Knegt et al., 2017). Although ≈ 20% of animal species are haplodiploid (comprising most *Hymenopterans*, some arthropods, thrips and *Hemipterans*, and several clades of beetles and mites; Crozier and Pamilo, 1996; Evans et al., 2004; de la Filia et al., 2015), little evolutionary theory has been developed specifically for speciation in haplodiploids (Koevoets and Beukeboom, 2009). Under haplodiploidy with arrhenotoky (hereafter simply haplodiploidy; Suomalainen et al., 1987), males develop from the mother's unfertilized eggs and are haploid, whereas eggs fertilized by fathers result in diploid females. Since this mode of inheritance is, from a theoretical viewpoint, similar to that of the X/Z chromosome, most work on speciation of haplodiploids draws on the rich literature of sex chromosome evolution (Jablonka and Lamb, 1991; Presgraves, 2008; Johnson and Lachance, 2012; Lohse and Ross, 2015). An important similarity between haplodiploids and X/Z chromosomes is that recessive mutations in the haploid sex are exposed to selection, but they are masked in diploids. This is expected to lead to faster evolution in the sex chromosomes (Charlesworth et al., 1987) that may partly underlie the large-X effect (Presgraves, 2008). The large-X effect refers to the observation that the sex chromosomes seem to play a special role in speciation by acting as the strongest barrier for gene flow between hybridizing lineages across different species (Höllinger and Hermisson, 2017). Similarly, haplodiploid species have been suggested to acquire reproductive isolation earlier and speciate faster than diploid species (Lohse and Ross, 2015; Lima, 2014). Although the factors influencing haplodiploid and X/Z chromosome evolution are not expected to be exactly the same (e.g. movement of sexually antagonistic genes to the sex chromosomes, dosage compensation between the sex chromosomes and autosomes, and turnover of sex chromosomes cannot occur in haplodiploids; Abbott et al., 2017), by studying haplodiploid models we can both improve our understanding of how speciation happens in the large subgroup of the animal kingdom that is haplodiploid, and gain new insights into the role of X/Z chromosomes in speciation for diploid species.

Recent studies have shown that hybridization and resulting gene flow between diverging populations may be important players in the speciation process since signs of hybridization and introgression are being observed ubiquitously in natural populations (Mallet, 2005; Dieckmann and Doebeli, 1999; Schluter, 2009; Schluter and Conte, 2009; Seehausen et al., 2014). When a hybrid population is formed, various selective forces may act simultaneously to either increase or decrease hybrid fitness, which dictate the fate of the population. One commonly documented finding is hybrid incompatibility (Presgraves, 2008; Fraïsse et al., 2014; Chen et al., 2016), where combinations of alleles at different loci interact to confer poor fitness when combined in a hybrid individual (Bateson, 1909; Dobzhansky, 1936; Muller, 1942; Orr, 1995). In a hybrid population, the existence of hybrid incompatibility reduces the mean population fitness. This deficit can be resolved either through reinforcement (evolution of increased premating isolation to avoid production of unfit hybrids; Servedio and Noor, 2003) or by purging (demographic swamping leading to extinction of one of the local populations/species or reinstatement of the ancestral allele combinations; Wolf et al., 2001). On the other hand, hybridization can transfer adaptive genetic variation from one lineage to another (Heliconius Genome Consortium, 2012; Song et al., 2011; Whitney et al., 2010) and may result in overall heterosis (also known as hybrid vigor): a higher fitness of hybrids as compared to their parents (Schwarz et al., 2005; Chen, 2013; Bernardes et al., 2017). Heterosis can stabilize polymorphisms by conferring a fitness advantage to hybrids and thereby favor the maintenance of hybridization either through the improved exploitation of novel ecological niches or the masking of recessive deleterious mutations. Therefore hybrid incompatibility acts to avert ongoing hybridization while heterosis favors the maintenance of hybrids.

One example of the simultaneous action of hybridization-averse and hybridization-favoring forces is found in a hybrid population of *Formica polyctena* and *F. aquilonia* wood ants in Finland (Kulmuni et al., 2010; Kulmuni and Pamilo, 2014; Beresford et al., 2017). Here, it has been reported that hybrid (haploid) males do not survive to adulthood, whereas (diploid) females have higher survivorship when they carry many introgressed alleles as heterozygotes (i.e., heterozygous for alleles originating from one of the parental species in a genomic background otherwise from the other parental species). Thus, a combination of hybrid incompatibility and heterosis seems to dictate the dynamics of the population in a ploidy-specific manner: hybrid haploid males suffer a fitness cost while diploid hybrid females can have a selective advantage over parental ones. Here, the differences in ploidy create an apparent sexual conflict (sensu Arnqvist and Rowe, 2005) between haploid males and diploid females , because their fitness landscapes (i.e., the complex relationship between genotypes and fitness created via hybrid incompatibility and heterozygote advantage) are different. This conflict is absent if the same rugged fitness landscape occurs in diploid autosomes.

When both hybridization-averse and hybridization-favoring forces are acting, the long-term resolution of a hybridizing population is difficult to foresee: will hybridization eventually result in either complete speciation or extinction of one of the populations involved? Alternatively, can it represent an equilibrium maintained stably on an evolutionary time scale? Furthermore, will the probability of these outcomes depend on ploidy? In other words, is one of these outcomes more probable when interacting genes are found on a “haplodiploid” X/Z chromosome than when they exist on a “diploid” autosome?

We here develop and analyze a population-genetic model of an isolated hybrid population in which both hybridization-averse and hybridization-favoring forces are acting, and we study the evolutionary outcomes in both haplodiploid and (fully) diploid genetic systems. The rich dynamics of the haplodiploid model can result in four possible evolutionary stable states depending on the strength of heterozygote advantage *versus* hybrid incompatibility, the strength of recombination, and the degree of assortative mating. This includes a case of symmetric coexistence (where all diversity is maintained) in which both alleles can be maintained despite the segregating hybrid incompatibility, and in which long-term hybridization is favored. We find that the dynamics differ between haplodiploid and diploid systems and that, unlike in previous models of sexual conflict in haplodiploid populations (Kraaijeveld, 2009; Albert and Otto, 2005), the conflict is not necessarily resolved in favor of the females. Indeed, a compromise may be reached at which the average fitness of females is decreased to rescue part of the fitness of males. Moreover, evaluation of the model using the data from the natural hybrid population suggests that, under the assumption of an equilibrium, the

Finnish ant population may represent an example of compromise between male costs and female benefits through asymmetric coexistence. We discuss our findings with respect to the long-term effects of hybridization, the potential for speciation in haplodiploid versus diploid species, and with respect to their relevance for X- or Z-linked alleles in diploid individuals.

Materials and Methods

The model

We model an isolated haplodiploid or diploid hybrid population with individuals from two founder populations P_+ and P_-. Note that throughout the manuscript, we preferentially refer to (sub-)populations rather than species; in those instances in which we use the term 'species' it is in order to emphasize that the two populations have diverged sufficiently for (potentially strong) hybrid incompatibility to exist. We assume discrete generations and consider two loci, **A** and **B**. Each locus has two alleles, the '+' allele (A_+ or B_+) inherited from population P_+ and the '$-$' allele (A_- or B_-) inherited from population P_-. We refer to 'hybrids' as individuals that carry two alleles from each of the two parental populations and cannot be assigned to either parental background. We refer to 'introgressed' individuals as those genotypes for which three of the four alleles are from the same parental population; these genotypes are identical to those produced by hybridization followed by backcrossing. We ignore new or recurrent mutation and genetic drift. Thus, male and female populations are of effectively infinite size; selection modifies the relative abundance of the different haplotypes/genotypes but not the number of individuals (soft selection). The life cycle is as follows (Fig. 1; see also Table 1 for a list of model parameters); consistent with the recursions defined below, we begin the life cycle at the adult stage:

1. mating, either randomly or via genotype matching with assortment strength α as detailed below;
2. recombination (in diploid individuals) at rate ρ;
3. viability (or survival) selection, where heterosis is modeled as a heterozygote advantage, σ, and hybrid incompatibility is modeled as a fully recessive negative epistasis, γ_1 and γ_2 (further details are provided below and in Figure 2).

Viability selection

The fitness landscape described here (Fig. 2) is inspired by the situation observed in Finnish *Formica* ants (Kulmuni et al., 2010; Kulmuni and Pamilo, 2014; Beresford et al., 2017). There, the authors discovered heterosis in the diploid females but recessive incompatibilities expressed in the haploid males. This creates a situation in which the same alleles that are favored in heterozygous females are selected against in hybrid haploid males and homozygous hybrid females. In the haplodiploid genetic system, males possess only one copy of each locus so they cannot be heterozygous and, therefore, cannot experience heterozygote advantage (Fig. 2(b)). Therefore, the fitness landscape with heterozygote advantage and recessive hybrid incompatibility expresses itself as an apparent sexual conflict when sexes differ in ploidy, as in haplodiploids or for X/Z chromosomes.

In our model, selection for heterozygous individuals is multiplicative with respect to the number of heterozygous loci: introgressed individuals with one heterozygous locus have fitness $1 + \sigma$, whereas diploid hybrid individuals that are heterozygous at both loci have

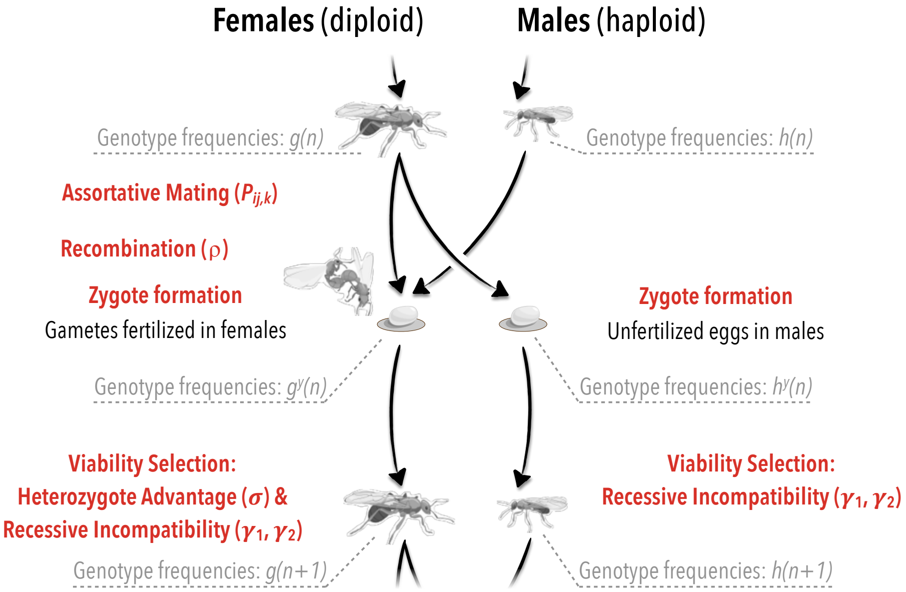


Figure 1: Illustration of the haplodiploid life cycle and its parametization

Table 1: List of model parameters.

Symbol	Parameter	Limits
σ, ω	**Strength of heterozygote advantage**, resulting in fitness $\omega = (1+\sigma)$ or $\omega^2 = (1+\sigma)^2$ of introgressed or double heterozygous diploid hybrids, respectively.	$\omega - 1 = \sigma > 0$
γ_1, γ_2	**Strength of fully recessive negative epistasis**, resulting in fitness $(1-\gamma_1)$ for A_+B_- homozygous diploid hybrids and A_+B_- hybrid haploid males, and $(1-\gamma_2)$ for A_-B_+ homozygous diploid hybrids and A_-B_+ hybrid haploid males.	$0 \leq \gamma_1, \gamma_2 \leq 1$
ρ	**Recombination rate** between locus **A** and **B**.	$0 \leq \rho \leq 0.5$
α	**Strength of assortment** via genotype matching, where $\alpha = 0$ represents random mating, $\alpha > 0$ represents assortative mating among conspecifics, and $\alpha < 0$ represents assortative mating between heterospecifics.	$-1 \leq \alpha \leq 1$

survivorship $(1+\sigma)^2$ (Fig. 2(a)). Finally, the recessive epistatic incompatibility parameter γ_1 acts on individuals homozygous or haploid for the A_+B_- haplotype, and γ_2 acts on individuals homozygous or haploid for the A_-B_+ haplotype (without loss of generality, we assume $\gamma_1 \geq \gamma_2$). Thus, epistasis in this model can be asymmetric, reflecting, for example, two Dobzhansky-Muller incompatibilities of different strength that have accumulated at a negligible recombination distance between the same chromosome pairs. Note that when $\gamma_1 = \gamma_2 = 1$, haploid hybrid males and homozygous hybrid zygotes are produced but do not survive to adulthood and that the classical case of a single Dobzhansky-Muller incompatibility is recovered when $\gamma_2 = 0$.

Assortative mating

Prezygotic isolation via assortative mating is an important mechanism that could mediate the detrimental effects to the population caused by the co-occurence of heterozygote advantage and epistasis modeled here. In the Finnish wood ant population that inspired our model (Kulmuni and Pamilo, 2014), almost all egg-laying queens collected had been inseminated by males of the same genetic group, indicating that prezygotic isolation barriers are likely operating to result in assortative mating. In this case, assortative mating could arise via choosiness of mating partners, via genotype-dependent development times, or via other post-mating prezygotic mechanisms. We implemented assortment via genotype matching (reviewed in Kopp et al. (2017)), where the proportion of matings depends on the genetic distance between two mating partners (and their respective frequencies in the population). We define the genetic distance between the genotypes of a mating pair as the average Hamming distance, i.e. the number of differences between 2 aligned sequences of characters, between all possible pairs of haplotypes with one parter from each sex. We use quadratic assortment (e.g., De Cara et al., 2008), which results in assortative mating without costs of choosiness but with sexual selection. The mating probability of a pair of male and female genotypes, $P_{ij,k}$ depends on the genetic distance between the two mates, the choosiness of the female, and the abundance of the different haplotype and genotypes as detailed below.

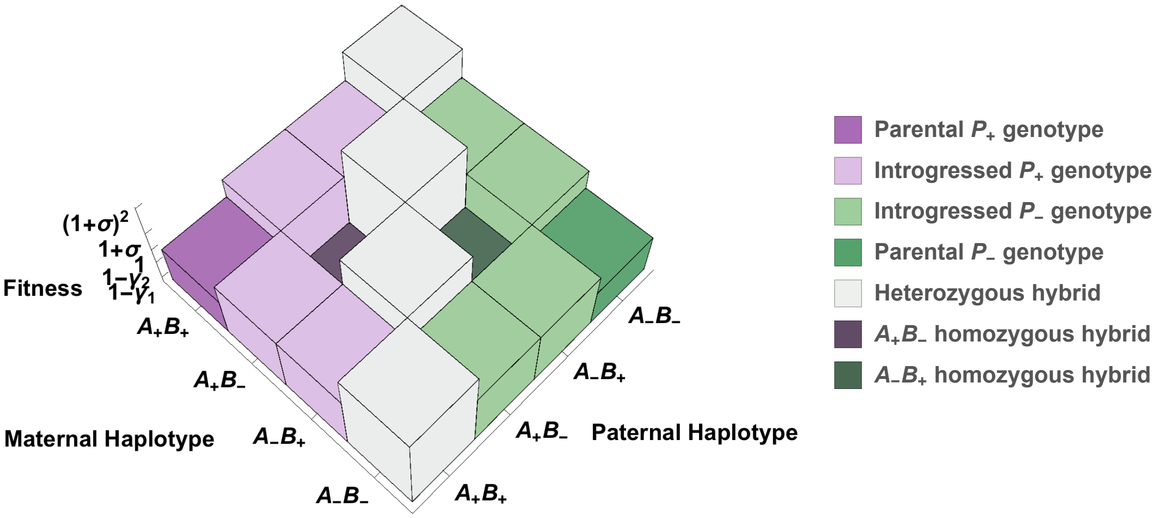
Mathematical modeling and analysis

In a given generation n, the frequencies of the male and female adults are given by $h_k(n)$ and $g_{ij}(n)$, respectively, with i and k indicating the haplotype received maternally and j the one of paternal origin. Without loss of generality, we assign index $i = 1$ to haplotype A_+B_+, index $i = 2$ to haplotype A_+B_-, $i = 3$ to haplotype A_-B_+ and, $i = 4$ to A_-B_-. Below, we describe the modeled life cycle (illustrated in Fig. S1) which determines how frequencies change from one generation to the next.

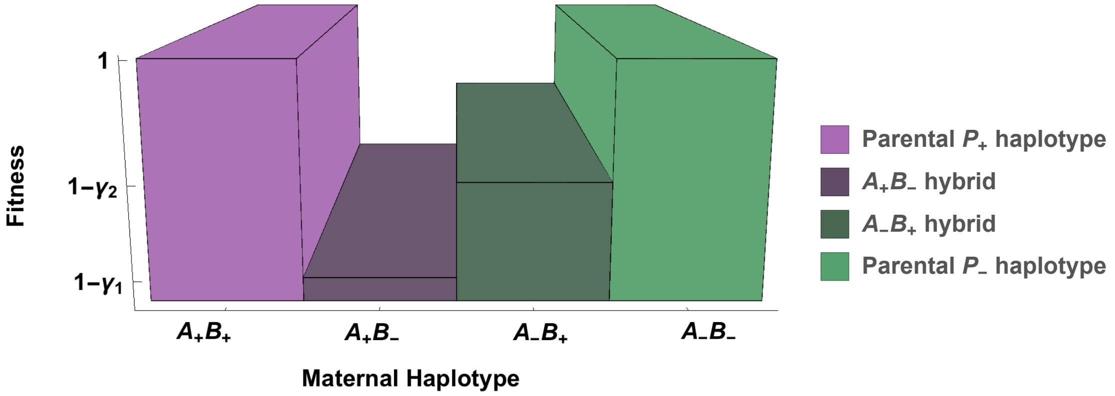
1. As detailed in figure 1 the first step of the life cycle is the mating between two individuals. The mating probability between an ij female and a k male is given by:

$$P_{ij,k}(n) = \frac{(1-\alpha^{\frac{d_{i,k}+d_{j,k}}{2}})g_{ij}(n)h_k(n)}{\sum_i\sum_j\sum_k(1-\alpha^{\frac{d_{i,k}+d_{j,k}}{2}})g_{ij}(n)h_k(n)} \tag{1}$$

   with $d_{i,k}$ the Hamming distance between two haplotypes. Note that for $\alpha = 0$, this simplifies to random mating and thus becomes equivalent to the dynamics described in Supplementary material (S7).



(a) Fitness Landscape for Diploid Individuals



(b) Fitness Landscape for Haploid Males

Figure 2: Three-dimensional fitness landscapes for the (a) diploid and (b) haploid genotypes. Panel a) corresponds to females in the haplodiploid model and all individuals in the diploid model. Individuals heterozygous at both loci (heterozygous hybrids) reside on a high fitness ridge (in white), whereas individuals homozygous at both loci (homozygous hybrids) suffer from reduced fitness due to negative epistasis. Panel b) shows the fitness landscape for haploid individuals (i.e. males) in the haplodiploid model. This landscape is identical to a transect from Panel a) for genotypes homozygous at both loci.

2. The next step is the formation of the zygote. Recombination happens only in females. We denote the frequency of newly born females as $g^y_{ik}(n+1)$.

$$\begin{cases} g^y_{ik}(n+1) = & \frac{1}{2}\sum_{j=1}^{4}\left(P_{ij,k}(n)+P_{ji,k}(n)\right) - \frac{\rho}{2}\Delta_k(n) \text{ if } i \in \{1,4\} \\ g^y_{ik}(n+1) = & \frac{1}{2}\sum_{j=1}^{4}\left(P_{ij,k}(n)+P_{ji,k}(n)\right) + \frac{\rho}{2}\Delta_k(n) \text{ if } i \in \{2,3\} \end{cases} \tag{2}$$

   with $\Delta_k(n) = P_{14,k}(n) + P_{41,k}(n) - P_{23,k}(n) - P_{32,k}(n)$.

   Males are composed from unfertilized female gametes, which have undergone recombination. The frequencies of newborn males are given by $h^y_k(n)$:

$$\begin{array}{rl} h^y_k(n_y) = & \frac{1}{2}\sum_{j=1}^{4}\left(g_{kj}(n)+g_{jk}(n)\right) - \frac{\rho}{2}\tau(n) \text{ if } k \in \{1,4\} \\ h^y_k(n_y) = & \frac{1}{2}\sum_{j=1}^{4}\left(g_{kj}(n)+g_{jk}(n)\right) + \frac{\rho}{2}\tau(n) \text{ if } k \in \{2,3\} \end{array} \tag{3}$$

   with $\tau(n) = g_{14}(n) + g_{41}(n) - g_{23}(n) - g_{32}(n)$.

3. Individuals of both sexes are under viability selection. The frequencies of male and female adults of the next generations are given by

$$h_k(n+1) = \frac{w^m_k h^y_k(n)}{\sum_{k=1}^{4} w^m_k h^y_k(n)} \tag{4}$$

   with w^m_i the fitness of haplotype i in males and:

$$g_{ij}(n+1) = \frac{w^f_{ij} g^y_{ij}(n)}{\sum_{i=1}^{4}\sum_{j=1}^{4} w^f_{ij} g^y_{ij}(n)} \tag{5}$$

   where w^f_{ij} denotes the fitness of the ij genotype. Note that there are no parental effects: $w^f_{ij} = w^f_{ji}$; we maintain the distinction only for modeling convenience.

The complete recursion for females is obtained by substituting $g^y_{ij}(n)$ by its expression given in (2) in (5) and $P_{ij,k}(n)$ by (1). The complete recursion for males is given by substituting h^y_i by its expression given in (3) in (4). For $\alpha = 0$, the detailed recursion is given in Supplement (S7). Note that we use a different point of the life cycle (the gamete frequencies) as this is more easily tractable due to the reduced number of variables.

The diploid model can be obtained by applying equations (2) and (5) to males as well, with the corresponding relevant substitutions.

For the analysis, we focus on the equilibrium of the system defined by:

$$\forall \{i,j,k\} \in \{1,2,3,4\}^3, g_{ij}(n+1) = g_{ij}(n) \text{ and } h_k(n+1) = h_k(n). \tag{6}$$

These equilibria can either be obtained by solving the system of equations presented above numerically, or by focusing on some of the known and potentially biological relevant equilibria, like fixation of a given haplotype. The stability of the equilibria is then obtained by computing the Eigenvalues of the Jacobian matrix at the focal equilibrium. If the absolute value of all Eigenvalues are below 1, the equilibrium is locally stable. For a more detailed explanation, see Otto and Day (2007, Chap. 7). We use this method to derive necessary and sufficient conditions for the existence and stability of the different evolutionary outcomes.

Simulations

Derivations, simulations, and data fitting were performed in *Mathematica* (v 10.4.1.0; Wolfram Research, Inc., 2016). To enable complete reproducibility of the results, we provide an Online Supplement that documents all steps of the analysis as well as the code used for simulations and figures. Equilibrium genotype frequencies were obtained numerically when possible, or based on simulations until the differences between genotype frequencies of two consecutive generations were smaller than 10^{-8} (or stopped after 10^5 generations without convergence).

Fitting the model to a natural ant population

To compare our model with data from the natural, hybridizing Finnish ant population, we estimated the different genotype frequencies of parental *F. polyctena*-like and *F. aquilonia*-like individuals from the data. Assuming that the natural population is at equilibrium, we fit the data (Table S2) to the model by calculating the sum of squared differences between the observed data and predicted equilibrium frequencies. Complete details of data estimation and model fitting are given in the Supplementary Methods and Supplementary Results.

Results

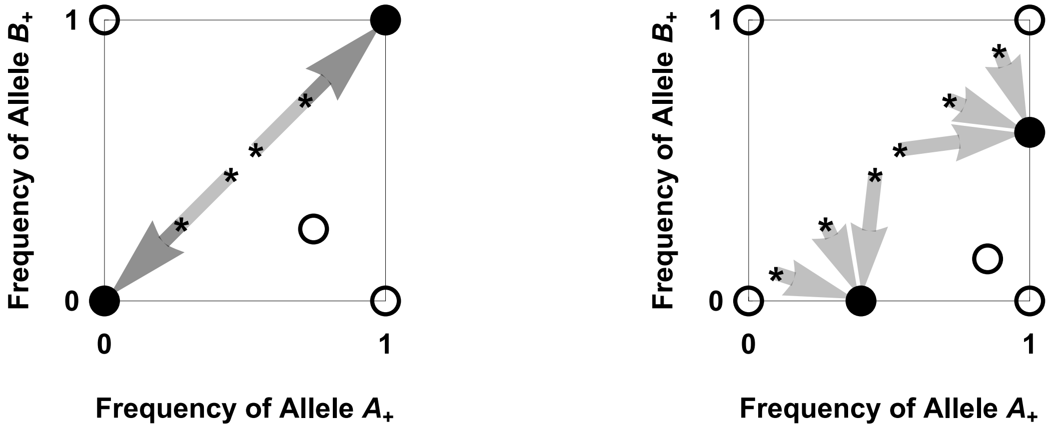
In this section, we describe the dynamics of a hybrid population under our model, with a particular focus on quantifying the differences between the haplodiploid and the diploid model. Two parameter domains are of particular interest:

1. The case of free recombination and strong epistasis (i.e., large γ_1, γ_2) most likely resembles that of the natural ant hybrid population that inspired the model. Here, the hybrid incompatibility loci are located on different chromosomes, and epistasis is strong enough to erase a large fraction of male zygotes during development.

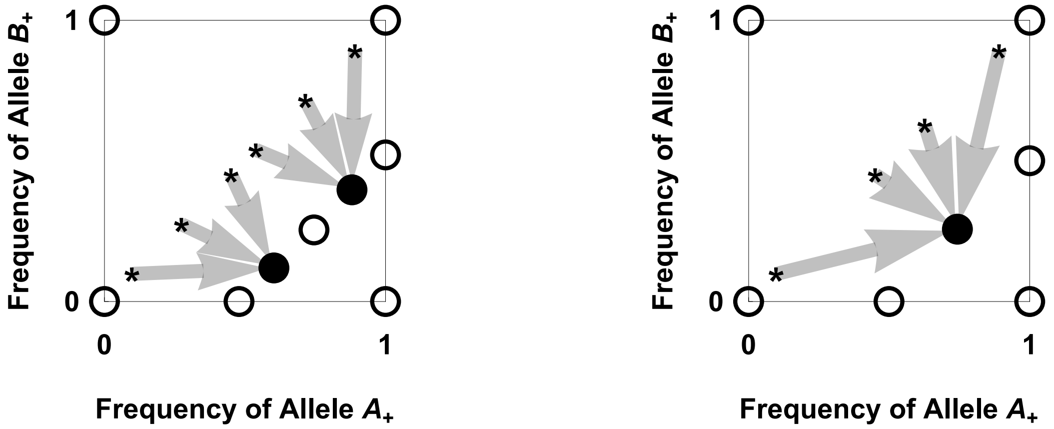
2. The case of low recombination is most relevant for the effects of a fitness landscape with epistasis (i.e., a "rugged" landscape) in X or Z chromosomes. Here, epistasis could arise, for example, through interactions between regulatory regions and their respective genes.

Evolutionary scenarios

Below, we describe four different types of evolutionary stable states (i.e., equilibrium scenarios) of the model, which represent long-term solutions to the opposing selective pressures of the hybridization-averse force of recessive negative epistasis and the hybridization-favoring heterozygote advantage. The population will attain these equilibria if no further pre- or post-zygotic barriers or other functional mutations appear. Next, we provide various necessary and sufficient analytical conditions for these scenarios. Figure 3 illustrates the potential equilibria by means of phase diagrams.



(a) Exclusion (b) Single-Locus Polymorphism



(c) Asymmetric Coexistence (d) Symmetric Coexistence

Figure 3: Phase-plane diagrams illustrating possible evolutionary scenarios in the haplodiploid model. The filled black dots show locally stable equilibria and the empty dots show unstable ones. The gray arrows show the basin of attraction starting from secondary contact scenarios (black asterisks on the line at $p_{B_+} = p_{A_+}$). Panel (a) illustrates exclusion: There are 2 external locally stable equilibria, each corresponding to the fixation of a parental population haplotype. (Here, $\sigma = 0.02$, $\gamma_1 = 0.9$, $\gamma_2 = 0.11$, $\rho = 0.5$, and $\alpha = 0$.) Panel (b) represents a single-locus polymorphism. Only one locus is polymorphic, leading to the maintenance of the weaker of the two incompatibilities (the A_-B_+ interaction). (Here, $\sigma = 0.009$, $\gamma_1 = 0.11$, $\gamma_2 = 0.002$, $\rho = 0.5$, and $\alpha = 0$.) Panel (c) corresponds to asymmetric coexistence. Two internal equilibria are locally stable, with one allele close to fixation. This scenario minimize the expression of the strongest interaction A_+B_-. (Here, $\sigma = 0.03$, $\gamma_1 = 0.11$, $\gamma_2 = 0.0013$, $\rho = 0.5$, and $\alpha = 0$.) Panel (d) shows symmetric coexistence. Frequencies of alleles A_- and B_- are symmetric around 0.5, with $p_{B_+} = 1 - p_{A_+}$. This scenario maximizes the formation of female heterozygous hybrids. (Here, $\sigma = 0.09$, $\gamma_1 = 0.3$, $\gamma_2 = 10^{-4}$, $\rho = 0.5$, and $\alpha = 0$.)

Exclusion

The *exclusion* scenario corresponds to the hybrid population becoming identical to one of the two parental populations, either P_+ or P_-, and the other parental population being therefore excluded. It occurs when both alleles from one of the founder subpopulations are purged, leading to a monomorphic stable state of the population (Fig. 3(a)). In this case, the initial frequency of A_+B_+ versus A_-B_- individuals mainly determines the outcome (i.e., the population is swamped by the majority subpopulation). As a rule of thumb, this outcome is observed when recombination is frequent and when the hybridization-averse force of negative epistasis is strong as compared with the hybridization-favoring heterozygote advantage ($\gamma_1, \gamma_2 \gg \sigma$).

With regard to the apparent sexual/ploidy conflict in the haplodiploid model, exclusion can be interpreted as a victory of the haploid males because all polymorphism is lost and no low-fitness hybrid males are produced. Conversely, since all polymorphism is lost, diploid females "lose" in this case and neither high-fitness introgressed (i.e., those individuals carrying only one 'foreign' allele) nor highest-fitness heterozygous hybrid females are produced. As discussed below, exclusion is never a possible outcome in the diploid model, in which there are no differences in ploidy.

Single-locus polymorphism

A *single-locus polymorphism* occurs when one allele is purged from the population but the other locus remains polymorphic at equilibrium (Fig. 3(b)). Because this is possible for either of the two loci, two such equilibria exist simultaneously, which are reached depending on the initial haplotype frequencies. This outcome is observed when recombination is frequent, epistasis is asymmetric ($\gamma_1 \neq \gamma_2$), and heterozygote advantage is small ($\gamma_1 \gg \sigma$). Like asymmetric coexistence below, this case represents a compromise between the hybridization-averse and hybridization-favoring forces of negative epistasis and heterozygote advantage, and is reached by maximizing the number of introgressed individuals of one founder subpopulation.

In the haplodiploid model, this scenario can be seen as a haploid-dominated compromise. Since one locus is fixed, one epistatic interaction has disappeared and few low-fitness hybrid males are produced. In females, high-fitness introgressed female frequencies are maximized but, since one locus is fixed, the highest-fitness heterozygous hybrid female genotypes are no longer available.

The single-locus polymorphism is never stable in the diploid model, i.e., when the ploidy difference is removed from the model. In a diploid population that resides transiently at single-locus polymorphism, a rare mutant at the second locus will always begin as heterozygote and therefore reap the advantage of being a heterozygote hybrid long before it suffers the epistatic cost of being a homozygote hybrid.

Asymmetric coexistence

"Asymmetric" coexistence occurs when all four haplotypes remain in the population and the frequency of introgressed individuals of one founder subpopulation is maximized (Fig. 3(c)). Because this can be achieved in two ways, two possible equilibria reside off the diagonal line $p_B = 1 - p_A$ (where p_A and p_B denote the allele frequencies of the '$-$' allele at the respective locus), and the initial contribution of different haplotypes determines which equilibrium will be attained. Like the single-locus polymorphism, this equilibrium represents a compromise between hybridization-averse and hybridization-favoring forces that is reached by maximizing the number of introgressed individuals. Our simulations demonstrate that

this scenario is rarely present in haplodiploids, and it generally involves asymmetric epistasis and intermediate-strength heterozygote advantage.

In the haplodiploid model, asymmetric coexistence can be seen as a compromise that is dominated by the diploids. Unlike in the single-locus polymorphism scenario, both loci are polymorphic and some double-heterozygous hybrid females are produced. But, unlike the symmetric coexistence scenario described below, females are not victorious over males because such high-fitness hybrid females are produced only at low frequencies.

Symmetric coexistence

Symmetric coexistence occurs when a locally stable equilibrium exists on the diagonal $p_B = 1 - p_A$, such that the number of heterozygous hybrids is maximized (Fig. 3(d)). Our notion of "symmetric" refers to the total fraction of alleles from the P_+ and P_- founder populations segregating at equilibrium, which is equal in this case. Here, prolonged hybridization is a mutual best-case scenario for both populations. This equilibrium is most likely when recombination is weak or when the hybridization-favoring force of heterozygote advantage is strong as compared with the hybridization-averse negative epistasis ($\sigma \geq \gamma_1, \gamma_2$). In the haplodiploid model, symmetric coexistence represents a victory for the diploids, because they maximize their own fitness without regard to the production of unfit hybrid haploids.

The four evolutionary stable states described above usually result in either a single, globally stable equilibrium (in the case of symmetric coexistence) or a bistable system, in which two locally stable equilibria exist. In rare cases and close to bifurcation points, we observe cases of tristability, which are further described in Figure S2.

Stability analysis of the model

Although the model dynamics are too complex to derive general analytical solutions, we were able to perform stability analyses for specific cases, which yield information about the general behavior of the model. In the following, our use of '>' and '<' does not necessarily imply strict inequalities; we merely did not explicitly study the limiting cases. For ease of notation, we refer to heterozygote advantage in terms of ω below; recall that $\omega = 1 + \sigma$.

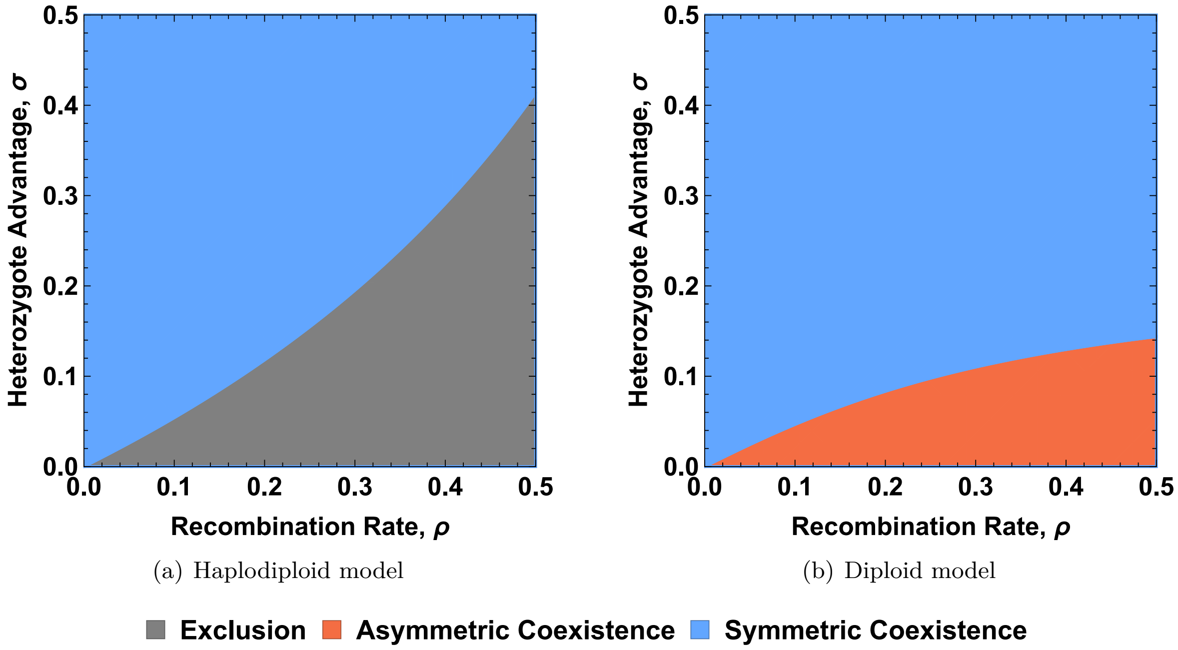
Conditions for symmetric coexistence when epistasis is lethal

We begin by describing the equilibrium structure when epistasis is lethal, i.e. $\gamma_1 = \gamma_2 = 1$; this case may resemble that in the natural ant population, in which most hybrid males do not survive to reproduce. For the haplodiploid model, we obtain a full analytic solution of the identity, existence and stability of equilibria. Here, only two outcomes are possible: symmetric coexistence and exclusion (Fig. 4(a)). As necessary and sufficient criterion for exclusion, we obtain

$$\rho > \frac{\omega^2 - 1}{\omega^2}. \qquad (7)$$

Thus, exclusion is only possible if heterozygote advantage is not too strong, and if recombination is breaking up gametes sufficiently often to significantly harm the haploid males.

For the diploid model, we can show that no boundary equilibrium is ever stable; asymmetric and symmetric coexistence are the only two possible outcomes. Although it was not possible to perform a stability analysis on the internal equilibria, we were able to propose a



(a) Haplodiploid model

(b) Diploid model

Figure 4: Symmetric coexistence can be locally stable if the heterozygote advantage, σ, is strong enough to compensate for recombination breaking up the parental haplotypes. Here we assume that epistasis is symmetric and lethal ($\gamma_1 = \gamma_2 = 1$). Panel (a) is an illustration of the condition for haplodiploids given in equation (7) and panel (b) of equation (8) for diploids.

condition for asymmetric coexistence, which has been evaluated numerically:

$$\rho > \frac{(\omega^2-1)(2\omega^4-6\omega^3+\omega^2+6\omega-2)}{\omega^2\left(2\omega^2-4\omega+1\right)\left(2\omega^2-3\right)} + 2\sqrt{\frac{(\omega-1)^5(\omega+1)^2(\omega^3-\omega^2-3\omega+1)}{\omega^4\left(2\omega^2-4\omega+1\right)^2\left(2\omega^2-3\right)^2}}. \qquad (8)$$

Although this expression is not very telling, its illustration in Figure 4(b) demonstrates how different this criterion is from that of the haplodiploid model. In the diploid model, males and females evolve on the same fitness landscape. Therefore, both males and females benefit from heterozygote advantage. This reduces the influence of the hybrid incompatibility on the optimal location of the population in genotype space, which thereby makes asymmetric coexistence less likely. Indeed, a heterozygote advantage of $\omega - 1 = \sigma >\approx 0.14$ is sufficient to ensure symmetric coexistence for all recombination rates, whereas in the haplodiploid model, $\sigma > \sqrt{2} - 1 \approx\ 0.41$ is necessary for symmetric coexistence independent of the recombination rate.

General stability conditions in the haplodiploid model

Using the results derived for the case of lethal epistasis, and by means of critical examination of the existence and stability conditions that we were able to compute analytically, we arrived at several illustrative conjectures delimiting the evolutionary outcomes in the haplodiploid model when epistasis is not lethal ($\gamma_1, \gamma_2 \neq 1$). These were all confirmed by extensive numerical simulations (see Mathematica Online Supplement). Note that assortative mating was not considered here.

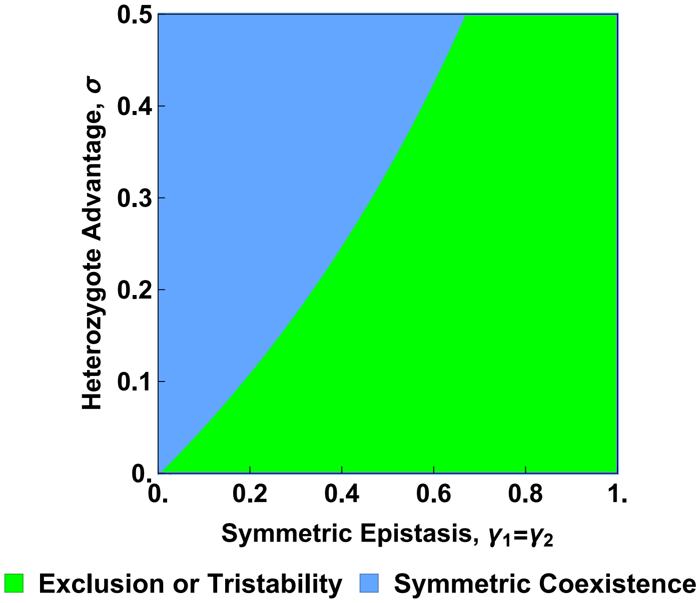


Figure 5: In haplodiploids, symmetric coexistence requires that heterozygote advantage, σ, is strong enough to both compensate for recombination such that the condition in equation 10 is fulfilled (see also Fig. 4(a)), and to overcome the deleterious effects of epistasis, as expressed by condition 11 for symmetric epistasis.

Firstly, strong heterozygote advantage can always override the effect of epistasis. Specifically, if

$$\omega > \sqrt{2}, \tag{9}$$

the evolutionary outcome is always symmetric coexistence, regardless of the values of γ_1 and γ_2. This is true not only for a single pair of interacting loci, but also for an arbitrary number of independent incompatibility pairs, because the detrimental effects caused by each incompatibility pair are eventually resolved independently (see also the section on multiple loci below). This result can be deduced from equation (7) for $\rho = 0.5$ and therefore corresponds to an upper bound: if heterozygote advantage is very strong, recombination no longer affects the outcome.

Secondly, recombination is a key player to determine whether compromise or exclusion can occur. In particular,

$$\rho < \frac{\omega^2 - 1}{\omega^2} \tag{10}$$

is a sufficient condition for the observation of symmetric coexistence, independent of the strength and symmetry of epistasis. This makes intuitive sense, because hybrid incompatibility is masked until gametes are broken up by recombination.

Thirdly, for symmetric epistasis ($\gamma_1 = \gamma_2$), there are three possible equilibrium patterns: symmetric coexistence, exclusion, and tristability of the two former types of equilibria. A necessary and sufficient condition for observation of anything but symmetric coexistence is

$$\omega < \sqrt{2} \quad \text{and} \quad \rho > \frac{\omega^2 - 1}{\omega^2} \quad \text{and} \quad \gamma_1 = \gamma_2 > \frac{2(\omega - 1)}{\omega}. \tag{11}$$

If the recombination rate ρ and the epistatic effects γ_1, γ_2 are very close to this limit, there is tristability; if they are far away, there is exclusion (cf. Fig. 5).

Finally, for asymmetric epistasis ($\gamma_1 \neq \gamma_2$), the dynamics display the whole range of possible evolutionary outcomes: symmetric coexistence, asymmetric coexistence, single-locus polymorphism, exclusion, as well as tristability of exclusion *and* symmetric coexistence, and single-locus polymorphism *and* symmetric coexistence. The local stability criterion for the stability of the monomorphic equilibria (i.e., the criterion for exclusion, or tristability of exclusion and symmetric coexistence) is

$$\omega < \sqrt{2} \quad \text{and} \quad \rho > \frac{\omega^2 - 1}{\omega^2} \quad \text{and} \quad \gamma_2 > \frac{2(\omega - 1)}{\omega}. \tag{12}$$

Thus, if epistasis is strong as compared with heterozygote advantage, no degree of asymmetry is sufficient to promote a compromise between males and females (i.e., single-locus polymorphism or asymmetric coexistence). In fact, we observe the following necessary (but not sufficient) condition for a single-locus polymorphism:

$$\omega < \sqrt{2} \quad \text{and} \quad \rho > \frac{\omega^2 - 1}{\omega^2} \quad \text{and} \quad \gamma_1 > \frac{2(\omega - 1)}{\omega} \quad \text{and} \quad \gamma_2 < \frac{2(\omega - 1)}{\omega}. \tag{13}$$

Hence, only a tight balance between the selective pressures of epistasis and heterozygote advantage in combination with asymmetry of the hybrid incompatibility promotes a long-term equilibrium with compromise.

An extension to multiple loci

Incompatibilities involving four loci

Above, we have demonstrated that recombination is an essential player when determining whether exclusion or coexistence is the long-term outcome in the haplodiploid dynamics. In order to see how our results change in the (biologically relevant) case of multiple hybrid incompatibilities, we implemented the dynamics for four loci. Given the complexity of the system, we considered only lethal incompatibilities, i.e. $\gamma_i = 1$ for all interactions i. With this extension, we consider two scenarios. Firstly, in the *"pairwise"* case we consider pairs of independent hybrid incompatibilities, where we assume that the incompatible loci are located next to each other (locus **A** interacts with locus **B** at recombination distance ρ_{12}, and locus **C** with locus **D** at recombination distance ρ_{34}), which leaves four viable male haplotypes ($A_+B_+C_+D_+$, $A_+B_+C_-D_-$, $A_-B_-C_+D_+$ and $A_-B_-C_-D_-$). Secondly, in the *"network"* case we assume that all loci interact such that only two viable male haplotypes exist $A_+B_+C_+D_+$ and $A_-B_-C_-D_-$. In both cases, heterozygote advantage is defined as before, now acting on all four loci multiplicatively.

Under this model, we derived the conditions under which exclusion (the purging of all foreign alleles resulting in a monomorphic equilibrium) is locally stable (cf. Mathematica Online Supplement). For the pairwise case, exclusion is stable only if heterozygote advantage is relatively weak:

$$\omega < \min\left[\frac{1}{\sqrt{1-\rho_{12}}}, \frac{1}{\sqrt{1-\rho_{34}}}\right], \tag{14}$$

where ρ_{ij} is the recombination rate between neighboring loci i and j. Note that this is independent of the recombination rate between non-interacting loci, here ρ_{23}. If $\rho_{12} = \rho_{34}$, this expression is equivalent to equation 7 (Fig. 4(a)). Overall, this condition indicates that exclusion, which we define as the fixation of one of the parental haplotypes, is less likely with four interacting loci than with two. This is because the fate of the two pairs of incompatibilities is decided independently, and exclusion requires that both pairs of incopatibilities fix for the same parental haplotype.

For the network case, the condition for stability of exclusion (see also Fig. S3) is

$$\omega < ((1-\rho_{12})(1-\rho_{23})(1-\rho_{34}))^{-\frac{1}{4}} . \tag{15}$$

In this scenario, exclusion is a more likely outcome with two pairs of incompatibilities than with one. This is because there are more unfit intermediate types in this scenario as compared with the pairwise model. Specifically in males,14 out of the 16 possible haplotypes do not survive to adulthood. To compensate for this fitness cost, any alternative evolutionary outcome requires strong heterozygote advantage.

Incompatibilities involving an arbitrary number of loci

From the results for two and four loci, we derived a conjecture that generalizes to an arbitrary number of loci. For the pairwise case, equation 14 can be generalized to

$$\omega < \min\left[\frac{1}{\sqrt{1-\rho_{ij}}}\right], \tag{16}$$

with i and j representing neighboring interacting loci. Note that this result holds only if interacting loci are next to each other on the same chromosome, or if all loci are unlinked (in which case it simplifies to $\omega < \sqrt{2}$).

For the network case, equation (15) generalizes to

$$\omega < \left(\prod_{\substack{i=1\\ j=i+1}}^{n-1} (1-\rho_{ij})\right)^{-\frac{1}{n}}, \tag{17}$$

with i and j neighboring loci and n the total number of loci in the network. Unlike in the pairwise case, the results for the network case do not depend on the genetic architecture (here, the ordering of loci along the genome).

We can therefore deduce that, for the pairwise case, exclusion becomes increasingly unlikely as the number of pairs of independent hybrid incompatibilities involved in the genetic barrier increases. Conversely, the opposite result is observed for the network case: more loci make exclusion a more likely outcome, but each additional interaction contributes less (cf. Fig. S3).

Increased assortative mating counteracts recombination and heterozygote advantage

Increasing the strength of assortative mating, $\alpha > 0$, counteracts the hybridization-favoring effect of heterozygote advantage, because matings between individuals with the same genotype are more common under stronger, positive assortment. Under sufficiently large positive α, exclusion is unavoidable. In general, increasing α leads to less maintenance of polymorphism in the population (Fig. S4). Conversely, when $\alpha < 0$, which means that individuals prefer to mate with those whose genotype is most different from their own, polymorphism is more likely to be maintained in the population.

Also with assortative mating, recombination remains a key player in determining the evolutionary outcome. When $\alpha < 0$ and recombination is small, symmetric coexistence is possible even in the absence of heterozygote advantage (i.e., $\sigma = 0$; Fig. S4). Indeed, under these conditions and assuming epistasis is very strong, (almost) all hybrid males are dead and only parental males survive. This ‘disassortative’ mating ($\alpha < 0$) creates a bias for the rare male haplotype. For example, if one female genotype increases in frequency, it will seek mainly the males of the other parental haplotype to reproduce with (which are currently rare, as their frequency is directly tied to the frequency of the females in the previous generation. This will increase their reproductive success, which leads to an increase of this haplotype frequency. Therefore, under this mate choice regime, we would observe a stable population composed almost exclusively of the A_+B_+ and A_-B_- haplotypes.

Differences between the haplodiploid and the diploid systems

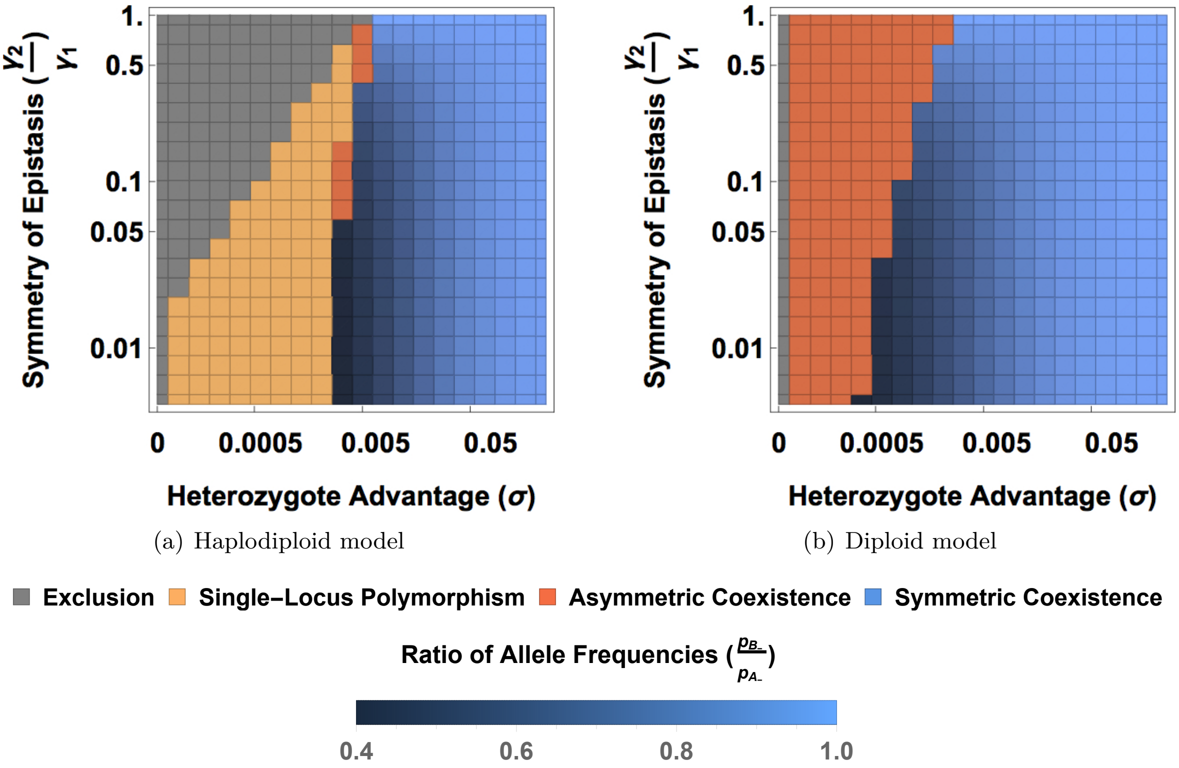
As described above and illustrated in Figure 6, the resulting haplodiploid dynamics display a wider range of possible evolutionary outcomes than the diploid dynamics. Because both males and females profit from heterozygote advantage in the diploid model, polymorphism is always maintained; in other words, even the smallest amount of heterozygote advantage promotes the creation or maintenance of diversity in diploids (Table S3). Conversely, in the haplodiploid model, polymorphism can be lost either at one or both loci, resulting in a single-locus polymorphism or exclusion. Thus, alleles responsible for incompatibilities are more effectively purged in the haplodiploid model.

In the diploid model, a single-locus polymorphism is never stable: Assume locus A is polymorphic and locus B is fixed for allele B_+. Then, a new mutant carrying allele B_- will always have a selective advantage regardless of the genotype in which it first appears (Table S3). In contrast, in the haplodiploid model, this is no longer true as the mutant carrying allele B_- will have a much lower fitness in males when associated to allele A_+. Therefore, if the cost of generating this unfit haplotype in males overrides the advantage in females, and allele A_+ is at high frequency, then invasion of the B_+ mutant may be prevented, leading to the stability of the single-locus polymorphism.

When polymorphism is maintained at both loci at equilibrium (i.e., asymmetric and symmetric coexistence), epistasis creates associations between the compatible alleles which results in elevated linkage disequilibrium (LD). Recombination breaks the association between alleles, thus high recombination decreases normalized LD (D', where $D' = \frac{LD}{D_{\max}}$ (Lewontin, 1964); Fig. S5). D' increases with the strength of heterozygote advantage at low recombination rates because it maximizes the discrepancy between highly fit double-heterozygote females on the one hand that can, under low recombination rate, still produce many fit male offspring and introgressed females on the other, who are less fit and produce many unfit hybrid males

In Figure S6, we compare the normalized LD (i.e. D') between the haplodiploid and diploid models. When polymorphism is maintained at both loci in both the haplodiploid and diploid model, normalized LD is always larger in haplodiploids than diploids. The difference in normalized LD between haplodiploids and diploids is maximized for intermediate recombination rates, where recombination is strong enough to create unfit hybrid genotypes, but not efficient enough to break the associations that are generated. Due to the increased selection against hybrid incompatibility in haploid males in the haplodiploid model, the normalized LD is usually 2-3 times higher in the haplodiploid as compared with the diploid model.

Thus, the hybrid incompatibility leaves a statistical signature in a population, even if the population finds itself at an equilibrium. The increased association across the genome, exhibited if the interacting loci are on the same chromosome, may also result in an underestimate of the recombination rate. Although both the diploid and the haplodiploid models display the elevated LD signal, it is much more pronounced in the haplodiploid scenario. This is because only an eighth of the possible diploid male genotypes suffer the cost of the incompatibility as compared to half of the possible haploid male genotypes.



(a) Haplodiploid model (b) Diploid model

Figure 6: More evolutionary outcomes are possible in (a) the haplodiploid than (b) the diploid model. The y-axis shows the degree of asymmetry of epistasis, displayed as the ratio of the two epistasis parameters ($\frac{\gamma_2}{\gamma_1}$) for a constant value of $\gamma_1 = 0.01$. For symmetric coexistence, the locally stable equilibrium can be at any point on the diagonal $p_{B_-} = 1 - p_{A_-}$, where p_{A_-} and p_{B_-} denote the allele frequencies of the $-$ allele at the respective locus. Blue shading illustrates the location of the equilibrium at symmetric coexistence: darker shades correspond to a bigger disparity in allele frequencies. This is the case when the asymmetry of the two epistasis parameters is large (i.e. smaller values on the y-axis) because smaller values of γ_2 favor the A_-B_+ haplotype over the A_+B_- haplotype. (Here, $\gamma_1 = 0.01, \rho = 0.5, \alpha = 0$.)

Discussion

Multiple recent studies have highlighted the pervasive nature of hybridization and its potential consequences for diversification and speciation (Abbott et al., 2013; Runemark et al., 2017; Montecinos et al., 2017). We here modeled the fate of a hybrid population in a scenario in which hybridization is simultaneously favored and selected against, inspired by a natural population of hybrid ants that simultaneously displays heterosis and hybrid incompatibility. In addition, both adaptive introgression and hybrid incompatibilities have been identified in natural systems (Heliconius Genome Consortium, 2012; Whitney et al., 2015; Corbett-Detig et al., 2013) and it is therefore likely that both processes may occur simultaneously during a single hybridization event. Furthermore, we were interested in comparing the long-term evolution of populations exposed to these opposing selective pressures under different ploidies (haplodiploid versus diploid), since it has been argued that haplodiploids might speciate more easily than diploids (Lohse and Ross, 2015). Finally, the comparison of ploidies can also be transferred to the case of diploid species with sex chromosomes, in which the described fitness landscape results in the diploid dynamics on the autosomes, and in the haplodiploid dynamics on the X/Z chromosome.

Our model considers a population in which heterozygote advantage and hybrid incompatibility act simultaneously on the same pair of loci, which creates a rugged fitness landscape with a ridge of high-fitness heterozygote genotypes, adjacent to which there are holes of incompatible double homozygotes (Fig. 2(a)). In haplodiploids, haploid males cannot profit from heterozygote advantage but suffer strongly from hybrid incompatibility (Fig. 2(b)). This results in a conflict of ploidies/sexes over the optimal location in the fitness landscape, because haploid males survive best if one parental haplotype is fixed whereas diploid females profit from maximum heterozygosity. Although females suffer from the same incompatibility as males, their presence is mainly masked in the diploid individuals because of the recessivity of the hybrid incompatibility. This is similar to Haldane's rule (Charlesworth et al., 1987; Koevoets and Beukeboom, 2009).

How ploidy matters

We found that, in the haplodiploid model, there exist four different stable outcomes of the conflict over hybrid status (Fig. 3): exclusion, where "males/haploids win"; symmetric coexistence, where "females/diploids win"; and two outcomes, single-locus polymorphism and asymmetric coexistence, where a compromise between male costs and female benefits is mediated by high frequencies of introgressed females. In fact, since low-frequency heterozygotes are favored both in males and in females in the diploid model, while only suffering the hybrid cost if introgressed alleles rise to high frequencies, exclusion and single-locus polymorphism never occur in the diploid model, which reduces the number of possible outcomes to asymmetric and symmetric coexistence. Therefore, consistent with Pamilo (1979); Pamilo and Crozier (1981); Patten et al. (2015), we found that introgression and maintenance of polymorphism, and thus long-term hybridization, are less likely in haplodiploids as compared to diploids.

Prior work has found that in haplodiploid species traditional sexual conflict tends to be resolved in favor of females because genes spend two thirds of their time in females (Albert and Otto, 2005). In our model, the co-occurrence of heterozygote advantage and hybrid incompatibility also creates an apparent sexual conflict that is caused by the difference in ploidy between the sexes. For several scenarios, we here derived the conditions for whether this conflict is resolved in favor of diploid females or haploid males. We find, that in addition to the strength of selection, recombination is a major player (cf. Fig. 4 and equation 12);

only if recombination breaks up gametes, the hybrid incompatibility is expressed. With free recombination, i.e., if the interacting genes are found on separate chromosomes, heterozygote advantage has to be very strong to counteract the hybrid incompatibility. We find that it has to be on the same order of magnitude as the strength of the incompatibility, but can be slightly lower in its absolute value. For example, heterozygote advantage with strength 41% is sufficient to result in symmetric coexistence even if the incompatibility is lethal (Fig. 4B). Thus, under consideration of absolute magnitude across the full parameter range, our results are consistent with prior work. However, reported cases and potential mechanisms of hybrid incompatibility indicate that large effects are feasible, whereas observed cases of heterozygote advantage or heterosis of large effect are relatively rare (Hedrick, 2012). Therefore, it may well be that under natural circumstances, the conflict modeled here may indeed be likely to be resolved via purging of at least one incompatible allele and thus in favor of males/haploids.

As expected in the presence of epistasis, we observed that linkage disequilibrium (LD) is elevated at all polymorphic stable states (i.e., for symmetric and asymmetric coexistence) both in the diploid and haplodiploid models, especially at intermediate recombination rates. This is particularly true for haplodiploids, which display about 2-3 times the LD of the diploid model with the same parameters. Transferred to the context of X/Z chromosomes, this is consistent with observations of larger LD on the X chromosome as compared with autosomes (Wall et al., 2002; Sandor et al., 2006; Li and Merilä, 2010). It has been argued that this is because selection is more effective on X-linked loci: recessive deleterious mutations are more visible to selection in haploid individuals (Charlesworth et al., 1987). However, a hybrid incompatibility accompanied by heterosis/heterozygote advantage as in our model may not be purged but create a continuous high-LD signal in an equilibrium population. This can potentially result in less efficient recombination and in underestimates of recombination rates on X chromosomes (because recombined individuals are not observed).

Generalization to multiple incompatibilities

Exclusion remains a stable solution when we extend the model to multiple loci and incompatibilities. We describe an interesting difference between multiple independent pairs of incompatibilities, and multiple loci that all interact with each other: in the latter case, exclusion becomes increasingly probable because the number of viable males decreases. This scenario of higher-order epistasis has recently received attention with regards to speciation (Paixão et al., 2014; Fraïsse et al., 2014; Kulmuni and Westram, 2017), and it will be interesting in the future to identify molecular scenarios (for example, involving biological pathways) that could result in such incompatibilities. In contrast, exclusion becomes less likely in the case of independent incompatibility pairs, where each incompatibility has to be purged independently, and in the same direction, for exclusion to occur. Here, mechanisms that reduce the recombination rate, such as inversions, could potentially invade and tilt the balance towards coexistence and thus maintenance of polymorphism in the hybrid population. It is important to note that the independent purging of incompatibilities, which leads to a decreasing probability of exclusion with increasingly many incompatibility pairs, is only true in effectively infinite-sized populations. In small populations, we expect that exclusion becomes a more likely scenario, especially if lethal incompatibility pairs are present.

Model assumptions

We chose a classical population-genetic modeling approach (Bürger, 2000; Nagylaki et al., 1992) to study how the co-occurence of heterozygote advantage and hybrid incompatibility affect the long-term dynamics of a hybrid population. By treating the problem in a deterministic framework and considering only two loci throughout most of the manuscript, we greatly oversimplify the situation in the natural population that inspired our model. However, at the same time this allowed us to gain a general insight, (often by means of analytical expressions), into how opposing selective pressures in genomes may be resolved, and to contrast these outcomes between haplodiploid and diploid systems. In addition to some obvious mechanisms at play in natural populations, which we ignore in our model (e.g., random genetic drift), some extensions of the model could be interesting to elaborate on in the future. For example, the ant populations represent networks of interacting nests with many queens per nest, but potentially different mating flight timing that depends, for example, on sun exposure in the spring. Thus, for the purpose of population-genetic inference of the evolutionary history (and potential evolutionary fate) of the hybrid ant population in Finland, it would be desirable to incorporate population structure, uneven sex ratios at birth, and sex-biased dispersal into the model, and obtain population-genomic data to infer evolutionary parameters.

Is the natural population at an equilibrium of asymmetric coexistence?

Model fitting results (see Supplementary Methods, Results, and Discussion) are inconclusive about the fate of the natural ant population that inspired our model. Our results suggest that the natural population might be approaching an evolutionary outcome that allows a compromise between male and female interests; either as single-locus polymorphism or via asymmetric coexistence. In particular, our model is able to explain the unusual skew in the population, where *F. aquilonia*-like parental genotypes far outnumber *F. polyctena*-like genotypes (see Supplement). Furthermore, the high recombination rates and strong prezygotic mechanisms operating in the natural population (Kulmuni et al., 2010; Kulmuni and Pamilo, 2014), are consistent with a parameter domain in our models at which asymmetric coexistence can be stably maintained over a wide range of values of female hybrid advantage. More complex models, for example including more than two incompatibility loci, may be better able to explain the high frequencies of introgressed as compared to parental females observed in the natural hybrid population. As argued in the Results, interactions at or between multiple loci should result in steeper differences of introgressed-allele frequencies across life stages than our model is able to produce.

Implications for hybrid speciation

Our model illustrates how the co-occurrence of heterozygote advantage and hybrid incompatibility affects haplodiploid and diploid populations. We can hypothesize how these different outcomes may provide an engine to hybrid speciation, or which other long-term evolutionary scenarios we expect to arise. The case of exclusion, which is possible only in the haplodiploid model, will lead to loss of diversity in the hybrid population, and, in the two-locus case, should result in the reversion of the hybrid population into one of its parental species. However, if multiple pairs of interacting loci are resolved independently, they may be purged randomly towards either parent, which could result in a true hybrid species that is isolated from both its parental species (Buerkle et al., 2000; Butlin and Ritchie, 2013; Schumer et al., 2015). In fact, our finding that exclusion is less likely to occur in populations with multiple pairs of interacting loci may result from exactly this mechanism, but it is beyond the scope of this manuscript to explore this further.

The long-term fate of the population is less straightforward to anticipate in the case of polymorphic stable equilibria. For any of these, heterozygote advantage is strong enough to stabilize the polymorphism either at one or both loci. Without further occurrence of functional mutations, males (in the haplodiploid model) and double-homozygotes for the incompatible alleles will continue to suffer a potentially large fitness cost. Mechanisms that could reduce this cost would be increased assortative mating or decreased recombination. However, neither of these would necessarily cause isolation from the parental species, unless they involved additional hybrid incompatibilities which isolate the hybrid population from its parental species. Alternatively, mutations that lower the hybrid fitness cost could invade, which would result in a weakening of species barriers and promote further introgression from the parental species. This indicates that any scenario in which polymorphic equilibria are stable may indeed be an unlikely candidate for hybrid speciation. Considering that such stable polymorphism (either as symmetric or asymmetric coexistence) is the only possible outcome in the diploid model, this results in the prediction that hybrid speciation would be more likely in a haplodiploid scenario. This is an interesting observation that is in line with other predictions that haplodiploids speciate more easily, that X/Z chromosomes are engines of speciation (Lima, 2014), and that hybrid speciation is rare (Schumer et al., 2014).

Relevance of the model for sex chromosomes

Haplodiploids and X/Z chromosomes have a similar mode of inheritance, where one sex carries a single copy of the chromosome, and the other carries two copies. Therefore, our results apply equally to cases of X-to-X or Z-to-Z hybrid incompatibilities (Lohse and Ross, 2015). Although haplodiploid systems do not include all of the unique evolutionary phenomena exhibited by sex chromosomes (Abbott et al., 2017), our results for haplodiploids are relevant for sex chromosomes. Our model predicts the long-term evolution of a population under the simultaneous influence of heterozygote advantage and hybrid incompatibility, and indicates the signatures that this type of fitness landscape could leave depending on whether it finds itself on an X chromosome or an autosome.

Firstly, the complex selection pressure imposed by the co-occurrence of heterozygote advantage and hybrid incompatibility manifests itself as an apparent sexual conflict on the X chromosome/in haplodiploids. This conflict is caused by the ploidy difference between the sexes. Here, the same fitness landscape that would be masked on an autosome and result in a stable polymorphism, creates a signal of sexually antagonistic selection on an X chromosome. Most importantly, this signal is created without the need for direct sexually antagonistic selection on single functional genes that have a sex-specific antagonistic effect. Thus, our model proposes an additional mechanism by which sex chromosomes can appear as hotspot of sexual conflict (e.g., Gibson et al., 2002; Pischedda and Chippindale, 2006).

Secondly, we find that purging of incompatibilities is more likely in the haplodiploid model, and thus on X/Z chromosomes. This is consistent with the faster-X theory (Charlesworth et al., 1987). However, only if recombination is strong enough, incompatibilities will become visible to selection and purged in the presence of heterozygote advantage. If they are not purged, they may persist as a long-term polymorphism, invisible to most empirical approaches, and confound population-genetic inference by creating signals of elevated linkage disequilibrium.

Conclusion

Hybridization is observed frequently in natural populations, and can have both deleterious and advantageous effects. We here show how diverse outcomes can be produced even under a rather simple model of a single hybrid population, in which heterozygote advantage and hybrid incompatibility are occurring at the same time. Consistent with previous theory on haplodiploids and X/Z chromosomes, we found that incompatible alleles are more likely to be purged in a haplodiploid than in a diploid model. Nevertheless, our results suggest that long-term hybridization can occur even in the presence of hybrid incompatibility, and if there are many incompatible pairs or many loci involved in the incompatibility. The evolutionary fate of the Finnish hybrid ant population that inspired our model is difficult to predict; further population-genetic analysis will be necessary to gain a more complete picture of its structure and evolutionary history.

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Data Accessibility

The complete documentation of all steps of the analysis is available as a Mathematica Online Supplement. Ant colony data is provided as Supplementary Table S1; genotype frequency data were obtained from Kulmuni and Pamilo (2014).

Author Contributions

CB, JK, and RB designed research, AB and CB developed the models, AHG performed simulations and data analysis, all authors interpreted the results and wrote the manuscript.

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Supplement for: Conflict between heterozygote advantage and hybrid breakdown in haplodiploids (and sex chromosomes)

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Supplementary Methods

Modeling of the life cycle in the absence of assortative mating

In the absence of assortative mating (i.e. $\alpha = 0$), equations (1)-(5) still hold. Nevertheless, tracking genotypes is cumbersome and not necessary in this context (as the production of gametes is independent of their probability of forming a zygote). Therefore, we present here the system of equations used to derive the random mating case. The main difference is where we place the observation point in the life cycle. In the main manuscript, we observe the genotype frequencies of adults and track them over time. Here, we track the frequencies of the gametes (the point in the life cycle when both sexes are haploid), reducing the previous system of 18 variables to 6.

In a given generation n, the frequencies of the male and female gametes are given by $\eta_k(n)$ and $\theta_i(n)$, respectively. Below, we present the modeled life cycle, in the absence of assortative mating, and how frequencies change from one generation to the next:

1. The first step is the formation of the zygote. In the absence of assortative mating, zygote formation depends only on the frequency of the different gametes in the population. In females, the frequency of a zygote carrying the ij genotype, with haplotype i inherited from the mother and j from the father is given by:

$$\theta^z_{ij}(n) = \theta_i(n) * \eta_j(n) \tag{S1}$$

Males are formed from unfertilized female gametes. Therefore, the frequency of zygote males reflects perfectly the frequency of female gametes:

$$\eta^z_k(n) = \theta_k(n) \tag{S2}$$

2. Individuals of both sex are under viability (or survival) selection. The frequencies of female and male adults are given by $\theta_{ij}^{a}(n)$ and $\eta_{i}^{a}(n_a)$, respectively:

$$\theta_{ij}^{a}(n) = \frac{w_{ij}^{f}\theta_{ij}^{z}(n)}{\sum_{i=1}^{4}\sum_{j=1}^{4} w_{ij}^{f}\theta_{ij}^{z}(n)} \tag{S3}$$

with w_{ij}^{f} the fitness of the ij genotype. Note that there are no parental effects: $w_{ij}^{f} = w_{ji}^{f}$; we maintain the distinction only for modeling convenience and:

$$\eta_{k}^{a}(n) = \frac{w_{k}^{m}\eta_{k}^{z}(n)}{\sum_{k=1}^{4} w_{k}^{m}\eta_{k}^{z}(n)} \tag{S4}$$

with w_{k}^{m} the fitness of haplotype k in males.

3. The last step corresponds to the production of gametes. As males are haploid, the gametes produced in the next generation reflect perfectly the distribution of adult males:

$$\eta_k(n+1) = \eta_{k}^{a}(n) \tag{S5}$$

Adult females produce eggs. Recombination happens during this stage. The frequency of the female gametes of the next generation, $f_{i}^{f}(n+1)$, is given by:

$$\begin{cases} \theta_i(n+1) = & \frac{1}{2}\sum_{j=1}^{4}\left(\theta_{ij}^{a}(n) + \theta_{ji}^{a}(n)\right) - \frac{\rho}{2}\psi(n) \text{ if } i \in \{1,4\} \\ \theta_i(n+1) = & \frac{1}{2}\sum_{j=1}^{4}\left(\theta_{ij}^{a}(n) + \theta_{ji}^{a}(n)\right) + \frac{\rho}{2}\psi(n) \text{ if } i \in \{2,3\} \end{cases} \tag{S6}$$

with $\psi(n) = \theta_{14}^{a}(n) + \theta_{41}^{a}(n) - \theta_{23}^{a}(n) - \theta_{32}^{a}(n)$.

By combining the different equations detailed above (i.e., substituting $\theta_{ij}^{a}(n)$ in equation (S6) and $\theta_{ij}^{z}(n)$ in (S3) for the female recursion and $\eta_{k}^{a}(n)$ in (S5) as well as $\eta_{k}^{z}(n)$ in (S4) for the male case), one obtains the following recursion when making the different fitness terms explicit:

$$\left\{\begin{aligned}
\theta_1(n+1) &= -\tfrac{1}{w^f}\left((\sigma+1)(-(\theta_2(n)+\theta_3(n)-1)\sigma\eta_1(n)+(\theta_2(n)+\theta_3(n)-1)\rho(\sigma+1)\eta_1(n)\right.\\
&\quad +\eta_1(n)+(\theta_3(n)\eta_2(n)+\theta_2(n)\eta_3(n))\rho(\sigma+1))+\theta_1(n)\left(-(2\eta_1(n)+\eta_2(n)+\eta_3(n)-1)\sigma^2\right.\\
&\quad \left.\left.-(4\eta_1(n)+\eta_2(n)+\eta_3(n)-2)\sigma+(2\eta_1(n)+\eta_2(n)+\eta_3(n)-1)\rho(\sigma+1)^2+1\right)\right)\\[2ex]
\theta_2(n+1) &= \tfrac{1}{w^f}\left((\sigma+1)(((\theta_3(n)-1)\eta_1(n)+\theta_1(n)(2\eta_1(n)+\eta_3(n)-1))\rho(\sigma+1)\right.\\
&\quad +\eta_2(n)(\theta_1(n)\rho(\sigma+1)+\theta_3(n)(\sigma\rho+\rho-\sigma)-1))+\theta_2(n)\left(\eta_1(n)\rho(\sigma+1)^2\right.\\
&\quad \left.\left.+\eta_3(n)(\sigma\rho+\rho-\sigma)(\sigma+1)+2\eta_2(n)\sigma-\sigma+2\eta_2(n)\gamma_1-1\right)\right)\\[2ex]
\theta_3(n+1) &= \tfrac{1}{w^f}\left((\sigma+1)(((\theta_2(n)-1)\eta_1(n)+\theta_1(n)(2\eta_1(n)+\eta_2(n)-1))\rho(\sigma+1)\right.\\
&\quad +\eta_3(n)(\theta_1(n)\rho(\sigma+1)+\theta_2(n)(\sigma\rho+\rho-\sigma)-1))+\theta_3(n)\left(\eta_1(n)\rho(\sigma+1)^2\right.\\
&\quad \left.\left.+\eta_2(n)(\sigma\rho+\rho-\sigma)(\sigma+1)+2\eta_3(n)\sigma-\sigma+2\eta_3(n)\gamma_2-1\right)\right)\\[2ex]
\eta_1(n+1) &= -\tfrac{\theta_1(n)}{\theta_2(n)\gamma_1+\theta_3(n)\gamma_2-1}\\[2ex]
\eta_2(n+1) &= \tfrac{\theta_2(n)(\gamma_1-1)}{\theta_2(n)\gamma_1+\theta_3(n)\gamma_2-1}\\[2ex]
\eta_3(n+1) &= \tfrac{\theta_3(n)(\gamma_2-1)}{\theta_2(n)\gamma_1+\theta_3(n)\gamma_2-1}
\end{aligned}\right. \tag{S7}$$

with w^f the mean fitness of the female population:

$$\begin{aligned}
w^f &= 2\left(\theta_3(n)\eta_1(n)\sigma^2-\eta_1(n)\sigma^2-\theta_3(n)\eta_2(n)\sigma^2-\theta_3(n)\sigma+2\theta_3(n)\eta_1(n)\sigma-2\eta_1(n)\sigma-\eta_2(n)\sigma\right.\\
&\quad +2\theta_3(n)\eta_3(n)\sigma-\eta_3(n)\sigma+\theta_1(n)(2\eta_1(n)+\eta_2(n)+\eta_3(n)-1)(\sigma+2)\sigma+\theta_2(n)\left((\eta_1(n)-\eta_3(n))\sigma^2\right.\\
&\quad \left.\left.+(2\eta_1(n)+2\eta_2(n)-1)\sigma+\eta_2(n)\gamma_1\right)+\theta_3(n)\eta_3(n)\gamma_2-1\right)
\end{aligned} \tag{S8}$$

Estimating genotype frequencies from a natural ant population

In order to compare our model with data from the natural, hybridizing Finnish ant population, we estimated the different genotype frequencies of parental *F. polyctena*-like and *F. aquilonia*-like individuals at pre-selection and post-selection life stages for males and females (Fig. S1(a)). We did not estimate the frequencies of introgressed or hybrid individuals. We used the genotype frequencies at different life-stages estimated in Kulmuni and Pamilo (2014) from nine microsatellite loci. For males, eggs were used to estimate pre-selection frequencies; the sum of adults and reproductive fathers was used to estimate post-selection frequencies. For females, eggs were used for pre-selection frequencies and the sum of young and old queens was used for post-selection frequencies. We used two different estimates for the number of parental females: individuals with exactly zero loci heterozygous for an introgressed allele, and individuals with one or more loci homozygous for the parental allele (i.e., the "diagnostic allele" in Kulmuni and Pamilo, 2014). In order to make these data comparable to our model, we rescaled the genotype frequencies such that 10.3% of the population is from the *F. polyctena*-like sub-population and 89.7% from the *F. aquilonia*-like sub-population, as estimated from the observed abundances of *F. polyctena*-like and *F. aquilonia*-like individuals from nests in the hybrid population collected between 1996-2012 (Table S1). Assuming that the natural population is at equilibrium, we fit the data (Table S2) to the model by calculating the sum of squared differences between the observed data and predicted equilibrium frequencies from 40600 parameter combinations.

Supplementary Results

Fitting the model to natural population frequencies

We compared the pre- and post-selection haplodiploid model (Fig. S1(a)) predictions with the estimated genotype frequencies of the natural, hybridizing *Formica* wood ant population for eggs and reproductive life-stages of males and females (Table S2). The model predictions from the best-fit models are shown in Figures S7 and S8. The best-fit models had parameter values corresponding to single-locus polymorphism or asymmetric coexistence, regardless of how the female frequencies were estimated (Fig. S9). Since these outcomes can occur at a variety of parameter combinations, we were not able to infer any specific parameter estimates other than that large values appear to be preferred for γ_1 and recombination (Fig. S10-S13), consistent with the genomic architecture of the natural population, where multiple incompatibilities are likely to be spread across chromosomes (Kulmuni and Pamilo, 2014). Our model predicts less change in the genotype frequencies before vs. after selection as compared to the differential observed in the data for eggs vs. reproductive adults (Fig. S7(c) and S8(c)).

Supplementary Discussion

We fitted our model to the data from the natural ant population described in Kulmuni and Pamilo (2014) and Table S1 in a rather crude approach. In the fitting procedure, we ignored that the data contain information from marker loci rather than the selected alleles, and we summarized the data in categories to resemble our case of a two-locus interaction. Our model fitting results indicate that the unequal ratio of *F. polyctena*-like and *F. aquilona*-like types that is observed in the natural population could represent a stable equilibrium of asymmetric coexistence. In fact, the high recombination rates among diagnostic alleles and strong prezygotic mechanisms producing within-group zygotes exhibited in the natural population (Kulmuni et al., 2010; Kulmuni and Pamilo, 2014) correspond with an area in the parameter space where asymmetric coexistence can be stably maintained over a wide range of values for female hybrid advantage.

Our model fit does not perform well at predicting the number of introgressed and hybrid females in the population. We were not able to estimate the population frequencies for introgressed and hybrid females with data from Kulmuni and Pamilo (2014), but we know from Kulmuni et al. (2010) that the vast majority of both *F. polyctena*-like and *F. aquilonia*-like females exhibit some introgression. Contrary to this observation in the natural population, our model fit predicts that introgressed *F. polyctena*-like females should be rare ($< 15\%$) and that pure *F. aquilona*-like females should be only slightly less common than the introgressed *F. polyctena*-like females (Fig. S8).

Supplementary Tables

Table S1: Table of adult frequencies for ant colonies in Långholmen in southern Finland. Individuals were genotyped and assigned to W- or R-type, where W indicates *F. aquilonia*-like parental individuals and R indicates *F. polyctena*-like parental individuals. Mean frequencies of *F. aquilonia*-like and *F. polyctena*-like types were calculated across castes and sampling years.

Sampling year	**Nest code**	**Caste**	**No. W ind.**	**No. R ind.**	**Freq. W**	**Freq. R**
1996	108_Year96	worker	7	0	1	0
1996	110_Year96	worker	14	0	1	0
1996	111_Year96	worker	6	0	1	0
1996	113_Year96	worker	0	4	0	1
1996	114_Year96	worker	6	0	1	0
1996	115_Year96	worker	6	0	1	0
1996	116_Year96	worker	7	0	1	0
1996	117_Year96	worker	1	0	1	0
1996	19_Year96	worker	7	0	1	0
1996	23_Year96	worker	7	0	1	0
1996	24_Year96	worker	7	0	1	0
1996	25_Year96	worker	1	2	0.333	0.667
1996	29_Year96	worker	5	3	0.625	0.375
1996	48_Year96	worker	6	0	1	0
2005	FA1	worker	4	0	1	0
2005	FA10	worker	4	0	1	0
2005	FA11	worker	4	0	1	0
2010	FA12	worker	2	36	0.298	0.702
2005	FA12	worker	15	4		
2005	FA13	worker	3	0	1	0
2005	FA14	worker	4	0	1	0
2005	FA15	worker	4	0	1	0
2005	FA16	worker	4	0	1	0
2008	FA17	queen (gyne)	10	0	1	0
2005	FA17	worker	4	0		
2008	FA18	queen (gyne)	19	0	1	0
2005	FA18	worker	4	0		
2008	FA19	queen (gyne)	2	0	1	0
2005	FA19	worker	4	0		
2005	FA2	worker	4	0	1	0

Continued on next page

Table S1 – continued from previous page

Sampling year	**Nest code**	**Caste**	**No. W ind.**	**No. R ind.**	**Freq. W**	**Freq. R**
2005	FA20	worker	4	0	1	0
2005	FA21	worker	4	0	1	0
2005	FA22	worker	4	0	1	0
2005	FA23	worker	4	0	1	0
2008	FA24	queen (gyne)	1	0	1	0
2005	FA24	worker	4	0		
2008	FA25	queen (gyne)	12	0	1	0
2012	FA26	worker	4	1	0.800	0.200
2012	FA27	worker	3	0	1	0
2012	FA29	worker	4	0	1	0
2005	FA3	worker	12	5	0.706	0.294
2012	FA31	worker	5	0	1	0
2012	FA32	worker	2	1	0.667	0.333
2012	FA33	worker	5	0	1	0
2012	FA35	worker	5	0	1	0
2012	FA39	worker	5	0	1	0
2010	FA4	worker	0	74	0.0645	0.935
2005	FA4	worker	6	13		
2005	FA5	worker	4	0	1	0
2005	FA6	worker	4	0	1	0
2005	FA7	worker	3	0	1	0
2008	FA8	queen (gyne)	1	0	1	0
2005	FA8	worker	4	0		
2005	FA9	worker	4	0	1	0
2014	FAuus2014A	worker	5	0	1	0
2004	Nest2	queen (gyne)	4	0	1	0
2004	Nest3	queen (gyne)	57	4	0.934	0.0667
2004	Nest4	queen (gyne)	6	0	1	0
2004	Nest5	queen (gyne)	6	21	0.222	0.778
Mean					**0.897**	**0.103**

Table S2: Table of estimated genotype frequencies used for data fitting. This data was calculated using the colony data from Table S1 above and the within-group genotype frequencies from Tables 1 & S7 of Kulmuni and Pamilo (2014). Following this same reference, “Introgressed” females refers to indviduals inferred to be purebred based on having no loci heterozygous for introgressed alleles. “Diagnostic” females refers to individuals inferred to be purebred based on having at least one locus homozygous for diagnostic alleles.

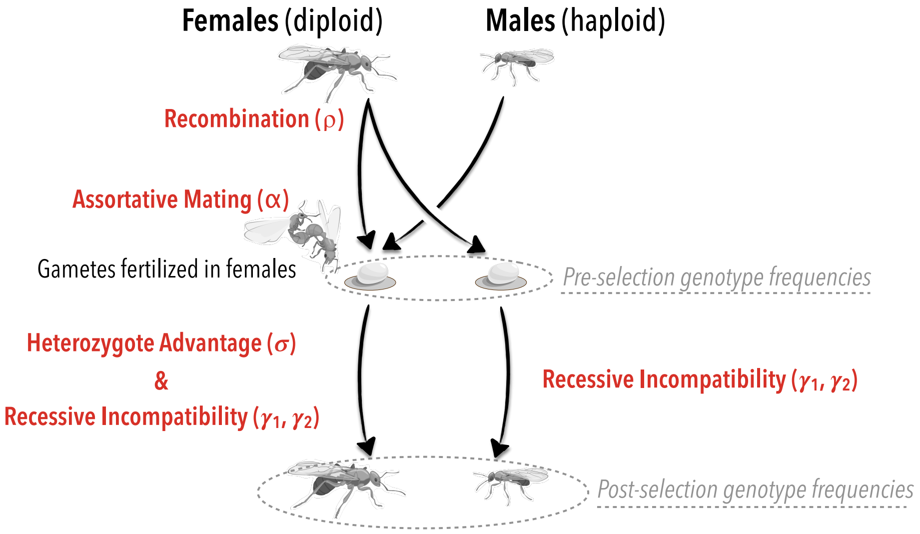
Males		
“Types”	**Before selection (Eggs)**	**After selection (Reproductive males)**
Parental *F. aquilonia*-like	0.637	0.828
Parental *F. polynecta*-like	0.0412	0.102
Summed hybrids	0.322	0.0701

“Introgressed” Females		
“Types”	**Before selection (Eggs)**	**After selection (Young and old queens)**
Parental *F. aquilonia*-like	0.511	0.424
Parental *F. polynecta*-like	0.0216	0
Summed all others	0.467	0.576
“Diagnostic” Females		
“Types”	**Before selection (Eggs)**	**After selection (Young and old queens)**
Parental *F. aquilonia*-like	0.314	0.189
Parental *F. polynecta*-like	0.0834	0.00214
Summed all others	0.603	0.809

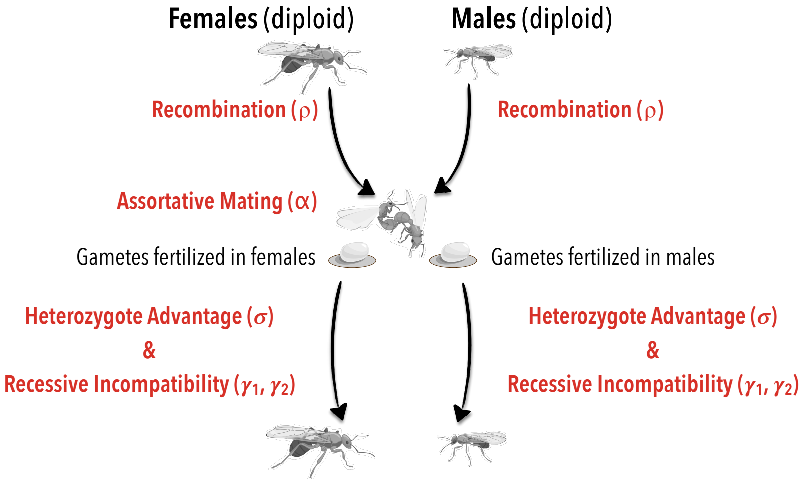
Table S3: Table that demonstrates why single-locus polymorphism can be invaded in diploids. This serves to explain why single-locus polymorphism is never stable in diploids.

Genotype	**Mutant**	**Fitness of the mutant / fitness of the mutated genotype**
$A_+A_+B_+B_+$	$A_-A_+B_+B_+$	$(1+\sigma) > 1$
$A_+A_+B_+B_-$	$A_-A_+B_+B_-$	$(1+\sigma) > 1$
$A_+A_+B_-B_-$	$A_-A_+B_-B_-$	$(1+\sigma)/(1-\gamma_1) > 1$
A_+B_+	A_-B_+	$(1-\gamma_2) < 1$
A_+B_-	A_-B_-	$1/(1-\gamma_1) > 1$

Supplementary Figures

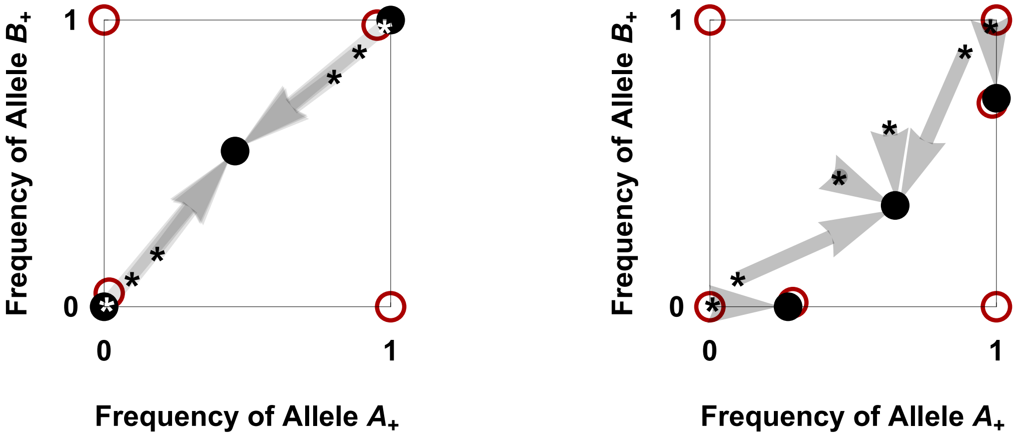


(a) Haplodiploid system



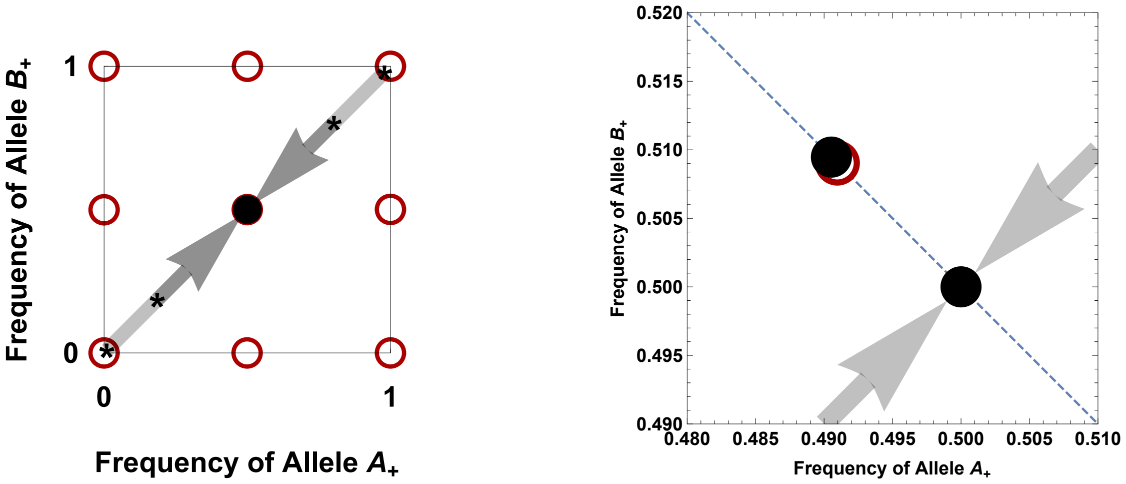
(b) Diploid system

Figure S1: Panel (a) shows the lifecycle of haplodiploids, panel (b) shows the lifecycle of diploids. Events that occur in either females and/or males are illustrated separately on the left and right sides, respectively, in order to highlight the differences between the lifecycles. The pre- and post-selection genotype frequencies for haplodiploids are indicated because they were used for model fitting.



(a) Tristability of Exclusion and Symmetric Coexistence.

(b) Tristability of Single-Locus Polymorphism and Symmetric Coexistence



(c) Symmetric Coexistence with Bistability

(d) Inset of Symmetric Coexistence with Bistability

Figure S2: Phase-plane diagrams of evolutionary scenarios in the haplodiploid model that are not discussed in the main text. Figures are as described in figure 3 except that unstable equilibia are red. Panel (a): $\sigma = 0.05$, $\gamma_1 = 0.2$, $\gamma_2 = 0.11$, $\rho = 0.099$, $\alpha = 0$. Panel (b): $\sigma = 0.143$, $\gamma_1 = 0.46$, $\gamma_2 = 0.083$, $\rho = 0.455$, $\alpha = 0$. Panel (c): $\sigma = 0.2$, $\gamma_1 = 0.019$, $\gamma_2 = 0.011$, $\rho = 0.000001$, $\alpha = 0$. Panel (d): inset of panel (c) with a dashed line at $y = 1 - x$.

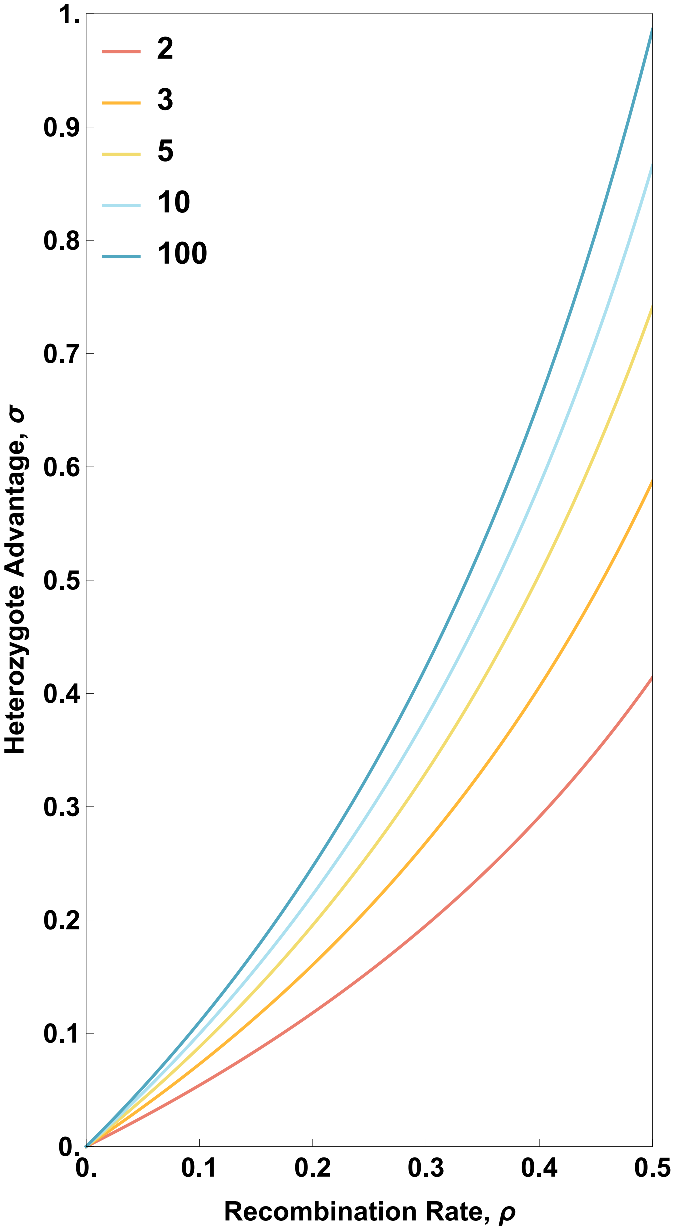


Figure S3: Conditions for stability of exclusion in the network case for haplodiploids with an increasing number of loci, as indicated in the legend. Exclusion represents a locally stable equilibrium for any parameter combination below the curve.

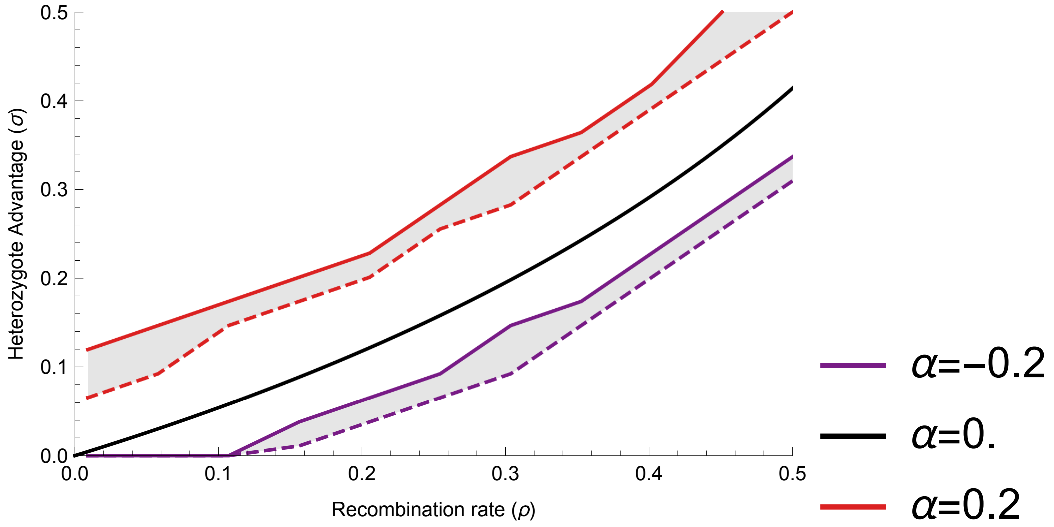
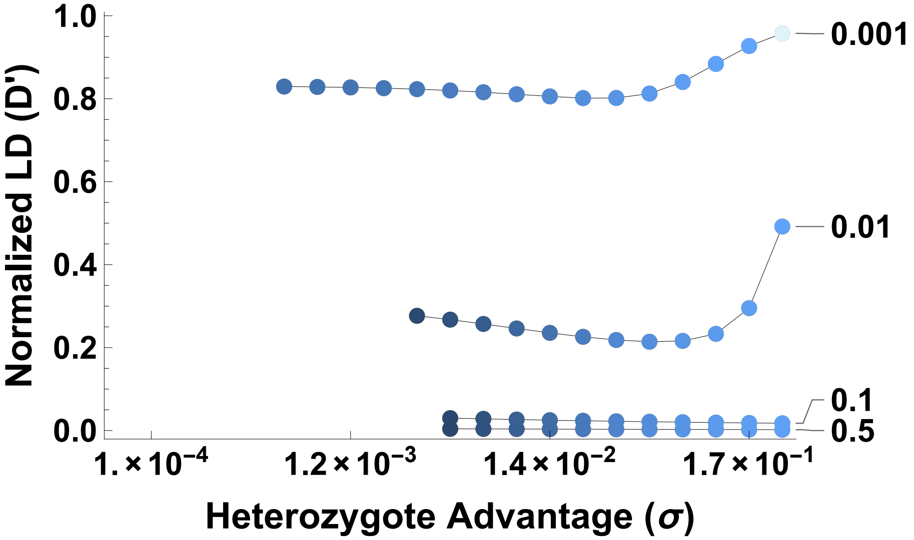
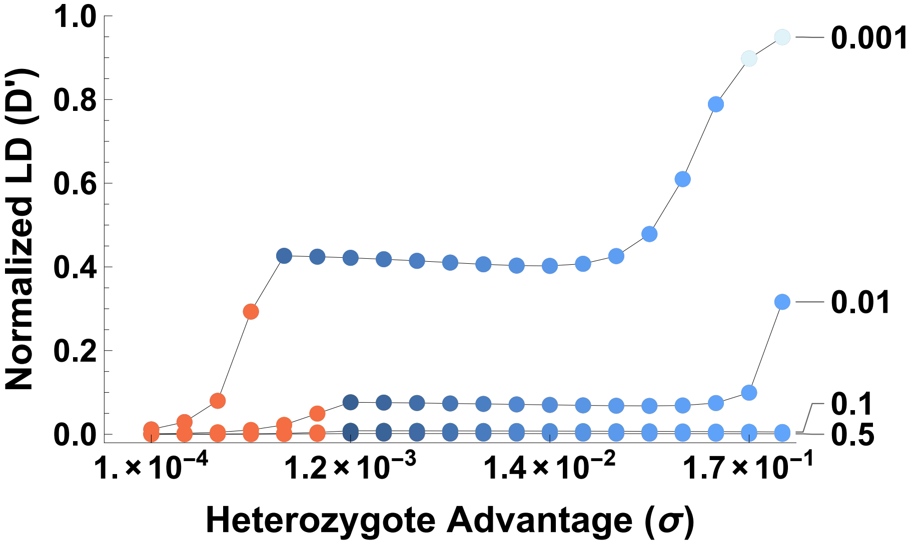


Figure S4: Plot of recombination (ρ) vs heterozygote advantage (σ) for lethal epistasis ($\gamma_1 = \gamma_2 = 1$) and varying strength of assortment, α. Solid lines show values at and above which symmetric coexistence occurs; dashed lines show values at and below which exclusion occurs; the shaded region between the solid and dashed lines shows values where asymmetric coexistence occurs. The result random mating ($\alpha = 0$) is given in equation 7 and so the black line is exactly the same as figure 4(a). This figure was generated with a precision of only ≈ 0.05 units of σ.



(a) Haplodiploids



(b) Diploids

Figure S5: The effect of heterozygote advantage on the normalized linkage disequilibrium ($D' = \frac{LD}{D_{\max}}$) for (a) haplodiploids and (b) diploids under varying recombination rates (values for ρ indicated at right of plot). Each point is shaded according to its evolutionary outcome following the color-scheme in figure 6. Normalization of LD is required since allele frequencies at the two loci can vary considerably (see shading of blue points in the plots above and in figure 6A). No values are shown for the single-locus polymorphism or exclusion outcomes because LD cannot exist when polymorphism is lost at one or both loci. ($\gamma_1 = 0.01, \gamma_2 = 0.002, \alpha = 0$).

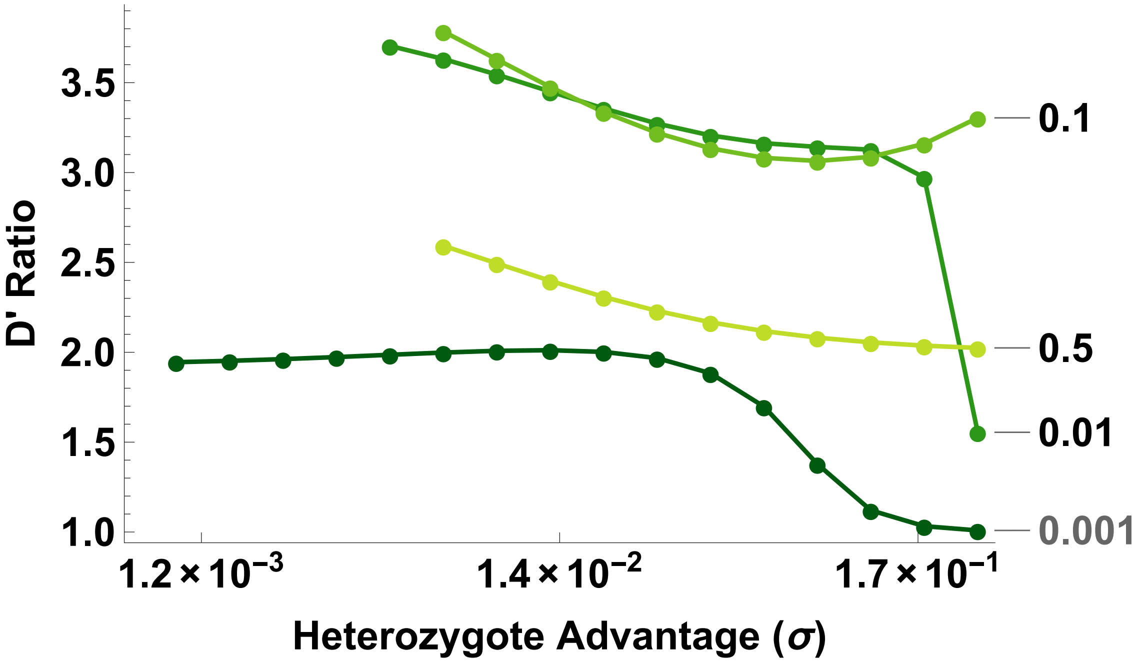
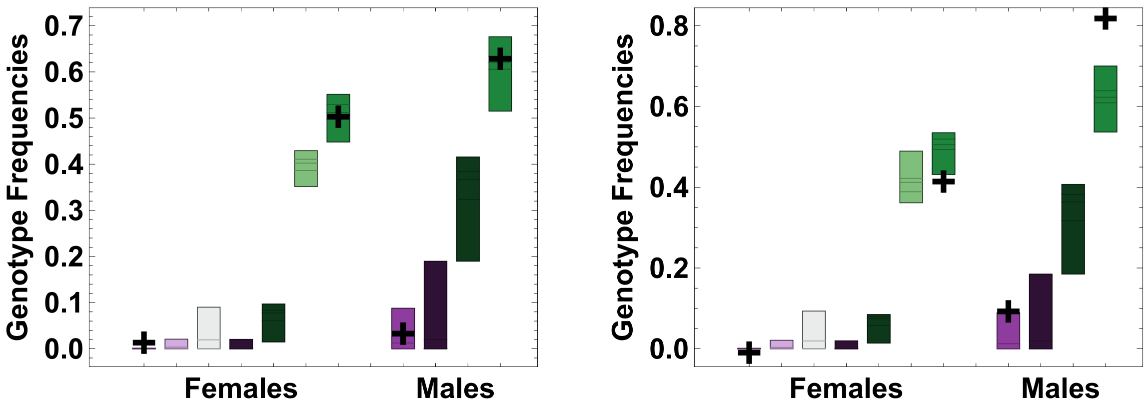
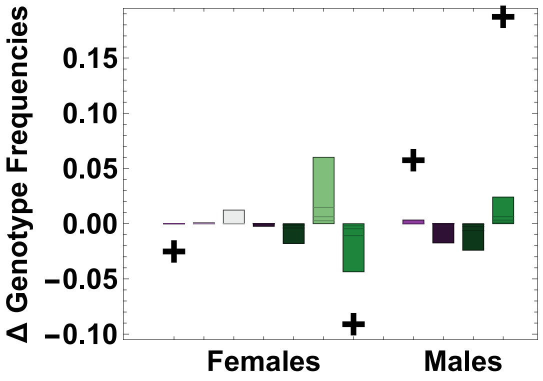


Figure S6: The effect of heterozygote advantage on the ratio of normalized linkage disequilibrium for haplodiploids over diploids ($\frac{D'_{\text{haplodiploids}}}{D'_{\text{diploids}}}$) under varying recombination rates. A ratio greater than 1 indicates more LD in haplodiploids; when polymorphism is maintained at both alleles, haplodiploids always have more or equal LD to diploids. Intermediate recombination values maximize the ratio. ($\gamma_1 = 0.01, \gamma_2 = 0.002, \alpha = 0$)



(a) Before viability selection

(b) After viability selection

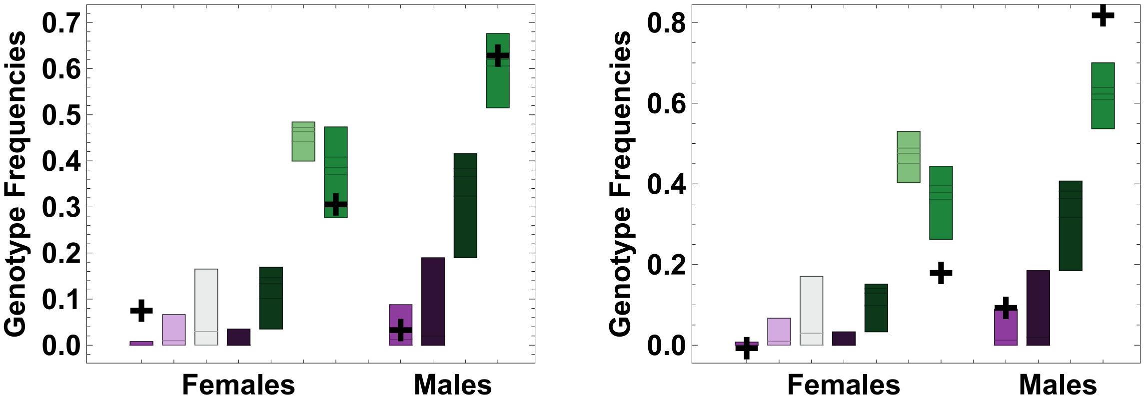


(c) Genotype frequency difference

🟪 **F. polyctena–like Parental** 🟪 **F. polyctena–like Introgressed** ⬜ **Heterozygous Hybrid** ⬛ **A_pB_a Homozygous Hybrid**

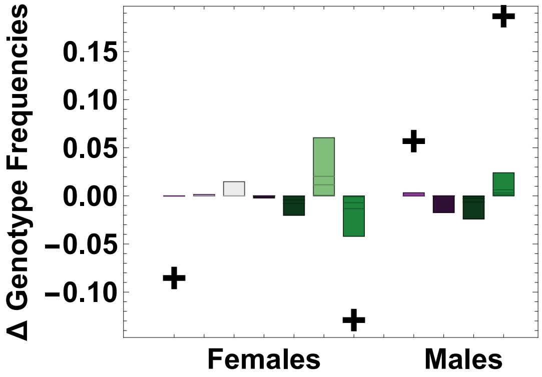
⬛ **A_aB_p Homozygous Hybrid** 🟩 **F. aquilonia–like Introgressed** 🟩 **F. aquilonia–like Parental**

Figure S7: Comparison of model predictions (boxplots) to the data used for fitting the model (+) shows that the model is able to capture the high frequency of *F. aquilona*-like alleles (green shades) in the population. Boxplots show the genotype frequencies for females and males that are predicted from the distribution of the best fitting models. Model predictions before selection, after selection, and delta selection (after selection − before selection). For "introgressed markers" data with random mating ($\alpha = 0$).



(a) Before viability selection

(b) After viability selection

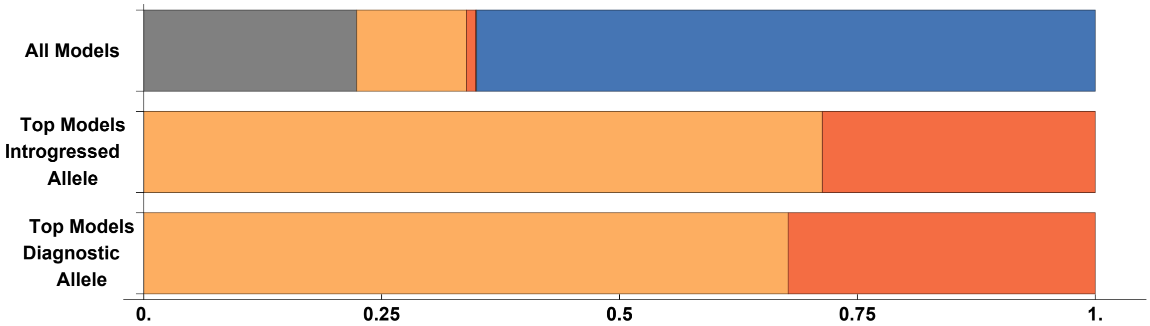


(c) Genotype frequency difference

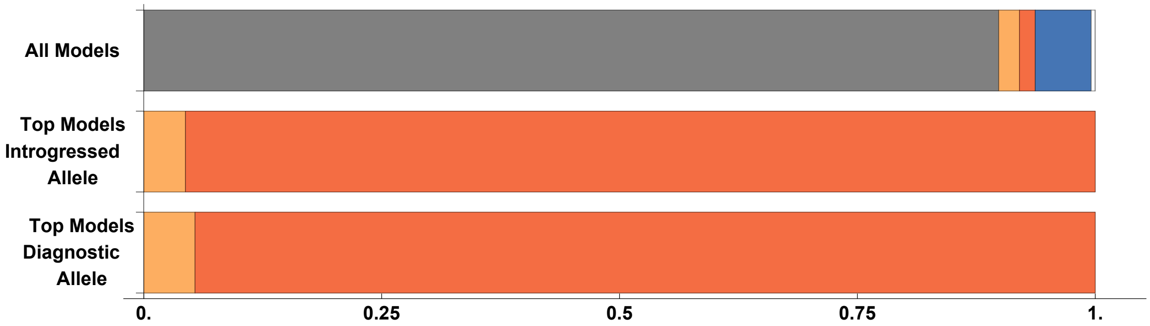
🟪 **F. polyctena–like Parental** 🟪 **F. polyctena–like Introgressed** ⬜ **Heterozygous Hybrid** ⬛ **A_pB_a Homozygous Hybrid**

🟩 **A_aB_p Homozygous Hybrid** 🟩 **F. aquilonia–like Introgressed** 🟩 **F. aquilonia–like Parental**

Figure S8: Comparison of model predictions (boxplots) to the data used for fitting the model (+) shows that the model is able to capture the high frequency of *F. aquilona*-like alleles (green shades) in the population. Boxplots show the genotype frequencies for females and males that are predicted from the distribution of the best fitting models. In this case parental genotype frequencies (shown on plot as +) are estimated using individuals with one or more loci homozygous for the parental allele ("diagnostic markers" data). Model predictions before selection, after selection, and delta selection (after selection − before selection). For "diagnostic markers" data with random mating ($\alpha = 0$).

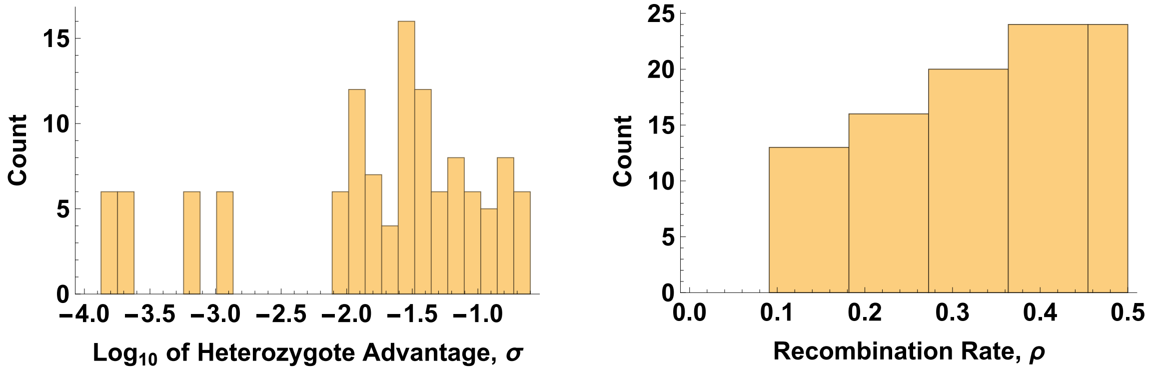


(a) Models with random mating ($\alpha = 0$)

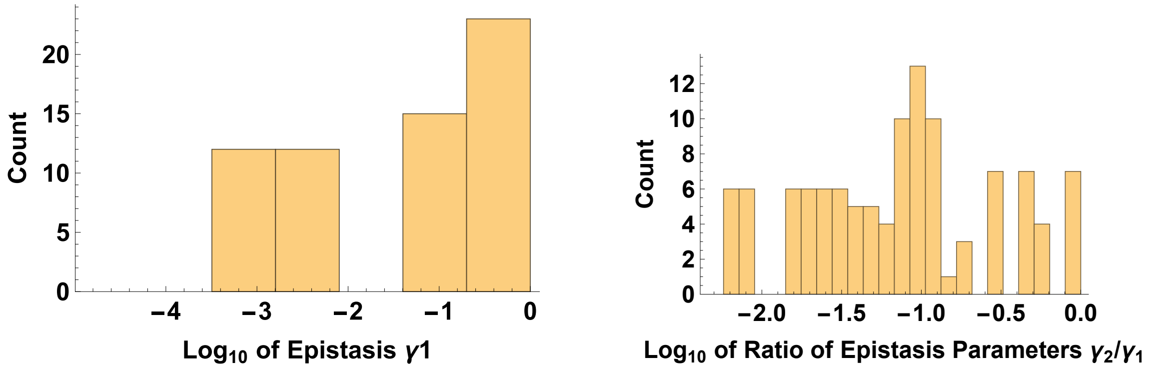


(b) Models with assortative mating

Figure S9: Bar plots show the proportion of parameter combinations that correspond to different evolutionary outcomes. “All models” is for all parameter combinations investigated, “Top models introgressed allele” is for model fitting to the “introgressed markers” data, and “Top models diagnostic allele” is for model fitting to the “diagnostic markers” data.

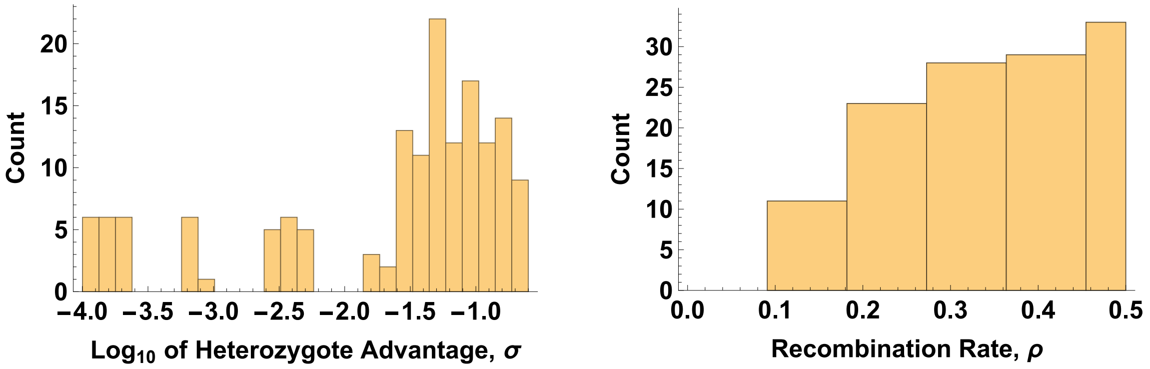


(a) Heterozygote advantage (b) Recombination



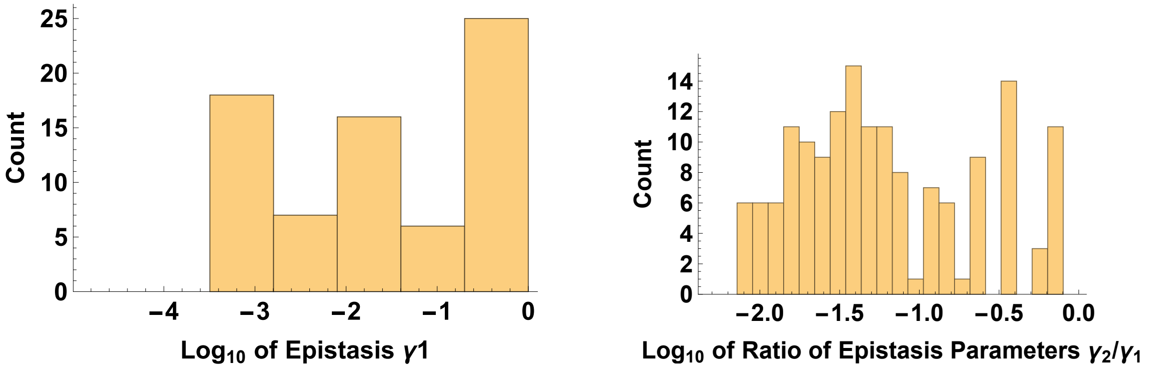
(c) Strength of negative epistasis γ_1 (d) Asymmetry of negative epistasis ($\frac{\gamma_2}{\gamma_1}$)

Figure S10: Distribution of the estimated parameter values for the model fitting "introgressed markers" data with random mating ($\alpha = 0$).



(a) Heterozygote advantage

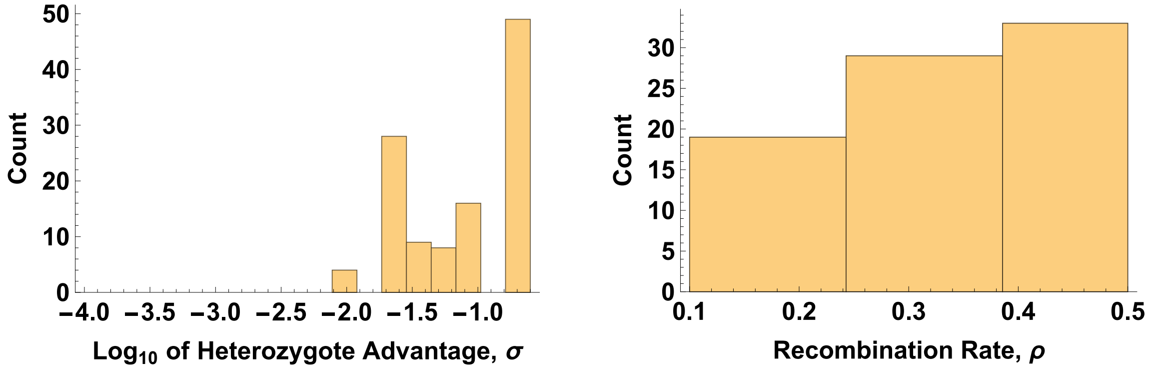
(b) Recombination



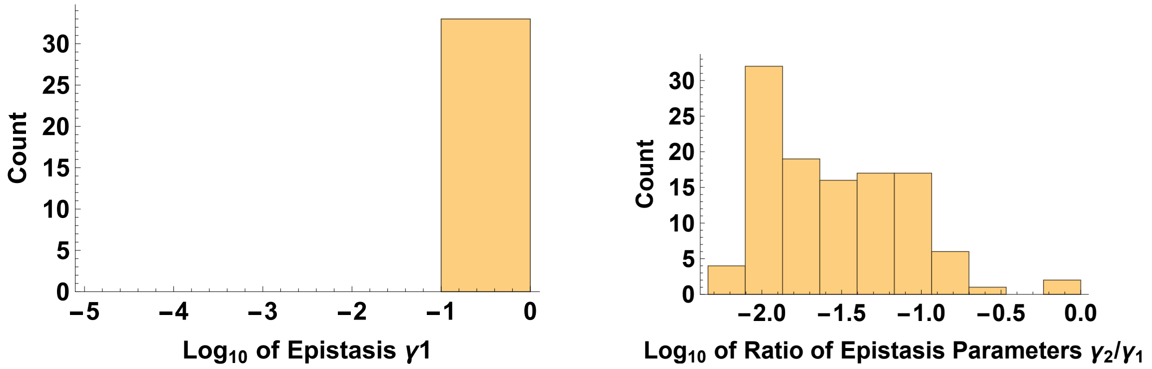
(c) Strength of negative epistasis γ_1

(d) Asymmetry of negative epistasis ($\frac{\gamma_2}{\gamma_1}$)

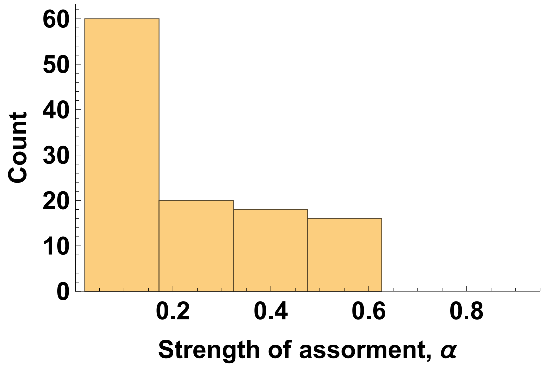
Figure S11: Distribution of the estimated parameter values for the model fitting "diagnostic markers" data with random mating ($\alpha = 0$).



(a) Heterozygote advantage (b) Recombination

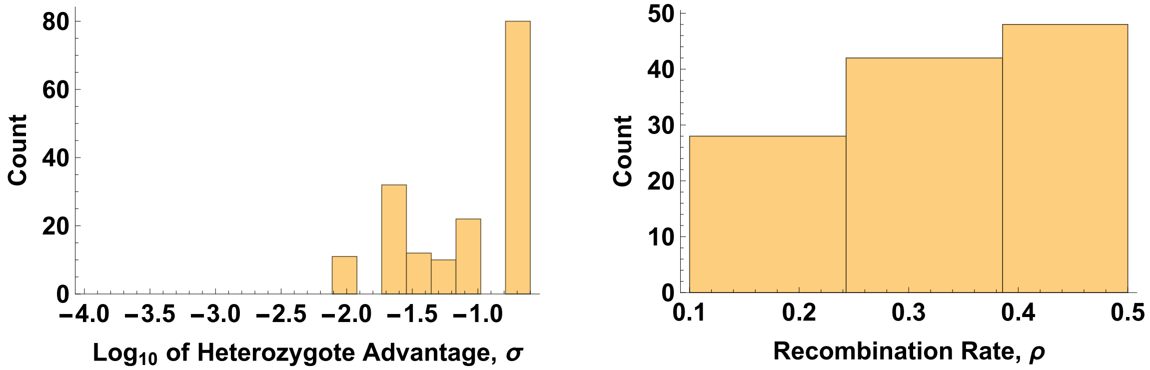


(c) Strength of negative epistasis γ_1 (d) Asymmetry of negative epistasis $(\frac{\gamma_2}{\gamma_1})$



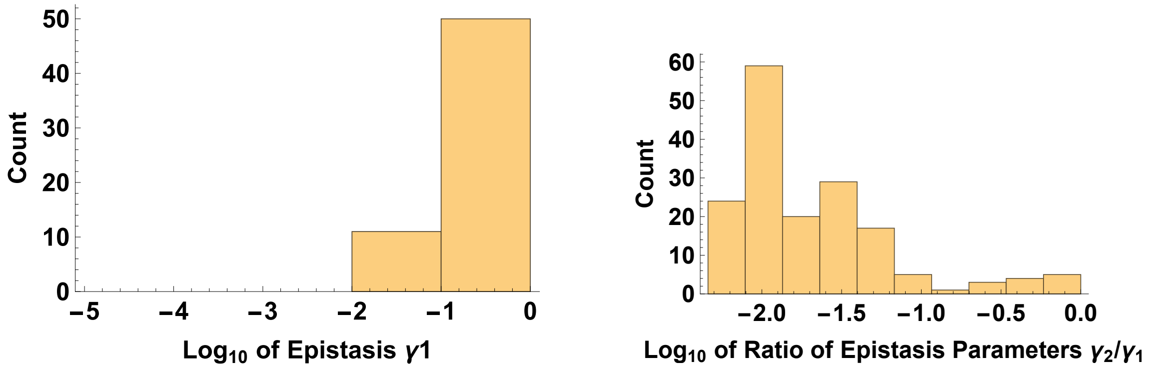
(e) Strength of assortment

Figure S12: Distribution of the estimated parameter values for the model fitting “introgressed markers” data with assortative mating.



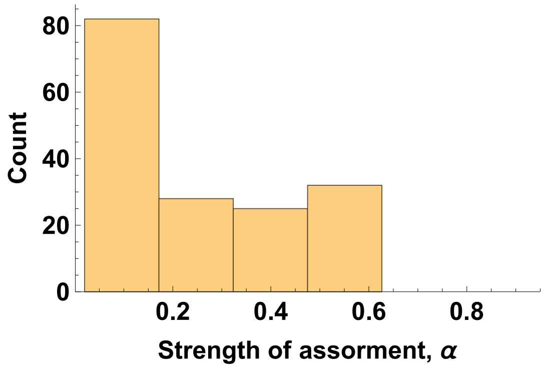
(a) Heterozygote advantage

(b) Recombination



(c) Strength of negative epistasis γ_1

(d) Asymmetry of negative epistasis ($\frac{\gamma_2}{\gamma_1}$)



(e) Strength of assortment

Figure S13: Distribution of the estimated parameter values for the model fitting "diagnostic markers" data with assortative mating.

References

J Kulmuni and P Pamilo. Introgression in hybrid ants is favored in females but selected against in males. *Proceedings of the National Academy of Sciences*, 111(35):12805–10, 2014. doi: 10.1073/pnas.1323045111.

J Kulmuni, B Seifert, and P Pamilo. Segregation distortion causes large-scale differences between male and female genomes in hybrid ants. *Proceedings of the National Academy of Sciences*, 107(16):7371–6, 2010. doi: 10.1073/pnas.0912409107.

Mathematica Online Supplement for “Conflict between heterozygote advantage and hybrid breakdown in haplodiploids (and sex chromosomes)”

The executable version of this file is available here: https://www.dropbox.com/s/w6jcx30im5t5597/Ant-hybrids_Mathematica_file_for_re-submission.nb?dl=0

Author contributions for coding and analysis

Chapter 1: CB
Chapter 2: AHG with help from AB
Chapter 3: CB
Chapter 4: AB
Chapter 5: AHG with help from CB, AB
Chapter 6: AHG

Chapter 1: Specifying the model

Dynamics without assortment

Life cycle for discrete dynamics & multiplicative selection

Before we begin, here is a handy function to improve display of lists:

```
grid[tab_] := Grid[tab, ItemSize → Full] (* this way it pretends that
  the document is of infinite width and doesn't break lines in tables *)
```

Assume that we have female gamete frequencies

```
gamF = {g1, g2, g3, g4};
```

and adult male frequencies

```
hapM = {h1, h2, h3, h4};
```

These create the next generation of female genotypes

```
genF = Table[gamF[[i]] hapM[[j]], {i, 4}, {j, 4}] // Flatten
```

```
{g1 h1, g1 h2, g1 h3, g1 h4, g2 h1, g2 h2, g2 h3,
 g2 h4, g3 h1, g3 h2, g3 h3, g3 h4, g4 h1, g4 h2, g4 h3, g4 h4}
```

and male genotypes/haplotypes (which are simply the female gamete frequencies).

```
genM = gamF
```

```
{g1, g2, g3, g4}
```

At first we will write down the model for general epistasis, but then study asymmetric recessive epistasis throughout the manuscript.

```
epistasisRecessiveAsymmetric =
  {e"01" → 0, e"10" → 0, e"01,10" → 0, e"01,01" → γ01, e"10,10" → γ10};
(* This is what we are going to use mainly from now on *)
```

Viability selection in males

Male frequencies are entirely determined by female gamete frequencies in the previous generation.

```
selectionMatrixMales = {1, 1 - e"01,01", 1 - e"10,10", 1};
(* notation indicates types of conflict,
here doubled such that haploids suffer as much as homozygous diploids *)
meanFitnessMales = Total[selectionMatrixMales gamF];
malesAfterSelection = selectionMatrixMales gamF / meanFitnessMales
```

$$\left\{\frac{g1}{g1+g4+g2\left(1-e_{01,01}\right)+g3\left(1-e_{10,10}\right)},\ \frac{g2\left(1-e_{01,01}\right)}{g1+g4+g2\left(1-e_{01,01}\right)+g3\left(1-e_{10,10}\right)},\ \frac{g3\left(1-e_{10,10}\right)}{g1+g4+g2\left(1-e_{01,01}\right)+g3\left(1-e_{10,10}\right)},\ \frac{g4}{g1+g4+g2\left(1-e_{01,01}\right)+g3\left(1-e_{10,10}\right)}\right\}$$

Viability selection in females, based on genotypes

To allow for strong selection, this scheme should be multiplicative. Also, we can integrate different types of epistasis. This is the general form:

```
selectionMatrixFemales = {{1, (1 - e"01") (1 + s), (1 - e"10") (1 + s), (1 + s)^2 (1 - e"01,10")},
   {(1 + s) (1 - e"01"), (1 - e"01,01"), (1 + s)^2 (1 - e"01,10"), (1 + s) (1 - e"01")},
   {(1 + s) (1 - e"10"), (1 + s)^2 (1 - e"01,10"), (1 - e"10,10"), (1 + s) (1 - e"10")},
   {(1 + s)^2 (1 - e"01,10"), (1 + s) (1 - e"01"), (1 + s) (1 - e"10"), 1}};
wShow = Prepend[selectionMatrixFemales, {{A0, B0}, {A0, B1}, {A1, B0}, {A1, B1}}];
Grid[MapThread[Prepend,
  {wShow, {"Haplotypes", {A0, B0}, {A0, B1}, {A1, B0}, {A1, B1}}}], Frame → All]
```

Haplotypes	{A0, B0}	{A0, B1}	{A1, B0}	{A1, B1}
{A0, B0}	1	$(1+s)\left(1-e_{01}\right)$	$(1+s)\left(1-e_{10}\right)$	$(1+s)^2\left(1-e_{01,10}\right)$
{A0, B1}	$(1+s)\left(1-e_{01}\right)$	$1-e_{01,01}$	$(1+s)^2\left(1-e_{01,10}\right)$	$(1+s)\left(1-e_{01}\right)$
{A1, B0}	$(1+s)\left(1-e_{10}\right)$	$(1+s)^2\left(1-e_{01,10}\right)$	$1-e_{10,10}$	$(1+s)\left(1-e_{10}\right)$
{A1, B1}	$(1+s)^2\left(1-e_{01,10}\right)$	$(1+s)\left(1-e_{01}\right)$	$(1+s)\left(1-e_{10}\right)$	1

Selection of genotypes happens as follows

```
femaleGenotypesAfterSelectionBeforeNormalization =
  Table[selectionMatrixFemales[[i, j]] gamF[[i]] hapM[[j]], {i, 4}, {j, 4}] // Flatten;
meanFitnessFemales = Total[femaleGenotypesAfterSelectionBeforeNormalization];
femaleGenotypesAfterSelection =
  femaleGenotypesAfterSelectionBeforeNormalization / meanFitnessFemales // Simplify;
```

```
femaleGenotypesAfterSelection // Column
```

$$-\Big((g1\,h1)\Big/\Big(-g1\,h1-g4\,h4+g2\,h1\,(1+s)\left(-1+e_{01}\right)+g1\,h2\,(1+s)\left(-1+e_{01}\right)+ g4\,h2\,(1+s)\left(-1+e_{01}\right)+g2\,h4\,(1+s)\left(-1+e_{01}\right)+g2\,h2\left(-1+e_{01,01}\right)+ g4\,h1\,(1+s)^2\left(-1+e_{01,10}\right)+g3\,h2\,(1+s)^2\left(-1+e_{01,10}\right)+g2\,h3\,(1+s)^2\left(-1+e_{01,10}\right)+ g1\,h4\,(1+s)^2\left(-1+e_{01,10}\right)+g3\,h1\,(1+s)\left(-1+e_{10}\right)+g1\,h3\,(1+s)\left(-1+e_{10}\right)+ g4\,h3\,(1+s)\left(-1+e_{10}\right)+g3\,h4\,(1+s)\left(-1+e_{10}\right)+g3\,h3\left(-1+e_{10,10}\right)\Big)\Big)$$

$$\begin{aligned}&-\big((\text{g1 h2 } (1+s)\ (1-e_{01}))\big)\ \big/\\&\quad\big(-\text{g1 h1}-\text{g4 h4}+\text{g2 h1 } (1+s)\ (-1+e_{01})+\text{g1 h2 } (1+s)\ (-1+e_{01})+\text{g4 h2 } (1+s)\ (-1+e_{01})+\\&\qquad\text{g2 h4 } (1+s)\ (-1+e_{01})+\text{g2 h2 } \left(-1+e_{01,01}\right)+\text{g4 h1 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g3 h2 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g2 h3 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g1 h4 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g3 h1 } (1+s)\ (-1+e_{10})+\text{g1 h3 } (1+s)\ (-1+e_{10})+\\&\qquad\text{g4 h3 } (1+s)\ (-1+e_{10})+\text{g3 h4 } (1+s)\ (-1+e_{10})+\text{g3 h3 } \left(-1+e_{10,10}\right)\big)\big)\end{aligned}$$

$$\begin{aligned}&-\big((\text{g1 h3 } (1+s)\ (1-e_{10}))\big)\ \big/\\&\quad\big(-\text{g1 h1}-\text{g4 h4}+\text{g2 h1 } (1+s)\ (-1+e_{01})+\text{g1 h2 } (1+s)\ (-1+e_{01})+\text{g4 h2 } (1+s)\ (-1+e_{01})+\\&\qquad\text{g2 h4 } (1+s)\ (-1+e_{01})+\text{g2 h2 } \left(-1+e_{01,01}\right)+\text{g4 h1 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g3 h2 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g2 h3 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g1 h4 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g3 h1 } (1+s)\ (-1+e_{10})+\text{g1 h3 } (1+s)\ (-1+e_{10})+\\&\qquad\text{g4 h3 } (1+s)\ (-1+e_{10})+\text{g3 h4 } (1+s)\ (-1+e_{10})+\text{g3 h3 } \left(-1+e_{10,10}\right)\big)\big)\end{aligned}$$

$$\begin{aligned}&-\big(\big(\text{g1 h4 } (1+s)^2\ \left(1-e_{01,10}\right)\big)\big)\ \big/\\&\quad\big(-\text{g1 h1}-\text{g4 h4}+\text{g2 h1 } (1+s)\ (-1+e_{01})+\text{g1 h2 } (1+s)\ (-1+e_{01})+\text{g4 h2 } (1+s)\ (-1+e_{01})+\\&\qquad\text{g2 h4 } (1+s)\ (-1+e_{01})+\text{g2 h2 } \left(-1+e_{01,01}\right)+\text{g4 h1 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g3 h2 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g2 h3 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g1 h4 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g3 h1 } (1+s)\ (-1+e_{10})+\text{g1 h3 } (1+s)\ (-1+e_{10})+\\&\qquad\text{g4 h3 } (1+s)\ (-1+e_{10})+\text{g3 h4 } (1+s)\ (-1+e_{10})+\text{g3 h3 } \left(-1+e_{10,10}\right)\big)\big)\end{aligned}$$

$$\begin{aligned}&-\big((\text{g2 h1 } (1+s)\ (1-e_{01}))\big)\ \big/\\&\quad\big(-\text{g1 h1}-\text{g4 h4}+\text{g2 h1 } (1+s)\ (-1+e_{01})+\text{g1 h2 } (1+s)\ (-1+e_{01})+\text{g4 h2 } (1+s)\ (-1+e_{01})+\\&\qquad\text{g2 h4 } (1+s)\ (-1+e_{01})+\text{g2 h2 } \left(-1+e_{01,01}\right)+\text{g4 h1 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g3 h2 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g2 h3 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g1 h4 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g3 h1 } (1+s)\ (-1+e_{10})+\text{g1 h3 } (1+s)\ (-1+e_{10})+\\&\qquad\text{g4 h3 } (1+s)\ (-1+e_{10})+\text{g3 h4 } (1+s)\ (-1+e_{10})+\text{g3 h3 } \left(-1+e_{10,10}\right)\big)\big)\end{aligned}$$

$$\begin{aligned}&-\big(\big(\text{g2 h2 } \left(1-e_{01,01}\right)\big)\big)\ \big/\\&\quad\big(-\text{g1 h1}-\text{g4 h4}+\text{g2 h1 } (1+s)\ (-1+e_{01})+\text{g1 h2 } (1+s)\ (-1+e_{01})+\text{g4 h2 } (1+s)\ (-1+e_{01})+\\&\qquad\text{g2 h4 } (1+s)\ (-1+e_{01})+\text{g2 h2 } \left(-1+e_{01,01}\right)+\text{g4 h1 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g3 h2 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g2 h3 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g1 h4 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g3 h1 } (1+s)\ (-1+e_{10})+\text{g1 h3 } (1+s)\ (-1+e_{10})+\\&\qquad\text{g4 h3 } (1+s)\ (-1+e_{10})+\text{g3 h4 } (1+s)\ (-1+e_{10})+\text{g3 h3 } \left(-1+e_{10,10}\right)\big)\big)\end{aligned}$$

$$\begin{aligned}&-\big(\big(\text{g2 h3 } (1+s)^2\ \left(1-e_{01,10}\right)\big)\big)\ \big/\\&\quad\big(-\text{g1 h1}-\text{g4 h4}+\text{g2 h1 } (1+s)\ (-1+e_{01})+\text{g1 h2 } (1+s)\ (-1+e_{01})+\text{g4 h2 } (1+s)\ (-1+e_{01})+\\&\qquad\text{g2 h4 } (1+s)\ (-1+e_{01})+\text{g2 h2 } \left(-1+e_{01,01}\right)+\text{g4 h1 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g3 h2 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g2 h3 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g1 h4 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g3 h1 } (1+s)\ (-1+e_{10})+\text{g1 h3 } (1+s)\ (-1+e_{10})+\\&\qquad\text{g4 h3 } (1+s)\ (-1+e_{10})+\text{g3 h4 } (1+s)\ (-1+e_{10})+\text{g3 h3 } \left(-1+e_{10,10}\right)\big)\big)\end{aligned}$$

$$\begin{aligned}&-\big((\text{g2 h4 } (1+s)\ (1-e_{01}))\big)\ \big/\\&\quad\big(-\text{g1 h1}-\text{g4 h4}+\text{g2 h1 } (1+s)\ (-1+e_{01})+\text{g1 h2 } (1+s)\ (-1+e_{01})+\text{g4 h2 } (1+s)\ (-1+e_{01})+\\&\qquad\text{g2 h4 } (1+s)\ (-1+e_{01})+\text{g2 h2 } \left(-1+e_{01,01}\right)+\text{g4 h1 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g3 h2 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g2 h3 } (1+s)^2\ \left(-1+e_{01,10}\right)+\\&\qquad\text{g1 h4 } (1+s)^2\ \left(-1+e_{01,10}\right)+\text{g3 h1 } (1+s)\ (-1+e_{10})+\text{g1 h3 } (1+s)\ (-1+e_{10})+\\&\qquad\text{g4 h3 } (1+s)\ (-1+e_{10})+\text{g3 h4 } (1+s)\ (-1+e_{10})+\text{g3 h3 } \left(-1+e_{10,10}\right)\big)\big)\end{aligned}$$

$$-\left(\left(g3\,h1\,(1+s)\,(1-e_{10})\right)/\left(-g1\,h1-g4\,h4+g2\,h1\,(1+s)\,(-1+e_{01})+g1\,h2\,(1+s)\,(-1+e_{01})+g4\,h2\,(1+s)\,(-1+e_{01})+g2\,h4\,(1+s)\,(-1+e_{01})+g2\,h2\,\left(-1+e_{01,01}\right)+g4\,h1\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h2\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g2\,h3\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g1\,h4\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h1\,(1+s)\,(-1+e_{10})+g1\,h3\,(1+s)\,(-1+e_{10})+g4\,h3\,(1+s)\,(-1+e_{10})+g3\,h4\,(1+s)\,(-1+e_{10})+g3\,h3\,\left(-1+e_{10,10}\right)\right)\right)$$

$$-\left(\left(g3\,h2\,(1+s)^{2}\,\left(1-e_{01,10}\right)\right)/\left(-g1\,h1-g4\,h4+g2\,h1\,(1+s)\,(-1+e_{01})+g1\,h2\,(1+s)\,(-1+e_{01})+g4\,h2\,(1+s)\,(-1+e_{01})+g2\,h4\,(1+s)\,(-1+e_{01})+g2\,h2\,\left(-1+e_{01,01}\right)+g4\,h1\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h2\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g2\,h3\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g1\,h4\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h1\,(1+s)\,(-1+e_{10})+g1\,h3\,(1+s)\,(-1+e_{10})+g4\,h3\,(1+s)\,(-1+e_{10})+g3\,h4\,(1+s)\,(-1+e_{10})+g3\,h3\,\left(-1+e_{10,10}\right)\right)\right)$$

$$-\left(\left(g3\,h3\,\left(1-e_{10,10}\right)\right)/\left(-g1\,h1-g4\,h4+g2\,h1\,(1+s)\,(-1+e_{01})+g1\,h2\,(1+s)\,(-1+e_{01})+g4\,h2\,(1+s)\,(-1+e_{01})+g2\,h4\,(1+s)\,(-1+e_{01})+g2\,h2\,\left(-1+e_{01,01}\right)+g4\,h1\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h2\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g2\,h3\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g1\,h4\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h1\,(1+s)\,(-1+e_{10})+g1\,h3\,(1+s)\,(-1+e_{10})+g4\,h3\,(1+s)\,(-1+e_{10})+g3\,h4\,(1+s)\,(-1+e_{10})+g3\,h3\,\left(-1+e_{10,10}\right)\right)\right)$$

$$-\left(\left(g3\,h4\,(1+s)\,(1-e_{10})\right)/\left(-g1\,h1-g4\,h4+g2\,h1\,(1+s)\,(-1+e_{01})+g1\,h2\,(1+s)\,(-1+e_{01})+g4\,h2\,(1+s)\,(-1+e_{01})+g2\,h4\,(1+s)\,(-1+e_{01})+g2\,h2\,\left(-1+e_{01,01}\right)+g4\,h1\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h2\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g2\,h3\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g1\,h4\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h1\,(1+s)\,(-1+e_{10})+g1\,h3\,(1+s)\,(-1+e_{10})+g4\,h3\,(1+s)\,(-1+e_{10})+g3\,h4\,(1+s)\,(-1+e_{10})+g3\,h3\,\left(-1+e_{10,10}\right)\right)\right)$$

$$-\left(\left(g4\,h1\,(1+s)^{2}\,\left(1-e_{01,10}\right)\right)/\left(-g1\,h1-g4\,h4+g2\,h1\,(1+s)\,(-1+e_{01})+g1\,h2\,(1+s)\,(-1+e_{01})+g4\,h2\,(1+s)\,(-1+e_{01})+g2\,h4\,(1+s)\,(-1+e_{01})+g2\,h2\,\left(-1+e_{01,01}\right)+g4\,h1\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h2\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g2\,h3\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g1\,h4\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h1\,(1+s)\,(-1+e_{10})+g1\,h3\,(1+s)\,(-1+e_{10})+g4\,h3\,(1+s)\,(-1+e_{10})+g3\,h4\,(1+s)\,(-1+e_{10})+g3\,h3\,\left(-1+e_{10,10}\right)\right)\right)$$

$$-\left(\left(g4\,h2\,(1+s)\,(1-e_{01})\right)/\left(-g1\,h1-g4\,h4+g2\,h1\,(1+s)\,(-1+e_{01})+g1\,h2\,(1+s)\,(-1+e_{01})+g4\,h2\,(1+s)\,(-1+e_{01})+g2\,h4\,(1+s)\,(-1+e_{01})+g2\,h2\,\left(-1+e_{01,01}\right)+g4\,h1\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h2\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g2\,h3\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g1\,h4\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h1\,(1+s)\,(-1+e_{10})+g1\,h3\,(1+s)\,(-1+e_{10})+g4\,h3\,(1+s)\,(-1+e_{10})+g3\,h4\,(1+s)\,(-1+e_{10})+g3\,h3\,\left(-1+e_{10,10}\right)\right)\right)$$

$$-\left(\left(g4\,h3\,(1+s)\,(1-e_{10})\right)/\left(-g1\,h1-g4\,h4+g2\,h1\,(1+s)\,(-1+e_{01})+g1\,h2\,(1+s)\,(-1+e_{01})+g4\,h2\,(1+s)\,(-1+e_{01})+g2\,h4\,(1+s)\,(-1+e_{01})+g2\,h2\,\left(-1+e_{01,01}\right)+g4\,h1\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h2\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g2\,h3\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g1\,h4\,(1+s)^{2}\,\left(-1+e_{01,10}\right)+g3\,h1\,(1+s)\,(-1+e_{10})+g1\,h3\,(1+s)\,(-1+e_{10})+g4\,h3\,(1+s)\,(-1+e_{10})+g3\,h4\,(1+s)\,(-1+e_{10})+g3\,h3\,\left(-1+e_{10,10}\right)\right)\right)$$

$$\begin{aligned}-\Big(\left(g4\ h4\right)\Big/\Big(&-g1\ h1-g4\ h4+g2\ h1\ (1+s)\ (-1+e_{01})+g1\ h2\ (1+s)\ (-1+e_{01})+\\&g4\ h2\ (1+s)\ (-1+e_{01})+g2\ h4\ (1+s)\ (-1+e_{01})+g2\ h2\ \left(-1+e_{01,01}\right)+\\&g4\ h1\ (1+s)^2\ \left(-1+e_{01,10}\right)+g3\ h2\ (1+s)^2\ \left(-1+e_{01,10}\right)+g2\ h3\ (1+s)^2\ \left(-1+e_{01,10}\right)+\\&g1\ h4\ (1+s)^2\ \left(-1+e_{01,10}\right)+g3\ h1\ (1+s)\ (-1+e_{10})+g1\ h3\ (1+s)\ (-1+e_{10})+\\&g4\ h3\ (1+s)\ (-1+e_{10})+g3\ h4\ (1+s)\ (-1+e_{10})+g3\ h3\ \left(-1+e_{10,10}\right)\Big)\Big)\end{aligned}$$

Recombination

Define different haplotypes and genotypes

```
haplotypes = Tuples[{0, 1}, 2]
genotypes = Tuples[haplotypes, 2]
```

```
{{0, 0}, {0, 1}, {1, 0}, {1, 1}}
```

```
{{{0, 0}, {0, 0}}, {{0, 0}, {0, 1}}, {{0, 0}, {1, 0}}, {{0, 0}, {1, 1}},
 {{0, 1}, {0, 0}}, {{0, 1}, {0, 1}}, {{0, 1}, {1, 0}}, {{0, 1}, {1, 1}},
 {{1, 0}, {0, 0}}, {{1, 0}, {0, 1}}, {{1, 0}, {1, 0}}, {{1, 0}, {1, 1}},
 {{1, 1}, {0, 0}}, {{1, 1}, {0, 1}}, {{1, 1}, {1, 0}}, {{1, 1}, {1, 1}}}
```

Define general frequency vectors

```
genFemale = Table[genotype_k, {k, genotypes}]
gametes = Table[gamete_k, {k, haplotypes}]
```

$$\begin{aligned}\{&\text{genotype}_{\{\{0,0\},\{0,0\}\}},\ \text{genotype}_{\{\{0,0\},\{0,1\}\}},\ \text{genotype}_{\{\{0,0\},\{1,0\}\}},\ \text{genotype}_{\{\{0,0\},\{1,1\}\}},\\&\text{genotype}_{\{\{0,1\},\{0,0\}\}},\ \text{genotype}_{\{\{0,1\},\{0,1\}\}},\ \text{genotype}_{\{\{0,1\},\{1,0\}\}},\ \text{genotype}_{\{\{0,1\},\{1,1\}\}},\\&\text{genotype}_{\{\{1,0\},\{0,0\}\}},\ \text{genotype}_{\{\{1,0\},\{0,1\}\}},\ \text{genotype}_{\{\{1,0\},\{1,0\}\}},\ \text{genotype}_{\{\{1,0\},\{1,1\}\}},\\&\text{genotype}_{\{\{1,1\},\{0,0\}\}},\ \text{genotype}_{\{\{1,1\},\{0,1\}\}},\ \text{genotype}_{\{\{1,1\},\{1,0\}\}},\ \text{genotype}_{\{\{1,1\},\{1,1\}\}}\}\end{aligned}$$

$$\{\text{gamete}_{\{0,0\}},\ \text{gamete}_{\{0,1\}},\ \text{gamete}_{\{1,0\}},\ \text{gamete}_{\{1,1\}}\}$$

Now make gametes out of genotypes after selection

```
recombination = gamete_J_ ⧴
  1 / 2 Sum[(1 - r) (genotype_{J,X} + genotype_{X,J}) + r (genotype_{{J[[1]],X[[2]]},{X[[1]],J[[2]]}} +
        genotype_{{X[[1]],J[[2]]},{J[[1]],X[[2]]}}), {X, haplotypes}]
```

$$\begin{aligned}\text{gamete}_{J\_} \mapsto \frac{1}{2}\sum_{X}^{\text{haplotypes}}\Big(&(1-r)\ \left(\text{genotype}_{\{J,X\}}+\text{genotype}_{\{X,J\}}\right)+\\&r\ \left(\text{genotype}_{\{\{J[\![1]\!],X[\![2]\!]\},\{X[\![1]\!],J[\![2]\!]\}\}}+\text{genotype}_{\{\{X[\![1]\!],J[\![2]\!]\},\{J[\![1]\!],X[\![2]\!]\}\}}\right)\Big)\end{aligned}$$

Here is the printout of what happens:

```
gametes /. recombination // FullSimplify
```

$$\begin{aligned}\Big\{&\tfrac{1}{2}\big(2\,\text{genotype}_{\{\{0,0\},\{0,0\}\}}+\text{genotype}_{\{\{0,0\},\{0,1\}\}}+\text{genotype}_{\{\{0,0\},\{1,0\}\}}-\\&\quad(-1+r)\,\text{genotype}_{\{\{0,0\},\{1,1\}\}}+\text{genotype}_{\{\{0,1\},\{0,0\}\}}+r\,\text{genotype}_{\{\{0,1\},\{1,0\}\}}+\\&\quad\text{genotype}_{\{\{1,0\},\{0,0\}\}}+r\,\text{genotype}_{\{\{1,0\},\{0,1\}\}}-(-1+r)\,\text{genotype}_{\{\{1,1\},\{0,0\}\}}\big),\\&\tfrac{1}{2}\big(\text{genotype}_{\{\{0,0\},\{0,1\}\}}+r\,\text{genotype}_{\{\{0,0\},\{1,1\}\}}+\text{genotype}_{\{\{0,1\},\{0,0\}\}}+\\&\quad2\,\text{genotype}_{\{\{0,1\},\{0,1\}\}}-(-1+r)\,\text{genotype}_{\{\{0,1\},\{1,0\}\}}+\text{genotype}_{\{\{0,1\},\{1,1\}\}}-\\&\quad(-1+r)\,\text{genotype}_{\{\{1,0\},\{0,1\}\}}+r\,\text{genotype}_{\{\{1,1\},\{0,0\}\}}+\text{genotype}_{\{\{1,1\},\{0,1\}\}}\big),\\&\tfrac{1}{2}\big(\text{genotype}_{\{\{0,0\},\{1,0\}\}}+r\,\text{genotype}_{\{\{0,0\},\{1,1\}\}}-(-1+r)\,\text{genotype}_{\{\{0,1\},\{1,0\}\}}+\\&\quad\text{genotype}_{\{\{1,0\},\{0,0\}\}}-(-1+r)\,\text{genotype}_{\{\{1,0\},\{0,1\}\}}+2\,\text{genotype}_{\{\{1,0\},\{1,0\}\}}+\\&\quad\text{genotype}_{\{\{1,0\},\{1,1\}\}}+r\,\text{genotype}_{\{\{1,1\},\{0,0\}\}}+\text{genotype}_{\{\{1,1\},\{1,0\}\}}\big),\\&\tfrac{1}{2}\big(-(-1+r)\,\text{genotype}_{\{\{0,0\},\{1,1\}\}}+\text{genotype}_{\{\{0,1\},\{1,1\}\}}+\text{genotype}_{\{\{1,0\},\{1,1\}\}}+\\&\quad r\,\big(\text{genotype}_{\{\{0,1\},\{1,0\}\}}+\text{genotype}_{\{\{1,0\},\{0,1\}\}}-\text{genotype}_{\{\{1,1\},\{0,0\}\}}\big)+\\&\quad\text{genotype}_{\{\{1,1\},\{0,0\}\}}+\text{genotype}_{\{\{1,1\},\{0,1\}\}}+\text{genotype}_{\{\{1,1\},\{1,0\}\}}+2\,\text{genotype}_{\{\{1,1\},\{1,1\}\}}\big)\Big\}\end{aligned}$$

As a test, combine selection and recombination in females, and try some special cases.

```
femaleLifeCycle = gametes /. recombination /.
    Thread[genFemale → femaleGenotypesAfterSelection] // Simplify;
```

No selection or recombination

```
femaleLifeCycle /. s → 0 /. epistasisRecessiveAsymmetric /. γ01 → 0 /. γ10 → 0 /. r → 0 /.
  Thread[hapM -> gamF] // FullSimplify
```

$$\left\{\frac{g1}{g1+g2+g3+g4},\ \frac{g2}{g1+g2+g3+g4},\ \frac{g3}{g1+g2+g3+g4},\ \frac{g4}{g1+g2+g3+g4}\right\}$$

```
femaleLifeCycle /. s → 0 /. epistasisRecessiveAsymmetric /. γ01 → 1 / 4 /. γ10 → 1 / 2 /.
   r → 0 /. Thread[hapM -> gamF] // FullSimplify
```

$$\begin{aligned}\Big\{&(4\,g1\,(g1+g2+g3+g4))\Big/\\&\quad\left(4\,g1^2+3\,g2^2+8\,g2\,g3+2\,g3^2+8\,(g2+g3)\,g4+4\,g4^2+8\,g1\,(g2+g3+g4)\right),\\&(g2\,(4\,g1+3\,g2+4\,(g3+g4)))\Big/\\&\quad\left(4\,g1^2+3\,g2^2+8\,g2\,g3+2\,g3^2+8\,(g2+g3)\,g4+4\,g4^2+8\,g1\,(g2+g3+g4)\right),\\&(2\,g3\,(2\,g1+2\,g2+g3+2\,g4))\Big/\\&\quad\left(4\,g1^2+3\,g2^2+8\,g2\,g3+2\,g3^2+8\,(g2+g3)\,g4+4\,g4^2+8\,g1\,(g2+g3+g4)\right),\\&(4\,g4\,(g1+g2+g3+g4))\Big/\\&\quad\left(4\,g1^2+3\,g2^2+8\,g2\,g3+2\,g3^2+8\,(g2+g3)\,g4+4\,g4^2+8\,g1\,(g2+g3+g4)\right)\Big\}\end{aligned}$$

Lethal epistasis and no recombination

```
femaleLifeCycle /. s → 0 /. epistasisRecessiveAsymmetric /. r → 0 /. γ01 → 1 /. γ10 → 1 /.
   Thread[hapM -> gamF] // FullSimplify
```

$$\left\{\frac{g1\ (g1+g2+g3+g4)}{g1^2+2\ g2\ (g3+g4)+2\ g1\ (g2+g3+g4)+g4\ (2\ g3+g4)},\ \frac{g2\ (g1+g3+g4)}{g1^2+2\ g2\ (g3+g4)+2\ g1\ (g2+g3+g4)+g4\ (2\ g3+g4)},\ \frac{g3\ (g1+g2+g4)}{g1^2+2\ g2\ (g3+g4)+2\ g1\ (g2+g3+g4)+g4\ (2\ g3+g4)},\ \frac{g4\ (g1+g2+g3+g4)}{g1^2+2\ g2\ (g3+g4)+2\ g1\ (g2+g3+g4)+g4\ (2\ g3+g4)}\right\}$$

Death of all heterozygotes

```
femaleLifeCycle /. s → -1 /. epistasisRecessiveAsymmetric /. γ10 → 0 /. γ01 → 0 /.
   Thread[hapM -> gamF] // FullSimplify
```

$$\left\{\frac{g1^2}{g1^2+g2^2+g3^2+g4^2},\ \frac{g2^2}{g1^2+g2^2+g3^2+g4^2},\ \frac{g3^2}{g1^2+g2^2+g3^2+g4^2},\ \frac{g4^2}{g1^2+g2^2+g3^2+g4^2}\right\}$$

Death of heterozygotes & incompatibility

```
femaleLifeCycle /. s → -1 /. epistasisRecessiveAsymmetric /. γ10 → 1 /. γ01 → 1 /.
   Thread[hapM -> gamF] // FullSimplify
```

$$\left\{\frac{g1^2}{g1^2+g4^2},\ 0,\ 0,\ \frac{g4^2}{g1^2+g4^2}\right\}$$

Makes all sense.

Dynamics as functions of haplotype frequencies

Here we define functions that describe the dynamics int he haplodiploid model.

Haplodiploid dynamics as function of female gametes and male frequencies after selection

```
dynamics = {
    (* the female gamete frequencies in the next generation are the following *)
    gametes /. recombination /. Thread[genFemale → femaleGenotypesAfterSelection],
    (* new male frequencies after selection
     are the female gamete frequencies after male selection *)
    malesAfterSelection
   } /. epistasisRecessiveAsymmetric // Simplify
```

```
{{(g1 (2 h1 + (1 + s) (h2 + h3 - h4 (-1 + r) (1 + s))) +
      (1 + s) (-g4 h1 (-1 + r) (1 + s) + g3 (h1 + h2 r (1 + s)) + g2 (h1 + h3 r (1 + s)))) /
    (2 (g3 h1 + g4 h1 + g3 h2 + g4 h2 + g3 h3 + g4 h3 + g3 h4 + g4 h4 + g3 h1 s + 2 g4 h1 s + 2 g3 h2 s +
        g4 h2 s + g4 h3 s + g3 h4 s + g4 h1 s^2 + g3 h2 s^2 + g1 (h1 + (1 + s) (h2 + h3 + h4 + h4 s)) +
        g2 (h2 + h1 (1 + s) + (1 + s) (h3 + h4 + h3 s) - h2 γ01) - g3 h3 γ10)),
   ((1 + s) (-g3 h2 (-1 + r) (1 + s) + g4 (h2 + h1 r (1 + s)) + g1 (h2 + h4 r (1 + s))) +
     g2 (h1 (1 + s) - (1 + s) (-h4 + h3 (-1 + r) (1 + s)) - 2 h2 (-1 + γ01))) /
    (2 (g3 h1 + g4 h1 + g3 h2 + g4 h2 + g3 h3 + g4 h3 + g3 h4 + g4 h4 + g3 h1 s + 2 g4 h1 s + 2 g3 h2 s +
        g4 h2 s + g4 h3 s + g3 h4 s + g4 h1 s^2 + g3 h2 s^2 + g1 (h1 + (1 + s) (h2 + h3 + h4 + h4 s)) +
        g2 (h2 + h1 (1 + s) + (1 + s) (h3 + h4 + h3 s) - h2 γ01) - g3 h3 γ10)),
   ((1 + s) (-g2 h3 (-1 + r) (1 + s) + g4 (h3 + h1 r (1 + s)) + g1 (h3 + h4 r (1 + s))) +
     g3 (2 h3 + h4 + h4 s + h1 (1 + s) - h2 (-1 + r) (1 + s)^2 - 2 h3 γ10)) /
    (2 (g3 h1 + g4 h1 + g3 h2 + g4 h2 + g3 h3 + g4 h3 + g3 h4 + g4 h4 + g3 h1 s + 2 g4 h1 s + 2 g3 h2 s +
        g4 h2 s + g4 h3 s + g3 h4 s + g4 h1 s^2 + g3 h2 s^2 + g1 (h1 + (1 + s) (h2 + h3 + h4 + h4 s)) +
        g2 (h2 + h1 (1 + s) + (1 + s) (h3 + h4 + h3 s) - h2 γ01) - g3 h3 γ10)),
   (g4 (h2 + h3 + 2 h4 + h2 s + h3 s - h1 (-1 + r) (1 + s)^2) +
      (1 + s) (-g1 h4 (-1 + r) (1 + s) + g3 (h4 + h2 r (1 + s)) + g2 (h4 + h3 r (1 + s)))) /
    (2 (g3 h1 + g4 h1 + g3 h2 + g4 h2 + g3 h3 + g4 h3 + g3 h4 + g4 h4 + g3 h1 s + 2 g4 h1 s + 2 g3 h2 s +
        g4 h2 s + g4 h3 s + g3 h4 s + g4 h1 s^2 + g3 h2 s^2 + g1 (h1 + (1 + s) (h2 + h3 + h4 + h4 s)) +
        g2 (h2 + h1 (1 + s) + (1 + s) (h3 + h4 + h3 s) - h2 γ01) - g3 h3 γ10))},
  {                g1                                  g2 - g2 γ01
   ────────────────────────────────── , ────────────────────────────────── ,
   g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10  g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10
              g3 - g3 γ10
   ────────────────────────────────── ,
   g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10
                  g4
   ──────────────────────────────────}}
   g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10
```

```
haplotypeDynamicsX[1][{s_, γ01_, γ10_, r_}][
  {femaleGametes_, maleHaplotypesAfterSelection_}] :=
 {{(g1 (2 h1 + (1 + s) (h2 + h3 - h4 (-1 + r) (1 + s))) +
          (1 + s) (-g4 h1 (-1 + r) (1 + s) + g3 (h1 + h2 r (1 + s)) + g2 (h1 + h3 r (1 + s)))) /
      (2 (g3 h1 + g4 h1 + g3 h2 + g4 h2 + g3 h3 + g4 h3 + g3 h4 + g4 h4 + g3 h1 s +
           2 g4 h1 s + 2 g3 h2 s + g4 h2 s + g4 h3 s + g3 h4 s + g4 h1 s^2 +
           g3 h2 s^2 + g1 (h1 + (1 + s) (h2 + h3 + h4 + h4 s)) +
           g2 (h2 + h1 (1 + s) + (1 + s) (h3 + h4 + h3 s) - h2 γ01) - g3 h3 γ10)),
    ((1 + s) (-g3 h2 (-1 + r) (1 + s) + g4 (h2 + h1 r (1 + s)) + g1 (h2 + h4 r (1 + s))) +
        g2 (h1 (1 + s) - (1 + s) (-h4 + h3 (-1 + r) (1 + s)) - 2 h2 (-1 + γ01))) /
      (2 (g3 h1 + g4 h1 + g3 h2 + g4 h2 + g3 h3 + g4 h3 + g3 h4 + g4 h4 + g3 h1 s +
           2 g4 h1 s + 2 g3 h2 s + g4 h2 s + g4 h3 s + g3 h4 s + g4 h1 s^2 +
           g3 h2 s^2 + g1 (h1 + (1 + s) (h2 + h3 + h4 + h4 s)) +
           g2 (h2 + h1 (1 + s) + (1 + s) (h3 + h4 + h3 s) - h2 γ01) - g3 h3 γ10)),
    ((1 + s) (-g2 h3 (-1 + r) (1 + s) + g4 (h3 + h1 r (1 + s)) + g1 (h3 + h4 r (1 + s))) +
        g3 (2 h3 + h4 + h4 s + h1 (1 + s) - h2 (-1 + r) (1 + s)^2 - 2 h3 γ10)) /
      (2 (g3 h1 + g4 h1 + g3 h2 + g4 h2 + g3 h3 + g4 h3 + g3 h4 + g4 h4 + g3 h1 s +
           2 g4 h1 s + 2 g3 h2 s + g4 h2 s + g4 h3 s + g3 h4 s + g4 h1 s^2 +
           g3 h2 s^2 + g1 (h1 + (1 + s) (h2 + h3 + h4 + h4 s)) +
           g2 (h2 + h1 (1 + s) + (1 + s) (h3 + h4 + h3 s) - h2 γ01) - g3 h3 γ10)),
    (g4 (h2 + h3 + 2 h4 + h2 s + h3 s - h1 (-1 + r) (1 + s)^2) + (1 + s)
          (-g1 h4 (-1 + r) (1 + s) + g3 (h4 + h2 r (1 + s)) + g2 (h4 + h3 r (1 + s)))) /
      (2 (g3 h1 + g4 h1 + g3 h2 + g4 h2 + g3 h3 + g4 h3 + g3 h4 + g4 h4 + g3 h1 s +
           2 g4 h1 s + 2 g3 h2 s + g4 h2 s + g4 h3 s + g3 h4 s + g4 h1 s^2 +
           g3 h2 s^2 + g1 (h1 + (1 + s) (h2 + h3 + h4 + h4 s)) +
           g2 (h2 + h1 (1 + s) + (1 + s) (h3 + h4 + h3 s) - h2 γ01) - g3 h3 γ10))},
   {                g1                                  g2 - g2 γ01
    ------------------------------------ , ------------------------------------ ,
    g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10    g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10
              g3 - g3 γ10
    ------------------------------------ ,
    g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10
                  g4
    ------------------------------------ }} /.
    g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10
   Thread[gamF → femaleGametes] /. Thread[
   hapM →
    maleHaplotypesAfterSelection]
```

But we can get rid of 2 variables here because frequencies sum up to 1.

```
dynamics[[All, 1 ;; 3]] /. {g4 → 1 - g1 - g2 - g3, h4 → 1 - h1 - h2 - h3} // Simplify
```

```
{{-(((1 + s) (h1 - (-1 + g2 + g3) h1 s + (-1 + g2 + g3) h1 r (1 + s) + (g3 h2 + g2 h3) r (1 + s)) +
        g1 (1 - (-2 + 4 h1 + h2 + h3) s - (-1 + 2 h1 + h2 + h3) s^2 + (-1 + 2 h1 + h2 + h3) r (1 + s)^2)) /
      (2 (-1 - g3 s - 2 h1 s + 2 g3 h1 s - h2 s - h3 s + 2 g3 h3 s - h1 s^2 +
          g3 h1 s^2 - g3 h2 s^2 + g1 (-1 + 2 h1 + h2 + h3) s (2 + s) +
          g2 ((-1 + 2 h1 + 2 h2) s + (h1 - h3) s^2 + h2 γ01) + g3 h3 γ10))),
  ((1 + s) (((-1 + g3) h1 + g1 (-1 + 2 h1 + h3)) r (1 + s) + h2 (-1 + g1 r (1 + s) + g3 (r - s + r s))) +
     g2 (-1 - s + 2 h2 s + h1 r (1 + s)^2 + h3 (1 + s) (r - s + r s) + 2 h2 γ01)) /
    (2 (-1 - g3 s - 2 h1 s + 2 g3 h1 s - h2 s - h3 s + 2 g3 h3 s - h1 s^2 +
        g3 h1 s^2 - g3 h2 s^2 + g1 (-1 + 2 h1 + h2 + h3) s (2 + s) +
        g2 ((-1 + 2 h1 + 2 h2) s + (h1 - h3) s^2 + h2 γ01) + g3 h3 γ10)),
  ((1 + s) (((-1 + g2) h1 + g1 (-1 + 2 h1 + h2)) r (1 + s) + h3 (-1 + g1 r (1 + s) + g2 (r - s + r s))) +
     g3 (-1 - s + 2 h3 s + h1 r (1 + s)^2 + h2 (1 + s) (r - s + r s) + 2 h3 γ10)) /
    (2 (-1 - g3 s - 2 h1 s + 2 g3 h1 s - h2 s - h3 s + 2 g3 h3 s - h1 s^2 +
        g3 h1 s^2 - g3 h2 s^2 + g1 (-1 + 2 h1 + h2 + h3) s (2 + s) +
        g2 ((-1 + 2 h1 + 2 h2) s + (h1 - h3) s^2 + h2 γ01) + g3 h3 γ10))},
 {-          g1                   g2 (-1 + γ01)              g3 (-1 + γ10)
    ------------------------ , ------------------------ , ------------------------}}
    -1 + g2 γ01 + g3 γ10       -1 + g2 γ01 + g3 γ10       -1 + g2 γ01 + g3 γ10
```

```
haplotypeDynamics[1][{s_, γ01_, γ10_, r_}][
   {femaleGametes_, maleHaplotypesAfterSelection_}] :=
  {{-((g1 (1 - (-2 + 4 h1 + h2 + h3) s - (-1 + 2 h1 + h2 + h3) s^2 + (-1 + 2 h1 + h2 + h3) r (1 + s)^2) +
              (1 + s) ((g3 h2 + g2 h3) r (1 + s) + h1 (1 - (-1 + g2 + g3) s +
                        (-1 + g2 + g3) r (1 + s)))) / (2 (-1 - g3 s - 2 h1 s + 2 g3 h1 s - h2 s - h3 s +
                2 g3 h3 s - h1 s^2 + g3 h1 s^2 - g3 h2 s^2 + g1 (-1 + 2 h1 + h2 + h3) s (2 + s) +
                g2 ((-1 + 2 h1 + 2 h2) s + (h1 - h3) s^2 + h2 γ01) + g3 h3 γ10))),
      ((1 + s) (((-1 + g3) h1 + g1 (-1 + 2 h1 + h3)) r (1 + s) +
             h2 (-1 + g1 r (1 + s) + g3 (r - s + r s))) +
          g2 (-1 - s + 2 h2 s + h1 r (1 + s)^2 + h3 (1 + s) (r - s + r s) + 2 h2 γ01)) /
        (2 (-1 - g3 s - 2 h1 s + 2 g3 h1 s - h2 s - h3 s + 2 g3 h3 s - h1 s^2 +
            g3 h1 s^2 - g3 h2 s^2 + g1 (-1 + 2 h1 + h2 + h3) s (2 + s) +
            g2 ((-1 + 2 h1 + 2 h2) s + (h1 - h3) s^2 + h2 γ01) + g3 h3 γ10)),
      ((1 + s) (((-1 + g2) h1 + g1 (-1 + 2 h1 + h2)) r (1 + s) +
             h3 (-1 + g1 r (1 + s) + g2 (r - s + r s))) +
          g3 (-1 - s + 2 h3 s + h1 r (1 + s)^2 + h2 (1 + s) (r - s + r s) + 2 h3 γ10)) /
        (2 (-1 - g3 s - 2 h1 s + 2 g3 h1 s - h2 s - h3 s + 2 g3 h3 s - h1 s^2 +
            g3 h1 s^2 - g3 h2 s^2 + g1 (-1 + 2 h1 + h2 + h3) s (2 + s) +
            g2 ((-1 + 2 h1 + 2 h2) s + (h1 - h3) s^2 + h2 γ01) + g3 h3 γ10))},
     {-          g1                   g2 (-1 + γ01)              g3 (-1 + γ10)
        ------------------------ , ------------------------ , ------------------------}} /.
        -1 + g2 γ01 + g3 γ10       -1 + g2 γ01 + g3 γ10       -1 + g2 γ01 + g3 γ10
    Thread[gamF[[1 ;; 3]] → femaleGametes] /.
   Thread[
    hapM[[1 ;; 3]] →
     maleHaplotypesAfterSelection]
```

Diploid dynamics as function of female gametes

```
dynamics =
 (* the female gamete frequencies in the next generation are the following *)
 gametes /. recombination /. Thread[genFemale → femaleGenotypesAfterSelection] /.
    epistasisRecessiveAsymmetric /. Thread[hapM → gamF] // Simplify
```

```
{(g1^2 + g2 g3 r (1 + s)^2 + g1 (1 + s) (g2 + g3 - g4 (-1 + r) (1 + s))) /
   (g1^2 + g3^2 + 2 g3 g4 + g4^2 + 2 g3 g4 s + 2 g2 (1 + s) (g3 + g4 + g3 s) +
     2 g1 (1 + s) (g2 + g3 + g4 + g4 s) - g2^2 (-1 + γ01) - g3^2 γ10),
 (g1 (1 + s) (g2 + g4 r (1 + s)) + g2 (g2 - (1 + s) (-g4 + g3 (-1 + r) (1 + s)) - g2 γ01)) /
   (g1^2 + g3^2 + 2 g3 g4 + g4^2 + 2 g3 g4 s + 2 g2 (1 + s) (g3 + g4 + g3 s) +
     2 g1 (1 + s) (g2 + g3 + g4 + g4 s) - g2^2 (-1 + γ01) - g3^2 γ10),
 (g1 (1 + s) (g3 + g4 r (1 + s)) + g3 (g3 + g4 + g4 s - g2 (-1 + r) (1 + s)^2 - g3 γ10)) /
   (g1^2 + g3^2 + 2 g3 g4 + g4^2 + 2 g3 g4 s + 2 g2 (1 + s) (g3 + g4 + g3 s) +
     2 g1 (1 + s) (g2 + g3 + g4 + g4 s) - g2^2 (-1 + γ01) - g3^2 γ10),
 (-g1 g4 (-1 + r) (1 + s)^2 + g4 (g3 + g4 + g3 s) + g2 (1 + s) (g4 + g3 r (1 + s))) /
   (g1^2 + g3^2 + 2 g3 g4 + g4^2 + 2 g3 g4 s + 2 g2 (1 + s) (g3 + g4 + g3 s) +
     2 g1 (1 + s) (g2 + g3 + g4 + g4 s) - g2^2 (-1 + γ01) - g3^2 γ10)}
```

Index 1 stands for the haplodiploid model, index 2 stands for the diploid model. We write down the complete (but redundant) version too (with an X), but only for checking.

```
haplotypeDynamicsX[2][{s_, γ01_, γ10_, r_}][gametes_] :=
 {(g1^2 + g2 g3 r (1 + s)^2 + g1 (1 + s) (g2 + g3 - g4 (-1 + r) (1 + s))) /
    (g1^2 + g3^2 + 2 g3 g4 + g4^2 + 2 g3 g4 s + 2 g2 (1 + s) (g3 + g4 + g3 s) +
      2 g1 (1 + s) (g2 + g3 + g4 + g4 s) - g2^2 (-1 + γ01) - g3^2 γ10),
   (g1 (1 + s) (g2 + g4 r (1 + s)) + g2 (g2 - (1 + s) (-g4 + g3 (-1 + r) (1 + s)) - g2 γ01)) /
    (g1^2 + g3^2 + 2 g3 g4 + g4^2 + 2 g3 g4 s + 2 g2 (1 + s) (g3 + g4 + g3 s) +
      2 g1 (1 + s) (g2 + g3 + g4 + g4 s) - g2^2 (-1 + γ01) - g3^2 γ10),
   (g1 (1 + s) (g3 + g4 r (1 + s)) + g3 (g3 + g4 + g4 s - g2 (-1 + r) (1 + s)^2 - g3 γ10)) /
    (g1^2 + g3^2 + 2 g3 g4 + g4^2 + 2 g3 g4 s + 2 g2 (1 + s) (g3 + g4 + g3 s) +
      2 g1 (1 + s) (g2 + g3 + g4 + g4 s) - g2^2 (-1 + γ01) - g3^2 γ10),
   (-g1 g4 (-1 + r) (1 + s)^2 + g4 (g3 + g4 + g3 s) + g2 (1 + s) (g4 + g3 r (1 + s))) /
    (g1^2 + g3^2 + 2 g3 g4 + g4^2 + 2 g3 g4 s + 2 g2 (1 + s) (g3 + g4 + g3 s) +
      2 g1 (1 + s) (g2 + g3 + g4 + g4 s) - g2^2 (-1 + γ01) - g3^2 γ10)} /. Thread[gamF → gametes]
```

Get rid of redunancy

```
dynamics[[1 ;; 3]] /. g4 → 1 - g1 - g2 - g3 // Simplify
```

```
{-((g2 g3 r (1 + s)^2 + g1 (1 + s) (1 - (-1 + g2 + g3) s + (-1 + g2 + g3) r (1 + s)) +
       g1^2 (r (1 + s)^2 - s (2 + s)))) / (-1 - 2 g3 s + 2 g3^2 s + 2 g1^2 s (2 + s) +
       2 g1 (-1 + g2 + g3) s (2 + s) - 2 g2 s (1 + g3 s) + g2^2 (2 s + γ01) + g3^2 γ10)),
 (g1 (-1 + g1 + g3) r (1 + s)^2 + g2 (1 + s) (-1 + g1 r (1 + s) + g3 (r - s + r s)) + g2^2 (s + γ01)) /
   (-1 - 2 g3 s + 2 g3^2 s + 2 g1^2 s (2 + s) +
     2 g1 (-1 + g2 + g3) s (2 + s) - 2 g2 s (1 + g3 s) + g2^2 (2 s + γ01) + g3^2 γ10),
 (g1 (-1 + g1 + g2) r (1 + s)^2 + g3 (1 + s) (-1 + g1 r (1 + s) + g2 (r - s + r s)) + g3^2 (s + γ10)) /
   (-1 - 2 g3 s + 2 g3^2 s + 2 g1^2 s (2 + s) +
     2 g1 (-1 + g2 + g3) s (2 + s) - 2 g2 s (1 + g3 s) + g2^2 (2 s + γ01) + g3^2 γ10)}
```

```
haplotypeDynamics[2][{s_, γ01_, γ10_, r_}][gametes_] :=
  {- ((g2 g3 r (1 + s)^2 + g1 (1 + s) (1 - (-1 + g2 + g3) s + (-1 + g2 + g3) r (1 + s)) +
          g1^2 (r (1 + s)^2 - s (2 + s))) / (-1 - 2 g3 s + 2 g3^2 s + 2 g1^2 s (2 + s) +
          2 g1 (-1 + g2 + g3) s (2 + s) - 2 g2 s (1 + g3 s) + g2^2 (2 s + γ01) + g3^2 γ10)),
    (g1 (-1 + g1 + g3) r (1 + s)^2 + g2 (1 + s) (-1 + g1 r (1 + s) + g3 (r - s + r s)) + g2^2 (s + γ01)) /
     (-1 - 2 g3 s + 2 g3^2 s + 2 g1^2 s (2 + s) + 2 g1 (-1 + g2 + g3) s (2 + s) -
       2 g2 s (1 + g3 s) + g2^2 (2 s + γ01) + g3^2 γ10),
    (g1 (-1 + g1 + g2) r (1 + s)^2 + g3 (1 + s) (-1 + g1 r (1 + s) + g2 (r - s + r s)) + g3^2 (s + γ10)) /
     (-1 - 2 g3 s + 2 g3^2 s + 2 g1^2 s (2 + s) + 2 g1 (-1 + g2 + g3) s (2 + s) - 2 g2 s (1 + g3 s) +
       g2^2 (2 s + γ01) + g3^2 γ10)} /. Thread[gamF[[1 ;; 3]] → gametes]
```

Haploid dynamics

For completeness we write down the haploid dynamics too.

```
dynamics =
 (gametes /. recombination /. Thread[genFemale → Flatten[Table[malesAfterSelection〚i〛
            malesAfterSelection〚j〛, {i, 4}, {j, 4}]]] /.
      epistasisRecessiveAsymmetric /. g4 → 1 - g1 - g2 - g3 // Simplify)〚1 ;; 3〛
```

```
{(g1^2 r + g2 g3 r (-1 + γ01) (-1 + γ10) + g1 (1 + (-1 + g2 + g3) r - g2 γ01 - g3 γ10)) /
   (-1 + g2 γ01 + g3 γ10)^2,
  (-g1 (-1 + g1 + g3) r + g2^2 (-1 + γ01) γ01 - g2 (g1 r + (-1 + γ01) (1 + g3 r (-1 + γ10) - g3 γ10))) /
   (-1 + g2 γ01 + g3 γ10)^2,
  (-g1 (-1 + g1 + g2) r - g3 (g1 r + (1 + g2 r (-1 + γ01) - g2 γ01) (-1 + γ10)) + g3^2 (-1 + γ10) γ10) /
   (-1 + g2 γ01 + g3 γ10)^2}
```

```
haplotypeDynamics[0][{s_, γ01_, γ10_, r_}][gametes_] :=
 {(g1^2 r + g2 g3 r (-1 + γ01) (-1 + γ10) + g1 (1 + (-1 + g2 + g3) r - g2 γ01 - g3 γ10)) /
     (-1 + g2 γ01 + g3 γ10)^2, (-g1 (-1 + g1 + g3) r + g2^2 (-1 + γ01) γ01 -
       g2 (g1 r + (-1 + γ01) (1 + g3 (r (-1 + γ10) - γ10)))) / (-1 + g2 γ01 + g3 γ10)^2,
    (-g1 (-1 + g1 + g2) r - g3 (g1 r + (1 + g2 (r (-1 + γ01) - γ01)) (-1 + γ10)) +
       g3^2 (-1 + γ10) γ10) / (-1 + g2 γ01 + g3 γ10)^2} /. Thread[gamF[[1 ;; 3]] → gametes]
```

Dynamics as functions of allele frequencies

Here, we translate the haplotype dynamics into allele frequency dynamics. That can be useful for analytical work later.

Transfer rules

p is the frequency of 1 at locus A/0, q is the frequency of allele 1 at locus B/1.

```
transferpRulegFemales =
 Solve[{pf == g3 + g4, qf == g2 + g4, LDf == g1 g4 - g2 g3, g1 + g2 + g3 + g4 == 1},
   {g1, g2, g3, g4}] // Flatten
transferpRulegMales = Solve[{pm == h3 + h4, qm == h2 + h4, LDm == h1 h4 - h2 h3,
     h1 + h2 + h3 + h4 == 1}, {h1, h2, h3, h4}] // Flatten
```

```
{g1 → 1 + LDf - pf - qf + pf qf, g2 → - LDf + qf - pf qf, g3 → - LDf + pf - pf qf, g4 → LDf + pf qf}
```

```
{h1 → 1 + LDm - pm - qm + pm qm, h2 → - LDm + qm - pm qm, h3 → - LDm + pm - pm qm, h4 → LDm + pm qm}
```

Conversion function

```
transferAlleleToHaplotype[1][{{pf_, qf_, LDf_}, {pm_, qm_, LDm_}}] :=
 {{1 + LDf - pf - qf + pf qf, -LDf + qf - pf qf, -LDf + pf - pf qf},
  {1 + LDm - pm - qm + pm qm, -LDm + qm - pm qm, -LDm + pm - pm qm}}
transferHaplotypeToAllele[1][{{g1_, g2_ , g3_}, {h1_, h2_, h3_}}] :=
 {{1 - g1 - g2, 1 - g1 - g3, g1 (1 - g1 - g2 - g3) - g2 g3},
  {1 - h1 - h2, 1 - h1 - h3, h1 (1 - h1 - h2 - h3) - h2 h3}}
transferAlleleToHaplotype[2][{pf_, qf_, LDf_}] :=
 {1 + LDf - pf - qf + pf qf, -LDf + qf - pf qf, -LDf + pf - pf qf}
transferHaplotypeToAllele[2][{g1_, g2_ , g3_}] :=
 {1 - g1 - g2, 1 - g1 - g3, g1 (1 - g1 - g2 - g3) - g2 g3}
```

Haplodiploid dynamics of allele frequencies and LD

```
dynamics = {
    (* the female gamete frequencies in the next generation are the following *)
    gametes /. recombination /. Thread[genFemale → femaleGenotypesAfterSelection],
    (* new male frequencies after selection
     are the female gamete frequencies after male selection *)
    malesAfterSelection
   } /. epistasisRecessiveAsymmetric // Simplify;

dynamicsPQ =
 Table[{dynamics[[k, 3]] + dynamics[[k, 4]], dynamics[[k, 2]] + dynamics[[k, 4]],
     dynamics[[k, 1]] dynamics[[k, 4]] - dynamics[[k, 3]] dynamics[[k, 2]]}, {k, 2}] /.
   transferpRulegFemales /. transferpRulegMales // Simplify
```

```
{{(LDf s + LDm s - 2 LDm qf s - 2 LDf qm s +
     LDf s^2 + LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 - 2 LDf LDm γ10 +
     pm (1 + (1 + qf + qm - 2 qf qm) s + (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2 - 2 LDf (-1 + qm) γ10) +
     pf (1 + (1 - 2 pm + qf + qm - 2 qf qm) s + (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qf - qm + 2 qf qm)) s^2 -
        2 pm γ10 - 2 LDm (-1 + qf) γ10 + 2 pm qf γ10 + 2 pm qm γ10 - 2 pm qf qm γ10)) /
   (2 (1 + qf s + qm s - 2 qf qm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 -
       LDf LDm γ01 + LDm qf γ01 + LDf qm γ01 - qf qm γ01 - LDf LDm γ10 +
       pf (s - 2 pm s + (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qf - qm + 2 qf qm)) s^2 + qf qm γ01 - pm qf qm
            γ01 - pm γ10 + pm qf γ10 + pm qm γ10 - pm qf qm γ10 + LDm (γ10 - qf (γ01 + γ10))) +
       pm (s + (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2 + qf qm γ01 + LDf (γ10 - qm (γ01 + γ10))))),
  (LDf s + LDm s - 2 LDm pf s - 2 LDf pm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 -
     2 LDm pf s^2 - 2 LDf pm s^2 - 2 LDf LDm γ01 +
     qm (1 + (1 + pf + pm - 2 pf pm) s + (pf + pm - 2 pf pm + LDf (-2 + 4 pm)) s^2 - 2 LDf (-1 + pm) γ01) +
     qf (1 + (1 + pf + pm - 2 pf pm - 2 qm) s + (LDm (-2 + 4 pf) + (-pf - pm + 2 pf pm) (-1 + 2 qm)) s^2 -
        2 LDm (-1 + pf) γ01 - 2 qm γ01 + 2 pf qm γ01 + 2 pm qm γ01 - 2 pf pm qm γ01)) /
   (2 (1 + qf s + qm s - 2 qf qm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 -
       LDf LDm γ01 + LDm qf γ01 + LDf qm γ01 - qf qm γ01 - LDf LDm γ10 +
       pf (s - 2 pm s + (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qf - qm + 2 qf qm)) s^2 + qf qm γ01 - pm qf qm
            γ01 - pm γ10 + pm qf γ10 + pm qm γ10 - pm qf qm γ10 + LDm (γ10 - qf (γ01 + γ10))) +
       pm (s + (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2 + qf qm γ01 + LDf (γ10 - qm (γ01 + γ10))))),
  (((LDf + pf qf) (-2 LDm + pm + qm - 2 pm qm + 2 (LDm + pm qm) - (LDm + pm (-1 + qm)) s -
```

```
            (LDm + (-1 + pm) qm) s - (LDm + (-1 + pm) (-1 + qm)) (-1 + r) (1 + s)^2) +
        (1 + s) (-(LDf + (-1 + pf) (-1 + qf)) (LDm + pm qm) (-1 + r) (1 + s) +
            (-LDf + qf - pf qf) (LDm + pm qm - (LDm + pm (-1 + qm)) r (1 + s)) +
            (-LDf + pf - pf qf) (LDm + pm qm - (LDm + (-1 + pm) qm) r (1 + s))))
     ((LDf + (-1 + pf) (-1 + qf)) (2 (LDm + (-1 + pm) (-1 + qm)) +
            (1 + s) (-2 LDm + pm + qm - 2 pm qm - (LDm + pm qm) (-1 + r) (1 + s))) +
        (1 + s) (-(LDf + pf qf) (LDm + (-1 + pm) (-1 + qm)) (-1 + r) (1 + s) +
            (-LDf + qf - pf qf) (1 + LDm - pm - qm + pm qm - (LDm + pm (-1 + qm)) r (1 + s)) +
            (-LDf + pf - pf qf) (1 + LDm - pm - qm + pm qm - (LDm + (-1 + pm) qm) r (1 + s)))) -
    ((1 + s) (-(LDf + pf (-1 + qf)) (LDm + (-1 + pm) qm) (-1 + r) (1 + s) +
            (LDf + pf qf) (-LDm + qm - pm qm + (LDm + (-1 + pm) (-1 + qm)) r (1 + s)) +
            (LDf + (-1 + pf) (-1 + qf)) (qm + LDm (-1 + r + r s) + pm qm (-1 + r + r s))) +
        (-LDf + qf - pf qf) ((LDm + (-1 + pm) (-1 + qm)) (1 + s) - (1 + s) (-LDm - pm qm -
                (LDm + pm (-1 + qm)) (-1 + r) (1 + s)) + 2 (LDm + (-1 + pm) qm) (-1 + γ01)))
     ((1 + s) (-(LDf + (-1 + pf) qf) (LDm + pm (-1 + qm)) (-1 + r) (1 + s) +
            (LDf + pf qf) (-LDm + pm - pm qm + (LDm + (-1 + pm) (-1 + qm)) r (1 + s)) +
            (LDf + (-1 + pf) (-1 + qf)) (pm + LDm (-1 + r + r s) + pm qm (-1 + r + r s))) +
        (-LDf + pf - pf qf) (LDm - 2 (LDm + pm (-1 + qm)) + pm qm + (LDm + pm qm) s +
            (LDm + (-1 + pm) (-1 + qm)) (1 + s) +
            (LDm + (-1 + pm) qm) (-1 + r) (1 + s)^2 + 2 (LDm + pm (-1 + qm)) γ10))) /
   (4 (1 + qf s + qm s - 2 qf qm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 -
         LDf LDm γ01 + LDm qf γ01 + LDf qm γ01 - qf qm γ01 - LDf LDm γ10 + pf (s - 2 pm s +
             (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qf - qm + 2 qf qm)) s^2 + qf qm γ01 - pm qf qm γ01 -
            pm γ10 + pm qf γ10 + pm qm γ10 - pm qf qm γ10 + LDm (γ10 - qf (γ01 + γ10))) + pm (s +
             (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2 + qf qm γ01 + LDf (γ10 - qm (γ01 + γ10))))^2)},
               pf + LDf γ10 + pf (-1 + qf) γ10
 {------------------------------------------------------------ ,
   1 + (-1 + pf) qf γ01 - pf γ10 + pf qf γ10 + LDf (γ01 + γ10)
               qf + LDf γ01 + (-1 + pf) qf γ01
  ------------------------------------------------------------ ,
   1 + (-1 + pf) qf γ01 - pf γ10 + pf qf γ10 + LDf (γ01 + γ10)
  (-(-1 + pf) pf (-1 + qf) qf (γ01 (-1 + γ10) - γ10) +
      LDf^2 (γ01 + γ10 - γ01 γ10) -
      LDf (-1 + pf (-1 + 2 qf) (γ01 (-1 + γ10) - γ10) + qf (γ01 + γ10 - γ01 γ10))) /
   (1 + (-1 + pf) qf γ01 - pf γ10 + pf qf γ10 + LDf (γ01 + γ10))^2}}
```

```
alleleDynamics[1][{s_, γ01_, γ10_, r_}][{{pf_, qf_, LDf_}, {pm_, qm_, LDm_}}] :=
 {{(LDf s + LDm s - 2 LDm qf s - 2 LDf qm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 -
        2 LDm qf s^2 - 2 LDf qm s^2 - 2 LDf LDm γ10 + pm (1 + (1 + qf + qm - 2 qf qm) s +
              (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2 - 2 LDf (-1 + qm) γ10) +
        pf (1 + (1 - 2 pm + qf + qm - 2 qf qm) s + (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qf - qm + 2 qf qm))
              s^2 - 2 pm γ10 - 2 LDm (-1 + qf) γ10 + 2 pm qf γ10 + 2 pm qm γ10 - 2 pm qf qm γ10)) /
     (2 (1 + qf s + qm s - 2 qf qm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 -
          LDf LDm γ01 + LDm qf γ01 + LDf qm γ01 - qf qm γ01 - LDf LDm γ10 + pf (s - 2 pm s +
              (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qf - qm + 2 qf qm)) s^2 + qf qm γ01 - pm qf qm γ01 -
              pm γ10 + pm qf γ10 + pm qm γ10 - pm qf qm γ10 + LDm (γ10 - qf (γ01 + γ10))) + pm (s +
              (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2 + qf qm γ01 + LDf (γ10 - qm (γ01 + γ10))))),
```

```
   (LDf s + LDm s - 2 LDm pf s - 2 LDf pm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 - 2 LDm pf s^2 -
      2 LDf pm s^2 - 2 LDf LDm γ01 + qm (1 + (1 + pf + pm - 2 pf pm) s +
           (pf + pm - 2 pf pm + LDf (-2 + 4 pm)) s^2 - 2 LDf (-1 + pm) γ01) +
      qf (1 + (1 + pf + pm - 2 pf pm - 2 qm) s + (LDm (-2 + 4 pf) + (-pf - pm + 2 pf pm) (-1 + 2 qm))
           s^2 - 2 LDm (-1 + pf) γ01 - 2 qm γ01 + 2 pf qm γ01 + 2 pm qm γ01 - 2 pf pm qm γ01)) /
    (2 (1 + qf s + qm s - 2 qf qm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 -
         LDf LDm γ01 + LDm qf γ01 + LDf qm γ01 - qf qm γ01 - LDf LDm γ10 + pf (s - 2 pm s +
              (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qf - qm + 2 qf qm)) s^2 + qf qm γ01 - pm qf qm γ01 -
              pm γ10 + pm qf γ10 + pm qm γ10 - pm qf qm γ10 + LDm (γ10 - qf (γ01 + γ10))) + pm (s +
              (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2 + qf qm γ01 + LDf (γ10 - qm (γ01 + γ10))))),
   (((LDf + pf qf) (-2 LDm + pm + qm - 2 pm qm + 2 (LDm + pm qm) - (LDm + pm (-1 + qm)) s -
               (LDm + (-1 + pm) qm) s - (LDm + (-1 + pm) (-1 + qm)) (-1 + r) (1 + s)^2) +
           (1 + s) (- (LDf + (-1 + pf) (-1 + qf)) (LDm + pm qm) (-1 + r) (1 + s) +
               (-LDf + qf - pf qf) (LDm + pm qm - (LDm + pm (-1 + qm)) r (1 + s)) +
               (-LDf + pf - pf qf) (LDm + pm qm - (LDm + (-1 + pm) qm) r (1 + s))))
        ((LDf + (-1 + pf) (-1 + qf)) (2 (LDm + (-1 + pm) (-1 + qm)) +
               (1 + s) (-2 LDm + pm + qm - 2 pm qm - (LDm + pm qm) (-1 + r) (1 + s))) +
           (1 + s) (- (LDf + pf qf) (LDm + (-1 + pm) (-1 + qm)) (-1 + r) (1 + s) +
               (-LDf + qf - pf qf) (1 + LDm - pm - qm + pm qm - (LDm + pm (-1 + qm)) r (1 + s)) +
               (-LDf + pf - pf qf) (1 + LDm - pm - qm + pm qm - (LDm + (-1 + pm) qm) r (1 + s)))) -
      ((1 + s) (- (LDf + pf (-1 + qf)) (LDm + (-1 + pm) qm) (-1 + r) (1 + s) +
               (LDf + pf qf) (-LDm + qm - pm qm + (LDm + (-1 + pm) (-1 + qm)) r (1 + s)) +
               (LDf + (-1 + pf) (-1 + qf)) (-LDm + qm - pm qm + (LDm + pm qm) r (1 + s))) +
           (-LDf + qf - pf qf) ((LDm + (-1 + pm) (-1 + qm)) (1 + s) - (1 + s) (-LDm - pm qm -
                    (LDm + pm (-1 + qm)) (-1 + r) (1 + s)) + 2 (LDm + (-1 + pm) qm) (-1 + γ01)))
        ((1 + s) (- (LDf + (-1 + pf) qf) (LDm + pm (-1 + qm)) (-1 + r) (1 + s) +
               (LDf + pf qf) (-LDm + pm - pm qm + (LDm + (-1 + pm) (-1 + qm)) r (1 + s)) +
               (LDf + (-1 + pf) (-1 + qf)) (-LDm + pm - pm qm + (LDm + pm qm) r (1 + s))) +
           (-LDf + pf - pf qf) (LDm - 2 (LDm + pm (-1 + qm)) + pm qm +
               (LDm + pm qm) s + (LDm + (-1 + pm) (-1 + qm)) (1 + s) +
               (LDm + (-1 + pm) qm) (-1 + r) (1 + s)^2 + 2 (LDm + pm (-1 + qm)) γ10))) /
    (4 (1 + qf s + qm s - 2 qf qm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 -
          2 LDf qm s^2 - LDf LDm γ01 + LDm qf γ01 + LDf qm γ01 - qf qm γ01 - LDf LDm γ10 +
          pf (s - 2 pm s + (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qf - qm + 2 qf qm)) s^2 +
              qf qm γ01 - pm qf qm γ01 - pm γ10 + pm qf γ10 + pm qm γ10 - pm qf qm γ10 +
              LDm (γ10 - qf (γ01 + γ10))) + pm (s + (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2 +
              qf qm γ01 + LDf (γ10 - qm (γ01 + γ10))))^2)},
 {(LDf γ10 + pf (1 + (-1 + qf) γ10)) / (1 - pf γ10 + LDf (γ01 + γ10) +
      qf ((-1 + pf) γ01 + pf γ10)),
  (LDf γ01 + qf (1 + (-1 + pf) γ01)) / (1 - pf γ10 + LDf (γ01 + γ10) +
      qf ((-1 + pf) γ01 + pf γ10)),
  (- (-1 + pf) pf (-1 + qf) qf (γ01 (-1 + γ10) - γ10) + LDf^2 (γ01 + γ10 - γ01 γ10) -
      LDf (-1 + pf (-1 + 2 qf) (γ01 (-1 + γ10) - γ10) + qf (γ01 + γ10 - γ01 γ10))) /
   (1 - pf γ10 + LDf (γ01 + γ10) + qf ((-1 + pf) γ01 + pf γ10))^2}}
```

Diploid dynamics of allele frequencies and LD

```
dynamics =
  (* the female gamete frequencies in the next generation are the following *)
  gametes /. recombination /. Thread[genFemale → femaleGenotypesAfterSelection] /.
     epistasisRecessiveAsymmetric /. Thread[hapM → gamF] // Simplify;

dynamicsPQ = {dynamics[[3]] + dynamics[[4]], dynamics[[2]] + dynamics[[4]],
     dynamics[[1]] dynamics[[4]] - dynamics[[3]] dynamics[[2]]} /.
    transferpRulegFemales // Simplify
```

$$
\begin{aligned}
&\{(\text{LDf}\,(s - 2\,\text{qf}\,s + (1 + 2\,\text{LDf} - 2\,\text{qf})\,s^2 - \text{LDf}\,\gamma 10) + \\
&\quad \text{pf}\,(1 + (1 + 2\,\text{qf} - 2\,\text{qf}^2)\,s + 2\,(-\text{LDf} + \text{qf} + 2\,\text{LDf}\,\text{qf} - \text{qf}^2)\,s^2 - 2\,\text{LDf}\,(-1 + \text{qf})\,\gamma 10) + \\
&\quad \text{pf}^2\,(-s + 2\,(-1 + \text{qf})\,\text{qf}\,s^2 - (-1 + \text{qf})^2\,\gamma 10))\,/ \\
&\ (1 + 2\,\text{LDf}\,s^2 + 4\,\text{LDf}^2\,s^2 - \text{LDf}^2\,\gamma 01 - \text{qf}^2\,(2\,s + \gamma 01) + 2\,\text{qf}\,(s - 2\,\text{LDf}\,s^2 + \text{LDf}\,\gamma 01) - \\
&\quad \text{LDf}^2\,\gamma 10 + \text{pf}^2\,(-2\,s + 4\,(-1 + \text{qf})\,\text{qf}\,s^2 - \gamma 10 + 2\,\text{qf}\,\gamma 10 - \text{qf}^2\,(\gamma 01 + \gamma 10)) + \\
&\quad 2\,\text{pf}\,(s + 2\,(-\text{LDf} + \text{qf} + 2\,\text{LDf}\,\text{qf} - \text{qf}^2)\,s^2 + \text{qf}^2\,\gamma 01 + \text{LDf}\,(\gamma 10 - \text{qf}\,(\gamma 01 + \gamma 10)))), \\
&\ (\text{LDf}\,(s - 2\,\text{pf}\,s + (1 + 2\,\text{LDf} - 2\,\text{pf})\,s^2 - \text{LDf}\,\gamma 01) + \\
&\quad \text{qf}\,(1 + (1 + 2\,\text{pf} - 2\,\text{pf}^2)\,s + 2\,(-\text{LDf} + \text{pf} + 2\,\text{LDf}\,\text{pf} - \text{pf}^2)\,s^2 - 2\,\text{LDf}\,(-1 + \text{pf})\,\gamma 01) + \\
&\quad \text{qf}^2\,(-s + 2\,(-1 + \text{pf})\,\text{pf}\,s^2 - (-1 + \text{pf})^2\,\gamma 01))\,/ \\
&\ (1 + 2\,\text{LDf}\,s^2 + 4\,\text{LDf}^2\,s^2 - \text{LDf}^2\,\gamma 01 - \text{qf}^2\,(2\,s + \gamma 01) + 2\,\text{qf}\,(s - 2\,\text{LDf}\,s^2 + \text{LDf}\,\gamma 01) - \\
&\quad \text{LDf}^2\,\gamma 10 + \text{pf}^2\,(-2\,s + 4\,(-1 + \text{qf})\,\text{qf}\,s^2 - \gamma 10 + 2\,\text{qf}\,\gamma 10 - \text{qf}^2\,(\gamma 01 + \gamma 10)) + \\
&\quad 2\,\text{pf}\,(s + 2\,(-\text{LDf} + \text{qf} + 2\,\text{LDf}\,\text{qf} - \text{qf}^2)\,s^2 + \text{qf}^2\,\gamma 01 + \text{LDf}\,(\gamma 10 - \text{qf}\,(\gamma 01 + \gamma 10)))), \\
&\ ((\text{LDf}^2\,s^2 + \text{pf}\,\text{qf}\,(-1 + (-1 + \text{pf})\,s)\,(-1 + (-1 + \text{qf})\,s) - \\
&\qquad \text{LDf}\,(-1 + (-2 + \text{pf} + \text{qf})\,s + (-1 + \text{pf} + \text{qf} - 2\,\text{pf}\,\text{qf})\,s^2 + r\,(1 + s)^2)) \\
&\quad\ (\text{LDf}^2\,s^2 + (-1 + \text{pf})\,(-1 + \text{qf})\,(1 + \text{pf}\,s)\,(1 + \text{qf}\,s) + \\
&\qquad \text{LDf}\,(1 + \text{qf}\,s + s^2 - \text{qf}\,s^2 - r\,(1 + s)^2 + \text{pf}\,s\,(1 - s + 2\,\text{qf}\,s))) - \\
&\quad ((\text{LDf} + (-1 + \text{pf})\,(-1 + \text{qf}))\,(1 + s)\,(\text{qf} + \text{LDf}\,(-1 + r + r\,s) + \text{pf}\,\text{qf}\,(-1 + r + r\,s)) + \\
&\qquad (-\text{LDf} + \text{qf} - \text{pf}\,\text{qf})\,(\text{qf} + \text{LDf}\,s + \text{pf}\,\text{qf}\,s + (\text{LDf} + \text{pf}\,(-1 + \text{qf}))\,(-1 + r)\,(1 + s) + \\
&\qquad\quad (\text{LDf} + \text{pf}\,(-1 + \text{qf}))\,(-1 + r)\,s\,(1 + s) + \text{LDf}\,\gamma 01 + (-1 + \text{pf})\,\text{qf}\,\gamma 01)) \\
&\quad ((\text{LDf} + (-1 + \text{pf})\,(-1 + \text{qf}))\,(1 + s)\,(\text{pf} + \text{LDf}\,(-1 + r + r\,s) + \text{pf}\,\text{qf}\,(-1 + r + r\,s)) + \\
&\qquad (-\text{LDf} + \text{pf} - \text{pf}\,\text{qf})\,(\text{pf} + (\text{LDf} + \text{pf}\,\text{qf})\,s + \\
&\qquad\quad (\text{LDf} + (-1 + \text{pf})\,\text{qf})\,(-1 + r)\,(1 + s)^2 + (\text{LDf} + \text{pf}\,(-1 + \text{qf}))\,\gamma 10)))\,/ \\
&\ (1 + 2\,\text{LDf}\,s^2 + 4\,\text{LDf}^2\,s^2 - \text{LDf}^2\,\gamma 01 - \text{qf}^2\,(2\,s + \gamma 01) + 2\,\text{qf}\,(s - 2\,\text{LDf}\,s^2 + \text{LDf}\,\gamma 01) - \\
&\quad \text{LDf}^2\,\gamma 10 + \text{pf}^2\,(-2\,s + 4\,(-1 + \text{qf})\,\text{qf}\,s^2 - \gamma 10 + 2\,\text{qf}\,\gamma 10 - \text{qf}^2\,(\gamma 01 + \gamma 10)) + \\
&\quad 2\,\text{pf}\,(s + 2\,(-\text{LDf} + \text{qf} + 2\,\text{LDf}\,\text{qf} - \text{qf}^2)\,s^2 + \text{qf}^2\,\gamma 01 + \text{LDf}\,(\gamma 10 - \text{qf}\,(\gamma 01 + \gamma 10))))^2\}
\end{aligned}
$$

```
alleleDynamics[2][{s_, γ01_, γ10_, r_}][{pf_, qf_, LDf_}
   (* of course these are general frequencies, no just in females *)] :=
  {(LDf (s - 2 qf s + (1 + 2 LDf - 2 qf) s^2 - LDf γ10) +
       pf (1 + (1 + 2 qf - 2 qf^2) s + 2 (-LDf + qf + 2 LDf qf - qf^2) s^2 - 2 LDf (-1 + qf) γ10) +
       pf^2 (-s + 2 (-1 + qf) qf s^2 - (-1 + qf)^2 γ10)) /
     (1 + 2 LDf s^2 + 4 LDf^2 s^2 - LDf^2 γ01 - qf^2 (2 s + γ01) + 2 qf (s - 2 LDf s^2 + LDf γ01) -
       LDf^2 γ10 + pf^2 (-2 s + 4 (-1 + qf) qf s^2 - γ10 + 2 qf γ10 - qf^2 (γ01 + γ10)) +
       2 pf (s + 2 (-LDf + qf + 2 LDf qf - qf^2) s^2 + qf^2 γ01 + LDf (γ10 - qf (γ01 + γ10)))),
   (LDf (s - 2 pf s + (1 + 2 LDf - 2 pf) s^2 - LDf γ01) +
       qf (1 + (1 + 2 pf - 2 pf^2) s + 2 (-LDf + pf + 2 LDf pf - pf^2) s^2 - 2 LDf (-1 + pf) γ01) +
       qf^2 (-s + 2 (-1 + pf) pf s^2 - (-1 + pf)^2 γ01)) /
     (1 + 2 LDf s^2 + 4 LDf^2 s^2 - LDf^2 γ01 - qf^2 (2 s + γ01) + 2 qf (s - 2 LDf s^2 + LDf γ01) -
       LDf^2 γ10 + pf^2 (-2 s + 4 (-1 + qf) qf s^2 - γ10 + 2 qf γ10 - qf^2 (γ01 + γ10)) +
       2 pf (s + 2 (-LDf + qf + 2 LDf qf - qf^2) s^2 + qf^2 γ01 + LDf (γ10 - qf (γ01 + γ10)))),
   ((LDf^2 s^2 + pf qf (-1 + (-1 + pf) s) (-1 + (-1 + qf) s) -
          LDf (-1 + (-2 + pf + qf) s + (-1 + pf + qf - 2 pf qf) s^2 + r (1 + s)^2))
        (LDf^2 s^2 + (-1 + pf) (-1 + qf) (1 + pf s) (1 + qf s) +
          LDf (1 + qf s + s^2 - qf s^2 - r (1 + s)^2 + pf s (1 - s + 2 qf s))) -
       ((LDf + (-1 + pf) (-1 + qf)) (1 + s) (-LDf + qf - pf qf + (LDf + pf qf) r (1 + s)) +
          (-LDf + qf - pf qf) (-LDf + qf - pf qf - (1 + s)
                (-LDf - pf qf - (LDf + pf (-1 + qf)) (-1 + r) (1 + s)) + (LDf + (-1 + pf) qf) γ01))
        ((LDf + (-1 + pf) (-1 + qf)) (1 + s) (-LDf + pf - pf qf + (LDf + pf qf) r (1 + s)) +
          (-LDf + pf - pf qf) (pf + (LDf + pf qf) s +
              (LDf + (-1 + pf) qf) (-1 + r) (1 + s)^2 + (LDf + pf (-1 + qf)) γ10))) /
     (1 + 2 LDf s^2 + 4 LDf^2 s^2 - LDf^2 γ01 - qf^2 (2 s + γ01) + 2 qf (s - 2 LDf s^2 + LDf γ01) -
        LDf^2 γ10 + pf^2 (-2 s + 4 (-1 + qf) qf s^2 - γ10 + 2 qf γ10 - qf^2 (γ01 + γ10)) +
        2 pf (s + 2 (-LDf + qf + 2 LDf qf - qf^2) s^2 + qf^2 γ01 + LDf (γ10 - qf (γ01 + γ10))))^2}
```

Haploid dynamics of allele frequencies and LD

```
dynamics = gametes /. recombination /. Thread[genFemale →
        Flatten[Table[malesAfterSelection⟦i⟧ malesAfterSelection⟦j⟧, {i, 4}, {j, 4}]]] /.
    epistasisRecessiveAsymmetric // Simplify
```

```
{(g1^2 + g2 g3 r (-1 + γ01) (-1 + γ10) + g1 (g2 + g3 + g4 - g4 r - g2 γ01 - g3 γ10)) /
   (g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10)^2,
  (g1 (g2 + g4 r - g2 γ01) + g2 (-1 + γ01) (-g4 + g2 (-1 + γ01) + g3 (-1 + r + γ10 - r γ10))) /
   (g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10)^2,
  (g1 (g3 + g4 r - g3 γ10) - g3 (-1 + γ10) (g3 + g4 + g2 (-1 + r) (-1 + γ01) - g3 γ10)) /
   (g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10)^2,
  (g1 (g4 - g4 r) + g4 (g3 + g4 - g3 γ10) - g2 (-1 + γ01) (g4 + g3 r - g3 r γ10)) /
   (g1 + g2 + g3 + g4 - g2 γ01 - g3 γ10)^2}
```

```
dynamicsPQ = {dynamics[[3]] + dynamics[[4]], dynamics[[2]] + dynamics[[4]],
    dynamics[[1]] dynamics[[4]] - dynamics[[3]] dynamics[[2]]} /.
   transferpRulegFemales // Simplify
```

```
                    pf + LDf γ10 + pf (-1 + qf) γ10
{―――――――――――――――――――――――――――――――――――――――――――――――――――――――――――――――――――,
 1 + (-1 + pf) qf γ01 - pf γ10 + pf qf γ10 + LDf (γ01 + γ10)
                    qf + LDf γ01 + (-1 + pf) qf γ01
 ―――――――――――――――――――――――――――――――――――――――――――――――――――――――――――――――――――,
 1 + (-1 + pf) qf γ01 - pf γ10 + pf qf γ10 + LDf (γ01 + γ10)
 ((-1 + r) (LDf^2 (γ01 (-1 + γ10) - γ10) + (-1 + pf) pf (-1 + qf) qf (γ01 (-1 + γ10) - γ10) +
      LDf (-1 + pf (-1 + 2 qf) (γ01 (-1 + γ10) - γ10) + qf (γ01 + γ10 - γ01 γ10)))) /
  (1 + (-1 + pf) qf γ01 - pf γ10 + pf qf γ10 + LDf (γ01 + γ10))^2}
```

```
alleleDynamics[0][{s_, γ01_, γ10_, r_}][{pf_, qf_, LDf_}
  (* of course these are general frequencies, not just in females *)] :=
 {(LDf γ10 + pf (1 + (-1 + qf) γ10)) / (1 - pf γ10 + LDf (γ01 + γ10) +
      qf ((-1 + pf) γ01 + pf γ10)), (LDf γ01 + qf (1 + (-1 + pf) γ01)) /
    (1 - pf γ10 + LDf (γ01 + γ10) + qf ((-1 + pf) γ01 + pf γ10)),
  ((-1 + r) (LDf^2 (γ01 (-1 + γ10) - γ10) + (-1 + pf) pf (-1 + qf) qf (γ01 (-1 + γ10) - γ10) +
       LDf (-1 + pf (-1 + 2 qf) (γ01 (-1 + γ10) - γ10) + qf (γ01 + γ10 - γ01 γ10)))) /
    (1 - pf γ10 + LDf (γ01 + γ10) + qf ((-1 + pf) γ01 + pf γ10))^2}
```

Some sanity checks of dynamical equations

Make sure to use the X when you want to enter full haplotypes.

```
haplotypeDynamicsX[1][{0, 0, 0, 0}][{{0.5, 0.4, 0.1, 0}, {0.25, 0.25, 0.25, 0.25}}]
haplotypeDynamics[1][{0, 0, 0, 0}][{{0.5, 0.4, 0.1}, {0.25, 0.25, 0.25}}]
```

```
{{0.375, 0.325, 0.175, 0.125}, {0.5, 0.4, 0.1, 0.}}

{{0.375, 0.325, 0.175}, {0.5, 0.4, 0.1}}
```

Iterate dynamics

Should not change if all pars are 0

```
startfreq = {0.5, 0.4, 0.1, 0};
pars = {0, 0, 0, 0};
freq = startfreq;
Do[freq = haplotypeDynamicsX[2][pars][freq];
 Print[freq],
 {k, 5}]
```

```
{0.5, 0.4, 0.1, 0.}

{0.5, 0.4, 0.1, 0.}

{0.5, 0.4, 0.1, 0.}

{0.5, 0.4, 0.1, 0.}

{0.5, 0.4, 0.1, 0.}
```

```
startfreq = {{0.5, 0.4, 0.1, 0}, {0.5, 0.4, 0.1, 0}};
pars = {0, 0, 0, 0};
freq = startfreq;
Do[freq = haplotypeDynamicsX[1][pars][freq];
 Print[freq],
 {k, 5}]
```

```
{{0.5, 0.4, 0.1, 0.}, {0.5, 0.4, 0.1, 0.}}

{{0.5, 0.4, 0.1, 0.}, {0.5, 0.4, 0.1, 0.}}

{{0.5, 0.4, 0.1, 0.}, {0.5, 0.4, 0.1, 0.}}

{{0.5, 0.4, 0.1, 0.}, {0.5, 0.4, 0.1, 0.}}

{{0.5, 0.4, 0.1, 0.}, {0.5, 0.4, 0.1, 0.}}
```

```
startfreq = {0.5, 0.4, 0, 0.1};
pars = {0.4, 1, 1, 1 / 3};
freq = startfreq;
Do[freq = haplotypeDynamicsX[2][pars][freq] // Chop;
 If[IntegerQ[k / 1000], Print[freq]; Print[Total[freq]]],
 {k, 5000}]
transferHaplotypeToAllele[2][freq⟦1 ;; 3⟧]
```

```
{0.2913, 0.2087, 0.2087, 0.2913}

1.

{0.2913, 0.2087, 0.2087, 0.2913}

1.

{0.2913, 0.2087, 0.2087, 0.2913}

1.

{0.2913, 0.2087, 0.2087, 0.2913}

1.

{0.2913, 0.2087, 0.2087, 0.2913}

1.

{0.5, 0.5, 0.0412997}
```

Should go to exclusion with only γ

```
startfreq = {0.5, 0.4, 0, 0.1};
pars = {0, 0.2, 0.2, 1 / 2};
freq = startfreq;
Do[freq = haplotypeDynamicsX[2][pars][freq] // Chop;
 If[IntegerQ[k / 1000], Print[freq]; Print[Total[freq]]],
 {k, 5000}]
```

```
{0.989231, 0.00538911, 0.00535054, 0.0000292745}

1.

{0.994777, 0.0026125, 0.00260356, 6.85181 × 10^-6}

1.

{0.99656, 0.00172064, 0.00171678, 2.96825 × 10^-6}

1.

{0.997437, 0.00128196, 0.00127982, 1.64659 × 10^-6}

1.

{0.997958, 0.00102125, 0.0010199, 1.04456 × 10^-6}

1.
```

Because of the recessivity it is really slow at the end. It’s much faster for haplodiploids:

```
startfreq = {{0.5, 0.4, 0, 0.1}, {0.5, 0.4, 0, 0.1}};
pars = {0, 0.2, 0.2, 1 / 2};
freq = startfreq;
Do[freq = haplotypeDynamicsX[1][pars][freq] // Chop;
 If[IntegerQ[k / 1000], Print[freq]],
 {k, 5000}]
transferHaplotypeToAllele[1][freq[[All, 1 ;; 3]]]
```

```
{{1., 0, 0, 0}, {1., 0, 0, 0}}

{{1., 0, 0, 0}, {1., 0, 0, 0}}

{{1., 0, 0, 0}, {1., 0, 0, 0}}

{{1., 0, 0, 0}, {1., 0, 0, 0}}

{{1., 0, 0, 0}, {1., 0, 0, 0}}

{{0., 0., 0.}, {0., 0., 0.}}
```

```
startfreq = {{0.1, 0, 0, 0.9}, {0.1, 0, 0, 0.9}};
pars = {0, 0.3, 1, 1 / 7}; (* "asymm. DMI!" *)
freq = startfreq;
Do[freq = haplotypeDynamicsX[1][pars][freq] // Chop;
 If[IntegerQ[k / 1000], Print[freq]],
 {k, 5000}]
transferHaplotypeToAllele[1][freq[[All, 1 ;; 3]]]
```

```
{{0, 0, 0, 1.}, {0, 0, 0, 1.}}

{{0, 0, 0, 1.}, {0, 0, 0, 1.}}

{{0, 0, 0, 1.}, {0, 0, 0, 1.}}

{{0, 0, 0, 1.}, {0, 0, 0, 1.}}

{{0, 0, 0, 1.}, {0, 0, 0, 1.}}

{{1, 1, 0}, {1, 1, 0}}
```

```
startfreq = {{0.1, 0, 0, 0.9}, {0.1, 0, 0, 0.9}};
pars = {.61, 0, 1, 1 / 2}; (* "asymm. DMI!" *)
freq = startfreq;
Do[freq = haplotypeDynamicsX[1][pars][freq] // Chop;
 If[IntegerQ[k / 1000], Print[freq]],
 {k, 5000}]
transferHaplotypeToAllele[1][freq[[All, 1 ;; 3]]]
```

```
{{0.23736, 0.42985, 0.0954301, 0.23736}, {0.262401, 0.475198, 0, 0.262401}}

{{0.23736, 0.42985, 0.0954301, 0.23736}, {0.262401, 0.475198, 0, 0.262401}}

{{0.23736, 0.42985, 0.0954301, 0.23736}, {0.262401, 0.475198, 0, 0.262401}}

{{0.23736, 0.42985, 0.0954301, 0.23736}, {0.262401, 0.475198, 0, 0.262401}}

{{0.23736, 0.42985, 0.0954301, 0.23736}, {0.262401, 0.475198, 0, 0.262401}}

{{0.33279, 0.66721, 0.0153192}, {0.262401, 0.737599, 0.0688543}}
```

Define Jacobian

```
JacobianAllele[1][par_][x_] :=
 D[Flatten[alleleDynamics[1][par][{{pf, qf, LDf}, {pm, qm, LDm}}], 2],
   {{pf, qf, LDf, pm, qm, LDm}}] /. x
JacobianAllele[2][par_][x_] :=
 D[alleleDynamics[2][par][{pf, qf, LDf}], {{pf, qf, LDf}}] /. x
JacobianHaplotype[1][par_][x_] :=
 D[Flatten[haplotypeDynamics[1][par][{{g1, g2, g3}, {h1, h2, h3}}], 2],
   {{g1, g2, g3, h1, h2, h3}}] /. x
JacobianHaplotype[2][par_][x_] :=
 D[haplotypeDynamics[2][par][{g1, g2, g3}], {{g1, g2, g3}}] /. x
JacobianAllele[0][par_][x_] :=
 D[alleleDynamics[0][par][{pf, qf, LDf}], {{pf, qf, LDf}}] /. x
JacobianHaplotype[0][par_][x_] :=
 D[haplotypeDynamics[0][par][{g1, g2, g3}], {{g1, g2, g3}}] /. x
```

As a test, we can compute the eigenvalues of a monomorphic equilibrium, both from a haplotype perspective and an allele perspective.

```
eig =
 Eigenvalues[JacobianAllele[2][{s, γ01, γ10, r}][{pf → 0, qf → 0, LDf → 0}]] // Simplify
eig = Eigenvalues[JacobianHaplotype[2][{s, γ01, γ10, r}][{g1 → 0, g2 → 0, g3 → 0}]] //
  Simplify
```

```
{1 + s, 1 + s, - (-1 + r) (1 + s)^2}

{1 + s, 1 + s, - (-1 + r) (1 + s)^2}
```

A function that determines equilibria and stability numerically

For haplodiploid model:

```
stableEquilibriaHaplotype[1, wp_: 30 (* set working precision; optional *)][
   par_ (* list of parameters: s, γ01, γ10, r *), noisey_: False] :=
 Module[{null, nonull, nullp, tempAllEq},
  (* Solve equation numerically, and only keep real-numbered solutions *)
```

```
null = Select[Quiet[Solve[haplotypeDynamics[1][par][{{g1, g2, g3}, {h1, h2, h3}}] -
      {{g1, g2, g3}, {h1, h2, h3}} ⩵ {{0, 0, 0}, {0, 0, 0}}, {g1, g2, g3, h1, h2, h3},
    WorkingPrecision → wp]], Im[#[[All, 2]]] ⩵ {0, 0, 0, 0, 0, 0} &];
(* Sometimes there are numerical instabilities that can be
 fixed by using Solve for these param combos *)

(* chop numbers close to 0 and 1 to these values *)
null[[All, All, 2]] = Chop[Chop[-1 + null[[All, All, 2]]] + 1];

(* option to print all the equilibria *)
If[noisey,
 allEquilibria = {};
 Do[
  tempAllEq = {{g1, g2, g3, h1, h2, h3} /. null[[i]],
    Eigenvalues[JacobianHaplotype[1][par][null[[i]]]]};
  If[(* all valid equilibria must have coordinates between 0 and 1 *)
   Abs[tempAllEq[[1, 1]] - 1 / 2] ≤ 1 / 2
    && Abs[tempAllEq[[1, 2]] - 1 / 2] ≤ 1 / 2
    && Abs[tempAllEq[[1, 3]] - 1 / 2] ≤ 1 / 2
    && Abs[tempAllEq[[1, 4]] - 1 / 2] ≤ 1 / 2
    && Abs[tempAllEq[[1, 5]] - 1 / 2] ≤ 1 / 2
    && Abs[tempAllEq[[1, 6]] - 1 / 2] ≤ 1 / 2
     (* they should not sum up to
      more than 1 (within the limits of numerical error) *)
    && Total[tempAllEq[[1]]] ≤ 2 + 10^-6,
   AppendTo[allEquilibria, tempAllEq];
  ];
  , {i, 1, Length[null]}];
];

(* select stable equilibria as follows *)
null = Select[DeleteDuplicates[null],
   (* all valid equilibria must have coordinates between 0 and 1 *)
  Abs[#[[1, 2]] - 1 / 2] ≤ 1 / 2
    && Abs[#[[2, 2]] - 1 / 2] ≤ 1 / 2
    && Abs[#[[3, 2]] - 1 / 2] ≤ 1 / 2
    && Abs[#[[4, 2]] - 1 / 2] ≤ 1 / 2
    && Abs[#[[5, 2]] - 1 / 2] ≤ 1 / 2
    && Abs[#[[6, 2]] - 1 / 2] ≤ 1 / 2
     (* they should not sum up to
      more than 1 (within the limits of numerical error) *)
    && Total[#[[All, 2]]] ≤ 2 + 10^-6
     (* and their eigenvalues should be all smaller than one -
      criterion for local stability *)
    && Max[Abs[Re[Chop[Eigenvalues[JacobianHaplotype[1][par][#]]]]]] ≤ 1 &];
(* This bit is for troubleshooting, prints each coord
  with its respective eigenvalue before they are filtered out below
  For[i=1,i≤ Length[null],i++,
   Print[{null[[i]],Eigenvalues[JacobianHaplotype[1][par][null[[i]]]]}];
```

```
    ];
  *)

  (* count number of stable equilibria *)
  nonull = Length[null];
  (* sort without any real reason  *)
  null = Sort[{{g1, g2, g3}, {h1, h2, h3}} /. null];
  (* convert into allele frequencies and sort
   (makes more sense here bc this will sort by allele frequency of A) *)
  nullp = Sort[transferHaplotypeToAllele[1] /@ null] // Chop;
  (* OUTPUT: *)
  {nonull (* number of stable equilibria *),
   Ceiling[Max[null[[All, 1, 1]] null[[All, 1, 2]] null[[All, 1, 3]]]]
   (* prints 1 if there is a stable internal equilibrium *),
   null (* list of coordinates of haplotype frequencies *),
   nullp (* list of coordinates of allele frequencies *)}
 ]
```

For diploid model:

```
stableEquilibriaHaplotype[2, wp_: 30 (* set working precision; optional *)][
  par_ (* list of parameters *), noisey_: False] :=
 Module[{null, nonull, nullp, tempAllEq},
  (* Solve equation numerically, and only keep real-numbered solutions *)
  null = Select[
    Quiet[Solve[haplotypeDynamics[2][par][{g1, g2, g3}] - {g1, g2, g3} == {0, 0, 0},
      {g1, g2, g3}, WorkingPrecision → wp]], Im[#[[All, 2]]] == {0, 0, 0} &];
  (* chop numbers close to 0 and 1 to these values *)
  null[[All, All, 2]] = Chop[Chop[-1 + null[[All, All, 2]]] + 1];

  (* option to print all the equilibria *)
  If[noisey,
   allEquilibria = {};
   Do[
    tempAllEq = {{g1, g2, g3} /. null[[i]],
      Eigenvalues[JacobianHaplotype[2][par][null[[i]]]]};
    If[(* all valid equilibria must have coordinates between 0 and 1 *)
     Abs[tempAllEq[[1, 1]] - 1 / 2] ≤ 1 / 2
      && Abs[tempAllEq[[1, 2]] - 1 / 2] ≤ 1 / 2
      && Abs[tempAllEq[[1, 3]] - 1 / 2] ≤ 1 / 2
      (* they should not sum up to
       more than 1 (within the limits of numerical error) *)
      && Total[tempAllEq[[1]]] ≤ 1 + 10^-6,
     AppendTo[allEquilibria, tempAllEq];
    ];
    , {i, 1, Length[null]}];
  ];

  (* select stable equilibria as follows *)
```

```
  null = Select[DeleteDuplicates[null],
     (* all valid equilibria must have coordinates between 0 and 1 *)
     Abs[#[[1, 2]] - 1 / 2] ≤ 1 / 2
       && Abs[#[[2, 2]] - 1 / 2] ≤ 1 / 2
       && Abs[#[[3, 2]] - 1 / 2] ≤ 1 / 2
       (* they should not sum up to
        more than 1 (within the limits of numerical error) *)
       && Total[#[[All, 2]]] ≤ 2 + 10^-6
       (* and their eigenvalues should be all smaller than zero -
        criterion for local stability *)
       && Max[Abs[Re[Chop[ Eigenvalues[JacobianHaplotype[2][par][#]] ]]]] ≤ 1 &];
  (* count number of stable equilibria *)
  nonull = Length[null];
  (* sort without any real reason  *)
  null = Sort[{g1, g2, g3} /. null];
  (* convert into allele frequencies and sort
    (makes more sense here bc this will sort by allele frequency of A) *)
  nullp = Sort[transferHaplotypeToAllele[2] /@ null] // Chop;
  (* OUTPUT: *)
  {nonull (* number of stable equilibria *),
    Ceiling[Max[null[[All, 1]] null[[All, 2]] null[[All, 3]]]]
    (* prints 1 if there is a stable internal equilibrium *),
    null (* list of coordinates of haplotype frequencies *),
    nullp (* list of coordinates of allele frequencies *)}
 ]
```

Some checks

```
Round[stableEquilibriaHaplotype[1][{0.3, 0, 1, 0.5}], 10^-6] // N
```

```
{1., 1., {{{0.2096, 0.52539, 0.05541}, {0.221895, 0.55621, 0.}}},
  {{{0.26501, 0.73499, 0.01482}, {0.221895, 0.778105, 0.049237}}}}
```

```
Round[stableEquilibriaHaplotype[2][{0.1, 0.01, 0.05, 0.5}], 10^-6] // N
```

```
{1., 1., {{0.251079, 0.268493, 0.229349}}, {{0.480428, 0.519572, 0.001462}}}
```

Looks like we can also find (tri-/)bistability here! (??)

```
Round[stableEquilibriaHaplotype[1][{0.05, 0.9, 0.01, 0.1}], 10^-6] // N
```

```
{2., 0., {{{0., 0., 0.409049}, {0., 0., 0.406622}},
   {{0.590951, 0., 0.409049}, {0.593378, 0., 0.406622}}},
  {{{0.409049, 0., 0.}, {0.406622, 0., 0.}}, {{1., 0.590951, 0.}, {1., 0.593378, 0.}}}}
```

```
Round[stableEquilibriaHaplotype[1][{0.05, 0.8, 0.01, 0.1}], 10^-6] // N
```

```
{3., 1., {{{0., 0., 0.409049}, {0., 0., 0.406622}},
   {{0.238495, 0.015059, 0.50795}, {0.242651, 0.003064, 0.511633}},
   {{0.590951, 0., 0.409049}, {0.593378, 0., 0.406622}}},
  {{{0.409049, 0., 0.}, {0.406622, 0., 0.}}, {{0.746445, 0.253555, 0.049231},
    {0.754284, 0.245716, 0.057312}}, {{1., 0.590951, 0.}, {1., 0.593378, 0.}}}}
```

Dynamics with assortment

Life cycle with assortment via matching function

As compared with the no-preference version, we operate now on genotype and mating pair level rather than genotype and gamete. However, there are some redundancies with the above subsection where we define the dynamics without the preference.

```
haplotypes = Tuples[{0, 1}, 2]
genotypes = Tuples[haplotypes, 2]
```

```
{{0, 0}, {0, 1}, {1, 0}, {1, 1}}
```

```
{{{0, 0}, {0, 0}}, {{0, 0}, {0, 1}}, {{0, 0}, {1, 0}}, {{0, 0}, {1, 1}},
 {{0, 1}, {0, 0}}, {{0, 1}, {0, 1}}, {{0, 1}, {1, 0}}, {{0, 1}, {1, 1}},
 {{1, 0}, {0, 0}}, {{1, 0}, {0, 1}}, {{1, 0}, {1, 0}}, {{1, 0}, {1, 1}},
 {{1, 1}, {0, 0}}, {{1, 1}, {0, 1}}, {{1, 1}, {1, 0}}, {{1, 1}, {1, 1}}}
```

General genotypes of males and females:

```
genotypeFemale = Table[genotypeF_genotypes[[i]], {i, 16}]
genotypeMale = Table[genotypeM_haplotypes[[i]], {i, 4}]
```

```
{genotypeF_{{0,0},{0,0}}, genotypeF_{{0,0},{0,1}}, genotypeF_{{0,0},{1,0}}, genotypeF_{{0,0},{1,1}},
 genotypeF_{{0,1},{0,0}}, genotypeF_{{0,1},{0,1}}, genotypeF_{{0,1},{1,0}}, genotypeF_{{0,1},{1,1}},
 genotypeF_{{1,0},{0,0}}, genotypeF_{{1,0},{0,1}}, genotypeF_{{1,0},{1,0}}, genotypeF_{{1,0},{1,1}},
 genotypeF_{{1,1},{0,0}}, genotypeF_{{1,1},{0,1}}, genotypeF_{{1,1},{1,0}}, genotypeF_{{1,1},{1,1}}}
```

```
{genotypeM_{0,0}, genotypeM_{0,1}, genotypeM_{1,0}, genotypeM_{1,1}}
```

Later we will deal with general diploid genotypes:

```
genotypeDiploid = Table[genotypeD_genotypes[[i]], {i, 16}]
```

```
{genotypeD_{{0,0},{0,0}}, genotypeD_{{0,0},{0,1}}, genotypeD_{{0,0},{1,0}}, genotypeD_{{0,0},{1,1}},
 genotypeD_{{0,1},{0,0}}, genotypeD_{{0,1},{0,1}}, genotypeD_{{0,1},{1,0}}, genotypeD_{{0,1},{1,1}},
 genotypeD_{{1,0},{0,0}}, genotypeD_{{1,0},{0,1}}, genotypeD_{{1,0},{1,0}}, genotypeD_{{1,0},{1,1}},
 genotypeD_{{1,1},{0,0}}, genotypeD_{{1,1},{0,1}}, genotypeD_{{1,1},{1,0}}, genotypeD_{{1,1},{1,1}}}
```

We now also need the level of mating pairs:

```
matingPairs = Table[matingPair_{genotypes[[i]],haplotypes[[j]]}, {i, 16}, {j, 4}] // Flatten
```

```
{matingPair_{{0,0},{0,0}},{0,0}, matingPair_{{0,0},{0,0}},{0,1},
 matingPair_{{0,0},{0,0}},{1,0}, matingPair_{{0,0},{0,0}},{1,1},
 matingPair_{{0,0},{0,1}},{0,0}, matingPair_{{0,0},{0,1}},{0,1}, matingPair_{{0,0},{0,1}},{1,0},
 matingPair_{{0,0},{0,1}},{1,1}, matingPair_{{0,0},{1,0}},{0,0}, matingPair_{{0,0},{1,0}},{0,1},
 matingPair_{{0,0},{1,0}},{1,0}, matingPair_{{0,0},{1,0}},{1,1}, matingPair_{{0,0},{1,1}},{0,0},
 matingPair_{{0,0},{1,1}},{0,1}, matingPair_{{0,0},{1,1}},{1,0}, matingPair_{{0,0},{1,1}},{1,1},
 matingPair_{{0,1},{0,0}},{0,0}, matingPair_{{0,1},{0,0}},{0,1}, matingPair_{{0,1},{0,0}},{1,0},
 matingPair_{{0,1},{0,0}},{1,1}, matingPair_{{0,1},{0,1}},{0,0}, matingPair_{{0,1},{0,1}},{0,1},
 matingPair_{{0,1},{0,1}},{1,0}, matingPair_{{0,1},{0,1}},{1,1}, matingPair_{{0,1},{1,0}},{0,0},
 matingPair_{{0,1},{1,0}},{0,1}, matingPair_{{0,1},{1,0}},{1,0}, matingPair_{{0,1},{1,0}},{1,1},
 matingPair_{{0,1},{1,1}},{0,0}, matingPair_{{0,1},{1,1}},{0,1}, matingPair_{{0,1},{1,1}},{1,0},
 matingPair_{{0,1},{1,1}},{1,1}, matingPair_{{1,0},{0,0}},{0,0}, matingPair_{{1,0},{0,0}},{0,1},
 matingPair_{{1,0},{0,0}},{1,0}, matingPair_{{1,0},{0,0}},{1,1}, matingPair_{{1,0},{0,1}},{0,0},
 matingPair_{{1,0},{0,1}},{0,1}, matingPair_{{1,0},{0,1}},{1,0}, matingPair_{{1,0},{0,1}},{1,1},
 matingPair_{{1,0},{1,0}},{0,0}, matingPair_{{1,0},{1,0}},{0,1}, matingPair_{{1,0},{1,0}},{1,0},
 matingPair_{{1,0},{1,0}},{1,1}, matingPair_{{1,0},{1,1}},{0,0}, matingPair_{{1,0},{1,1}},{0,1},
 matingPair_{{1,0},{1,1}},{1,0}, matingPair_{{1,0},{1,1}},{1,1}, matingPair_{{1,1},{0,0}},{0,0},
 matingPair_{{1,1},{0,0}},{0,1}, matingPair_{{1,1},{0,0}},{1,0}, matingPair_{{1,1},{0,0}},{1,1},
 matingPair_{{1,1},{0,1}},{0,0}, matingPair_{{1,1},{0,1}},{0,1}, matingPair_{{1,1},{0,1}},{1,0},
 matingPair_{{1,1},{0,1}},{1,1}, matingPair_{{1,1},{1,0}},{0,0}, matingPair_{{1,1},{1,0}},{0,1},
 matingPair_{{1,1},{1,0}},{1,0}, matingPair_{{1,1},{1,0}},{1,1}, matingPair_{{1,1},{1,1}},{0,0},
 matingPair_{{1,1},{1,1}},{0,1}, matingPair_{{1,1},{1,1}},{1,0}, matingPair_{{1,1},{1,1}},{1,1}}
```

and for the diploid case

```
matingPairsDiploid = Table[matingPair_{genotypes[[i]],genotypes[[j]]}, {i, 16}, {j, 16}] // Flatten;
```

Epistasis

Later, we will usually deal with the case of completely recessive epistasis (using parameter γ because ϵ is always handy for Taylor approximations)

```
epistasisRecessiveAsymmetric =
  {e_"01" → 0, e_"10" → 0, e_"01,10" → 0, e_"01,01" → γ01, e_"10,10" → γ10};
```

Viability selection in males

Note that the frequencies are purely determined by female gamete frequencies in the previous generation.

```
selectionMatrixMales = {1, 1 - e"01,01", 1 - e"10,10", 1};
(* notation indicates types of conflict,
here doubled such that haploids suffer as much as homozygous diploids *)
meanFitnessMales = Total[selectionMatrixMales genotypeMale]
malesAfterSelection = selectionMatrixMales genotypeMale / meanFitnessMales
```

$$\text{genotypeM}_{\{0,0\}} + (1 - e_{01,01})\ \text{genotypeM}_{\{0,1\}} + (1 - e_{10,10})\ \text{genotypeM}_{\{1,0\}} + \text{genotypeM}_{\{1,1\}}$$

$$\Big\{\text{genotypeM}_{\{0,0\}} \Big/ \left(\text{genotypeM}_{\{0,0\}} + (1 - e_{01,01})\ \text{genotypeM}_{\{0,1\}} + (1 - e_{10,10})\ \text{genotypeM}_{\{1,0\}} + \text{genotypeM}_{\{1,1\}}\right),$$
$$\left((1 - e_{01,01})\ \text{genotypeM}_{\{0,1\}}\right) \Big/ \left(\text{genotypeM}_{\{0,0\}} + (1 - e_{01,01})\ \text{genotypeM}_{\{0,1\}} + (1 - e_{10,10})\ \text{genotypeM}_{\{1,0\}} + \text{genotypeM}_{\{1,1\}}\right),$$
$$\left((1 - e_{10,10})\ \text{genotypeM}_{\{1,0\}}\right) \Big/ \left(\text{genotypeM}_{\{0,0\}} + (1 - e_{01,01})\ \text{genotypeM}_{\{0,1\}} + (1 - e_{10,10})\ \text{genotypeM}_{\{1,0\}} + \text{genotypeM}_{\{1,1\}}\right),\ \text{genotypeM}_{\{1,1\}} \Big/$$
$$\left(\text{genotypeM}_{\{0,0\}} + (1 - e_{01,01})\ \text{genotypeM}_{\{0,1\}} + (1 - e_{10,10})\ \text{genotypeM}_{\{1,0\}} + \text{genotypeM}_{\{1,1\}}\right)\Big\}$$

Viability selection in females, based on genotypes

For strong selection, this scheme should be multiplicative. Also, we can integrate different types of epistasis. This is the general form:

```
selectionMatrixFemales = {{1, (1 - e"01") (1 + s), (1 - e"10") (1 + s), (1 + s)^2 (1 - e"01,10")},
    {(1 + s) (1 - e"01"), (1 - e"01,01"), (1 + s)^2 (1 - e"01,10"), (1 + s) (1 - e"01")},
    {(1 + s) (1 - e"10"), (1 + s)^2 (1 - e"01,10"), (1 - e"10,10"), (1 + s) (1 - e"10")},
    {(1 + s)^2 (1 - e"01,10"), (1 + s) (1 - e"01"), (1 + s) (1 - e"10"), 1}};
selectionTableFemales = Flatten[selectionMatrixFemales];
wShow = Prepend[selectionMatrixFemales, {{A0, B0}, {A0, B1}, {A1, B0}, {A1, B1}}];
Grid[MapThread[Prepend,
  {wShow, {"Haplotypes", {A0, B0}, {A0, B1}, {A1, B0}, {A1, B1}}}], Frame → All]
```

Haplotypes	{A0, B0}	{A0, B1}	{A1, B0}	{A1, B1}
{A0, B0}	1	$(1+s)\ (1-e_{01})$	$(1+s)\ (1-e_{10})$	$(1+s)^2\ (1-e_{01,10})$
{A0, B1}	$(1+s)\ (1-e_{01})$	$1-e_{01,01}$	$(1+s)^2\ (1-e_{01,10})$	$(1+s)\ (1-e_{01})$
{A1, B0}	$(1+s)\ (1-e_{10})$	$(1+s)^2\ (1-e_{01,10})$	$1-e_{10,10}$	$(1+s)\ (1-e_{10})$
{A1, B1}	$(1+s)^2\ (1-e_{01,10})$	$(1+s)\ (1-e_{01})$	$(1+s)\ (1-e_{10})$	1

```
{genotypeFemale, selectionTableFemales} // grid
```

$\text{genotypeF}_{\{\{0,0\},\{0,0\}\}}$	$\text{genotypeF}_{\{\{0,0\},\{0,1\}\}}$	$\text{genotypeF}_{\{\{0,0\},\{1,0\}\}}$	$\text{genotypeF}_{\{\{0,0\},\{1,1\}\}}$	genotypeF
1	$(1+s)\ (1-e_{01})$	$(1+s)\ (1-e_{10})$	$(1+s)^2\ (1-e_{01,10})$	$(1+s)$

Selection of genotypes

```
femaleGenotypesAfterSelectionBeforeNormalization =
  selectionTableFemales genotypeFemale;
meanFitnessFemales = Total[femaleGenotypesAfterSelectionBeforeNormalization];
femaleGenotypesAfterSelection =
  femaleGenotypesAfterSelectionBeforeNormalization / meanFitnessFemales // Simplify;
```

```
femaleGenotypesAfterSelection[[1 ;; 3]] // Column
```

```
- (genotypeF_{{0,0},{0,0}} / (-genotypeF_{{0,0},{0,0}} + (1 + s) (-1 + e_{01}) genotypeF_{{0,0},{0,1}} +
      (1 + s) (-1 + e_{10}) genotypeF_{{0,0},{1,0}} + (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{0,0},{1,1}} +
      (1 + s) (-1 + e_{01}) genotypeF_{{0,1},{0,0}} + (-1 + e_{01,01}) genotypeF_{{0,1},{0,1}} +
      (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{0,1},{1,0}} + (1 + s) (-1 + e_{01}) genotypeF_{{0,1},{1,1}} +
      (1 + s) (-1 + e_{10}) genotypeF_{{1,0},{0,0}} + (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{1,0},{0,1}} +
      (-1 + e_{10,10}) genotypeF_{{1,0},{1,0}} + (1 + s) (-1 + e_{10}) genotypeF_{{1,0},{1,1}} +
      (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{1,1},{0,0}} + (1 + s) (-1 + e_{01}) genotypeF_{{1,1},{0,1}} +
      (1 + s) (-1 + e_{10}) genotypeF_{{1,1},{1,0}} - genotypeF_{{1,1},{1,1}}))
- (((1 + s) (1 - e_{01}) genotypeF_{{0,0},{0,1}}) /
    (-genotypeF_{{0,0},{0,0}} + (1 + s) (-1 + e_{01}) genotypeF_{{0,0},{0,1}} +
      (1 + s) (-1 + e_{10}) genotypeF_{{0,0},{1,0}} + (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{0,0},{1,1}} +
      (1 + s) (-1 + e_{01}) genotypeF_{{0,1},{0,0}} + (-1 + e_{01,01}) genotypeF_{{0,1},{0,1}} +
      (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{0,1},{1,0}} + (1 + s) (-1 + e_{01}) genotypeF_{{0,1},{1,1}} +
      (1 + s) (-1 + e_{10}) genotypeF_{{1,0},{0,0}} + (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{1,0},{0,1}} +
      (-1 + e_{10,10}) genotypeF_{{1,0},{1,0}} + (1 + s) (-1 + e_{10}) genotypeF_{{1,0},{1,1}} +
      (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{1,1},{0,0}} + (1 + s) (-1 + e_{01}) genotypeF_{{1,1},{0,1}} +
      (1 + s) (-1 + e_{10}) genotypeF_{{1,1},{1,0}} - genotypeF_{{1,1},{1,1}}))
- (((1 + s) (1 - e_{10}) genotypeF_{{0,0},{1,0}}) /
    (-genotypeF_{{0,0},{0,0}} + (1 + s) (-1 + e_{01}) genotypeF_{{0,0},{0,1}} +
      (1 + s) (-1 + e_{10}) genotypeF_{{0,0},{1,0}} + (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{0,0},{1,1}} +
      (1 + s) (-1 + e_{01}) genotypeF_{{0,1},{0,0}} + (-1 + e_{01,01}) genotypeF_{{0,1},{0,1}} +
      (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{0,1},{1,0}} + (1 + s) (-1 + e_{01}) genotypeF_{{0,1},{1,1}} +
      (1 + s) (-1 + e_{10}) genotypeF_{{1,0},{0,0}} + (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{1,0},{0,1}} +
      (-1 + e_{10,10}) genotypeF_{{1,0},{1,0}} + (1 + s) (-1 + e_{10}) genotypeF_{{1,0},{1,1}} +
      (1 + s)^2 (-1 + e_{01,10}) genotypeF_{{1,1},{0,0}} + (1 + s) (-1 + e_{01}) genotypeF_{{1,1},{0,1}} +
      (1 + s) (-1 + e_{10}) genotypeF_{{1,1},{1,0}} - genotypeF_{{1,1},{1,1}}))
```

That looks correct! The same is of course happening in the diploid model, we just need to replace the variable:

```
diploidGenotypesAfterSelection =
  femaleGenotypesAfterSelection /. {genotypeF_x_ → genotypeD_x};
```

Assortment and recombination

```
geneticDistance[F_, M_] := Total[Abs[Total[F] / 2 - M]]
(* Total[F] will sum the values inside each of the two "locus" tuples,
then divide this value by 2 because females have
 a genome that's twice the size of that of the males'.
For example, Total[{{0,0},{1,1}}]/2 will return {0.5,0.5}.
Then get the sum of the distances for female
 vs male at locus1 and female vs male at locus2. *)
```

For diploids

```
geneticDistanceDiploid[F_, M_] := Total[Abs[Total[F] - Total[M]] / 2]
```

```
geneticDistance[{{1, 1}, {0, 0}}, {0, 0}]
```

```
1
```

```
geneticDistanceDiploid[{{1, 1}, {0, 0}}, {{1, 1}, {1, 1}}]
```

```
1
```

Assortative mating

This is what they call “Gaussian assortative mating” in De Cara et al. 2008.

```
assortmentCoefficientsGaussian[F_, M_] := (1 - A)^geneticDistance[F,M]
```

And this is what they call “quadratic assortative mating”:

```
assortmentCoefficientsQuadratic[F_, M_] := 1 - A geneticDistance[F, M] / 2
assortmentCoefficientsQuadraticDiploid[F_, M_] := 1 - A geneticDistanceDiploid[F, M] / 2
```

We will be using quadratic assortment for now, because Gaussian assortative mating is problematic for introgressed females (for A=1, they would not be able to mate at all). The maximum assortment coefficient is 1 for both of these function, i.e. A ranges from 0 (random mating) to 1 (strong assortment, no mating with opposite type).

```
assortmentCoefficientsTable =
 Table[assortmentCoefficientsQuadratic[matingPairs[[i, 2]], matingPairs[[i, 3]]],
  {i, Length[matingPairs]}]
```

$$\Big\{1, 1-\frac{A}{2}, 1-\frac{A}{2}, 1-A, 1-\frac{A}{4}, 1-\frac{A}{4}, 1-\frac{3A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{2},$$
$$1-\frac{A}{2}, 1-\frac{A}{2}, 1-\frac{A}{2}, 1-\frac{A}{4}, 1-\frac{A}{4}, 1-\frac{3A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{2}, 1, 1-A, 1-\frac{A}{2}, 1-\frac{A}{2}, 1-\frac{A}{2},$$
$$1-\frac{A}{2}, 1-\frac{A}{2}, 1-\frac{3A}{4}, 1-\frac{A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{4}, 1-\frac{A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{2}, 1-\frac{A}{2},$$
$$1-\frac{A}{2}, 1-\frac{A}{2}, 1-\frac{A}{2}, 1-A, 1, 1-\frac{A}{2}, 1-\frac{3A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{4}, 1-\frac{A}{4}, 1-\frac{A}{2}, 1-\frac{A}{2}, 1-\frac{A}{2},$$
$$1-\frac{A}{2}, 1-\frac{3A}{4}, 1-\frac{A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{4}, 1-\frac{3A}{4}, 1-\frac{3A}{4}, 1-\frac{A}{4}, 1-\frac{A}{4}, 1-A, 1-\frac{A}{2}, 1-\frac{A}{2}, 1\Big\}$$

For diplo-diploids

```
assortmentCoefficientsTableDiploid =
  Table[assortmentCoefficientsQuadraticDiploid[matingPairsDiploid[[i, 2]],
    matingPairsDiploid[[i, 3]]], {i, Length[matingPairsDiploid]}];
```

Mating pairs are created from males and females after selection and then weighed by the assortment coefficients. Be aware that this is very slow, but the simplification is needed to subsequently speed up the simulation code.

```
matingPairFrequenciesBeforeNormalization =
  assortmentCoefficientsTable Flatten[Table[femaleGenotypesAfterSelection〚i〛
      malesAfterSelection〚j〛, {i, 16}, {j, 4}]] // Simplify;
totalForNormalization = Total[matingPairFrequenciesBeforeNormalization] // Simplify;
matingPairFrequencies =
  matingPairFrequenciesBeforeNormalization / totalForNormalization / Simplify;
matingPairFrequencies〚3〛
```

$$\begin{aligned}&\Big(4\left(1-\tfrac{A}{2}\right)\left(1-e_{10,10}\right)\text{genotypeF}_{\{\{0,0\},\{0,0\}\}}\\
&\quad\big(\text{genotypeF}_{\{\{0,0\},\{0,0\}\}}-(1+s)\,(-1+e_{01})\,\text{genotypeF}_{\{\{0,0\},\{0,1\}\}}+\\
&\qquad\text{genotypeF}_{\{\{0,0\},\{1,0\}\}}+\cdots 78\cdots+s\,\text{genotypeF}_{\{\{1,1\},\{1,0\}\}}-\\
&\qquad e_{10}\,\text{genotypeF}_{\{\{1,1\},\{1,0\}\}}-s\,e_{10}\,\text{genotypeF}_{\{\{1,1\},\{1,0\}\}}+\text{genotypeF}_{\{\{1,1\},\{1,1\}\}}\big)\\
&\quad\text{genotypeM}_{\{1,0\}}\,\big(\text{genotypeM}_{\{0,0\}}-\left(-1+e_{01,01}\right)\text{genotypeM}_{\{0,1\}}+\\
&\qquad\text{genotypeM}_{\{1,0\}}-e_{10,10}\,\text{genotypeM}_{\{1,0\}}+\text{genotypeM}_{\{1,1\}}\big)\Big)\Big/\\
&\Big(\text{Simplify}\,\big(-\text{genotypeF}_{\{\{0,0\},\{0,0\}\}}+(1+s)\,(-1+e_{01})\,\text{genotypeF}_{\{\{0,0\},\{0,1\}\}}+\\
&\qquad(1+s)\,(-1+e_{10})\,\text{genotypeF}_{\{\{0,0\},\{1,0\}\}}+\cdots 10\cdots+(1+s)\,(-1+e_{01})\\
&\qquad\;\text{genotypeF}_{\{\{1,1\},\{0,1\}\}}+(1+s)\,(-1+e_{10})\,\text{genotypeF}_{\{\{1,1\},\{1,0\}\}}-\text{genotypeF}_{\{\{1,1\},\{1,1\}\}}\big)\\
&\quad\big(\text{genotypeM}_{\{0,0\}}-\left(-1+e_{\cdots 7\cdots}\right)\cdots 1\cdots-\cdots 1\cdots+\text{genotypeM}_{\{1,1\}}\big)\\
&\quad\big(-4\,\text{genotypeF}_{\{\{0,0\},\{1,0\}\}}\,\text{genotypeM}_{\{0,0\}}+A\,\text{genotypeF}_{\{\{0,0\},\{1,0\}\}}\,\text{genotypeM}_{\{0,0\}}-\\
&\qquad 4\,s\,\text{genotypeF}_{\{\{0,0\},\{1,0\}\}}\,\text{genotypeM}_{\{0,0\}}+\cdots 1010\cdots\big)\Big)\end{aligned}$$

large output | show less | show more | show all | set size limit...

```
Sum[matingPairFrequencies〚i〛, {i, Length[matingPairs]}] // Simplify
```

```
1
```

Same for diploids:

```
matingPairFrequenciesDiploid = assortmentCoefficientsTableDiploid
   Flatten[Table[diploidGenotypesAfterSelection〚i〛
      diploidGenotypesAfterSelection〚j〛, {i, 16}, {j, 16}]];
matingPairFrequenciesDiploid〚3〛 // Simplify
```

$$\begin{aligned}&\left(\left(1-\frac{A}{4}\right)(1+s)\,(1-e_{10})\,\text{genotypeD}_{\{\{0,0\},\{0,0\}\}}\,\text{genotypeD}_{\{\{0,0\},\{1,0\}\}}\right)\Big/\\
&\big(-\text{genotypeD}_{\{\{0,0\},\{0,0\}\}}+(1+s)\,(-1+e_{01})\,\text{genotypeD}_{\{\{0,0\},\{0,1\}\}}+\\
&\quad(1+s)\,(-1+e_{10})\,\text{genotypeD}_{\{\{0,0\},\{1,0\}\}}+(1+s)^2\left(-1+e_{01,10}\right)\text{genotypeD}_{\{\{0,0\},\{1,1\}\}}+\\
&\quad(1+s)\,(-1+e_{01})\,\text{genotypeD}_{\{\{0,1\},\{0,0\}\}}+\left(-1+e_{01,01}\right)\text{genotypeD}_{\{\{0,1\},\{0,1\}\}}+\\
&\quad(1+s)^2\left(-1+e_{01,10}\right)\text{genotypeD}_{\{\{0,1\},\{1,0\}\}}+(1+s)\,(-1+e_{01})\,\text{genotypeD}_{\{\{0,1\},\{1,1\}\}}+\\
&\quad(1+s)\,(-1+e_{10})\,\text{genotypeD}_{\{\{1,0\},\{0,0\}\}}+(1+s)^2\left(-1+e_{01,10}\right)\text{genotypeD}_{\{\{1,0\},\{0,1\}\}}+\\
&\quad\left(-1+e_{10,10}\right)\text{genotypeD}_{\{\{1,0\},\{1,0\}\}}+(1+s)\,(-1+e_{10})\,\text{genotypeD}_{\{\{1,0\},\{1,1\}\}}+\\
&\quad(1+s)^2\left(-1+e_{01,10}\right)\text{genotypeD}_{\{\{1,1\},\{0,0\}\}}+(1+s)\,(-1+e_{01})\,\text{genotypeD}_{\{\{1,1\},\{0,1\}\}}+\\
&\quad(1+s)\,(-1+e_{10})\,\text{genotypeD}_{\{\{1,1\},\{1,0\}\}}-\text{genotypeD}_{\{\{1,1\},\{1,1\}\}}\big)^2\end{aligned}$$

```
matingPairFrequenciesDiploidBeforeNormalization =
  assortmentCoefficientsTableDiploid Flatten[Table[diploidGenotypesAfterSelection⟦i⟧
      diploidGenotypesAfterSelection⟦j⟧, {i, 16}, {j, 16}]] // Simplify;
totalForNormalizationDiploid = Total[
    matingPairFrequenciesDiploidBeforeNormalization] // Simplify;
matingPairFrequenciesDiploid = matingPairFrequenciesDiploidBeforeNormalization /
    totalForNormalizationDiploid // Simplify;
matingPairFrequenciesDiploid⟦
 3⟧
```

```
$Aborted
```

$$\begin{aligned}&\left(\left(1-\frac{A}{4}\right)(1+s)(1-e_{10})\,\text{genotypeD}_{\{\{0,0\},\{0,0\}\}}\,\text{genotypeD}_{\{\{0,0\},\{1,0\}\}}\right)\Big/\\&\Big(-\text{genotypeD}_{\{\{0,0\},\{0,0\}\}}+(1+s)(-1+e_{01})\,\text{genotypeD}_{\{\{0,0\},\{0,1\}\}}+\\&\quad(1+s)(-1+e_{10})\,\text{genotypeD}_{\{\{0,0\},\{1,0\}\}}+(1+s)^2(-1+e_{01,10})\,\text{genotypeD}_{\{\{0,0\},\{1,1\}\}}+\\&\quad(1+s)(-1+e_{01})\,\text{genotypeD}_{\{\{0,1\},\{0,0\}\}}+(-1+e_{01,01})\,\text{genotypeD}_{\{\{0,1\},\{0,1\}\}}+\\&\quad(1+s)^2(-1+e_{01,10})\,\text{genotypeD}_{\{\{0,1\},\{1,0\}\}}+(1+s)(-1+e_{01})\,\text{genotypeD}_{\{\{0,1\},\{1,1\}\}}+\\&\quad(1+s)(-1+e_{10})\,\text{genotypeD}_{\{\{1,0\},\{0,0\}\}}+(1+s)^2(-1+e_{01,10})\,\text{genotypeD}_{\{\{1,0\},\{0,1\}\}}+\\&\quad(-1+e_{10,10})\,\text{genotypeD}_{\{\{1,0\},\{1,0\}\}}+(1+s)(-1+e_{10})\,\text{genotypeD}_{\{\{1,0\},\{1,1\}\}}+\\&\quad(1+s)^2(-1+e_{01,10})\,\text{genotypeD}_{\{\{1,1\},\{0,0\}\}}+(1+s)(-1+e_{01})\,\text{genotypeD}_{\{\{1,1\},\{0,1\}\}}+\\&\quad(1+s)(-1+e_{10})\,\text{genotypeD}_{\{\{1,1\},\{1,0\}\}}-\text{genotypeD}_{\{\{1,1\},\{1,1\}\}}\Big)^2\end{aligned}$$

```
Sum[matingPairFrequenciesDiploid⟦i⟧, {i, Length[matingPairsDiploid]}] // Simplify
```

```
1
```

Recombination

Now, new females are created from recombined female gametes and male haplotypes of mating pairs.

```
makeNewFemale = genotypeF{J_,B_} :→ 1 / 2 Sum[(1 - r) (matingPair{J,X},B + matingPair{X,J},B) +
     r (matingPair{{J[[1]],X[[2]]},{X[[1]],J[[2]]}},B + matingPair{{X[[1]],J[[2]]},{J[[1]],X[[2]]}},B),
    {X, haplotypes}]
```

$$\begin{aligned}\text{genotypeF}_{\{J\_,B\_\}}:\rightarrow\frac{1}{2}\sum_{X}^{\text{haplotypes}}&\Big((1-r)\left(\text{matingPair}_{\{J,X\},B}+\text{matingPair}_{\{X,J\},B}\right)+\\&r\left(\text{matingPair}_{\{\{J\llbracket 1\rrbracket,X\llbracket 2\rrbracket\},\{X\llbracket 1\rrbracket,J\llbracket 2\rrbracket\}\},B}+\text{matingPair}_{\{\{X\llbracket 1\rrbracket,J\llbracket 2\rrbracket\},\{J\llbracket 1\rrbracket,X\llbracket 2\rrbracket\}\},B}\right)\Big)\end{aligned}$$

Males are created only from recombined female gametes.

```
makeNewMale = genotypeMJ_ :→
  1 / 2 Sum[(1 - r) (genotypeF{J,X} + genotypeF{X,J}) + r (genotypeF{{J[[1]],X[[2]]},{X[[1]],J[[2]]}} +
       genotypeF{{X[[1]],J[[2]]},{J[[1]],X[[2]]}}), {X, haplotypes}]
```

$$\begin{aligned}\text{genotypeM}_{J\_}:\rightarrow\frac{1}{2}\sum_{X}^{\text{haplotypes}}&\Big((1-r)\left(\text{genotypeF}_{\{J,X\}}+\text{genotypeF}_{\{X,J\}}\right)+\\&r\left(\text{genotypeF}_{\{\{J\llbracket 1\rrbracket,X\llbracket 2\rrbracket\},\{X\llbracket 1\rrbracket,J\llbracket 2\rrbracket\}\}}+\text{genotypeF}_{\{\{X\llbracket 1\rrbracket,J\llbracket 2\rrbracket\},\{J\llbracket 1\rrbracket,X\llbracket 2\rrbracket\}\}}\right)\Big)\end{aligned}$$

Try out:

```
genotypeF_{genotypes[[1]]} /. makeNewFemale
```

```
1/2 (2 (1 - r) matingPair_{{{0,0},{0,0}},{0,0}} + 2 r matingPair_{{{0,0},{0,0}},{0,0}} +
   (1 - r) (matingPair_{{{0,0},{0,1}},{0,0}} + matingPair_{{{0,1},{0,0}},{0,0}}) +
   r (matingPair_{{{0,0},{0,1}},{0,0}} + matingPair_{{{0,1},{0,0}},{0,0}}) +
   (1 - r) (matingPair_{{{0,0},{1,0}},{0,0}} + matingPair_{{{1,0},{0,0}},{0,0}}) +
   r (matingPair_{{{0,0},{1,0}},{0,0}} + matingPair_{{{1,0},{0,0}},{0,0}}) +
   r (matingPair_{{{0,1},{1,0}},{0,0}} + matingPair_{{{1,0},{0,1}},{0,0}}) +
   (1 - r) (matingPair_{{{0,0},{1,1}},{0,0}} + matingPair_{{{1,1},{0,0}},{0,0}}))
```

It is a bit more difficult to make new diploids, because both male and female parents can recombine:

```
makeNewDiploid = genotypeD_{{A_,B_}} :>
   1 / 4 Sum[(1 - r)^2 (* no rec in either parent *) (matingPair_{{A,X},{B,Y}} +
         matingPair_{{X,A},{B,Y}} + matingPair_{{A,X},{Y,B}} + matingPair_{{X,A},{Y,B}})
      + (1 - r) r (* rec in male parent *) (matingPair_{{A,X},{{B[[1]],Y[[2]]},{Y[[1]],B[[2]]}}} +
         matingPair_{{X,A},{{B[[1]],Y[[2]]},{Y[[1]],B[[2]]}}} + matingPair_{{X,A},{{Y[[1]],B[[2]]},{B[[1]],Y[[2]]}}} +
         matingPair_{{A,X},{{Y[[1]],B[[2]]},{B[[1]],Y[[2]]}}})
      + r (1 - r) (* rec in female parent *)
       (matingPair_{{{A[[1]],X[[2]]},{X[[1]],A[[2]]}},{B,Y}} + matingPair_{{{A[[1]],X[[2]]},{X[[1]],A[[2]]}},{Y,B}} +
         matingPair_{{{X[[1]],A[[2]]},{A[[1]],X[[2]]}},{B,Y}} + matingPair_{{{X[[1]],A[[2]]},{A[[1]],X[[2]]}},{Y,B}})
      + r^2 (* rec in both parents *)
       (matingPair_{{{A[[1]],X[[2]]},{X[[1]],A[[2]]}},{{B[[1]],Y[[2]]},{Y[[1]],B[[2]]}}} +
         matingPair_{{{A[[1]],X[[2]]},{X[[1]],A[[2]]}},{{Y[[1]],B[[2]]},{B[[1]],Y[[2]]}}} +
         matingPair_{{{X[[1]],A[[2]]},{A[[1]],X[[2]]}},{{B[[1]],Y[[2]]},{Y[[1]],B[[2]]}}} +
         matingPair_{{{X[[1]],A[[2]]},{A[[1]],X[[2]]}},{{Y[[1]],B[[2]]},{B[[1]],Y[[2]]}}}),
     {X, haplotypes}, {Y, haplotypes}];
```

We can now combine the pieces of the life cycle to the actual dynamics:

```
dynamicsUnnormalizedWithMatching = {(* new female genotype arises from *)
     genotypeFemale /. makeNewFemale(* recombination and sampling from
       mating pairs *) /. Thread[matingPairs → matingPairFrequencies]
     (* input of actual mating pair frequencies after selection *),
     (* new male genotype arises from *)
     genotypeMale /. makeNewMale(* recombination of female gametes *) /.
      Thread[genotypeFemale → femaleGenotypesAfterSelection]
      (* input of female frequencies after selection *)} /.
    epistasisRecessiveAsymmetric(* reduce epistasis coefficients *) // Simplify;
(* keep in mind that this has to be normalized
 to 1 *)
dynamicsTotal = Total /@ dynamicsUnnormalizedWithMatching // Simplify
 (* compute total for normalization *);
```

An example:

```
dynamicsUnnormalizedWithMatching⟦1, 1⟧
```

```
- (((-8 genotypeF{{0,0},{0,0}} +
        (1 + s) ((-4 + A) genotypeF{{0,0},{0,1}} + (-4 + A) genotypeF{{0,0},{1,0}} -
           4 genotypeF{{0,0},{1,1}} + 2 A genotypeF{{0,0},{1,1}} + 4 r genotypeF{{0,0},{1,1}} -
           2 A r genotypeF{{0,0},{1,1}} - 4 s genotypeF{{0,0},{1,1}} + 2 A s genotypeF{{0,0},{1,1}} +
           4 r s genotypeF{{0,0},{1,1}} - 2 A r s genotypeF{{0,0},{1,1}} - 4 genotypeF{{0,1},{0,0}} +
           A genotypeF{{0,1},{0,0}} - 4 r genotypeF{{0,1},{1,0}} + 2 A r genotypeF{{0,1},{1,0}} -
           4 r s genotypeF{{0,1},{1,0}} + 2 A r s genotypeF{{0,1},{1,0}} - 4 genotypeF{{1,0},{0,0}} +
           A genotypeF{{1,0},{0,0}} - 4 r genotypeF{{1,0},{0,1}} + 2 A r genotypeF{{1,0},{0,1}} -
           4 r s genotypeF{{1,0},{0,1}} + 2 A r s genotypeF{{1,0},{0,1}} -
           4 genotypeF{{1,1},{0,0}} + 2 A genotypeF{{1,1},{0,0}} + 4 r genotypeF{{1,1},{0,0}} -
           2 A r genotypeF{{1,1},{0,0}} - 4 s genotypeF{{1,1},{0,0}} + 2 A s genotypeF{{1,1},{0,0}} +
           4 r s genotypeF{{1,1},{0,0}} - 2 A r s genotypeF{{1,1},{0,0}})) genotypeM{0,0}) /
    (8 (genotypeF{{0,0},{0,0}} + (1 + s) genotypeF{{0,0},{0,1}} + genotypeF{{0,0},{1,0}} +
        s genotypeF{{0,0},{1,0}} + genotypeF{{0,0},{1,1}} +
        2 s genotypeF{{0,0},{1,1}} + s^2 genotypeF{{0,0},{1,1}} +
        genotypeF{{0,1},{0,0}} + s genotypeF{{0,1},{0,0}} + genotypeF{{0,1},{0,1}} -
        γ01 genotypeF{{0,1},{0,1}} + genotypeF{{0,1},{1,0}} + 2 s genotypeF{{0,1},{1,0}} +
        s^2 genotypeF{{0,1},{1,0}} + genotypeF{{0,1},{1,1}} + s genotypeF{{0,1},{1,1}} +
        genotypeF{{1,0},{0,0}} + s genotypeF{{1,0},{0,0}} + genotypeF{{1,0},{0,1}} +
        2 s genotypeF{{1,0},{0,1}} + s^2 genotypeF{{1,0},{0,1}} +
        genotypeF{{1,0},{1,0}} - γ10 genotypeF{{1,0},{1,0}} + genotypeF{{1,0},{1,1}} +
        s genotypeF{{1,0},{1,1}} + genotypeF{{1,1},{0,0}} + 2 s genotypeF{{1,1},{0,0}} +
        s^2 genotypeF{{1,1},{0,0}} + genotypeF{{1,1},{0,1}} + s genotypeF{{1,1},{0,1}} +
        genotypeF{{1,1},{1,0}} + s genotypeF{{1,1},{1,0}} + genotypeF{{1,1},{1,1}})
     (genotypeM{0,0} - (-1 + γ01) genotypeM{0,1} + genotypeM{1,0} -
        γ10 genotypeM{1,0} + genotypeM{1,1})))
```

This takes a while to run. You can save the dynamical equations for later, or cut a couple of simplification steps.

```
Import[ToString[NotebookDirectory[]] <> "dynamicsWithPref_saved"]
(* this imports the file called "dynamicsWithPref_saved"
 so long as it is in the same directory as this notebook *)
```

```
Import: File not found during Import.
```

```
$Failed
```

The diploid dynamics are slightly simpler:

```
dynamicsUnnormalizedWithMatchingDiploid = (* new female genotype arises from *)
  genotypeDiploid /. makeNewDiploid (* recombination and sampling from mating
       pairs *) /. Thread[matingPairsDiploid → matingPairFrequenciesDiploid]
     (* input of actual mating pair frequencies after selection *) /.
    epistasisRecessiveAsymmetric(* reduce epistasis coefficients *) // Simplify;
dynamicsTotalDiploid = Total /@ dynamicsUnnormalizedWithMatchingDiploid
  (* compute total for normalization *);
```

```
$Aborted
```

Dynamics as functions of haplotype frequencies

Haplodiploid dynamics as function of female gametes and male frequencies after selection

Create some genotype frequencies for testing purposes:

```
testF = RandomVariate[UniformDistribution[], 16];
testF = testF / Total[testF];
testM = RandomVariate[UniformDistribution[], 4];
testM = testM / Total[testM];
```

Dynamical equations:

```
dynamicsHaplodiploidWithMatching[{α_, σ_, γ1_, γ2_, R_}][
  {femaleGenotypes_, maleGenotypes_}] :=
 dynamicsUnnormalizedWithMatching / dynamicsTotal /.
    Thread[genotypeFemale → femaleGenotypes] /. Thread[
    genotypeMale → maleGenotypes] /. Thread[{A, s, γ01, γ10, r} -> {α, σ, γ1, γ2, R}]
```

Test:

```
dynamicsHaplodiploidWithMatching[{1, 0.1, 0.01, 0.02, 0.5}][{testF, testM}]
```

```
{{0.0840051, 0.0790078, 0.0348801, 0.0214843, 0.0918598, 0.175376, 0.0243312, 0.0530175,
  0.072139, 0.0358112, 0.0673231, 0.038687, 0.0319385, 0.090978, 0.0380982, 0.0610633},
 {0.209395, 0.315888, 0.239392, 0.235324}}
```

Diploid dynamics as function of gamete frequencies after selection

```
dynamicsDiploidWithMatching[{α_, σ_, γ1_, γ2_, R_}][genotypes_] :=
 dynamicsUnnormMatchingDiploidSimplified / dynamicsTotalDiploid /. Thread[
    genotypeDiploid → genotypes] /. Thread[{A, s, γ01, γ10, r} -> {α, σ, γ1, γ2, R}]
```

Test:

```
dynamicsDiploidWithMatching[{1, 0.1, 0.01, 0.02, 0.5}][testF] // N
```

```
{0.116377, 0.13204, 0.111305, 0.101934, 0.13204, 0.165403, 0.114043, 0.136624,
 0.111305, 0.114043, 0.132534, 0.112855, 0.101934, 0.136624, 0.112855, 0.130467}
```

You can also save everything in the notebook that you have calculated so far, in order to “resurrect” it later.

```
DumpSave[ToString[NotebookDirectory[]] <>
   "ant-dynamics_haplodiploid&diploid_with-preference.mx", "Global`"];
```

Chapter 2: Evolutionary scenarios

For the model without preference, use the function **stableEquilibriaHaplotype** to solve for all of the equilibria. Then investigate the stable equilibria in order to assign the given parameter combination to a specific evolutionary scenario.
Here are two functions (for haplodiploids and diploids seperately) that will classify the different evolutionary scenarios from a given parameter combination. Recall that parameter combinations must be inputted as a list in the following order: $\{\sigma, \gamma 1, \gamma 2, \rho\}$

```
IdentifyCase[pars_] := Module[{allMaleFreqs},
  equilOutput = stableEquilibriaHaplotype[1][pars];
  allMaleFreqs = Sort[Flatten@equilOutput[[4, All, 2, 1 ;; 2]]];

  (* Now catch the 6 possible cases as well as some putative error cases: *)
  Which[equilOutput[[1]] == 1
    && Abs[equilOutput[[4, 1, 1, 1]] - 0.5] < 0.01 &&
```

```
      Abs[equilOutput[[4, 1, 1, 2]] - 0.5] < 0.01,
     "F.5" (* females win with 0.5 allele freq for both loci *),
     equilOutput[[1]] == 1, "F", (* females win but NOT
      near 0.5 allele freq for both loci *)
     equilOutput[[1]] == 5, "MCF"(* depending on intial it's possible that males win,
     compromise, or females win *),
     equilOutput[[1]] == 2
      && allMaleFreqs == {0, 0, 1, 1}, "M" (* males win *),
     equilOutput[[1]] == 2
      && allMaleFreqs[[{1, 4}]] == {0, 1} && allMaleFreqs[[2 ;; 3]] ≠ {0, 1},
     "C" (* compromise *),
     equilOutput[[1]] == 2
      && Total@Abs[equilOutput[[4, 1, 1, 1 ;; 2]] - equilOutput[[4, 2, 1, 1 ;; 2]]] < 0.05
     (* stable equilibria are almost on top of each other *),
     "F2" (* near the bistability so 2 equilibria are
      almost about to converge to F case *),
     equilOutput[[1]] == 2
      && equilOutput[[2]] == 1, "A" (* asymmetric coexistence *),
     equilOutput[[1]] == 2,
     "weird bistable" (* if it's bistable but NEITHER C, M, nor A *),
     equilOutput[[1]] == 3
      && allMaleFreqs[[{1, 2, 5, 6}]] == {0, 0, 1, 1}
      && 0 < allMaleFreqs[[3]] < 1 && 0 < allMaleFreqs[[4]] < 1,
     "MC" (* depending on intial males win or compromise *),
     equilOutput[[1]] == 3
      && allMaleFreqs[[{1, 6}]] == {0, 1}
      && 0 < allMaleFreqs[[3]] < 1 && 0 < allMaleFreqs[[4]] < 1,
     "CF" (* depending on intial compromise or females win *),
     equilOutput[[1]] == 3, "weird tristable" (* if it'
      s tristable but NEITHER CF nor MC *),
     True, "weird other" (* none of the above cases are met *)]
  ]

IdentifyCaseDIPLOID[pars_] := Module[{},
   equilOutput = stableEquilibriaHaplotype[2][pars];

   Which[equilOutput[[1]] == 1
      && Abs[equilOutput[[4, 1, 1]] - 0.5] < 0.01 &&
      Abs[equilOutput[[4, 1, 2]] - 0.5] < 0.01 (* both loci near 0.5 *)
      && Chop[1 - equilOutput[[4, 1, 1]] - equilOutput[[4, 1, 2]] , 10^-6] == 0
     (* point sits on line y=1-x *),
     "F.5" (* coexistence near 0.5 allele freq for both loci *),
     equilOutput[[1]] == 1
      && Chop[1 - equilOutput[[4, 1, 1]] - equilOutput[[4, 1, 2]] , 10^-6] == 0
     (* point sits on line y=1-x *),
     "F" (* coexistence but not near 0.5 allele freq for both loci *),
     equilOutput[[1]] == 1 , "weird unistability",
     equilOutput[[1]] == 2
      && equilOutput[[4, 1, 1]] < 0.01 && equilOutput[[4, 1, 2]] < 0.01
      (* both loci within 1% of 0 or 1 allele freq *)
```

```
     && equilOutput[[4, 2, 1]] > 0.99 && equilOutput[[4, 2, 2]] > 0.99,
    "M"(* exclusion-like state *),
    equilOutput[[1]] == 2
     && Total@Abs[equilOutput[[4, 1, 1 ;; 2]] - equilOutput[[4, 2, 1 ;; 2]]] < 0.05
    (* stable equilibria are almost on top of each other *)
    , "F2" (* near the bistability so 2 equilibria are
     almost about to converge to F.5 case *),
    equilOutput[[1]] == 2
     && Chop[1 - equilOutput[[4, 1, 2]] - equilOutput[[4, 2, 1]], 10^-6] == 0 &&
     Chop[1 - equilOutput[[4, 1, 1]] - equilOutput[[4, 2, 2]], 10^-6] == 0
    (* equilibria are symmetrical within numerical precision*)
    , "A" (* asymmetric coexistence *),
    equilOutput[[1]] == 2 , "weird bistability",
    equilOutput[[1]] == 3 , "weird tristability"
   ]
  ]
```

Here are two functions (for haplodiploids and diploids seperately) that will plot the phase plane for a given parameter combination. Note that the phase plane diagrams given in the manuscript also show the basin of attraction. The basin of attraction was done by simulation; see Chapter 5 section “Basin of attraction” below.

```
PlotPhasePlane[pars_, PlotFemales_: False, allBlack_: True] :=
 Module[{equilFreqFemalesMales, unstableEquil, unstableHaps},
  (* get the equilibria *)
  equilFreqFemalesMales =
   stableEquilibriaHaplotype[1][pars, True][[4, All, All, 1 ;; 2]];
  (* calculate the allele freq for stable *)
  If[PlotFemales == True,
   (* just use the female allel freq *)
   stableFreq = equilFreqFemalesMales[[All, 1, All]];,
   (* use the allele freq for males and females combined *)
   stableFreq = 2 / 3 * equilFreqFemalesMales[[All, 1, All]] +
      1 / 3 * equilFreqFemalesMales[[All, 2, All]];
  ];

  unstableEquil = Select[DeleteDuplicates[allEquilibria],
     (* one of the eigenvalues should be bigger than one -
     criterion for local instability *)
     Max[Re[Chop[#[[2]] ]]] > 1 &][[All, 1]];
  (* keep just the equilibrium frequencies of the haplotypes *)
  (* count allele frequencies then combine by males and females *)
  unstableHaps = Partition[#, 3] & /@ unstableEquil;
  If[PlotFemales == True,
   (* just use the female allele freq *)
   unstableFreq =
     Thread[transferHaplotypeToAllele[1][unstableHaps]][[All, 1, 1 ;; 2]];,
   (* use the allele freq for males and females combined *)
   unstableFreq = Total[# * {2 / 3, 1 / 3}] & /@
      Thread[transferHaplotypeToAllele[1][unstableHaps]][[All, All, 1 ;; 2]];
  ];
```

```
  Which[allBlack == True,
   plot = Show[ListPlot[stableFreq, Frame → True, AspectRatio → 1,
      PlotRange → {{0, 1}, {0, 1}}, PlotRangeClipping → False, ImagePadding → 65,
      FrameTicks → {{{{0, "0  "}, {1, "1  "}}, None}, {{{0, "\n0"}, {1, "\n1"}}, None}},
      FrameLabel → (Style[#, FontSize → 14.5] & /@
         {"Frequency of Allele Aw", "Frequency of Allele Bw"}), PlotLabel → pars,
      LabelStyle → {FontFamily -> "Times", FontSize → 16}, ImageSize → 250],
     Graphics[{PointSize[0.15], Point[stableFreq]}],
     Graphics[{PointSize[0.15], Point[unstableFreq]}],
     Graphics[{White, PointSize[0.12], Point[unstableFreq]}]]
   ,
   allBlack == False,
   plot = Show[ListPlot[stableFreq, Frame → True, AspectRatio → 1,
      PlotRange → {{0, 1}, {0, 1}}, PlotRangeClipping → False, ImagePadding → 65,
      FrameTicks → {{{{0, "0  "}, {1, "1  "}}, None}, {{{0, "\n0"}, {1, "\n1"}}, None}},
      FrameLabel → (Style[#, FontSize → 14.5] & /@
         {"Frequency of Allele Aw", "Frequency of Allele Bw"}), PlotLabel → pars,
      LabelStyle → {FontFamily -> "Times", FontSize → 16}, ImageSize → 250],
     Graphics[{PointSize[0.15], Point[stableFreq]}],
     Graphics[{Darker[Red], PointSize[0.15], Point[unstableFreq]}],
     Graphics[{White, PointSize[0.12], Point[unstableFreq]}]]
  ];
  Return[plot];
 ]

PlotPhasePlaneDIPLOID[pars_] := Module[{unstableEquil, unstableFreq},
  (* get the equilibria *)
  stableFreq  = stableEquilibriaHaplotype[2][pars, True][[4, All, 1 ;; 2]];

  (* get the unstable equilibria *)
  unstableEquil = Select[DeleteDuplicates[allEquilibria],
     (* one of the eigenvalues should be bigger than one -
      criterion for local instability *)
    Max[Re[Chop[#[[2]] ]]] > 1 &][[All, 1]];
  (* keep just the equilibrium frequencies of the haplotypes *)
  (* convert to allele freq *)
  unstableFreq = Thread[transferHaplotypeToAllele[2][unstableEquil] ][[All, 1 ;; 2]];

  Show[ListPlot[stableFreq, Frame → True, AspectRatio → 1,
    PlotRange → {{0, 1}, {0, 1}}, PlotRangePadding → 0.02, FrameLabel →
     {"Frequency of Allele 1 at Locus 1", "Frequency of Allele 1 at Locus 2"},
    PlotLabel → "Diploid " <> ToString@pars],
   Graphics[{PointSize[0.04], Point[stableFreq]}],
   Graphics[{Darker[Red], PointSize[0.025], Point[unstableFreq]}],
   Graphics[{White, PointSize[0.01], Point[unstableFreq]}]]
 ]
```

If α=0 (no preference) and we don't care about the time to convergence or any specific starting conditions, we can use solve to get the haplotype frequencies before and after selection, as well as the LD at the equilibria.

```
noPrefEquilGenotypes[pars_, identifyCase_: False, summarizeGen_: True] :=
 Module[{equilOutput, allMaleFreqs, temp, out, gentempF, gentemp, gentempAfterSel,
   femalesPostSel, malesPostSel, LD}, (* pars are: σ, γ1, γ2, r *)
  equilOutput = stableEquilibriaHaplotype[1][pars // N];

  (* this is the part that gets the genotypes
   before and after selection from gamete frequencies *)
  temp = equilOutput[[3]] // N;
  out = {};
  (* functions to apply selection on newborns *)
  femalesPostSel = femaleGenotypesAfterSelection /. epistasisRecessiveAsymmetric /.
    Thread[{s, γ01, γ10} → pars[[1 ;; 3]]];
  malesPostSel = malesAfterSelection /. epistasisRecessiveAsymmetric /.
    Thread[{γ01, γ10} → pars[[2 ;; 3]]];

  Do[
   (* go from haplotype frequencies to genotype frequencies *)
   AppendTo[temp[[i, 1]], 1 - Total@temp[[i, 1]]];
   AppendTo[temp[[i, 2]], 1 - Total@temp[[i, 2]]];
   gentempF = Flatten[Table[temp[[i, 1, j]] * temp[[i, 2, k]], {j, 4}, {k, 4}]];
   gentemp = {gentempF, temp[[i, 1]]};
   (* apply selection on newborns *)
   gentempAfterSel = {femalesPostSel /. Thread[genotypeFemale → gentemp[[1]] ],
     malesPostSel /. Thread[genotypeMale → gentemp[[2]] ]};

   (* save to output *)
   If[summarizeGen == True,
    AppendTo[out, {Join[fem7Catfreq@gentemp, temp[[i, 1]]],
      Join[fem7Catfreq@gentempAfterSel, gentempAfterSel[[2]]]}],
    AppendTo[out, {gentemp , gentempAfterSel}]
   ],
   {i, Length@temp}];

  (* this is the part that categorizes what's going on at these param values *)
  If[identifyCase == True,
   allMaleFreqs = Sort[Flatten@equilOutput[[4, All, 2, 1 ;; 2]]];
   (* Now catch the 6 possible cases as well as some putative error cases: *)
   outputCase = Which[equilOutput[[1]] == 1
      && Abs[equilOutput[[4, 1, 1, 1]] - 0.5] < 0.01 && Abs[equilOutput[[4, 1, 1, 2]] - 0.5]
       0.01, "F.5" (* females win with 0.5 allele freq for both loci *),
     equilOutput[[1]] == 1, "F", (* females win but NOT near
      0.5 allele freq for both loci *)
     equilOutput[[1]] == 5, "MCF"(* depending on intial it's
      possible that males win, compromise, or females win *),
     equilOutput[[1]] == 2
      && allMaleFreqs == {0, 0, 1, 1}, "M" (* males win *),
     equilOutput[[1]] == 2
      && allMaleFreqs[[{1, 4}]] == {0, 1} && allMaleFreqs[[2 ;; 3]] ≠ {0, 1},
     "C" (* compromise; single locus polymorphism *),
```

```
        equilOutput[[1]] == 2
         && Total@Abs[equilOutput[[4, 1, 1, 1 ;; 2]] - equilOutput[[4, 2, 1, 1 ;; 2]]] < 0.05
        (* stable equilibria are almost on top of each other *),
        "F2" (* near the bistability so 2 equilibria are
         almost about to converge to F case *),
        equilOutput[[1]] == 2
         && equilOutput[[2]] == 1, "A" (* asymmetric coexistence *),
        equilOutput[[1]] == 2,
        "weird bistable" (* if it's bistable but NEITHER C, M, nor A *),
        equilOutput[[1]] == 3
         && allMaleFreqs[[{1, 2, 5, 6}]] == {0, 0, 1, 1}
         && 0 < allMaleFreqs[[3]] < 1 && 0 < allMaleFreqs[[4]] < 1,
        "MC" (* depending on intial males win or compromise *),
        equilOutput[[1]] == 3
         && allMaleFreqs[[{1, 6}]] == {0, 1}
         && 0 < allMaleFreqs[[3]] < 1 && 0 < allMaleFreqs[[4]] < 1,
        "CF" (* depending on intial compromise or females win *),
        equilOutput[[1]] == 3, "weird tristable" (* if it's
         tristable but NEITHER CF nor MC *),
        True, "weird other" (* none of the above cases are met *)];
          LD =
       Partition[Flatten[equilOutput[[4]]][[3 * Range[2 * Length@equilOutput[[4]]]]], 2];
          LD = (2 / 3) #[[1]] + (1 / 3) #[[2]] & /@ LD;
      (* weighted average among males and females *)
      Return[{out, outputCase, LD}],
      Return[out] (* this outputs a table of all equilibrium
       freq. First giving BEFORE selection freq then AFTER selection freq. *)
     ]
   ]
```

Chapter 3: Stability analysis of the model

Equilibria and stability analysis for *γ*=1 in haplodiploids

Write out dynamics for lethal epistasis:

```
alleleDynamics[1][{s, 1, 1, r}][{{pf, qf, LDf}, {pm, qm, LDm}}] -
   {{pf, qf, LDf}, {pm, qm, LDm}} // Flatten // Simplify
```

```
{-pf + (-2 LDf LDm + LDf s + LDm s - 2 LDm qf s -
      2 LDf qm s + LDf s^2 + LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 +
      pm (1 - 2 LDf (-1 + qm) + (1 + qf + qm - 2 qf qm) s + (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2) +
      pf (1 - 2 pm - 2 LDm (-1 + qf) + 2 pm qf + 2 pm qm - 2 pm qf qm + (1 - 2 pm + qf + qm - 2 qf qm) s +
          (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qm + qf (-1 + 2 qm))) s^2)) /
    (2 (1 - 2 LDf LDm + LDm qf + LDf qm - qf qm + qf s + qm s - 2 qf qm s + LDf s^2 +
          LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 +
          pm (LDf - 2 LDf qm + qf qm + s + (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2) +
          pf (LDm - pm - 2 LDm qf + pm qf + pm qm + qf qm - 2 pm qf qm + s - 2 pm s +
             (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qm + qf (-1 + 2 qm))) s^2))),
```

```
-qf + (-2 LDf LDm + LDf s + LDm s - 2 LDm pf s - 2 LDf pm s + LDf s^2 + LDm s^2 +
     4 LDf LDm s^2 - 2 LDm pf s^2 - 2 LDf pm s^2 +
     qm (1 - 2 LDf (-1 + pm) + (1 + pf + pm - 2 pf pm) s + (pf + pm - 2 pf pm + LDf (-2 + 4 pm)) s^2) +
     qf (1 - 2 LDm (-1 + pf) - 2 qm + 2 pf qm + 2 pm qm - 2 pf pm qm + (1 + pf + pm - 2 pf pm - 2 qm) s +
        (LDm (-2 + 4 pf) + (-pm + pf (-1 + 2 pm)) (-1 + 2 qm)) s^2)) /
   (2 (1 - 2 LDf LDm + LDm qf + LDf qm - qf qm + qf s + qm s - 2 qf qm s + LDf s^2 +
       LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 +
       pm (LDf - 2 LDf qm + qf qm + s + (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2) +
       pf (LDm - pm - 2 LDm qf + pm qf + pm qm + qf qm - 2 pm qf qm + s - 2 pm s +
          (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qm + qf (-1 + 2 qm))) s^2))),
-LDf + ((((LDf + pf qf) (-2 LDm + pm + qm - 2 pm qm + 2 (LDm + pm qm) - (LDm + pm (-1 + qm)) s -
            (LDm + (-1 + pm) qm) s - (LDm + (-1 + pm) (-1 + qm)) (-1 + r) (1 + s)^2) +
        (1 + s) (-(LDf + (-1 + pf) (-1 + qf)) (LDm + pm qm) (-1 + r) (1 + s) +
            (-LDf + qf - pf qf) (LDm + pm qm - (LDm + pm (-1 + qm)) r (1 + s)) +
            (-LDf + pf - pf qf) (LDm + pm qm - (LDm + (-1 + pm) qm) r (1 + s))))
      ((LDf + (-1 + pf) (-1 + qf)) (2 (LDm + (-1 + pm) (-1 + qm)) +
            (1 + s) (-2 LDm + pm + qm - 2 pm qm - (LDm + pm qm) (-1 + r) (1 + s))) +
        (1 + s) (-(LDf + pf qf) (LDm + (-1 + pm) (-1 + qm)) (-1 + r) (1 + s) +
            (-LDf + qf - pf qf) (1 + LDm - pm - qm + pm qm - (LDm + pm (-1 + qm)) r (1 + s)) +
            (-LDf + pf - pf qf) (1 + LDm - pm - qm + pm qm - (LDm + (-1 + pm) qm) r (1 + s)))) -
     (1 + s) (-(LDf + pf (-1 + qf)) (LDm + (-1 + pm) qm) (-1 + r) (1 + s) + (-LDf + qf - pf qf)
          (2 LDm + (-1 + pm) (-1 + qm) + pm qm + (LDm + pm (-1 + qm)) (-1 + r) (1 + s)) +
        (LDf + pf qf) (-LDm + qm - pm qm + (LDm + (-1 + pm) (-1 + qm)) r (1 + s)) +
        (LDf + (-1 + pf) (-1 + qf)) (qm + LDm (-1 + r + r s) + pm qm (-1 + r + r s)))
      ((-LDf + pf - pf qf) (LDm + pm qm + (LDm + pm qm) s + (LDm + (-1 + pm) (-1 + qm)) (1 + s) +
            (LDm + (-1 + pm) qm) (-1 + r) (1 + s)^2) +
        (1 + s) (-(LDf + (-1 + pf) qf) (LDm + pm (-1 + qm)) (-1 + r) (1 + s) +
            (LDf + pf qf) (-LDm + pm - pm qm + (LDm + (-1 + pm) (-1 + qm)) r (1 + s)) +
            (LDf + (-1 + pf) (-1 + qf)) (pm + LDm (-1 + r + r s) + pm qm (-1 + r + r s))))) /
   (4 (1 - 2 LDf LDm + LDm qf + LDf qm - qf qm + qf s + qm s - 2 qf qm s + LDf s^2 +
        LDm s^2 + 4 LDf LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 +
        pm (LDf - 2 LDf qm + qf qm + s + (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2) +
        pf (LDm - pm - 2 LDm qf + pm qf + pm qm + qf qm - 2 pm qf qm + s - 2 pm s +
           (LDm (-2 + 4 qf) + (-1 + 2 pm) (-qm + qf (-1 + 2 qm))) s^2))^2),
                 LDf + pf qf                         LDf + pf qf
-pm + ----------------------------- , ----------------------------- -
       1 + 2 LDf - pf - qf + 2 pf qf   1 + 2 LDf - pf - qf + 2 pf qf
  qm,
-LDm +
  (LDf + LDf^2 - LDf qf +
      (-1 + pf) pf (-1 + qf) qf + LDf pf (-1 + 2 qf)) /
   (1 + 2 LDf - qf + pf (-1 + 2 qf))^2}
```

Find equilibria:

```
sols =
  Solve[Thread[{-pf + (-2 LDf LDm + LDf s + LDm s - 2 LDm qf s - 2 LDf qm s + LDf s^2 + LDm s^2 + 4 LDf
            LDm s^2 - 2 LDm qf s^2 - 2 LDf qm s^2 + pm (1 - 2 LDf (-1 + qm) +
               (1 + qf + qm - 2 qf qm) s + (qf + qm - 2 qf qm + LDf (-2 + 4 qm)) s^2) +
```

$$
\begin{aligned}
&pf \left(1 - 2\, pm - 2\, LDm \left(-1 + qf\right) + 2\, pm\, qf + 2\, pm\, qm - 2\, pm\, qf\, qm + \left(1 - 2\, pm + qf + \right.\right.\\
&\quad \left.\left. qm - 2\, qf\, qm\right) s + \left(LDm \left(-2 + 4\, qf\right) + (-1 + 2\, pm) \left(-qm + qf\, (-1 + 2\, qm)\right)\right) s^2\right) \Big/ \\
&\left(2 \left(1 - 2\, LDf\, LDm + LDm\, qf + LDf\, qm - qf\, qm + qf\, s + qm\, s - 2\, qf\, qm\, s + LDf\, s^2 + \right.\right.\\
&\quad LDm\, s^2 + 4\, LDf\, LDm\, s^2 - 2\, LDm\, qf\, s^2 - 2\, LDf\, qm\, s^2 + \\
&\quad pm \left(LDf - 2\, LDf\, qm + qf\, qm + s + \left(qf + qm - 2\, qf\, qm + LDf\, (-2 + 4\, qm)\right) s^2\right) + \\
&\quad pf \left(LDm - 2\, LDm\, qf + qf\, qm + pm \left(-1 + qf + qm - 2\, qf\, qm\right) + s - 2\, pm\right.\\
&\qquad \left.\left.\left. s + \left(LDm \left(-2 + 4\, qf\right) + (-1 + 2\, pm) \left(-qm + qf\, (-1 + 2\, qm)\right)\right) s^2\right)\right)\right), \\
&-qf + \left(-2\, LDf\, LDm + LDf\, s + LDm\, s - 2\, LDm\, pf\, s - 2\, LDf\, pm\, s + LDf\, s^2 + LDm\, s^2 + \right.\\
&\quad 4\, LDf\, LDm\, s^2 - 2\, LDm\, pf\, s^2 - 2\, LDf\, pm\, s^2 + qm \left(1 - 2\, LDf\, (-1 + pm) + \right.\\
&\qquad \left. \left(1 + pf + pm - 2\, pf\, pm\right) s + \left(pf + pm - 2\, pf\, pm + LDf\, (-2 + 4\, pm)\right) s^2\right) + \\
&\quad qf \left(1 - 2\, LDm \left(-1 + pf\right) - 2\, qm + 2\, pf\, qm + 2\, pm\, qm - 2\, pf\, pm\, qm + \left(1 + pf + pm - \right.\right.\\
&\qquad \left.\left.\left. 2\, pf\, pm - 2\, qm\right) s + \left(LDm \left(-2 + 4\, pf\right) + \left(-pm + pf\, (-1 + 2\, pm)\right) (-1 + 2\, qm)\right) s^2\right)\right) \Big/ \\
&\left(2 \left(1 - 2\, LDf\, LDm + LDm\, qf + LDf\, qm - qf\, qm + qf\, s + qm\, s - 2\, qf\, qm\, s + LDf\, s^2 + \right.\right.\\
&\quad LDm\, s^2 + 4\, LDf\, LDm\, s^2 - 2\, LDm\, qf\, s^2 - 2\, LDf\, qm\, s^2 + \\
&\quad pm \left(LDf - 2\, LDf\, qm + qf\, qm + s + \left(qf + qm - 2\, qf\, qm + LDf\, (-2 + 4\, qm)\right) s^2\right) + \\
&\quad pf \left(LDm - 2\, LDm\, qf + qf\, qm + pm \left(-1 + qf + qm - 2\, qf\, qm\right) + s - 2\, pm\right.\\
&\qquad \left.\left.\left. s + \left(LDm \left(-2 + 4\, qf\right) + (-1 + 2\, pm) \left(-qm + qf\, (-1 + 2\, qm)\right)\right) s^2\right)\right)\right), \\
&-LDf + \left(\left(\left(LDf + pf\, qf\right) \left(-2\, LDm + pm + qm - 2\, pm\, qm + 2\, (LDm + pm\, qm) - (LDm + pm\, (-1 + qm))\, s - \right.\right.\right.\\
&\qquad \left. (LDm + (-1 + pm)\, qm)\, s - (LDm + (-1 + pm)\, (-1 + qm))\, (-1 + r)\, (1 + s)^2\right) + \\
&\quad (1 + s) \left(-\left(LDf + \left(-1 + pf\right) \left(-1 + qf\right)\right) (LDm + pm\, qm)\, (-1 + r)\, (1 + s) + \right.\\
&\qquad \left(-LDf + qf - pf\, qf\right) (LDm + pm\, qm - (LDm + pm\, (-1 + qm))\, r\, (1 + s)) + \\
&\qquad \left.\left. \left(-LDf + pf - pf\, qf\right) (LDm + pm\, qm - (LDm + (-1 + pm)\, qm)\, r\, (1 + s))\right)\right) \\
&\quad \left(\left(LDf + \left(-1 + pf\right) \left(-1 + qf\right)\right) (2\, (LDm + (-1 + pm)\, (-1 + qm)) + (1 + s) \right.\\
&\qquad (-2\, LDm + pm + qm - 2\, pm\, qm - (LDm + pm\, qm)\, (-1 + r)\, (1 + s))) + \\
&\quad (1 + s) \left(-\left(LDf + pf\, qf\right) (LDm + (-1 + pm)\, (-1 + qm))\, (-1 + r)\, (1 + s) + \right.\\
&\qquad \left(-LDf + qf - pf\, qf\right) (1 + LDm - pm - qm + pm\, qm - (LDm + pm\, (-1 + qm))\, r\, (1 + s)) + \\
&\qquad \left.\left. \left(-LDf + pf - pf\, qf\right) (1 + LDm - pm - qm + pm\, qm - (LDm + (-1 + pm)\, qm)\, r\, (1 + s))\right)\right) - \\
&\quad (1 + s) \left(-\left(LDf + pf \left(-1 + qf\right)\right) (LDm + (-1 + pm)\, qm)\, (-1 + r)\, (1 + s) + \right.\\
&\qquad \left(-LDf + qf - pf\, qf\right) (2\, LDm + (-1 + pm)\, (-1 + qm) + \\
&\qquad\quad pm\, qm + (LDm + pm\, (-1 + qm))\, (-1 + r)\, (1 + s)) + \\
&\qquad \left(LDf + pf\, qf\right) (-LDm + qm - pm\, qm + (LDm + (-1 + pm)\, (-1 + qm))\, r\, (1 + s)) + \\
&\qquad \left. \left(LDf + \left(-1 + pf\right) \left(-1 + qf\right)\right) (-LDm + qm - pm\, qm + (LDm + pm\, qm)\, r\, (1 + s))\right) \\
&\quad \left(\left(-LDf + pf - pf\, qf\right) \left(LDm + pm\, qm + (LDm + pm\, qm)\, s + (LDm + (-1 + pm)\, (-1 + qm))\right.\right.\\
&\qquad \left. (1 + s) + (LDm + (-1 + pm)\, qm)\, (-1 + r)\, (1 + s)^2\right) + \\
&\quad (1 + s) \left(-\left(LDf + \left(-1 + pf\right) qf\right) (LDm + pm\, (-1 + qm))\, (-1 + r)\, (1 + s) + \right.\\
&\qquad \left(LDf + pf\, qf\right) (-LDm + pm - pm\, qm + (LDm + (-1 + pm)\, (-1 + qm))\, r\, (1 + s)) + \\
&\qquad \left.\left.\left. \left(LDf + \left(-1 + pf\right) \left(-1 + qf\right)\right) (-LDm + pm - pm\, qm + (LDm + pm\, qm)\, r\, (1 + s))\right)\right)\right) \Big/ \\
&\left(4 \left(1 - 2\, LDf\, LDm + LDm\, qf + LDf\, qm - qf\, qm + qf\, s + qm\, s - 2\, qf\, qm\, s + LDf\, s^2 + \right.\right.\\
&\quad LDm\, s^2 + 4\, LDf\, LDm\, s^2 - 2\, LDm\, qf\, s^2 - 2\, LDf\, qm\, s^2 + \\
&\quad pm \left(LDf - 2\, LDf\, qm + qf\, qm + s + \left(qf + qm - 2\, qf\, qm + LDf\, (-2 + 4\, qm)\right) s^2\right) + \\
&\quad pf \left(LDm - 2\, LDm\, qf + qf\, qm + pm \left(-1 + qf + qm - 2\, qf\, qm\right) + s - 2\, pm\, s + \right.\\
&\qquad \left.\left.\left. \left(LDm \left(-2 + 4\, qf\right) + (-1 + 2\, pm) \left(-qm + qf\, (-1 + 2\, qm)\right)\right) s^2\right)\right)^2\right), \\
&-pm + \frac{LDf + pf\, qf}{1 + 2\, LDf - pf - qf + 2\, pf\, qf}, \frac{LDf + pf\, qf}{1 + 2\, LDf - pf - qf + 2\, pf\, qf} - qm, \\
&-LDm + \\
&\left(LDf^2 + \left(-1 + pf\right) pf \left(-1 + qf\right) qf + LDf \left(1 - qf + pf \left(-1 + 2\, qf\right)\right)\right) \Big/
\end{aligned}
$$

```
      (1 + 2 LDf - qf + pf (-1 + 2 qf))^2} ==
    {0, 0, 0, 0, 0, 0}], {pf, qf, LDf, pm, qm,
  LDm}] // Simplify
```

Solve: Equations may not give solutions for all "solve" variables.

$$\left\{\left\{pf\to\frac{-1+s-2\,qf\,s}{2\,s},\ LDf\to\frac{qf\,\left(1+\left(-1+2\,qf\right)\,s\right)}{2\,s},\ pm\to 0,\ qm\to 0,\ LDm\to 0\right\},\right.$$

$$\left\{pf\to\frac{1}{2}\left(3-2\,qf+\frac{1}{s}\right),\ LDf\to\frac{\left(-1+qf\right)\,\left(-1+\left(-1+2\,qf\right)\,s\right)}{2\,s},\ pm\to 1,\ qm\to 1,\ LDm\to 0\right\},$$

$$\left\{pf\to 0,\ qf\to 0,\ LDf\to 0,\ pm\to 0,\ qm\to 0,\ LDm\to 0\right\},$$

$$\left\{pf\to\frac{-1+s}{2\,s},\ qf\to 0,\ LDf\to 0,\ pm\to 0,\ qm\to 0,\ LDm\to 0\right\},$$

$$\left\{pf\to\frac{1}{2}\left(3+\frac{1}{s}\right),\ qf\to 0,\ LDf\to\frac{1+s}{2\,s},\ pm\to 1,\ qm\to 1,\ LDm\to 0\right\},\ \left\{pf\to\frac{1}{2},\ qf\to\frac{1}{2},\right.$$

$$LDf\to-\frac{1}{4\,s^2}\left(1+s+r\,(1+s)^2+\sqrt{\left(r^2\,(1+s)^4-2\,r\,(1+s)^2\,\left(-1-s+s^2\right)+\left(1+s+s^2\right)^2\right)}\right),$$

$$\left.pm\to\frac{1}{2},\ qm\to\frac{1}{2},\ LDm\to\frac{1}{4}\right\},\ \left\{pf\to\frac{1}{2},\ qf\to\frac{1}{2},\right.$$

$$LDf\to-\frac{1}{4\,s^2}\left(1+s+r\,(1+s)^2-\sqrt{\left(r^2\,(1+s)^4-2\,r\,(1+s)^2\,\left(-1-s+s^2\right)+\left(1+s+s^2\right)^2\right)}\right),$$

$$\left.pm\to\frac{1}{2},\ qm\to\frac{1}{2},\ LDm\to\frac{1}{4}\right\},\ \left\{pf\to-\frac{1}{2\,s},\ qf\to\frac{1}{2},\ LDf\to\frac{1}{4\,s},\ pm\to 0,\ qm\to 0,\ LDm\to 0\right\},$$

$$\left\{pf\to 1+\frac{1}{2\,s},\ qf\to\frac{1}{2},\ LDf\to\frac{1}{4\,s},\ pm\to 1,\ qm\to 1,\ LDm\to 0\right\},$$

$$\left\{pf\to 1,\ qf\to 1,\ LDf\to 0,\ pm\to 1,\ qm\to 1,\ LDm\to 0\right\},$$

$$\left\{pf\to-\frac{1+s}{2\,s},\ qf\to 1,\ LDf\to\frac{1+s}{2\,s},\ pm\to 0,\ qm\to 0,\ LDm\to 0\right\},$$

$$\left.\left\{pf\to\frac{1+s}{2\,s},\ qf\to 1,\ LDf\to 0,\ pm\to 1,\ qm\to 1,\ LDm\to 0\right\}\right\}$$

For systematic exploration add solution for qf

$$\text{sols} = \left\{\left\{\text{pf} \to \frac{-1+s-2\,\text{qf}\,s}{2\,s},\ \text{qf} \to \text{qf},\ \text{LDf} \to \frac{\text{qf}\,\left(1+\left(-1+2\,\text{qf}\right)\,s\right)}{2\,s},\ \text{pm} \to 0,\ \text{qm} \to 0,\ \text{LDm} \to 0\right\},\right.$$

$$\left\{\text{pf} \to \frac{1}{2}\left(3-2\,\text{qf}+\frac{1}{s}\right),\ \text{qf} \to \text{qf},\ \text{LDf} \to \frac{\left(-1+\text{qf}\right)\,\left(-1+\left(-1+2\,\text{qf}\right)\,s\right)}{2\,s},\ \text{pm} \to 1,\ \text{qm} \to 1,\ \text{LDm} \to 0\right\},$$

$$\left\{\text{pf} \to 0,\ \text{qf} \to 0,\ \text{LDf} \to 0,\ \text{pm} \to 0,\ \text{qm} \to 0,\ \text{LDm} \to 0\right\},$$

$$\left\{\text{pf} \to \frac{-1+s}{2\,s},\ \text{qf} \to 0,\ \text{LDf} \to 0,\ \text{pm} \to 0,\ \text{qm} \to 0,\ \text{LDm} \to 0\right\},$$

$$\left\{\text{pf} \to \frac{1}{2}\left(3+\frac{1}{s}\right),\ \text{qf} \to 0,\ \text{LDf} \to \frac{1+s}{2\,s},\ \text{pm} \to 1,\ \text{qm} \to 1,\ \text{LDm} \to 0\right\},\ \left\{\text{pf} \to \frac{1}{2},\ \text{qf} \to \frac{1}{2},\right.$$

$$\text{LDf} \to -\frac{1}{4\,s^2}\left(1+s+r\,(1+s)^2+\sqrt{\left(r^2\,(1+s)^4-2\,r\,(1+s)^2\,\left(-1-s+s^2\right)+\left(1+s+s^2\right)^2\right)}\right),$$

$$\left.\text{pm} \to \frac{1}{2},\ \text{qm} \to \frac{1}{2},\ \text{LDm} \to \frac{1}{4}\right\},\ \left\{\text{pf} \to \frac{1}{2},\ \text{qf} \to \frac{1}{2},\right.$$

$$\text{LDf} \to -\frac{1}{4\,s^2}\left(1+s+r\,(1+s)^2-\sqrt{\left(r^2\,(1+s)^4-2\,r\,(1+s)^2\,\left(-1-s+s^2\right)+\left(1+s+s^2\right)^2\right)}\right),$$

$$\left.\text{pm} \to \frac{1}{2},\ \text{qm} \to \frac{1}{2},\ \text{LDm} \to \frac{1}{4}\right\},\ \left\{\text{pf} \to -\frac{1}{2\,s},\ \text{qf} \to \frac{1}{2},\ \text{LDf} \to \frac{1}{4\,s},\ \text{pm} \to 0,\ \text{qm} \to 0,\ \text{LDm} \to 0\right\},$$

$$\left\{\text{pf} \to 1+\frac{1}{2\,s},\ \text{qf} \to \frac{1}{2},\ \text{LDf} \to \frac{1}{4\,s},\ \text{pm} \to 1,\ \text{qm} \to 1,\ \text{LDm} \to 0\right\},$$

$$\left\{\text{pf} \to 1,\ \text{qf} \to 1,\ \text{LDf} \to 0,\ \text{pm} \to 1,\ \text{qm} \to 1,\ \text{LDm} \to 0\right\},$$

$$\left\{\text{pf} \to -\frac{1+s}{2\,s},\ \text{qf} \to 1,\ \text{LDf} \to \frac{1+s}{2\,s},\ \text{pm} \to 0,\ \text{qm} \to 0,\ \text{LDm} \to 0\right\},$$

$$\left.\left\{\text{pf} \to \frac{1+s}{2\,s},\ \text{qf} \to 1,\ \text{LDf} \to 0,\ \text{pm} \to 1,\ \text{qm} \to 1,\ \text{LDm} \to 0\right\}\right\}$$

$$\Big\{\Big\{pf \to \frac{-1+s-2\,qf\,s}{2\,s},\ qf \to qf,\ LDf \to \frac{qf\,\left(1+\left(-1+2\,qf\right)\,s\right)}{2\,s},\ pm \to 0,\ qm \to 0,\ LDm \to 0\Big\},$$

$$\Big\{pf \to \frac{1}{2}\left(3-2\,qf+\frac{1}{s}\right),\ qf \to qf,\ LDf \to \frac{\left(-1+qf\right)\,\left(-1+\left(-1+2\,qf\right)\,s\right)}{2\,s},\ pm \to 1,\ qm \to 1,\ LDm \to 0\Big\},$$

$$\{pf \to 0,\ qf \to 0,\ LDf \to 0,\ pm \to 0,\ qm \to 0,\ LDm \to 0\},$$

$$\Big\{pf \to \frac{-1+s}{2\,s},\ qf \to 0,\ LDf \to 0,\ pm \to 0,\ qm \to 0,\ LDm \to 0\Big\},$$

$$\Big\{pf \to \frac{1}{2}\left(3+\frac{1}{s}\right),\ qf \to 0,\ LDf \to \frac{1+s}{2\,s},\ pm \to 1,\ qm \to 1,\ LDm \to 0\Big\},\ \Big\{pf \to \frac{1}{2},\ qf \to \frac{1}{2},$$

$$LDf \to -\frac{1}{4\,s^2}\left(1+s+r\,(1+s)^2+\sqrt{r^2\,(1+s)^4-2\,r\,(1+s)^2\,\left(-1-s+s^2\right)+\left(1+s+s^2\right)^2}\right),$$

$$pm \to \frac{1}{2},\ qm \to \frac{1}{2},\ LDm \to \frac{1}{4}\Big\},\ \Big\{pf \to \frac{1}{2},\ qf \to \frac{1}{2},$$

$$LDf \to -\frac{1}{4\,s^2}\left(1+s+r\,(1+s)^2-\sqrt{r^2\,(1+s)^4-2\,r\,(1+s)^2\,\left(-1-s+s^2\right)+\left(1+s+s^2\right)^2}\right),$$

$$pm \to \frac{1}{2},\ qm \to \frac{1}{2},\ LDm \to \frac{1}{4}\Big\},\ \Big\{pf \to -\frac{1}{2\,s},\ qf \to \frac{1}{2},\ LDf \to \frac{1}{4\,s},\ pm \to 0,\ qm \to 0,\ LDm \to 0\Big\},$$

$$\Big\{pf \to 1+\frac{1}{2\,s},\ qf \to \frac{1}{2},\ LDf \to \frac{1}{4\,s},\ pm \to 1,\ qm \to 1,\ LDm \to 0\Big\},$$

$$\{pf \to 1,\ qf \to 1,\ LDf \to 0,\ pm \to 1,\ qm \to 1,\ LDm \to 0\},$$

$$\Big\{pf \to -\frac{1+s}{2\,s},\ qf \to 1,\ LDf \to \frac{1+s}{2\,s},\ pm \to 0,\ qm \to 0,\ LDm \to 0\Big\},$$

$$\Big\{pf \to \frac{1+s}{2\,s},\ qf \to 1,\ LDf \to 0,\ pm \to 1,\ qm \to 1,\ LDm \to 0\Big\}\Big\}$$

Test existence and stability (based on eigenvalues) for all solutions: updated

```
Do[Print[i];
 Print[sols[[i]]];
 Print[xxx = Reduce[0 ≤ sols[[i, 1, 2]] ≤ 1
     && 0 ≤ sols[[i, 2, 2]] ≤ 1
     && -1 / 4 ≤ sols[[i, 3, 2]] ≤ 1 / 4
     && 0 ≤ sols[[i, 4, 2]] ≤ 1
     && 0 ≤ sols[[i, 5, 2]] ≤ 1
     && -1 / 4 ≤ sols[[i, 6, 2]] ≤ 1 / 4
     && 0 ≤ s && 0 < r ≤ 1 / 2 && 0 ≤ qf ≤ 1]];
 If[xxx === False, Print["Does not exist."],
  eig = Eigenvalues[JacobianAllele[1][{s, 1, 1, r}][sols[[i]]]] // Simplify;
  Print["Stability condition: "];
  Print[Reduce[Table[Reduce[-1 ≤ eig[[k]] ≤ 1 && 0 ≤ s && 0 < r ≤ 1 / 2],
     {k, Length[eig]}]]]], {i, Length[sols]}]
```

1

$$\Big\{pf \to \frac{-1+s-2\,qf\,s}{2\,s},\ qf \to qf,\ LDf \to \frac{qf\,\left(1+\left(-1+2\,qf\right)\,s\right)}{2\,s},\ pm \to 0,\ qm \to 0,\ LDm \to 0\Big\}$$

$$0 < r \le \frac{1}{2}\ \&\&\ 0 \le qf < \frac{1}{2}\ \&\&\ s \ge -\frac{1}{-1+2\,qf}$$

Stability condition:

False

2

$$\left\{pf \to \frac{1}{2}\left(3-2\,qf+\frac{1}{s}\right),\ qf \to qf,\ LDf \to \frac{(-1+qf)\,(-1+(-1+2\,qf)\,s)}{2\,s},\ pm \to 1,\ qm \to 1,\ LDm \to 0\right\}$$

$$0<r\le\frac{1}{2}\,\&\&\,\frac{1}{2}<qf\le 1\,\&\&\,s\ge\frac{1}{-1+2\,qf}$$

Stability condition:

False

3

$$\{pf \to 0,\ qf \to 0,\ LDf \to 0,\ pm \to 0,\ qm \to 0,\ LDm \to 0\}$$

$$0<r\le\frac{1}{2}\,\&\&\,s\ge 0\,\&\&\,0\le qf\le 1$$

Stability condition:

$$\left(s==0\,\&\&\,0<r\le\frac{1}{2}\right)\,||\,\left(0<s<-1+\sqrt{2}\,\&\&\,\frac{2\,s+s^2}{1+2\,s+s^2}\le r\le\frac{1}{2}\right)\,||\,\left(s==-1+\sqrt{2}\,\&\&\,r==\frac{1}{2}\right)$$

4

$$\left\{pf \to \frac{-1+s}{2\,s},\ qf \to 0,\ LDf \to 0,\ pm \to 0,\ qm \to 0,\ LDm \to 0\right\}$$

$$0<r\le\frac{1}{2}\,\&\&\,s\ge 1\,\&\&\,0\le qf\le 1$$

Stability condition:

False

5

$$\left\{pf \to \frac{1}{2}\left(3+\frac{1}{s}\right),\ qf \to 0,\ LDf \to \frac{1+s}{2\,s},\ pm \to 1,\ qm \to 1,\ LDm \to 0\right\}$$

False

Does not exist.

6

$$\left\{pf \to \frac{1}{2},\ qf \to \frac{1}{2},\right.$$
$$LDf \to -\frac{1}{4\,s^2}\left(1+s+r\,(1+s)^2+\sqrt{r^2\,(1+s)^4-2\,r\,(1+s)^2\,(-1-s+s^2)+(1+s+s^2)^2}\right),$$
$$\left.pm \to \frac{1}{2},\ qm \to \frac{1}{2},\ LDm \to \frac{1}{4}\right\}$$

False

Does not exist.

7

$$\left\{pf \to \frac{1}{2},\ qf \to \frac{1}{2},\ LDf \to -\frac{1}{4\,s^2}\left(1+s+r\,(1+s)^2-\sqrt{r^2\,(1+s)^4-2\,r\,(1+s)^2\left(-1-s+s^2\right)+\left(1+s+s^2\right)^2}\right),\ pm \to \frac{1}{2},\ qm \to \frac{1}{2},\ LDm \to \frac{1}{4}\right\}$$

$$s > 0\ \&\&\ 0 < r \le \frac{1}{2}\ \&\&\ 0 \le qf \le 1$$

Stability condition:

$$\left(0 < s \le -1+\sqrt{2}\ \&\&\ 0 < r \le \frac{2\,s+s^2}{1+2\,s+s^2}\right)\ ||\ \left(s > -1+\sqrt{2}\ \&\&\ 0 < r \le \frac{1}{2}\right)$$

8

$$\left\{pf \to -\frac{1}{2\,s},\ qf \to \frac{1}{2},\ LDf \to \frac{1}{4\,s},\ pm \to 0,\ qm \to 0,\ LDm \to 0\right\}$$

False

Does not exist.

9

$$\left\{pf \to 1+\frac{1}{2\,s},\ qf \to \frac{1}{2},\ LDf \to \frac{1}{4\,s},\ pm \to 1,\ qm \to 1,\ LDm \to 0\right\}$$

False

Does not exist.

10

$$\{pf \to 1,\ qf \to 1,\ LDf \to 0,\ pm \to 1,\ qm \to 1,\ LDm \to 0\}$$

$$0 < r \le \frac{1}{2}\ \&\&\ s \ge 0\ \&\&\ 0 \le qf \le 1$$

Stability condition:

$$\left(s == 0\ \&\&\ 0 < r \le \frac{1}{2}\right)\ ||\ \left(0 < s < -1+\sqrt{2}\ \&\&\ \frac{2\,s+s^2}{1+2\,s+s^2} \le r \le \frac{1}{2}\right)\ ||\ \left(s == -1+\sqrt{2}\ \&\&\ r == \frac{1}{2}\right)$$

11

$$\left\{pf \to -\frac{1+s}{2\,s},\ qf \to 1,\ LDf \to \frac{1+s}{2\,s},\ pm \to 0,\ qm \to 0,\ LDm \to 0\right\}$$

False

Does not exist.

12

$$\left\{pf \to \frac{1+s}{2\,s},\ qf \to 1,\ LDf \to 0,\ pm \to 1,\ qm \to 1,\ LDm \to 0\right\}$$

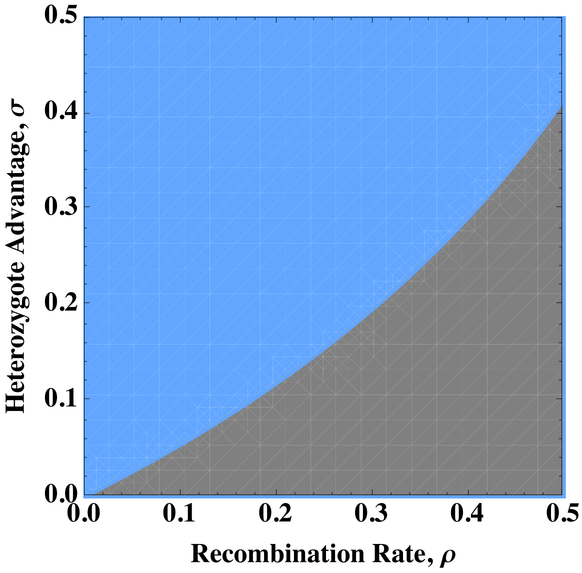
$$0 < r \le \frac{1}{2}\ \&\&\ s \ge 1\ \&\&\ 0 \le qf \le 1$$

Stability condition:

False

This is a plot of the solution for *γ*=1

```
(*PLOT42 HERE*)
xx = RegionPlot[
  {(s == 0 && 0 < r ≤ 1/2) || (0 < s < -1 + √2 && (2 s + s^2)/(1 + 2 s + s^2) ≤ r ≤ 1/2) || (s == -1 + √2 && r == 1/2),
   (0 < s ≤ -1 + √2 && 0 < r ≤ (2 s + s^2)/(1 + 2 s + s^2)) || (s > -1 + √2 && 0 < r ≤ 1/2)}, {r, 0, 0.5},
  {s, 0, 0.5}, FrameLabel → {"Recombination Rate, ρ", "Heterozygote Advantage, σ"},
  PlotRangePadding → None,
  (*PlotLegends→Placed[{"Exclusion","Symmetric coexistence"},{Center,Top}],*)
  PlotStyle → {GrayLevel[0.5], Hue[0.5945945945945946, 0.6166666666666667, 1]},
  BoundaryStyle → {GrayLevel[0.5], Hue[0.5945945945945946, 0.6166666666666667, 1]},
  ImageSize → 300, BaseStyle → {FontSize → 14, FontWeight → Bold},
  FrameStyle → Directive[Black]]
```



```
Export[ToString[NotebookDirectory[]] <> "analytic-limit-lethal-haplodiploid.pdf", xx]
```

Stability of monomorphic equilibria

This is the condition for local stability of exclusion. updated

```
eig = Eigenvalues[JacobianAllele[1][{s, γ1, γ2, r}][
    {pf → 0, qf → 0, LDf → 0, pm → 0, qm → 0, LDm → 0}]] /. s → w - 1 // Simplify
```

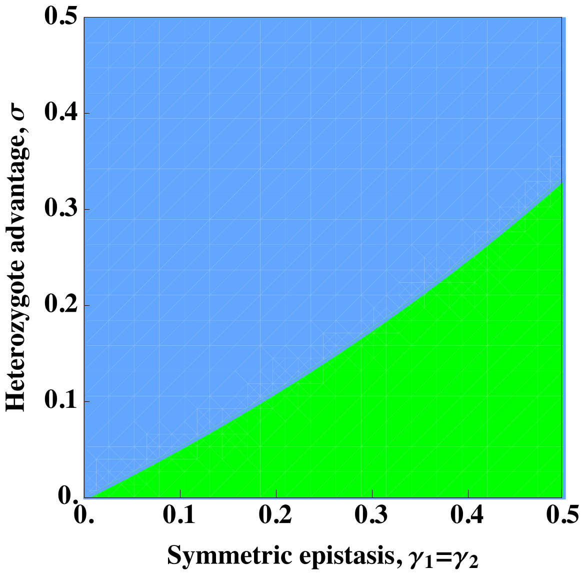
$$\left\{-\frac{1}{4} w \left((-1+r)\, w+\sqrt{(-1+r)\,\left(-8+(-1+r)\, w^2\right)}\right),\right.$$
$$\frac{1}{4} w \left(w-r\, w+\sqrt{(-1+r)\,\left(-8+(-1+r)\, w^2\right)}\right),\ \frac{1}{4}\left(w-\sqrt{w}\ \sqrt{8+w-8\,\gamma 1}\right),$$
$$\left.\frac{1}{4}\left(w+\sqrt{w}\ \sqrt{8+w-8\,\gamma 1}\right),\ \frac{1}{4}\left(w-\sqrt{w}\ \sqrt{8+w-8\,\gamma 2}\right),\ \frac{1}{4}\left(w+\sqrt{w}\ \sqrt{8+w-8\,\gamma 2}\right)\right\}$$

```
Reduce[
 Table[Reduce[-1 ≤ eig[[k]] ≤ 1 && √2 > w > 1 && (-1 + w^2)/w^2 < r ≤ 1 / 2 && 0 < γ2 < 1 && 0 < γ1 < 1],
  {k, Length[eig]}]]
```

$$1 < w < \sqrt{2} \;\&\&\; \frac{-2+2w}{w} \le \gamma 2 < 1 \;\&\&\; \frac{-2+2w}{w} \le \gamma 1 < 1 \;\&\&\; \frac{-1+w^2}{w^2} < r \le \frac{1}{2}$$

Plot solution

```
xx = RegionPlot[{γ > 2 s/(1 + s) && (-2 + 2 (s + 1))/(s + 1) ≤ γ ≤ (8 + s + 1)/8, γ < 2 s/(1 + s)}, {γ, 0, 0.5}, {s, 0, 0.5},
  FrameLabel → {"Symmetric epistasis, γ1=γ2", "Heterozygote advantage, σ"},
  PlotRangePadding → None, (*PlotLegends→
   Placed[{"Exclusion or tristability","Symmetric coexistence"},{Center,Top}],*)
  PlotStyle → {Green, Hue[0.5945945945945946, 0.6166666666666667, 1]},
  BoundaryStyle → {Green, Hue[0.5945945945945946, 0.6166666666666667, 1]},
  ImageSize → 300, BaseStyle → {FontSize → 14, FontWeight → Bold},
  FrameStyle → Directive[Black], PlotStyle → Automatic,
  FrameTicks → {{Range[0, 1, 0.1], None}, {Range[0, 1, 0.1], None}}]
```



```
Export[ToString[NotebookDirectory[]] <> "analytic-limit-symmetric-epistasis.pdf", xx]
```

```
legendxx = SwatchLegend[{Green, Hue[0.5945945945945946, 0.6166666666666667, 1]},
  {"Exclusion or Tristability", "Symmetric Coexistence"},
  LabelStyle -> {14, Bold}, LegendLayout → {"Row", 1}]
```

🟩 Exclusion or Tristability 🟦 Symmetric Coexistence

Equilibria and stability for γ=1 in diploids

Write out dynamics

```
alleleDynamics[2][{w - 1, 1, 1, r}][{pf, qf, LDf}] - {pf, qf, LDf} // Flatten // Simplify
```

```
{-pf + (pf^2 (1 - (-1 + qf)^2 + 2 (-1 + qf) qf (-1 + w)^2 - w) +
      LDf (w (-1 - 2 qf (-1 + w) + w) + LDf (1 - 4 w + 2 w^2)) +
      pf (w - 2 LDf (-2 + w) w + 2 qf (-1 + w) w - 2 qf^2 (-1 + w) w + 2 LDf qf (1 - 4 w + 2 w^2))) /
    (1 - 2 LDf^2 + qf^2 (1 - 2 w) + pf^2 (1 + 2 qf - 2 qf^2 + 4 (-1 + qf) qf (-1 + w)^2 - 2 w) +
      2 LDf (-1 + w)^2 + 4 LDf^2 (-1 + w)^2 + 2 qf (-1 + LDf - 2 LDf (-1 + w)^2 + w) +
      2 pf (-1 + LDf - 2 LDf qf + qf^2 + 2 (-LDf + qf + 2 LDf qf - qf^2) (-1 + w)^2 + w)),
 -qf + (LDf^2 (1 - 4 w + 2 w^2) + LDf (w (-1 + 4 qf + w - 2 qf w) + 2 pf (qf + w - 4 qf w - w^2 + 2 qf w^2)) +
      qf (w - qf w - 2 pf (1 + qf (-2 + w) - w) w + pf^2 (-2 (-1 + w) w + qf (1 - 4 w + 2 w^2)))) /
    (1 - 2 LDf^2 + qf^2 (1 - 2 w) + pf^2 (1 + 2 qf - 2 qf^2 + 4 (-1 + qf) qf (-1 + w)^2 - 2 w) +
      2 LDf (-1 + w)^2 + 4 LDf^2 (-1 + w)^2 + 2 qf (-1 + LDf - 2 LDf (-1 + w)^2 + w) +
      2 pf (-1 + LDf - 2 LDf qf + qf^2 + 2 (-LDf + qf + 2 LDf qf - qf^2) (-1 + w)^2 + w)),
 -LDf + (-w^2 (LDf^2 (-2 + w) + (-1 + pf) qf (-1 + pf + qf + pf qf (-2 + w) - pf w) +
         LDf (-1 + pf - qf (-3 + w) + 2 pf qf (-2 + w) - pf w + r w))
       (LDf^2 (-2 + w) + pf (-1 + qf) (-1 + pf + qf + pf qf (-2 + w) - qf w) +
         LDf (-1 + qf + pf (3 + 2 qf (-2 + w) - w) - qf w + r w)) +
      (pf qf (pf (-1 + w) - w) (qf (-1 + w) - w) + LDf^2 (-1 + w)^2 +
         LDf (pf (2 qf (-1 + w) - w) (-1 + w) + w (qf + w - qf w - r w)))
       ((-1 + pf) (-1 + qf) (1 + pf (-1 + w)) (1 + qf (-1 + w)) + LDf^2 (-1 + w)^2 +
         LDf (2 + pf (2 + 2 qf (-1 + w) - w) (-1 + w) - 2 w + w^2 - r w^2 - qf (2 - 3 w + w^2)))) /
    (1 - 2 LDf^2 + qf^2 (1 - 2 w) + pf^2 (1 + 2 qf - 2 qf^2 + 4 (-1 + qf) qf (-1 + w)^2 - 2 w) +
       2 LDf (-1 + w)^2 + 4 LDf^2 (-1 + w)^2 + 2 qf (-1 + LDf - 2 LDf (-1 + w)^2 + w) +
       2 pf (-1 + LDf - 2 LDf qf + qf^2 + 2 (-LDf + qf + 2 LDf qf - qf^2) (-1 + w)^2 + w))^2}
```

Try to find solutions:

```
sols = Solve[Thread[
   {-pf + (pf^2 (-(-1 + qf)^2 - s + 2 (-1 + qf) qf s^2) + LDf (-(-1 + 2 qf) s (1 + s) + LDf (-1 + 2 s^2)) +
          pf (-(1 + s) (-1 - 2 qf s + 2 qf^2 s) + LDf (2 - 2 s^2 + qf (-2 + 4 s^2))))) /
       (1 - 2 LDf^2 + 2 LDf s^2 + 4 LDf^2 s^2 - qf^2 (1 + 2 s) + 2 qf (LDf + s - 2 LDf s^2) +
          pf^2 (-1 + 2 qf - 2 qf^2 - 2 s + 4 (-1 + qf) qf s^2) +
          2 pf (LDf - 2 LDf qf + qf^2 + s + 2 (-LDf + qf + 2 LDf qf - qf^2) s^2)), -qf +
      (qf^2 (-(-1 + pf)^2 - s + 2 (-1 + pf) pf s^2) + LDf (-(-1 + 2 pf) s (1 + s) + LDf (-1 + 2 s^2)) +
          qf (-(1 + s) (-1 - 2 pf s + 2 pf^2 s) + LDf (2 - 2 s^2 + pf (-2 + 4 s^2))))) /
       (1 - 2 LDf^2 + 2 LDf s^2 + 4 LDf^2 s^2 - qf^2 (1 + 2 s) + 2 qf (LDf + s - 2 LDf s^2) +
          pf^2 (-1 + 2 qf - 2 qf^2 - 2 s + 4 (-1 + qf) qf s^2) +
          2 pf (LDf - 2 LDf qf + qf^2 + s + 2 (-LDf + qf + 2 LDf qf - qf^2) s^2)),
     -LDf + (-(1 + s) (LDf^2 (-1 + s) + (-1 + pf) qf (-1 + qf - pf qf - pf s + pf qf s) +
                LDf (-1 + r + qf (2 + 2 pf (-1 + s) - s) - pf s + r s)) ((LDf + (-1 + pf) (-1 + qf))
                 (1 + s) (-LDf + pf - pf qf + (LDf + pf qf) r (1 + s)) + (-LDf + pf - pf qf)
                 (LDf + pf + pf (-1 + qf) + (LDf + pf qf) s + (LDf + (-1 + pf) qf) (-1 + r) (1 + s)^2)) +
          (LDf^2 s^2 + pf qf (-1 + (-1 + pf) s) (-1 + (-1 + qf) s) - LDf (-1 + (-2 + pf + qf) s +
                   (-1 + pf + qf - 2 pf qf) s^2 + r (1 + s)^2)) (LDf^2 s^2 + (-1 + pf) (-1 + qf) (1 + pf s)
                 (1 + qf s) + LDf (1 + qf s + s^2 - qf s^2 - r (1 + s)^2 + pf s (1 - s + 2 qf s)))) /
       (1 - 2 LDf^2 + 2 LDf s^2 + 4 LDf^2 s^2 - qf^2 (1 + 2 s) + 2 qf (LDf + s - 2 LDf s^2) +
           pf^2 (-1 + 2 qf - 2 qf^2 - 2 s + 4 (-1 + qf) qf s^2) + 2 pf (LDf - 2 LDf qf + qf^2 +
                s + 2 (-LDf + qf + 2 LDf qf - qf^2) s^2))^2} == {0, 0, 0}], {pf, qf, LDf}]
```

```
$Aborted
```

This is not solvable with Mathematica's methods.

Try analysis of the internal equilibrium with $p_f = q_f$

```
alleleDynamics[2][{s, 1, 1, r}][{pf, pf, LDf}] - {pf, pf, LDf} // Flatten // Simplify
```

```
{-(((-1 + 2 pf) (LDf^2 (-1 + 2 s^2) + (-1 + pf) pf (pf - s - 2 pf s^2 + pf^2 (-1 + 2 s^2)) +
          LDf (s (1 + s) + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2)))) /
      (1 + 4 pf s + pf^3 (4 - 8 s^2) + LDf^2 (-2 + 4 s^2) + pf^4 (-2 + 4 s^2) + pf^2 (-2 - 4 s + 4 s^2) +
        2 LDf (s^2 + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2)))),
  -(((-1 + 2 pf) (LDf^2 (-1 + 2 s^2) + (-1 + pf) pf (pf - s - 2 pf s^2 + pf^2 (-1 + 2 s^2)) +
          LDf (s (1 + s) + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2)))) /
      (1 + 4 pf s + pf^3 (4 - 8 s^2) + LDf^2 (-2 + 4 s^2) + pf^4 (-2 + 4 s^2) + pf^2 (-2 - 4 s + 4 s^2) +
        2 LDf (s^2 + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2)))),
  -LDf + (-(1 + s)^2 (LDf^2 (-1 + s) + (-1 + pf) pf (-1 + pf + pf^2 (-1 + s) - pf s) +
           LDf (-1 + r - 2 pf (-1 + s) + 2 pf^2 (-1 + s) + r s))^2 +
       (LDf^2 s^2 + (-1 + pf)^2 (1 + pf s)^2 + LDf (1 - 2 pf (-1 + s) s + s^2 + 2 pf^2 s^2 - r (1 + s)^2))
        (LDf^2 s^2 + pf^2 (-1 + (-1 + pf) s)^2 -
          LDf (-1 + 2 (-1 + pf) s + (-1 + 2 pf - 2 pf^2) s^2 + r (1 + s)^2))) /
     (1 + 4 pf s + pf^3 (4 - 8 s^2) + LDf^2 (-2 + 4 s^2) + pf^4 (-2 + 4 s^2) + pf^2 (-2 - 4 s + 4 s^2) +
        2 LDf (s^2 + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2)))^2}
```

```
sols =
 Solve[Thread[{-(((-1 + 2 pf) (LDf^2 (-1 + 2 s^2) + (-1 + pf) pf (pf - s - 2 pf s^2 + pf^2 (-1 + 2 s^2)) +
          LDf (s (1 + s) + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2))))/
       (1 + 4 pf s + pf^3 (4 - 8 s^2) + LDf^2 (-2 + 4 s^2) + pf^4 (-2 + 4 s^2) +
         pf^2 (-2 - 4 s + 4 s^2) + 2 LDf (s^2 + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2)))),
     -(((-1 + 2 pf) (LDf^2 (-1 + 2 s^2) + (-1 + pf) pf (pf - s - 2 pf s^2 + pf^2 (-1 + 2 s^2)) +
          LDf (s (1 + s) + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2))))/
       (1 + 4 pf s + pf^3 (4 - 8 s^2) + LDf^2 (-2 + 4 s^2) + pf^4 (-2 + 4 s^2) +
         pf^2 (-2 - 4 s + 4 s^2) + 2 LDf (s^2 + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2)))),
     -LDf + (-(1 + s)^2 (LDf^2 (-1 + s) + (-1 + pf) pf (-1 + pf + pf^2 (-1 + s) - pf s) +
            LDf (-1 + r - 2 pf (-1 + s) + 2 pf^2 (-1 + s) + r s))^2 +
         (LDf^2 s^2 + (-1 + pf)^2 (1 + pf s)^2 + LDf (1 - 2 pf (-1 + s) s + s^2 + 2 pf^2 s^2 - r (1 + s)^2))
          (LDf^2 s^2 + pf^2 (-1 + (-1 + pf) s)^2 -
            LDf (-1 + 2 (-1 + pf) s + (-1 + 2 pf - 2 pf^2) s^2 + r (1 + s)^2)))/
       (1 + 4 pf s + pf^3 (4 - 8 s^2) + LDf^2 (-2 + 4 s^2) + pf^4 (-2 + 4 s^2) + pf^2 (-2 - 4 s + 4 s^2) +
          2 LDf (s^2 + pf (2 - 4 s^2) + pf^2 (-2 + 4 s^2)))^2} == {0, 0}], {pf, LDf}] // Simplify
```

sols =

$$
\begin{aligned}
&\Big\{\Big\{pf \to \frac{1}{2},\ qf \to \frac{1}{2},\ LDf \to \Big(2\times 2^{1/3} + 12\times 2^{1/3}\,r + 24\times 2^{1/3}\,r\,s - 6\times 2^{1/3}\,s^2 - 12\times 2^{1/3}\,r\,s^2 - 48\times 2^{1/3}\\
&\quad r\,s^3 + 6\times 2^{1/3}\,s^4 - 24\times 2^{1/3}\,r\,s^4 - \Big(2 - 9\,r - 18\,r\,s - 9\,s^2 + 9\,r\,s^2 + 36\,r\,s^3 + 9\,s^4 +\\
&\quad 18\,r\,s^4 + \frac{1}{16\,384}\Big(\sqrt{\Big(268\,435\,456\,\big(2 - 9\,s^2 + 9\,s^4 + 9\,r\,(1+s)^2\,(-1+2\,s^2)\big)^2 +}\\
&\quad \overline{\big(-256 + 768\,(-1+2\,s^2)\,(1 - 2\,s^2 + 8\,r\,(1+s)^2)\big)^3\Big)}\Big)\Big)^{1/3} +\\
&\quad 2^{2/3}\Big(2 - 9\,r - 18\,r\,s - 9\,s^2 + 9\,r\,s^2 + 36\,r\,s^3 + 9\,s^4 + 18\,r\,s^4 + \frac{1}{16\,384}\\
&\quad \Big(\sqrt{\Big(268\,435\,456\,\big(2 - 9\,s^2 + 9\,s^4 + 9\,r\,(1+s)^2\,(-1+2\,s^2)\big)^2 +}\\
&\quad \overline{\big(-256 + 768\,(-1+2\,s^2)\,(1 - 2\,s^2 + 8\,r\,(1+s)^2)\big)^3\Big)}\Big)\Big)^{2/3}\Big)\Big/\\
&\quad \Big(12\,(-1+2\,s^2)\,\Big(2 - 9\,r - 18\,r\,s - 9\,s^2 + 9\,r\,s^2 + 36\,r\,s^3 + 9\,s^4 + 18\,r\,s^4 +\\
&\quad \frac{1}{16\,384}\Big(\sqrt{\Big(268\,435\,456\,\big(2 - 9\,s^2 + 9\,s^4 + 9\,r\,(1+s)^2\,(-1+2\,s^2)\big)^2 +}\\
&\quad \overline{\big(-256 + 768\,(-1+2\,s^2)\,(1 - 2\,s^2 + 8\,r\,(1+s)^2)\big)^3\Big)}\Big)\Big)^{1/3}\Big)\Big\},\ \Big\{pf \to \frac{1}{2},\ qf \to \frac{1}{2},\\
&LDf \to \frac{1}{24\,(-1+2\,s^2)}\Big(-2 + \Big(2\times 2^{1/3}\,\big(1 + i\sqrt{3}\big)\,\big(-1 + 3\,s^2 - 3\,s^4 + 6\,r\,(1+s)^2\,(-1+2\,s^2)\big)\Big)\Big/\\
&\quad \Big(2 - 9\,r - 18\,r\,s - 9\,s^2 + 9\,r\,s^2 + 36\,r\,s^3 + 9\,s^4 + 18\,r\,s^4 +\\
&\quad \frac{1}{16\,384}\Big(\sqrt{\Big(268\,435\,456\,\big(2 - 9\,s^2 + 9\,s^4 + 9\,r\,(1+s)^2\,(-1+2\,s^2)\big)^2 +}\\
&\quad \overline{\big(-256 + 768\,(-1+2\,s^2)\,(1 - 2\,s^2 + 8\,r\,(1+s)^2)\big)^3\Big)}\Big)\Big)^{1/3} +\\
&\quad i\,2^{2/3}\,\big(i + \sqrt{3}\big)\,\Big(2 - 9\,r - 18\,r\,s - 9\,s^2 + 9\,r\,s^2 + 36\,r\,s^3 + 9\,s^4 + 18\,r\,s^4 +
\end{aligned}
$$

$$\frac{1}{16384}\left(\sqrt{\left(268435456\left(2-9s^2+9s^4+9r(1+s)^2\left(-1+2s^2\right)\right)^2+\right.}\right.$$

$$\left.\left.\left(-256+768\left(-1+2s^2\right)\left(1-2s^2+8r(1+s)^2\right)\right)^3\right)\right)\Bigg)^{1/3}\Bigg)\Bigg\},\ \left\{pf\to\frac{1}{2},\ qf\to\frac{1}{2},\right.$$

$$LDf\to-\frac{1}{24\left(-1+2s^2\right)}\left(2+\left(2\,i\,2^{1/3}\left(i+\sqrt{3}\right)\left(-1+3s^2-3s^4+6r(1+s)^2\left(-1+2s^2\right)\right)\right)\Big/\right.$$

$$\Bigg(2-9r-18rs-9s^2+9rs^2+36rs^3+9s^4+18rs^4+$$

$$\frac{1}{16384}\left(\sqrt{\left(268435456\left(2-9s^2+9s^4+9r(1+s)^2\left(-1+2s^2\right)\right)^2+\right.}\right.$$

$$\left.\left.\left(-256+768\left(-1+2s^2\right)\left(1-2s^2+8r(1+s)^2\right)\right)^3\right)\right)\Bigg)^{1/3}+$$

$$2^{2/3}\left(1+i\sqrt{3}\right)\Bigg(2-9r-18rs-9s^2+9rs^2+36rs^3+9s^4+18rs^4+$$

$$\frac{1}{16384}\left(\sqrt{\left(268435456\left(2-9s^2+9s^4+9r(1+s)^2\left(-1+2s^2\right)\right)^2+\right.}\right.$$

$$\left.\left.\left(-256+768\left(-1+2s^2\right)\left(1-2s^2+8r(1+s)^2\right)\right)^3\right)\right)\Bigg)^{1/3}\Bigg)\Bigg\},$$

$$\Bigg\{pf\to-\frac{1}{2\left(r(1+s)^2\left(-1+2s^2\right)+s\left(2+5s-s^3\right)\right)}\Bigg(-2s-5s^2+s^4-r(1+s)^2\left(-1+2s^2\right)+$$

$$\sqrt{\left(s^2\left(-2+s+s^2\right)^2+r^2(1+s)^2\left(1-4s-4s^2+8s^3+4s^4\right)+\right.}$$

$$\left.2rs\left(-2+3s+12s^2+s^3-6s^4-2s^5\right)\right)+s\sqrt{\left(s^2\left(-2+s+s^2\right)^2+\right.}$$

$$\left.r^2(1+s)^2\left(1-4s-4s^2+8s^3+4s^4\right)+2rs\left(-2+3s+12s^2+s^3-6s^4-2s^5\right)\right)\Bigg),$$

$$qf\to-\frac{1}{2\left(r(1+s)^2\left(-1+2s^2\right)+s\left(2+5s-s^3\right)\right)}\Bigg(-2s-5s^2+s^4-r(1+s)^2\left(-1+2s^2\right)+$$

$$\sqrt{\left(s^2\left(-2+s+s^2\right)^2+r^2(1+s)^2\left(1-4s-4s^2+8s^3+4s^4\right)+\right.}$$

$$\left.2rs\left(-2+3s+12s^2+s^3-6s^4-2s^5\right)\right)+s\sqrt{\left(s^2\left(-2+s+s^2\right)^2+\right.}$$

$$\left.r^2(1+s)^2\left(1-4s-4s^2+8s^3+4s^4\right)+2rs\left(-2+3s+12s^2+s^3-6s^4-2s^5\right)\right)\Bigg),$$

$$LDf\to\frac{s^3(2+s)\left(r(1+s)^2-s(2+s)\right)}{\left(r(1+s)^2\left(-1+2s^2\right)+s\left(2+5s-s^3\right)\right)^2}\Bigg\},\ \Bigg\{pf\to$$

$$\frac{1}{2\left(r(1+s)^2\left(-1+2s^2\right)+s\left(2+5s-s^3\right)\right)}$$

$$\Bigg(2s+5s^2-s^4+r(1+s)^2\left(-1+2s^2\right)+$$

$$\sqrt{\left(s^2\left(-2+s+s^2\right)^2+r^2(1+s)^2\left(1-4s-4s^2+8s^3+4s^4\right)+\right.}$$

$$\left.2rs\left(-2+3s+12s^2+s^3-6s^4-2s^5\right)\right)+s\sqrt{\left(s^2\left(-2+s+s^2\right)^2+\right.}$$

$$\left.r^2(1+s)^2\left(1-4s-4s^2+8s^3+4s^4\right)+2rs\left(-2+3s+12s^2+s^3-6s^4-2s^5\right)\right)\Bigg),$$

$$qf\to\frac{1}{2\left(r(1+s)^2\left(-1+2s^2\right)+s\left(2+5s-s^3\right)\right)}\Bigg(2s+5s^2-s^4+r(1+s)^2\left(-1+2s^2\right)+$$

$$\sqrt{\left(s^2\left(-2+s+s^2\right)^2+r^2(1+s)^2\left(1-4s-4s^2+8s^3+4s^4\right)+\right.}$$

$$\left.2rs\left(-2+3s+12s^2+s^3-6s^4-2s^5\right)\right)+s\sqrt{\left(s^2\left(-2+s+s^2\right)^2+\right.}$$

$$\left.r^2(1+s)^2\left(1-4s-4s^2+8s^3+4s^4\right)+2rs\left(-2+3s+12s^2+s^3-6s^4-2s^5\right)\right)\Bigg),$$

$$\texttt{LDf} \to \frac{s^3\,(2+s)\,\left(r\,(1+s)^2 - s\,(2+s)\right)}{\left(r\,(1+s)^2\,\left(-1+2\,s^2\right) + s\,\left(2+5\,s-s^3\right)\right)^2}\}\};$$

Check whether the last two yield the coordinates of the asymmetric-coexistence eq.

$$\frac{1}{2\,\left(r\,(1+s)^2\,\left(-1+2\,s^2\right)+s\,\left(2+5\,s-s^3\right)\right)}\left(2\,s+5\,s^2-s^4+r\,(1+s)^2\,\left(-1+2\,s^2\right)+\sqrt{\left(s^2\,\left(-2+s+s^2\right)^2+r^2\,(1+s)^2\,\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)+2\,r\,s\,\left(-2+3\,s+12\,s^2+s^3-6\,s^4-2\,s^5\right)\right)}+s\,\sqrt{\left(s^2\,\left(-2+s+s^2\right)^2+r^2\,(1+s)^2\,\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)+2\,r\,s\,\left(-2+3\,s+12\,s^2+s^3-6\,s^4-2\,s^5\right)\right)}\right)\;\texttt{/. \{r → 0.5, s → 0.1\} // N}$$

```
0.142524
```

$$-\frac{1}{2\,\left(r\,(1+s)^2\,\left(-1+2\,s^2\right)+s\,\left(2+5\,s-s^3\right)\right)}\left(-2\,s-5\,s^2+s^4-r\,(1+s)^2\,\left(-1+2\,s^2\right)+\sqrt{\left(s^2\,\left(-2+s+s^2\right)^2+r^2\,(1+s)^2\,\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)+2\,r\,s\,\left(-2+3\,s+12\,s^2+s^3-6\,s^4-2\,s^5\right)\right)}+s\,\sqrt{\left(s^2\,\left(-2+s+s^2\right)^2+r^2\,(1+s)^2\,\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)+2\,r\,s\,\left(-2+3\,s+12\,s^2+s^3-6\,s^4-2\,s^5\right)\right)}\right)\;\texttt{/. \{r → 0.5, s → 0.26\} // N}$$

```
-0.0265612
```

```
Round[stableEquilibriaHaplotype[2][{0.1, 1, 1, 0.25}], 10^-6] // N
```

```
{1., 1., {{0.319404, 0.180596, 0.180596}}, {{0.5, 0.5, 0.069404}}}
```

Yes, they do.

Try to do stability analysis - unsuccessful.

```
Do[Print[i];
Print[sols⟦i⟧];
 TimeConstrained[
  Print[xxx = Reduce[0 ≤ sols⟦i, 1, 2⟧ ≤ 1
      && 0 ≤ sols⟦i, 2, 2⟧ ≤ 1
      && -1 / 4 ≤ sols⟦i, 3, 2⟧ ≤ 1 / 4 && √2 - 1 ≥ s > 0 && 0 < r ≤ 1 / 2]];
  If[xxx === False, Print["Does not exist."],
   eig = Eigenvalues[JacobianAllele[2][{s, 1, 1, r}][sols[[i]]]] // Simplify;
   Print["Stability condition: "];
   Print[Reduce[Table[Reduce[eig⟦k⟧ ≤ 1 && 0 ≤ s && 0 < r ≤ 1 / 2], {k, Length[eig]}]]]],
  120, Print["Took too long to evaluate"]], {i, Length[sols]}]
```

Check when the coordinates of the equilibrium pass 0 & 1; this could be a potential criterion.

$$\text{Solve}\Big[\frac{1}{2\left(r\,(1+s)^2\left(-1+2\,s^2\right)+s\left(2+5\,s-s^3\right)\right)}\Big(2\,s+5\,s^2-s^4+r\,(1+s)^2\left(-1+2\,s^2\right)+\sqrt{\left(s^2\left(-2+s+s^2\right)^2+r^2\,(1+s)^2\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)+2\,r\,s\left(-2+3\,s+12\,s^2+s^3-6\,s^4-2\,s^5\right)\right)}+s\sqrt{\left(s^2\left(-2+s+s^2\right)^2+r^2\,(1+s)^2\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)+2\,r\,s\left(-2+3\,s+12\,s^2+s^3-6\,s^4-2\,s^5\right)\right)}\Big)=\!=1,\ r\Big]\ //\ \text{Simplify}$$

$$\left\{\left\{r\to\frac{s\,(2+s)}{(1+s)^2}\right\},\left\{r\to\frac{s\left(-2-3\,s+s^2+s^3\right)}{(1+s)^2\left(-1+2\,s^2\right)}\right\}\right\}$$

$$\text{Solve}\Big[-\frac{1}{2\left(r\,(1+s)^2\left(-1+2\,s^2\right)+s\left(2+5\,s-s^3\right)\right)}\Big(-2\,s-5\,s^2+s^4-r\,(1+s)^2\left(-1+2\,s^2\right)+\sqrt{\left(s^2\left(-2+s+s^2\right)^2+r^2\,(1+s)^2\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)+2\,r\,s\left(-2+3\,s+12\,s^2+s^3-6\,s^4-2\,s^5\right)\right)}+s\sqrt{\left(s^2\left(-2+s+s^2\right)^2+r^2\,(1+s)^2\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)+2\,r\,s\left(-2+3\,s+12\,s^2+s^3-6\,s^4-2\,s^5\right)\right)}\Big)=\!=0,\ r\Big]\ //\ \text{Simplify}$$

$$\left\{\left\{r\to\frac{s\,(2+s)}{(1+s)^2}\right\},\left\{r\to\frac{s\left(-2-3\,s+s^2+s^3\right)}{(1+s)^2\left(-1+2\,s^2\right)}\right\}\right\}$$

These are the criteria for existence of the “asymmetric coexistence” equilibrium.

Guess limit of stability from existence conditions above.

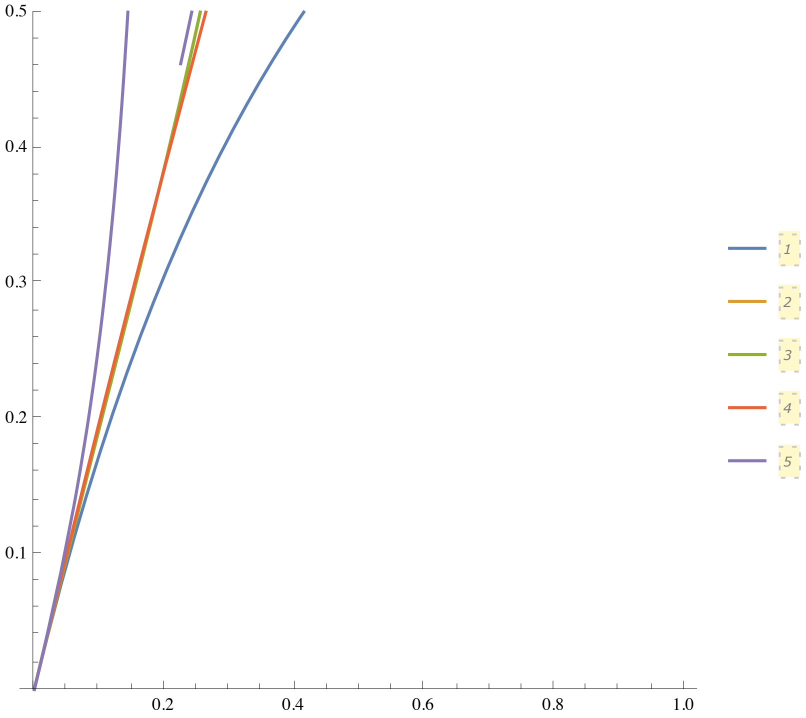
Plot possible conditions and see which ones make most sense.

$$\mathtt{Plot}\Big[\Big\{\frac{s\,(2+s)}{(1+s)^2},\ \frac{s\left(-2-3\,s+s^2+s^3\right)}{(1+s)^2\left(-1+2\,s^2\right)},\ \frac{-2\,s-3\,s^2+s^3+s^4}{-1-2\,s+s^2+4\,s^3+2\,s^4},$$

$$\frac{2\,s+5\,s^2-9\,s^4+2\,s^6}{(1+s)^2\left(-1+2\,s^2\right)^2}-2\,\sqrt{2}\,\sqrt{-\frac{-4\,s^5-8\,s^6+3\,s^7+11\,s^8+6\,s^9+s^{10}}{(1+s)^4\left(-1+2\,s^2\right)^4}}\,,$$

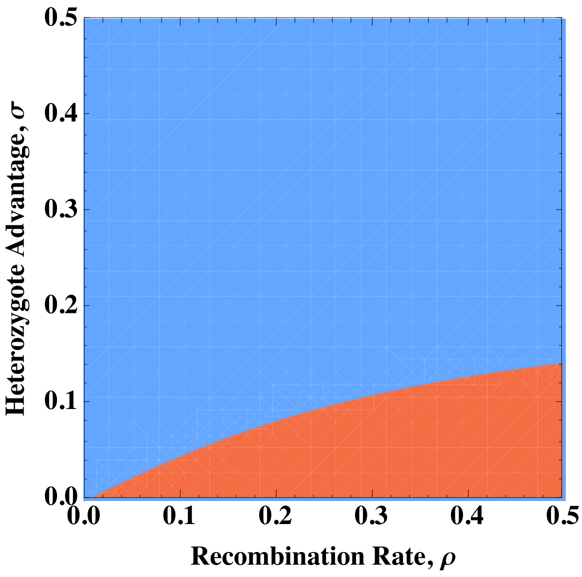
$$\frac{2\,s-3\,s^2-12\,s^3-s^4+6\,s^5+2\,s^6}{(1+s)^2\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)}+2\,\sqrt{-\frac{-8\,s^5-16\,s^6-2\,s^7+10\,s^8+6\,s^9+s^{10}}{(1+s)^4\left(1-4\,s-4\,s^2+8\,s^3+4\,s^4\right)^2}}\Big\},$$

```
{s, 0, 1}, PlotLegends → Automatic, PlotRange → {0, 0.5}, AspectRatio → 1]
```



Plot solution:

```
xx = RegionPlot[
  {(2 s - 3 s^2 - 12 s^3 - s^4 + 6 s^5 + 2 s^6)/((1 + s)^2 (1 - 4 s - 4 s^2 + 8 s^3 + 4 s^4)) + 2 Sqrt[-(-8 s^5 - 16 s^6 - 2 s^7 + 10 s^8 + 6 s^9 + s^10)/((1 + s)^4 (1 - 4 s - 4 s^2 + 8 s^3 + 4 s^4)^2)] < r && s < 0.15,
   (2 s - 3 s^2 - 12 s^3 - s^4 + 6 s^5 + 2 s^6)/((1 + s)^2 (1 - 4 s - 4 s^2 + 8 s^3 + 4 s^4)) + 2 Sqrt[-(-8 s^5 - 16 s^6 - 2 s^7 + 10 s^8 + 6 s^9 + s^10)/((1 + s)^4 (1 - 4 s - 4 s^2 + 8 s^3 + 4 s^4)^2)] > r ||
    s > 0.15}, {r, 0, 0.5}, {s, 0, 0.5},
  FrameLabel → {"Recombination Rate, ρ", "Heterozygote Advantage, σ"},
  PlotRangePadding → None, (*PlotLegends→
   Placed[{"Asymmetric coexistence","Symmetric coexistence"},{Center,Top}],*)
  ImageSize → 300, PlotStyle → {RGBColor[244 / 255, 109 / 255, 67 / 255],
    Hue[0.5945945945945946, 0.6166666666666667, 1]},
  BoundaryStyle → {RGBColor[244 / 255, 109 / 255, 67 / 255],
    Hue[0.5945945945945946, 0.6166666666666667, 1]},
  BaseStyle → {FontSize → 14, FontWeight → Bold}, FrameStyle → Directive[Black]]
```



```
legendxx = SwatchLegend[{GrayLevel[0.5], RGBColor[244 / 255, 109 / 255, 67 / 255],
    Hue[0.5945945945945946, 0.6166666666666667, 1]},
  {"Exclusion", "Asymmetric Coexistence", "Symmetric Coexistence"},
  LabelStyle -> {14, Bold}, LegendLayout → {"Row", 1}]
```

⬛ **Exclusion** 🟧 **Asymmetric Coexistence** 🟦 **Symmetric Coexistence**

```
Export[ToString[NotebookDirectory[]] <> "analytic-limit-lethal-diploid.pdf", xx]
Export[ToString[NotebookDirectory[]] <> "analytic-limit-lethal-legend.pdf", legendxx]
```

```
/Users/nando/Documents/finnish_hybrid_ants/results/analytic-limit-lethal-diploid.pdf
/Users/nando/Documents/finnish_hybrid_ants/results/analytic-limit-lethal-legend.pdf
```

Coordinates of SLPs

```
alleleDynamics[2][{s, 1, 1, r}][{pf, 0, 0}] - {pf, 0, 0} // Flatten // Simplify
```

$$\left\{\frac{\text{pf}\,(\text{s}-\text{pf}\,(1+2\,\text{s}))}{1+\text{pf}+2\,\text{pf}\,\text{s}},\ 0,\ 0\right\}$$

```
Solve[pf (s - pf (1 + 2 s))/(1 + pf + 2 pf s) == 0, pf] // Simplify
```

$$\left\{\{\text{pf}\to 0\},\ \left\{\text{pf}\to \frac{\text{s}}{1+2\,\text{s}}\right\}\right\}$$

No stable monomorphic or SLP equilibria

These are all monomorphic & SLP equilibria: updated

```
sols = {{pf → 0, qf → 0, LDf → 0}, {pf → 1, qf → 1, LDf → 0},
   {pf → 0, qf → s/(1 + 2 s), LDf → 0}, {pf → s/(1 + 2 s), qf → 0, LDf → 0}};
Do[Print[i];
 Print[sols[[i]]];
 Print[xxx = Reduce[0 ≤ sols[[i, 1, 2]] ≤ 1
     && 0 ≤ sols[[i, 2, 2]] ≤ 1
     && -1 / 4 ≤ sols[[i, 3, 2]] ≤ 1 / 4]];
 If[xxx === False, Print["Does not exist."],
  eig = Eigenvalues[JacobianAllele[2][{s, 1, 1, r}][sols[[i]]]] // Simplify;
  Print["Stability condition: "];
  Print[Reduce[Table[Reduce[-1 ≤ eig[[k]] ≤ 1 && 0 < s && 0 < r ≤ 1 / 2],
      {k, Length[eig]}]]]], {i, Length[sols]}]
```

```
1

{pf → 0, qf → 0, LDf → 0}

True

Stability condition:

False

2

{pf → 1, qf → 1, LDf → 0}

True

Stability condition:

False

3
```

$$\left\{\mathtt{pf} \to 0,\ \mathtt{qf} \to \frac{s}{1+2\,s},\ \mathtt{LDf} \to 0\right\}$$

```
s ≤ -1 || s ≥ 0

Stability condition:

False

4
```

$$\left\{\mathtt{pf} \to \frac{s}{1+2\,s},\ \mathtt{qf} \to 0,\ \mathtt{LDf} \to 0\right\}$$

```
s ≤ -1 || s ≥ 0

Stability condition:

False
```

Chapter 4: An extension to multiple loci

Main Functions

Function to generates gametes from diploid parents for four loci

```
CalculateHap[gen_, rho12_, rho23_, rho34_, rho21_, rho32_, rho43_] :=
 Module[{i1, i2, i3, i4, i1m, i2m, i3m, i4m,
   i1f, i2f, i3f, i4f, indicem, indicef, indice, hap},
  hap = Table[0, {i, 1, 16}];
  For [i1m = 0, i1m ≤ 1, i1m++,
   For[i2m = 0, i2m ≤ 1, i2m++,
     For [i3m = 0, i3m ≤ 1, i3m++,
       For[i4m = 0, i4m ≤ 1, i4m++,
         For[ i1f = 0, i1f ≤ 1, i1f++,
           For[ i2f = 0, i2f ≤ 1, i2f++,
             For[ i3f = 0, i3f ≤ 1, i3f++,
               For[i4f = 0, i4f ≤ 1, i4f++,
                 indicem = 8 * i1m + 4 * i2m + 2 * i3m + i4m;
                 indicef = 8 * i1f + 4 * i2f + 2 * i3f + i4f;
```

```
indice = 16 * indicem + indicef;
i1 = i1m + i1f;
i2 = i2m + i2f;
i3 = i3m + i3f;
i4 = i4m + i4f;
    If[i1 == 1 && (i2 == 1 || i3 == 1 || i4 == 1),
         If [(i4 ≠ 1 && i3 ≠ 1),
              hap[[indicem + 1]] =
   hap[[indicem + 1]] + rho21 * gen[[indice + 1]] / 2;
              hap[[indicef + 1]] = hap[[indicef + 1]] +
    rho21 * gen[[indice + 1]] / 2;
              indicem = 8 * i1m + 4 * i2f + 2 * i3f + i4f;
              indicef = 8 * i1f + 4 * i2m + 2 * i3m + i4m;
              hap[[indicem + 1]] =
   hap[[indicem + 1]] + rho12 * gen[[indice + 1]] / 2;
              hap[[indicef + 1]] = hap[[indicef + 1]] +
    rho12 * gen[[indice + 1]] / 2,
          If[(i4 ≠ 1),
               hap[[indicem + 1]] =
    hap[[indicem + 1]] + rho21 * rho32 * gen[[indice + 1]] / 2;
               hap[[indicef + 1]] = hap[[indicef + 1]] +
     rho21 * rho32 * gen[[indice + 1]] / 2;
               indicem = 8 * i1m + 4 * i2f + 2 * i3f + i4f;
               indicef = 8 * i1f + 4 * i2m + 2 * i3m + i4m;
               hap[[indicem + 1]] =
    hap[[indicem + 1]] + rho12 * rho32 * gen[[indice + 1]] / 2;
               hap[[indicef + 1]] = hap[[indicef + 1]] +
     rho12 * rho32 * gen[[indice + 1]] / 2;
               indicem = 8 * i1m + 4 * i2m + 2 * i3f + i4f;
               indicef = 8 * i1f + 4 * i2f + 2 * i3m + i4m;
               hap[[indicem + 1]] =
    hap[[indicem + 1]] + rho23 * rho21 * gen[[indice + 1]] / 2;
               hap[[indicef + 1]] = hap[[indicef + 1]] +
     rho23 * rho21 * gen[[indice + 1]] / 2;
               indicem = 8 * i1m + 4 * i2f + 2 * i3m + i4m;
               indicef = 8 * i1f + 4 * i2m + 2 * i3f + i4f;
               hap[[indicem + 1]] =
    hap[[indicem + 1]] + rho23 * rho12 * gen[[indice + 1]] / 2;
               hap[[indicef + 1]] = hap[[indicef + 1]] +
     rho23 * rho12 * gen[[indice + 1]] / 2,
           hap[[indicem + 1]] = hap[[indicem + 1]] +
     rho21 * rho32 * rho43 * gen[[indice + 1]] / 2;
           hap[[indicef + 1]] = hap[[indicef + 1]] +
     rho21 * rho32 * rho43 * gen[[indice + 1]] / 2;
           indicem = 8 * i1m + 4 * i2f + 2 * i3f + i4f;
           indicef = 8 * i1f + 4 * i2m + 2 * i3m + i4m;
           hap[[indicem + 1]] =
```

```
                                   hap[[indicem + 1]] + rho12 * rho32 * rho43 * gen[[indice + 1]] / 2;
                                         hap[[indicef + 1]] = hap[[indicef + 1]] +
                                    rho12 * rho32 * rho43 * gen[[indice + 1]] / 2;
                                         indicem = 8 * i1m + 4 * i2m + 2 * i3f + i4f;
                                         indicef = 8 * i1f + 4 * i2f + 2 * i3m + i4m;
                                         hap[[indicem + 1]] =
                                   hap[[indicem + 1]] + rho23 * rho21 * rho43 * gen[[indice + 1]] / 2;
                                         hap[[indicef + 1]] = hap[[indicef + 1]] +
                                    rho23 * rho21 * rho43 * gen[[indice + 1]] / 2;
                                         indicem = 8 * i1m + 4 * i2f + 2 * i3m + i4m;
                                         indicef = 8 * i1f + 4 * i2m + 2 * i3f + i4f;
                                         hap[[indicem + 1]] =
                                   hap[[indicem + 1]] + rho23 * rho12 * rho43 * gen[[indice + 1]] / 2;
                                         hap[[indicef + 1]] = hap[[indicef + 1]] +
                                    rho23 * rho12 * rho43 * gen[[indice + 1]] / 2;
                                         indicem = 8 * i1m + 4 * i2m + 2 * i3m + i4f;
                                         indicef = 8 * i1f + 4 * i2f + 2 * i3f + i4m;
                                         hap[[indicem + 1]] =
                                   hap[[indicem + 1]] + rho34 * rho32 * rho21 * gen[[indice + 1]] / 2;
                                         hap[[indicef + 1]] = hap[[indicef + 1]] +
                                    rho34 * rho32 * rho21 * gen[[indice + 1]] / 2;
                                         indicem = 8 * i1m + 4 * i2f + 2 * i3f + i4m;
                                         indicef = 8 * i1f + 4 * i2m + 2 * i3m + i4f;
                                         hap[[indicem + 1]] =
                                   hap[[indicem + 1]] + rho12 * rho32 * rho34 * gen[[indice + 1]] / 2;
                                         hap[[indicef + 1]] = hap[[indicef + 1]] +
                                    rho12 * rho32 * rho34 * gen[[indice + 1]] / 2;
                                         indicem = 8 * i1m + 4 * i2m + 2 * i3f + i4m;
                                         indicef = 8 * i1f + 4 * i2f + 2 * i3m + i4f;
                                         hap[[indicem + 1]] =
                                   hap[[indicem + 1]] + rho23 * rho21 * rho34 * gen[[indice + 1]] / 2;
                                         hap[[indicef + 1]] = hap[[indicef + 1]] +
                                    rho23 * rho21 * rho34 * gen[[indice + 1]] / 2;
                                         indicem = 8 * i1m + 4 * i2f + 2 * i3m + i4f;
                                         indicef = 8 * i1f + 4 * i2m + 2 * i3f + i4m;
                                         hap[[indicem + 1]] =
                                   hap[[indicem + 1]] + rho12 * rho23 * rho34 * gen[[indice + 1]] / 2;
                                         hap[[indicef + 1]] = hap[[indicef + 1]] +
                                    rho12 * rho23 * rho34 * gen[[indice + 1]] / 2]
                                     ],
                                    If[ (i2 == 1 && (i3 == 1 || i4 == 1)),
                                         If [(i4 ≠ 1),
                                              hap[[indicem + 1]] =
                                    hap[[indicem + 1]] + rho32 * gen[[indice + 1]] / 2;
                                              hap[[indicef + 1]] = hap[[indicef + 1]] +
                                     rho32 * gen[[indice + 1]] / 2;
                                              indicem = 8 * i1m + 4 * i2m + 2 * i3f + i4f;
```

```
                indicef = 8 * i1f + 4 * i2f + 2 * i3m + i4m;
                hap[[indicem + 1]] =
      hap[[indicem + 1]] + rho23 * gen[[indice + 1]] / 2;
                hap[[indicef + 1]] = hap[[indicef + 1]] +
       rho23 * gen[[indice + 1]] / 2,
            hap[[indicem + 1]] = hap[[indicem + 1]] +
       rho43 * rho32 * gen[[indice + 1]] / 2;
            hap[[indicef + 1]] = hap[[indicef + 1]] +
       rho43 * rho32 * gen[[indice + 1]] / 2;
            indicem = 8 * i1m + 4 * i2m + 2 * i3f + i4f;
            indicef = 8 * i1f + 4 * i2f + 2 * i3m + i4m;
            hap[[indicem + 1]] =
      hap[[indicem + 1]] + rho23 * rho43 * gen[[indice + 1]] / 2;
            hap[[indicef + 1]] = hap[[indicef + 1]] +
       rho23 * rho43 * gen[[indice + 1]] / 2;
            indicem = 8 * i1m + 4 * i2m + 2 * i3m + i4f;
            indicef = 8 * i1f + 4 * i2f + 2 * i3f + i4m;
            hap[[indicem + 1]] =
      hap[[indicem + 1]] + rho34 * rho32 * gen[[indice + 1]] / 2;
            hap[[indicef + 1]] = hap[[indicef + 1]] +
       rho34 * rho32 * gen[[indice + 1]] / 2;
            indicem = 8 * i1m + 4 * i2m + 2 * i3f + i4m;
            indicef = 8 * i1f + 4 * i2f + 2 * i3m + i4f;
            hap[[indicem + 1]] =
      hap[[indicem + 1]] + rho23 * rho34 * gen[[indice + 1]] / 2;
            hap[[indicef + 1]] = hap[[indicef + 1]] +
       rho23 * rho34 * gen[[indice + 1]] / 2;
            ],
       If[(i3 == 1 && i4 == 1),
             hap[[indicem + 1]] =
       hap[[indicem + 1]] + rho43 * gen[[indice + 1]] / 2;
             hap[[indicef + 1]] = hap[[indicef + 1]] +
        rho43 * gen[[indice + 1]] / 2;
             indicem = 8 * i1m + 4 * i2m + 2 * i3f + i4f;
             indicef = 8 * i1f + 4 * i2f + 2 * i3f + i4m;
             hap[[indicem + 1]] =
       hap[[indicem + 1]] + rho34 * gen[[indice + 1]] / 2;
             hap[[indicef + 1]] = hap[[indicef + 1]] +
        rho34 * gen[[indice + 1]] / 2,
         hap[[indicem + 1]] = hap[[indicem + 1]] +
        gen[[indice + 1]] / 2;
         hap[[indicef + 1]] = hap[[indicef + 1]] +
        gen[[indice + 1]] / 2
     ];
   ];
 ];
];
```

```
                ];
               (*];*)
              ];
            ];
          ];
        ];
      ];
    ];
    Return[hap]
  ]
```

Define the dynamics of the system with fertilization, followed by selection and then recombination. Only tracks the haplotype frequncies. Takes arbitrary fitness table for males and females

```
Dynamics4L[hapM4L_, gamF4L_, ρ12_, ρ23_, ρ34_, ρ21_, ρ32_, ρ43_, SelMale_,
  SelFemale_] := Module[{gemM4L, meanFitnessMales4L, malesAfterSelection4L,
   femaleGenotypesAfterSelectionBeforeNormalization4L, indicem, indicef, indice,
   i1, i2, i3, i4, meanFitnessFemales4L, femaleGenotypesAfterSelection4L, gemF4L},
  gemM4L = gamF4L;
  meanFitnessMales4L = Total[SelMale gamF4L];
  malesAfterSelection4L = SelMale gamF4L / meanFitnessMales4L;
  femaleGenotypesAfterSelectionBeforeNormalization4L = Table[0, 256];
  Do[
   indicem = 8 * i1m + 4 * i2m + 2 * i3m + i4m;
   indicef = 8 * i1f + 4 * i2f + 2 * i3f + i4f;
   indice = 16 * indicem + indicef;
   i1 = i1m + i1f;
   i2 = i2m + i2f;
   i3 = i3m + i3f;
   i4 = i4m + i4f;
   femaleGenotypesAfterSelectionBeforeNormalization4L[[indice + 1]] =
    SelFemale[[indice + 1]] * gamF4L[[indicef + 1]] * hapM4L[[indicem + 1]],
   {i1m, 0, 1}, {i2m, 0, 1}, {i3m, 0, 1}, {i4m, 0, 1}, {i1f, 0, 1},
   {i2f, 0, 1}, {i3f, 0, 1}, {i4f, 0, 1}];
  meanFitnessFemales4L = Total[femaleGenotypesAfterSelectionBeforeNormalization4L];
  femaleGenotypesAfterSelection4L =
   femaleGenotypesAfterSelectionBeforeNormalization4L / meanFitnessFemales4L;
  gemF4L = CalculateHap[femaleGenotypesAfterSelection4L,
    ρ12, ρ23, ρ34, ρ21, ρ32, ρ43];
  Return[{malesAfterSelection4L, gemF4L}]
 ]
```

The pairwise case: 2 independent DMIs

Define the fitness table for males

```
selectionMatrixMales4L =
 Table[(1 - Boole[(i1 == 0 && i2 == 1)] * ϵ"02") * (1 - Boole[(i1 == 1 && i2 == 0)] * ϵ"20")
    (1 - Boole[(i3 == 0 && i4 == 1)] * η"02") * (1 - Boole[(i3 == 1 && i4 == 0)] * η"20"),
   {i1, 0, 1}, {i2, 0, 1}, {i3, 0, 1}, {i4, 0, 1}] // Flatten
```

```
{1, 1 - η02, 1 - η20, 1, 1 - ϵ02, (1 - ϵ02) (1 - η02), (1 - ϵ02) (1 - η20), 1 - ϵ02,
 1 - ϵ20, (1 - ϵ20) (1 - η02), (1 - ϵ20) (1 - η20), 1 - ϵ20, 1, 1 - η02, 1 - η20, 1}
```

Define the fitness table for females

```
selectionMatrixFemales4L = Table[0, 256];
Do[
 indicem = 8 * i1m + 4 * i2m + 2 * i3m + i4m;
 indicef = 8 * i1f + 4 * i2f + 2 * i3f + i4f;
 indice = 16 * indicem + indicef;
 i1 = i1m + i1f;
 i2 = i2m + i2f;
 i3 = i3m + i3f;
 i4 = i4m + i4f;
 selectionMatrixFemales4L[[indice + 1]] = 1 * (1 + s1) ^ (Boole[i1 == 1] + Boole[i2 == 1]) *
    (1 + s2) ^ (Boole[i3 == 1] + Boole[i4 == 1]) * (1 - Boole[i2 - i1 == 1] * ϵ"01") *
    (1 - Boole[i1 - i2 == 1] * ϵ"10") * (1 - Boole[i1 == 0 && i2 == 2] * ϵ"02") * (1 - Boole[i1 == 2 &&
          i2 == 0] * ϵ"20") * (1 - Boole[i1 == 1 && i2 == 1] * ϵ"11") * (1 - Boole[i4 - i3 == 1] *
       η"01") * (1 - Boole[i3 - i4 == 1] * η"10") * (1 - Boole[i3 == 0 && i4 == 2] * η"02") *
    (1 - Boole[i3 == 2 && i4 == 0] * η"20") * (1 - Boole[i3 == 1 && i4 == 1] * η"11"), {i1m, 0, 1},
 {i2m, 0, 1}, {i3m, 0, 1}, {i4m, 0, 1}, {i1f, 0, 1}, {i2f, 0, 1}, {i3f, 0, 1}, {i4f, 0, 1}]
```

```
hapM4L = {h1, h2, h3, h4, h5, h6, h7, h8, h9, h10, h11, h12, h13, h14, h15, h16};
```

```
gamF4L = {g1, g2, g3, g4, g5, g6, g7, g8, g9, g10, g11, g12, g13, g14, g15, g16};
```

Display in which order the haplotypes are calculated

```
Do[Print[i1, i2, i3, i4], {i1, 0, 1}, {i2, 0, 1}, {i3, 0, 1}, {i4, 0, 1}]
```

```
0000

0001

0010

0011

0100

0101

0110

0111

1000

1001

1010

1011

1100

1101

1110

1111
```

Test for the dynamics for the second pair of loci

Check if the dynamics obtained matches with the 2 locus case define previously

```
StartCondf = {g1, g2, g3, g4, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0};
StartCondm = {h1, h2, h3, h4, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0};

test = Dynamics4L[StartCondm, StartCondf, ρ12, ρ23, ρ34,
     ρ21, ρ32, ρ43, selectionMatrixMales4L, selectionMatrixFemales4L] /.
    {η"01" → 0, η"10" → 0, η"11" → 0} // FullSimplify // Together;

$Aborted

claudiaversion = haplotypeDynamicsX[1][{s2, η"02", η"20", ρ34}][
   {{g1, g2, g3, g4}, {h1, h2, h3, h4}}] // FullSimplify;

claudiaversion[[2]] - test[[1, 1 ;; 4]] // FullSimplify

{0, 0, 0, 0}

claudiaversion[[1]] - test[[2, 1 ;; 4]] // FullSimplify

{0, 0, 0, 0}
```

Test for the dynamics for the first pair of loci

Check if the dynamics obtained matches with the 2 locus case define previously

```
StartCondf = {g1, 0, 0, 0, g2, 0, 0, 0, g3, 0, 0, 0, g4, 0, 0, 0};
StartCondm = {h1, 0, 0, 0, h2, 0, 0, 0, h3, 0, 0, 0, h4, 0, 0, 0};

test = Dynamics4L[StartCondm, StartCondf, ρ12,
     ρ23, ρ34, selectionMatrixMales4L, selectionMatrixFemales4L] /.
    {ϵ"01" → 0, ϵ"10" → 0, ϵ"11" → 0} // FullSimplify // Together;

claudiaversion = haplotypeDynamicsX[1][{s1, ϵ"02", ϵ"20", ρ12}][
   {{g1, g2, g3, g4}, {h1, h2, h3, h4}}] // FullSimplify;
```

```
claudiaversion[[2]] -
  {test[[1, 1]], test[[1, 5]], test[[1, 9]], test[[1, 13]]} // Simplify
```

```
{0, 0, 0, 0}
```

```
claudiaversion[[1]] - {test[[2, 1]], test[[2, 5]], test[[2, 9]], test[[2, 13]]} //
 FullSimplify
```

```
{0, 0, 0, 0}
```

```
Dynamic4LGen = Dynamics4L[gamF4L, hapM4L, ρ12, ρ23, ρ34,
   ρ21, ρ32, ρ43, selectionMatrixMales4L, selectionMatrixFemales4L];
```

```
Jac4LGen = D[Dynamic4LGen, {{g1, g2, g3, g4, g5, g6, g7, g8, g9, g10, g11, g12, g13, g14,
     g15, g16, h1, h2, h3, h4, h5, h6, h7, h8, h9, h10, h11, h12, h13, h14, h15, h16}}];
```

All heterozygote advantage are equal and epistasis is lethal

```
param = {s1 → s, s2 → s, ϵ"01" → 0, ϵ"10" → 0, ϵ"02" → 1,
   ϵ"20" -> 1, ϵ"11" → 0, η"01" → 0, η"10" → 0, η"02" → 1, η"20" -> 1, η"11" → 0};
```

```
SimplerDym = Dynamic4LGen /. param;
```

Define the Jacobian Matrix

```
Jac4LGen =
  D[Flatten[SimplerDym], {{g1, g2, g3, g4, g5, g6, g7, g8, g9, g10, g11, g12, g13, g14,
     g15, g16, h1, h2, h3, h4, h5, h6, h7, h8, h9, h10, h11, h12, h13, h14, h15, h16}}];
```

First case exclusion: 0000 haplotype

```
exclusion =
 {g1, g2, g3, g4, g5, g6, g7, g8, g9, g10, g11, g12, g13, g14, g15, g16, h1, h2, h3, h4,
    h5, h6, h7, h8, h9, h10, h11, h12, h13, h14, h15, h16} -> {1, 0, 0, 0, 0, 0, 0,
    0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0} // Thread
```

```
{g1 → 1, g2 → 0, g3 → 0, g4 → 0, g5 → 0, g6 → 0, g7 → 0, g8 → 0, g9 → 0, g10 → 0, g11 → 0,
 g12 → 0, g13 → 0, g14 → 0, g15 → 0, g16 → 0, h1 → 1, h2 → 0, h3 → 0, h4 → 0, h5 → 0, h6 → 0,
 h7 → 0, h8 → 0, h9 → 0, h10 → 0, h11 → 0, h12 → 0, h13 → 0, h14 → 0, h15 → 0, h16 → 0}
```

```
{g1 → 1, g2 → 0, g3 → 0, g4 → 0, g5 → 0, g6 → 0, g7 → 0, g8 → 0, g9 → 0, g10 → 0, g11 → 0,
 g12 → 0, g13 → 0, g14 → 0, g15 → 0, g16 → 0, h1 → 1, h2 → 0, h3 → 0, h4 → 0, h5 → 0, h6 → 0,
 h7 → 0, h8 → 0, h9 → 0, h10 → 0, h11 → 0, h12 → 0, h13 → 0, h14 → 0, h15 → 0, h16 → 0}
```

```
{g1 → 1, g2 → 0, g3 → 0, g4 → 0, g5 → 0, g6 → 0, g7 → 0, g8 → 0, g9 → 0, g10 → 0, g11 → 0,
 g12 → 0, g13 → 0, g14 → 0, g15 → 0, g16 → 0, h1 → 1, h2 → 0, h3 → 0, h4 → 0, h5 → 0, h6 → 0,
 h7 → 0, h8 → 0, h9 → 0, h10 → 0, h11 → 0, h12 → 0, h13 → 0, h14 → 0, h15 → 0, h16 → 0}
```

```
JacAtEcl = Jac4LGen /. {s → ω - 1} /. exclusion // Simplify
```

```
{{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
  0, 0, 0, 0, 0, 0, -1, 0, 0, 0, 0, 0, 0, 0, 0, -1, 0, 0, -1},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
```

$$\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0\},$$

$$\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0\},$$

$$\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0\},$$

$$\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0\},$$

$$\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1\},$$

$$\Big\{0, -\frac{\omega}{2}, -\frac{\omega}{2}, \frac{1}{2}(-2+\rho43)\,\omega^2, -\frac{\omega}{2}, \frac{1}{2}(-2+\rho23\,\rho34+\rho32\,\rho43)\,\omega^2, \frac{1}{2}(-2+\rho32)\,\omega^2,$$

$$\frac{1}{2}(-2+\rho32\,\rho43)\,\omega^3, -\frac{\omega}{2}, \frac{1}{2}(-2+\rho21\,\rho23\,\rho34+\rho12\,\rho32\,\rho34+\rho12\,\rho23\,\rho43+\rho21\,\rho32\,\rho43)\,\omega^2,$$

$$\frac{1}{2}(-2+\rho12\,\rho23+\rho21\,\rho32)\,\omega^2, \frac{1}{2}(-2+\rho12\,\rho23\,\rho43+\rho21\,\rho32\,\rho43)\,\omega^3, \frac{1}{2}(-2+\rho21)\,\omega^2,$$

$$\frac{1}{2}(-2+\rho21\,\rho23\,\rho34+\rho21\,\rho32\,\rho43)\,\omega^3, \frac{1}{2}(-2+\rho21\,\rho32)\,\omega^3, \frac{1}{2}(-2+\rho21\,\rho32\,\rho43)\,\omega^4,$$

$$0, -\frac{\omega}{2}, -\frac{\omega}{2}, \frac{1}{2}(-2+\rho43)\,\omega^2, -\frac{\omega}{2}, \frac{1}{2}(-2+\rho23\,\rho34+\rho32\,\rho43)\,\omega^2, \frac{1}{2}(-2+\rho32)\,\omega^2,$$

$$\frac{1}{2}(-2+\rho32\,\rho43)\,\omega^3, -\frac{\omega}{2}, \frac{1}{2}(-2+\rho21\,\rho23\,\rho34+\rho12\,\rho32\,\rho34+\rho12\,\rho23\,\rho43+\rho21\,\rho32\,\rho43)\,\omega^2,$$

$$\frac{1}{2}(-2+\rho12\,\rho23+\rho21\,\rho32)\,\omega^2, \frac{1}{2}(-2+\rho12\,\rho23\,\rho43+\rho21\,\rho32\,\rho43)\,\omega^3, \frac{1}{2}(-2+\rho21)\,\omega^2,$$

$$\frac{1}{2}(-2+\rho21\,\rho23\,\rho34+\rho21\,\rho32\,\rho43)\,\omega^3, \frac{1}{2}(-2+\rho21\,\rho32)\,\omega^3, \frac{1}{2}(-2+\rho21\,\rho32\,\rho43)\,\omega^4\Big\},$$

$$\Big\{0, \frac{\omega}{2}, 0, \frac{\rho34\,\omega^2}{2}, 0, \frac{1}{2}(\rho32\,\rho34+\rho23\,\rho43)\,\omega^2, 0, \frac{1}{2}\rho32\,\rho34\,\omega^3, 0,$$

$$\frac{1}{2}(\rho12\,\rho23\,\rho34+\rho21\,\rho32\,\rho34+\rho21\,\rho23\,\rho43+\rho12\,\rho32\,\rho43)\,\omega^2, 0,$$

$$\frac{1}{2}(\rho12\,\rho23+\rho21\,\rho32)\,\rho34\,\omega^3, 0, \frac{1}{2}\rho21\,(\rho32\,\rho34+\rho23\,\rho43)\,\omega^3, 0,$$

$$\frac{1}{2}\rho21\,\rho32\,\rho34\,\omega^4, 0, \frac{\omega}{2}, 0, \frac{\rho34\,\omega^2}{2}, 0, \frac{1}{2}(\rho32\,\rho34+\rho23\,\rho43)\,\omega^2, 0,$$

$$\frac{1}{2}\rho32\,\rho34\,\omega^3, 0, \frac{1}{2}(\rho12\,\rho23\,\rho34+\rho21\,\rho32\,\rho34+\rho21\,\rho23\,\rho43+\rho12\,\rho32\,\rho43)\,\omega^2, 0,$$

$$\frac{1}{2}(\rho12\,\rho23+\rho21\,\rho32)\,\rho34\,\omega^3, 0, \frac{1}{2}\rho21\,(\rho32\,\rho34+\rho23\,\rho43)\,\omega^3, 0, \frac{1}{2}\rho21\,\rho32\,\rho34\,\omega^4\Big\},$$

$$\Big\{0, 0, \frac{\omega}{2}, \frac{\rho34\,\omega^2}{2}, 0, 0, \frac{\rho23\,\omega^2}{2}, \frac{1}{2}\rho23\,\rho34\,\omega^3, 0, 0, \frac{1}{2}(\rho21\,\rho23+\rho12\,\rho32)\,\omega^2,$$

$$\frac{1}{2}(\rho21\,\rho23+\rho12\,\rho32)\,\rho34\,\omega^3, 0, 0, \frac{1}{2}\rho21\,\rho23\,\omega^3, \frac{1}{2}\rho21\,\rho23\,\rho34\,\omega^4, 0, 0,$$

$$\frac{\omega}{2}, \frac{\rho34\,\omega^2}{2}, 0, 0, \frac{\rho23\,\omega^2}{2}, \frac{1}{2}\rho23\,\rho34\,\omega^3, 0, 0, \frac{1}{2}(\rho21\,\rho23+\rho12\,\rho32)\,\omega^2,$$

$$\frac{1}{2}(\rho21\,\rho23+\rho12\,\rho32)\,\rho34\,\omega^3, 0, 0, \frac{1}{2}\rho21\,\rho23\,\omega^3, \frac{1}{2}\rho21\,\rho23\,\rho34\,\omega^4\Big\},$$

$$\Big\{0, 0, 0, \frac{\rho43\,\omega^2}{2}, 0, 0, 0, \frac{1}{2}\rho23\,\rho43\,\omega^3, 0, 0, 0, \frac{1}{2}(\rho21\,\rho23+\rho12\,\rho32)\,\rho43\,\omega^3,$$

$$0, 0, 0, \frac{1}{2}\rho21\,\rho23\,\rho43\,\omega^4, 0, 0, 0, \frac{\rho43\,\omega^2}{2}, 0, 0, 0, \frac{1}{2}\rho23\,\rho43\,\omega^3,$$

$$0, 0, 0, \frac{1}{2}(\rho21\,\rho23+\rho12\,\rho32)\,\rho43\,\omega^3, 0, 0, 0, \frac{1}{2}\rho21\,\rho23\,\rho43\,\omega^4\Big\},$$

$$\Big\{0, 0, 0, 0, \frac{\omega}{2}, \frac{1}{2}(\rho32\,\rho34+\rho23\,\rho43)\,\omega^2, \frac{\rho23\,\omega^2}{2}, \frac{1}{2}\rho23\,\rho43\,\omega^3, 0, 0, 0, 0,$$

$$\frac{\rho 12\,\omega^2}{2},\ \frac{1}{2}\rho 12\,(\rho 32\,\rho 34+\rho 23\,\rho 43)\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 23\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 23\,\rho 43\,\omega^4,\ 0,$$

$$0,\ 0,\ 0,\ \frac{\omega}{2},\ \frac{1}{2}(\rho 32\,\rho 34+\rho 23\,\rho 43)\,\omega^2,\ \frac{\rho 23\,\omega^2}{2},\ \frac{1}{2}\rho 23\,\rho 43\,\omega^3,\ 0,\ 0,\ 0,\ 0,$$

$$\frac{\rho 12\,\omega^2}{2},\ \frac{1}{2}\rho 12\,(\rho 32\,\rho 34+\rho 23\,\rho 43)\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 23\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 23\,\rho 43\,\omega^4\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(\rho 23\,\rho 34+\rho 32\,\rho 43)\,\omega^2,\ 0,\ \frac{1}{2}\rho 23\,\rho 34\,\omega^3,\ 0,\ 0,\ 0,\ 0,\ 0,$$

$$\frac{1}{2}\rho 12\,(\rho 23\,\rho 34+\rho 32\,\rho 43)\,\omega^3,\ 0,\ \frac{1}{2}\rho 12\,\rho 23\,\rho 34\,\omega^4,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(\rho 23\,\rho 34+\rho 32\,\rho 43)\,\omega^2,$$

$$0,\ \frac{1}{2}\rho 23\,\rho 34\,\omega^3,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}\rho 12\,(\rho 23\,\rho 34+\rho 32\,\rho 43)\,\omega^3,\ 0,\ \frac{1}{2}\rho 12\,\rho 23\,\rho 34\,\omega^4\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{\rho 32\,\omega^2}{2},\ \frac{1}{2}\rho 32\,\rho 34\,\omega^3,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}\rho 12\,\rho 32\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 32\,\rho 34\,\omega^4,$$

$$0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{\rho 32\,\omega^2}{2},\ \frac{1}{2}\rho 32\,\rho 34\,\omega^3,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}\rho 12\,\rho 32\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 32\,\rho 34\,\omega^4\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}\rho 32\,\rho 43\,\omega^3,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}\rho 12\,\rho 32\,\rho 43\,\omega^4,\ 0,$$

$$0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}\rho 32\,\rho 43\,\omega^3,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}\rho 12\,\rho 32\,\rho 43\,\omega^4\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{\omega}{2},\ \frac{1}{2}(\rho 12\,\rho 23\,\rho 34+\rho 21\,\rho 32\,\rho 34+\rho 21\,\rho 23\,\rho 43+\rho 12\,\rho 32\,\rho 43)\,\omega^2,$$

$$\frac{1}{2}(\rho 21\,\rho 23+\rho 12\,\rho 32)\,\omega^2,\ \frac{1}{2}(\rho 21\,\rho 23+\rho 12\,\rho 32)\,\rho 43\,\omega^3,\ \frac{\rho 12\,\omega^2}{2},$$

$$\frac{1}{2}\rho 12\,(\rho 23\,\rho 34+\rho 32\,\rho 43)\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 32\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 32\,\rho 43\,\omega^4,\ 0,\ 0,\ 0,\ 0,$$

$$0,\ 0,\ 0,\ 0,\ \frac{\omega}{2},\ \frac{1}{2}(\rho 12\,\rho 23\,\rho 34+\rho 21\,\rho 32\,\rho 34+\rho 21\,\rho 23\,\rho 43+\rho 12\,\rho 32\,\rho 43)\,\omega^2,$$

$$\frac{1}{2}(\rho 21\,\rho 23+\rho 12\,\rho 32)\,\omega^2,\ \frac{1}{2}(\rho 21\,\rho 23+\rho 12\,\rho 32)\,\rho 43\,\omega^3,\ \frac{\rho 12\,\omega^2}{2},$$

$$\frac{1}{2}\rho 12\,(\rho 23\,\rho 34+\rho 32\,\rho 43)\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 32\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 32\,\rho 43\,\omega^4\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(\rho 21\,\rho 23\,\rho 34+\rho 12\,\rho 32\,\rho 34+\rho 12\,\rho 23\,\rho 43+\rho 21\,\rho 32\,\rho 43)\,\omega^2,$$

$$0,\ \frac{1}{2}(\rho 21\,\rho 23+\rho 12\,\rho 32)\,\rho 34\,\omega^3,\ 0,\ \frac{1}{2}\rho 12\,(\rho 32\,\rho 34+\rho 23\,\rho 43)\,\omega^3,\ 0,\ \frac{1}{2}\rho 12\,\rho 32\,\rho 34\,\omega^4,$$

$$0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(\rho 21\,\rho 23\,\rho 34+\rho 12\,\rho 32\,\rho 34+\rho 12\,\rho 23\,\rho 43+\rho 21\,\rho 32\,\rho 43)\,\omega^2,$$

$$0,\ \frac{1}{2}(\rho 21\,\rho 23+\rho 12\,\rho 32)\,\rho 34\,\omega^3,\ 0,\ \frac{1}{2}\rho 12\,(\rho 32\,\rho 34+\rho 23\,\rho 43)\,\omega^3,\ 0,\ \frac{1}{2}\rho 12\,\rho 32\,\rho 34\,\omega^4\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(\rho 12\,\rho 23+\rho 21\,\rho 32)\,\omega^2,\ \frac{1}{2}(\rho 12\,\rho 23+\rho 21\,\rho 32)\,\rho 34\,\omega^3,\ 0,$$

$$0,\ \frac{1}{2}\rho 12\,\rho 23\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 23\,\rho 34\,\omega^4,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(\rho 12\,\rho 23+\rho 21\,\rho 32)\,\omega^2,$$

$$\frac{1}{2}(\rho 12\,\rho 23+\rho 21\,\rho 32)\,\rho 34\,\omega^3,\ 0,\ 0,\ \frac{1}{2}\rho 12\,\rho 23\,\omega^3,\ \frac{1}{2}\rho 12\,\rho 23\,\rho 34\,\omega^4\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(\rho 12\,\rho 23+\rho 21\,\rho 32)\,\rho 43\,\omega^3,\ 0,\ 0,\ 0,\ \frac{1}{2}\rho 12\,\rho 23\,\rho 43\,\omega^4,$$

$$0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{1}{2} (\rho 12\, \rho 23 + \rho 21\, \rho 32)\, \rho 43\, \omega^3, 0, 0, 0, \frac{1}{2} \rho 12\, \rho 23\, \rho 43\, \omega^4\Big\},$$

$$\Big\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{\rho 21\, \omega^2}{2}, \frac{1}{2} \rho 21\, (\rho 32\, \rho 34 + \rho 23\, \rho 43)\, \omega^3,$$

$$\frac{1}{2} \rho 21\, \rho 23\, \omega^3, \frac{1}{2} \rho 21\, \rho 23\, \rho 43\, \omega^4, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,$$

$$\frac{\rho 21\, \omega^2}{2}, \frac{1}{2} \rho 21\, (\rho 32\, \rho 34 + \rho 23\, \rho 43)\, \omega^3, \frac{1}{2} \rho 21\, \rho 23\, \omega^3, \frac{1}{2} \rho 21\, \rho 23\, \rho 43\, \omega^4\Big\},$$

$$\Big\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{1}{2} \rho 21\, (\rho 23\, \rho 34 + \rho 32\, \rho 43)\, \omega^3, 0, \frac{1}{2} \rho 21\, \rho 23\, \rho 34\, \omega^4,$$

$$0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{1}{2} \rho 21\, (\rho 23\, \rho 34 + \rho 32\, \rho 43)\, \omega^3, 0, \frac{1}{2} \rho 21\, \rho 23\, \rho 34\, \omega^4\Big\},$$

$$\Big\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{1}{2} \rho 21\, \rho 32\, \omega^3, \frac{1}{2} \rho 21\, \rho 32\, \rho 34\, \omega^4, 0,$$

$$0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{1}{2} \rho 21\, \rho 32\, \omega^3, \frac{1}{2} \rho 21\, \rho 32\, \rho 34\, \omega^4\Big\},$$

$$\Big\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{1}{2} \rho 21\, \rho 32\, \rho 43\, \omega^4, 0,$$

$$0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{1}{2} \rho 21\, \rho 32\, \rho 43\, \omega^4\Big\}\Big\}$$

```
JacAtEcl // Simplify // MatrixForm
```

$$\left(\begin{array}{cccccccc}
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & -\frac{\omega}{2} & -\frac{\omega}{2} & -\frac{1}{2}(1+\rho 34)\,\omega^2 & -\frac{\omega}{2} & \frac{1}{2}(-1-\rho 34+\rho 23\,(-1+2\,\rho 34))\,\omega^2 & -\frac{1}{2}(1+\rho 23)\,\omega^2 & \frac{1}{2}(-1+\rho 23\;(\\
0 & \frac{\omega}{2} & 0 & \frac{\rho 34\,\omega^2}{2} & 0 & \frac{1}{2}(\rho 23+\rho 34-2\,\rho 23\,\rho 34)\,\omega^2 & 0 & -\frac{1}{2}(-1 \\
0 & 0 & \frac{\omega}{2} & \frac{\rho 34\,\omega^2}{2} & 0 & 0 & \frac{\rho 23\,\omega^2}{2} & \frac{1}{2}\rho \\
0 & 0 & 0 & -\frac{1}{2}(-1+\rho 34)\,\omega^2 & 0 & 0 & 0 & -\frac{1}{2}\rho 23 \\
0 & 0 & 0 & 0 & \frac{\omega}{2} & \frac{1}{2}(\rho 23+\rho 34-2\,\rho 23\,\rho 34)\,\omega^2 & \frac{\rho 23\,\omega^2}{2} & -\frac{1}{2}\rho 23 \\
0 & 0 & 0 & 0 & 0 & \frac{1}{2}(1-\rho 34+\rho 23\,(-1+2\,\rho 34))\,\omega^2 & 0 & \frac{1}{2}\rho \\
0 & 0 & 0 & 0 & 0 & 0 & -\frac{1}{2}(-1+\rho 23)\,\omega^2 & -\frac{1}{2}(-1 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{2}(-1+\rho 2 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \\
0 & 0 & 0 & 0 & 0 & 0 & 0 &
\end{array}\right.$$

Calculate the Eigenvalues

```
eig = Eigenvalues[JacAtEcl]
```

$$\Big\{0,0,0,0,0,0,0,0,0,0,0,0,0,0,\frac{\omega}{2},\frac{\omega}{2},\frac{\omega}{2},\frac{\omega}{2},\frac{\rho 32\,\omega^2}{2},\frac{1}{2}(\rho 12\,\rho 23+\rho 21\,\rho 32)\,\omega^2,$$

$$\frac{1}{2}(\rho 23\,\rho 34+\rho 32\,\rho 43)\,\omega^2,\ \frac{1}{2}(\rho 21\,\rho 23\,\rho 34+\rho 12\,\rho 32\,\rho 34+\rho 12\,\rho 23\,\rho 43+\rho 21\,\rho 32\,\rho 43)\,\omega^2,$$

$$\frac{1}{2}\rho 21\,\rho 32\,\omega^3,\ \frac{1}{2}\rho 32\,\rho 43\,\omega^3,\ \frac{1}{2}(\rho 12\,\rho 23+\rho 21\,\rho 32)\,\rho 43\,\omega^3,\ \frac{1}{2}\rho 21\,(\rho 23\,\rho 34+\rho 32\,\rho 43)\,\omega^3,$$

$$\frac{1}{4}\left(\rho 21\,\omega^2-\sqrt{\rho 21}\,\omega\,\sqrt{8+\rho 21\,\omega^2}\right),\ \frac{1}{4}\left(\rho 21\,\omega^2+\sqrt{\rho 21}\,\omega\,\sqrt{8+\rho 21\,\omega^2}\right),$$

$$\frac{1}{4}\left(\rho 43\,\omega^2-\sqrt{\rho 43}\,\omega\,\sqrt{8+\rho 43\,\omega^2}\right),\ \frac{1}{4}\left(\rho 43\,\omega^2+\sqrt{\rho 43}\,\omega\,\sqrt{8+\rho 43\,\omega^2}\right),$$

$$\frac{1}{4}\left(\rho 21\,\rho 32\,\rho 43\,\omega^4-\sqrt{\rho 21}\,\sqrt{\rho 32}\,\sqrt{\rho 43}\,\omega^2\,\sqrt{8+\rho 21\,\rho 32\,\rho 43\,\omega^4}\right),$$

$$\frac{1}{4}\left(\rho 21\,\rho 32\,\rho 43\,\omega^4+\sqrt{\rho 21}\,\sqrt{\rho 32}\,\sqrt{\rho 43}\,\omega^2\,\sqrt{8+\rho 21\,\rho 32\,\rho 43\,\omega^4}\right)\Big\}$$

Finally replace ρ21 by 1-ρ12. This is done only now to avoid Mathematica using $\sqrt{}$(-1+ρ12) as an intermediate step

```
eig = eig /. {ρ21 → 1 - ρ12, ρ32 → 1 - ρ23, ρ43 → 1 - ρ34} // FullSimplify
```

$$\Big\{0,0,0,0,0,0,0,0,0,0,0,0,0,0,\frac{\omega}{2},\frac{\omega}{2},\frac{\omega}{2},\frac{\omega}{2},-\frac{1}{2}(-1+\rho 23)\,\omega^2,$$

$$\frac{1}{2}(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,\omega^2,\ \frac{1}{2}(1-\rho 34+\rho 23\,(-1+2\,\rho 34))\,\omega^2,$$

$$-\frac{1}{2}(-1+\rho 23+\rho 34-2\,\rho 23\,\rho 34+\rho 12\,(-1+2\,\rho 23)\,(-1+2\,\rho 34))\,\omega^2,\ \frac{1}{2}(-1+\rho 12)\,(-1+\rho 23)\,\omega^3,$$

$$\frac{1}{2}(-1+\rho 23)\,(-1+\rho 34)\,\omega^3,\ -\frac{1}{2}(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,(-1+\rho 34)\,\omega^3,$$

$$-\frac{1}{2}(-1+\rho 12)\,(1-\rho 34+\rho 23\,(-1+2\,\rho 34))\,\omega^3,\ -\frac{1}{4}\omega\left((-1+\rho 12)\,\omega+\sqrt{1-\rho 12}\,\sqrt{8-(-1+\rho 12)\,\omega^2}\right),$$

$$\frac{1}{4}\omega\left(\omega-\rho 12\,\omega+\sqrt{1-\rho 12}\,\sqrt{8-(-1+\rho 12)\,\omega^2}\right),$$

$$-\frac{1}{4}\omega\left((-1+\rho 34)\,\omega+\sqrt{1-\rho 34}\,\sqrt{8-(-1+\rho 34)\,\omega^2}\right),$$

$$\frac{1}{4}\omega\left(\omega-\rho 34\,\omega+\sqrt{1-\rho 34}\,\sqrt{8-(-1+\rho 34)\,\omega^2}\right),$$

$$\frac{1}{4}\Big(-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4-\sqrt{1-\rho 12}\,\sqrt{1-\rho 23}\,\sqrt{1-\rho 34}\,\omega^2$$

$$\sqrt{8-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4}\Big),\ \frac{1}{4}\Big(-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4+$$

$$\sqrt{1-\rho 12}\,\sqrt{1-\rho 23}\,\sqrt{1-\rho 34}\,\omega^2\,\sqrt{8-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4}\Big)\Big\}$$

$$\begin{aligned}\mathrm{eig} = \Big\{&0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{\omega}{2}, \frac{\omega}{2}, \frac{\omega}{2}, \frac{\omega}{2},\\
&-\frac{1}{2}(-1+\rho 23)\,\omega^2, \frac{1}{2}(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,\omega^2, \frac{1}{2}(1-\rho 34+\rho 23\,(-1+2\,\rho 34))\,\omega^2,\\
&-\frac{1}{2}(-1+\rho 23+\rho 34-2\,\rho 23\,\rho 34+\rho 12\,(-1+2\,\rho 23)\,(-1+2\,\rho 34))\,\omega^2,\\
&\frac{1}{2}(-1+\rho 12)\,(-1+\rho 23)\,\omega^3, \frac{1}{2}(-1+\rho 23)\,(-1+\rho 34)\,\omega^3,\\
&-\frac{1}{2}(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,(-1+\rho 34)\,\omega^3, -\frac{1}{2}(-1+\rho 12)\,(1-\rho 34+\rho 23\,(-1+2\,\rho 34))\,\omega^3,\\
&-\frac{1}{4}\omega\left((-1+\rho 12)\,\omega+\sqrt{1-\rho 12}\,\sqrt{8-(-1+\rho 12)\,\omega^2}\right),\\
&\frac{1}{4}\omega\left(\omega-\rho 12\,\omega+\sqrt{1-\rho 12}\,\sqrt{8-(-1+\rho 12)\,\omega^2}\right),\\
&-\frac{1}{4}\omega\left((-1+\rho 34)\,\omega+\sqrt{1-\rho 34}\,\sqrt{8-(-1+\rho 34)\,\omega^2}\right),\\
&\frac{1}{4}\omega\left(\omega-\rho 34\,\omega+\sqrt{1-\rho 34}\,\sqrt{8-(-1+\rho 34)\,\omega^2}\right),\\
&\frac{1}{4}\Big(-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4-\sqrt{1-\rho 12}\,\sqrt{1-\rho 23}\,\sqrt{1-\rho 34}\,\omega^2\\
&\quad\sqrt{8-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4}\Big), \frac{1}{4}\Big(-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4+\\
&\quad\sqrt{1-\rho 12}\,\sqrt{1-\rho 23}\,\sqrt{1-\rho 34}\,\omega^2\,\sqrt{8-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4}\Big)\Big\};\end{aligned}$$

If all loci are on different chromosomes

```
eig = Eigenvalues[JacAtEcl /.
    {ρ12 → 1 / 2, ρ23 → 1 / 2, ρ34 → 1 / 2, ρ21 → 1 / 2, ρ32 → 1 / 2, ρ43 → 1 / 2}] // FullSimplify
```

$$\begin{aligned}\Big\{&0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{\omega}{2}, \frac{\omega}{2}, \frac{\omega}{2}, \frac{\omega}{2}, \frac{\omega^2}{4}, \frac{\omega^2}{4}, \frac{\omega^2}{4}, \frac{\omega^2}{4}, \frac{\omega^3}{8}, \frac{\omega^3}{8},\\
&\frac{\omega^3}{8}, \frac{\omega^3}{8}, \frac{1}{32}\left(\omega^4-\omega^2\sqrt{64+\omega^4}\right), \frac{1}{32}\omega^2\left(\omega^2+\sqrt{64+\omega^4}\right), \frac{1}{8}\left(\omega^2-\sqrt{\omega^2\,(16+\omega^2)}\right),\\
&\frac{1}{8}\left(\omega^2-\sqrt{\omega^2\,(16+\omega^2)}\right), \frac{1}{8}\left(\omega^2+\sqrt{\omega^2\,(16+\omega^2)}\right), \frac{1}{8}\left(\omega^2+\sqrt{\omega^2\,(16+\omega^2)}\right)\Big\}\end{aligned}$$

Case 1 Independent pairs of loci

For simplicity we first check that all Eigenvalues are smaller than 1:

```
Apply[And, Thread[eig < 1]] /. {ρ12 -> r, ρ23 -> 1 / 2, ρ34 -> r} // Simplify
```

$$\begin{aligned}&\omega<2\;\&\&\;\omega^2<4\;\&\&\;(-1+r)^2\,\omega^4<8+(-1+r)\,\omega^2\sqrt{16+(-1+r)^2\,\omega^4}\;\&\&\\
&\sqrt{1-r}\;\omega\,\sqrt{8-(-1+r)\,\omega^2}<4+(-1+r)\,\omega^2\;\&\&\;(-1+r)\,\omega^2\left((-1+r)\,\omega^2+\sqrt{16+(-1+r)^2\,\omega^4}\right)<8\;\&\&\\
&4+r\,\omega^3>\omega^3\;\&\&\;4+r\,\omega^2+\sqrt{1-r}\;\omega\,\sqrt{8+\omega^2-r\,\omega^2}>\omega^2\end{aligned}$$

$$\mathtt{Reduce}\Big[\omega < 2 \;\&\&\; \omega^2 < 4 \;\&\&\; (-1+r)^2\,\omega^4 < 8 + (-1+r)\,\omega^2\,\sqrt{16+(-1+r)^2\,\omega^4} \;\&\&\; \\ \sqrt{1-r}\;\omega\,\sqrt{8-(-1+r)\,\omega^2} < 4 + (-1+r)\,\omega^2 \;\&\&\; \\ (-1+r)\,\omega^2\left((-1+r)\,\omega^2+\sqrt{16+(-1+r)^2\,\omega^4}\right) < 8 \;\&\&\; 4 + r\,\omega^3 > \omega^3 \;\&\&\; \\ 4 + r\,\omega^2 + \sqrt{1-r}\;\omega\,\sqrt{8+\omega^2-r\,\omega^2} > \omega^2 \;\&\&\; \omega > 1 \;\&\&\; 0 \le r \le 1/2,\ \omega,\ \mathtt{Reals}\Big]$$

$$0 < r \le \frac{1}{2} \;\&\&\; 1 < \omega < \sqrt{\frac{1}{1-r}}$$

Then we check that all Eigenvalues are larger than - 1 :

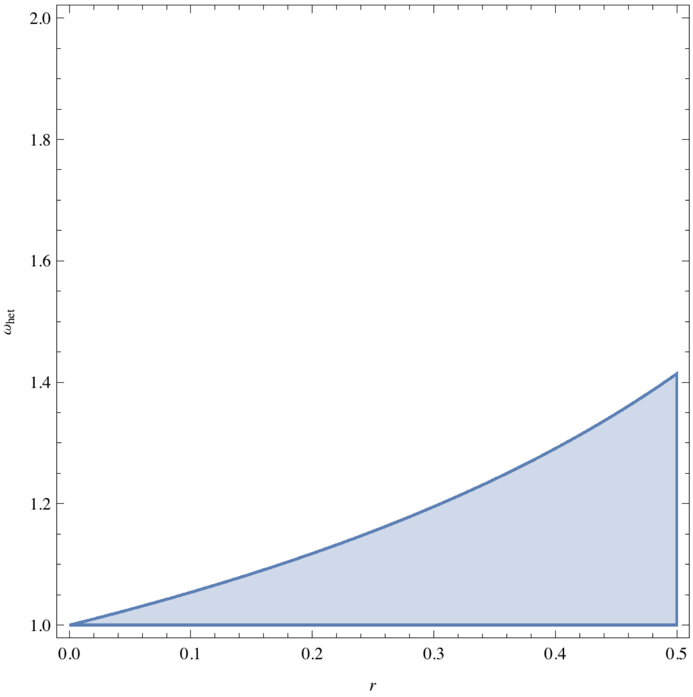
```
Apply[And, Thread[eig > -1]] /. {ρ12 -> r, ρ23 -> 1 / 2, ρ34 -> r} // Simplify
```

$$(-1+r)\,\omega^3 < 4 \;\&\&\; (-1+r)\,\omega^2\,\sqrt{16+(-1+r)^2\,\omega^4} < 8 + (-1+r)^2\,\omega^4 \;\&\&\; \\ \omega\left((-1+r)\,\omega+\sqrt{1-r}\,\sqrt{8-(-1+r)\,\omega^2}\right) < 4 \;\&\&\; 2+\omega > 0 \;\&\&\; 4+\omega^2 > 0 \;\&\&\; \\ 4+\sqrt{1-r}\;\omega\,\sqrt{8-(-1+r)\,\omega^2} > (-1+r)\,\omega^2 \;\&\&\; 8+(-1+r)^2\,\omega^4+(-1+r)\,\omega^2\,\sqrt{16+(-1+r)^2\,\omega^4} > 0$$

$$\mathtt{Reduce}\Big[(-1+r)\,\omega^3 < 4 \;\&\&\; (-1+r)\,\omega^2\,\sqrt{16+(-1+r)^2\,\omega^4} < 8 + (-1+r)^2\,\omega^4 \;\&\&\; \\ \omega\left((-1+r)\,\omega+\sqrt{1-r}\,\sqrt{8-(-1+r)\,\omega^2}\right) < 4 \;\&\&\; 2+\omega > 0 \;\&\&\; \\ 4+\omega^2 > 0 \;\&\&\; 4+\sqrt{1-r}\;\omega\,\sqrt{8-(-1+r)\,\omega^2} > (-1+r)\,\omega^2 \;\&\&\; \\ 8+(-1+r)^2\,\omega^4+(-1+r)\,\omega^2\,\sqrt{16+(-1+r)^2\,\omega^4} > 0 \;\&\&\; \omega > 1 \;\&\&\; 0 \le r \le 1/2,\ \omega,\ \mathtt{Reals}\Big]$$

$$0 \le r \le \frac{1}{2} \;\&\&\; \omega > 1$$

$$\begin{aligned}
&\texttt{RegionPlot}\Big[\omega < 2 \,\&\&\, \omega^2 < 4 \,\&\&\, (-1+r)^2\,\omega^4 < 8 + (-1+r)\,\omega^2\sqrt{16+(-1+r)^2\,\omega^4} \,\&\&\\
&\quad \sqrt{1-r}\;\omega\,\sqrt{8-(-1+r)\,\omega^2} < 4 + (-1+r)\,\omega^2 \,\&\&\\
&\quad (-1+r)\,\omega^2\left((-1+r)\,\omega^2 + \sqrt{16+(-1+r)^2\,\omega^4}\right) < 8 \,\&\&\, 4 + r\,\omega^3 > \omega^3 \,\&\&\\
&\quad 4 + r\,\omega^2 + \sqrt{1-r}\;\omega\,\sqrt{8+\omega^2-r\,\omega^2} > \omega^2 \,\&\&\, (-1+r)\,\omega^3 < 4 \,\&\&\\
&\quad (-1+r)\,\omega^2\sqrt{16+(-1+r)^2\,\omega^4} < 8 + (-1+r)^2\,\omega^4 \,\&\&\\
&\quad \omega\left((-1+r)\,\omega + \sqrt{1-r}\;\sqrt{8-(-1+r)\,\omega^2}\right) < 4 \,\&\&\, 2+\omega > 0 \,\&\&\\
&\quad 4+\omega^2 > 0 \,\&\&\, 4 + \sqrt{1-r}\;\omega\,\sqrt{8-(-1+r)\,\omega^2} > (-1+r)\,\omega^2 \,\&\&\\
&\quad 8 + (-1+r)^2\,\omega^4 + (-1+r)\,\omega^2\sqrt{16+(-1+r)^2\,\omega^4} > 0,\\
&\quad \{r,\,0,\,.5\},\;\{\omega,\,1,\,2\},\;\texttt{FrameLabel}\to\{r,\,\omega_{\text{het}}\}\Big]
\end{aligned}$$



Case 2 the second and third loci are in TL (r->0)

For simplicity we first check that all Eigenvalues are smaller than 1:

```
Apply[And, Thread[eig < 1]] /. {ρ12 -> r, ρ23 → 0, ρ34 -> r} // Simplify
```

$$\begin{aligned}
&\omega < 2 \,\&\&\, \omega^2 < 2 \,\&\&\, 2 + r\,\omega^2 > \omega^2 \,\&\&\, \left(1 - 2\,r + 2\,r^2\right)\omega^2 < 2 \,\&\&\, 2 + r\,\omega^3 > \omega^3 \,\&\&\, (-1+r)^2\,\omega^3 < 2 \,\&\&\\
&\quad 4 + r\,\omega^2 + \sqrt{1-r}\;\omega\,\sqrt{8+\omega^2-r\,\omega^2} > \omega^2 \,\&\&\, \sqrt{1-r}\;\omega\,\sqrt{8-(-1+r)\,\omega^2} < 4 + (-1+r)\,\omega^2 \,\&\&\\
&\quad (-1+r)\,\omega^2\left((-1+r)\,\omega^2 + \sqrt{8+(-1+r)^2\,\omega^4}\right) < 4 \,\&\&\, (-1+r)^2\,\omega^4 < 4 + (-1+r)\,\omega^2\sqrt{8+(-1+r)^2\,\omega^4}
\end{aligned}$$

$$\begin{aligned}&\mathbf{Reduce}\Big[\omega < 2 \;\&\&\; \omega^2 < 2 \;\&\&\; 2 + r\,\omega^2 > \omega^2 \;\&\&\; \left(1 - 2\,r + 2\,r^2\right)\omega^2 < 2 \;\&\&\\ &\quad 2 + r\,\omega^3 > \omega^3 \;\&\&\; (-1+r)^2\,\omega^3 < 2 \;\&\&\; 4 + r\,\omega^2 + \sqrt{1-r}\;\omega\,\sqrt{8 + \omega^2 - r\,\omega^2} > \omega^2 \;\&\&\\ &\quad \sqrt{1-r}\;\omega\,\sqrt{8 - (-1+r)\,\omega^2} < 4 + (-1+r)\,\omega^2 \;\&\&\; (-1+r)\,\omega^2\left((-1+r)\,\omega^2 + \sqrt{8 + (-1+r)^2\,\omega^4}\right) < 4 \;\&\&\\ &\quad (-1+r)^2\,\omega^4 < 4 + (-1+r)\,\omega^2\,\sqrt{8 + (-1+r)^2\,\omega^4} \;\&\&\; \omega > 1 \;\&\&\; 0 \le r \le 1/2,\; \mathbf{Reals}\Big]\end{aligned}$$

$$1 < \omega < \sqrt{2} \;\&\&\; \frac{-1+\omega^2}{\omega^2} < r \le \frac{1}{2}$$

Then we check that all Eigenvalues are larger than - 1 :

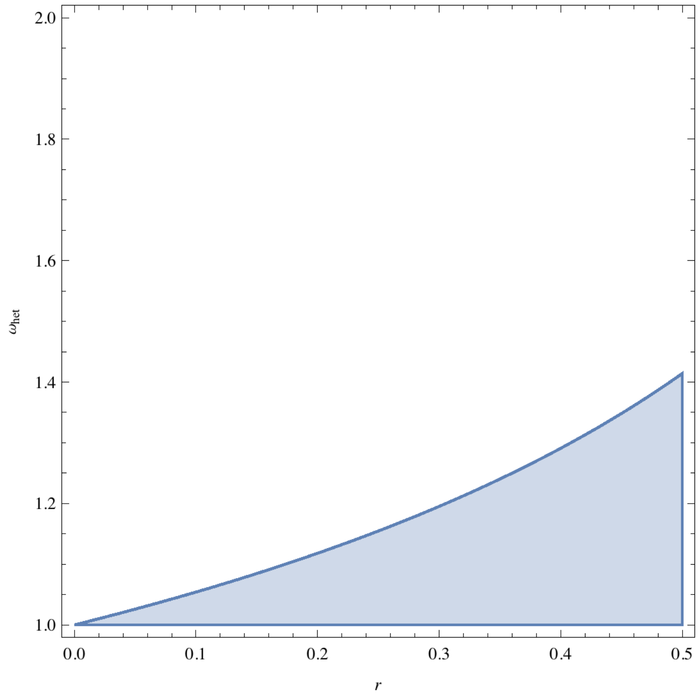
```
Apply[And, Thread[eig > -1]] /. {ρ12 -> r, ρ23 → 0, ρ34 -> r} // Simplify
```

$$\begin{aligned}&2 + \omega > 0 \;\&\&\; 2 + \omega^2 > 0 \;\&\&\; (-1+r)\,\omega^2 < 2 \;\&\&\\ &\;2 + \left(1 - 2\,r + 2\,r^2\right)\omega^2 > 0 \;\&\&\; (-1+r)\,\omega^3 < 2 \;\&\&\; 2 + (-1+r)^2\,\omega^3 > 0 \;\&\&\\ &\;\omega\left((-1+r)\,\omega + \sqrt{1-r}\;\sqrt{8 - (-1+r)\,\omega^2}\right) < 4 \;\&\&\; 4 + \sqrt{1-r}\;\omega\,\sqrt{8 - (-1+r)\,\omega^2} > (-1+r)\,\omega^2 \;\&\&\\ &\;4 + (-1+r)^2\,\omega^4 + (-1+r)\,\omega^2\,\sqrt{8 + (-1+r)^2\,\omega^4} > 0 \;\&\&\; (-1+r)\,\omega^2\,\sqrt{8 + (-1+r)^2\,\omega^4} < 4 + (-1+r)^2\,\omega^4\end{aligned}$$

$$\begin{aligned}&\mathbf{Reduce}\Big[2 + \omega > 0 \;\&\&\; 2 + \omega^2 > 0 \;\&\&\; (-1+r)\,\omega^2 < 2 \;\&\&\\ &\quad 2 + \left(1 - 2\,r + 2\,r^2\right)\omega^2 > 0 \;\&\&\; (-1+r)\,\omega^3 < 2 \;\&\&\; 2 + (-1+r)^2\,\omega^3 > 0 \;\&\&\\ &\quad \omega\left((-1+r)\,\omega + \sqrt{1-r}\;\sqrt{8 - (-1+r)\,\omega^2}\right) < 4 \;\&\&\; 4 + \sqrt{1-r}\;\omega\,\sqrt{8 - (-1+r)\,\omega^2} > (-1+r)\,\omega^2 \;\&\&\\ &\quad 4 + (-1+r)^2\,\omega^4 + (-1+r)\,\omega^2\,\sqrt{8 + (-1+r)^2\,\omega^4} > 0 \;\&\&\\ &\quad (-1+r)\,\omega^2\,\sqrt{8 + (-1+r)^2\,\omega^4} < 4 + (-1+r)^2\,\omega^4 \;\&\&\; \omega > 1 \;\&\&\; 0 \le r \le 1/2,\; \mathbf{Reals}\Big]\end{aligned}$$

$$\omega > 1 \;\&\&\; 0 \le r \le \frac{1}{2}$$

```
RegionPlot[ω < 2 && ω^2 < 2 && 2 + r ω^2 > ω^2 && (1 - 2 r + 2 r^2) ω^2 < 2 &&
  2 + r ω^3 > ω^3 && (-1 + r)^2 ω^3 < 2 && 4 + r ω^2 + √(1 - r) ω √(8 + ω^2 - r ω^2) > ω^2 &&
  √(1 - r) ω √(8 - (-1 + r) ω^2) < 4 + (-1 + r) ω^2 && (-1 + r) ω^2 ((-1 + r) ω^2 + √(8 + (-1 + r)^2 ω^4)) < 4 &&
  (-1 + r)^2 ω^4 < 4 + (-1 + r) ω^2 √(8 + (-1 + r)^2 ω^4), {r, 0, .5}, {ω, 1, 2}, FrameLabel → {r, ω_het}]
```



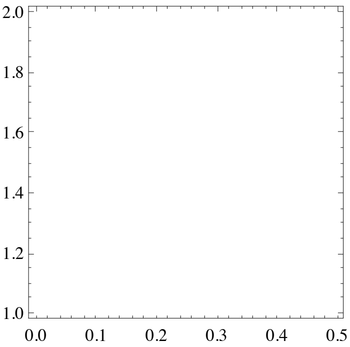
Case 3 : General case

```
Apply[And, Thread[-1 < eig < 1]] // FullSimplify
```

```
$Aborted
```

```
Table[RegionPlot[ω < 2 && 2 + ρ23 ω^2 > ω^2 &&
   (1 - ρ23 + ρ12 (-1 + 2 ρ23)) ω^2 < 2 && (1 - ρ34 + ρ23 (-1 + 2 ρ34)) ω^2 < 2 &&
   2 + (-1 + ρ23 + ρ34 - 2 ρ23 ρ34 + ρ12 (-1 + 2 ρ23) (-1 + 2 ρ34)) ω^2 > 0 &&
   (-1 + ρ12) (-1 + ρ23) ω^3 < 2 && (-1 + ρ23) (-1 + ρ34) ω^3 < 2 &&
   2 + (1 - ρ23 + ρ12 (-1 + 2 ρ23)) (-1 + ρ34) ω^3 > 0 &&
   2 + (-1 + ρ12) (1 - ρ34 + ρ23 (-1 + 2 ρ34)) ω^3 > 0 &&
   4 + ρ12 ω^2 + √(1 - ρ12) ω √(8 + ω^2 - ρ12 ω^2) > ω^2 && √(1 - ρ12) ω √(8 - (-1 + ρ12) ω^2) <
    4 + (-1 + ρ12) ω^2 && 4 + ρ34 ω^2 + √(1 - ρ34) ω √(8 + ω^2 - ρ34 ω^2) > ω^2 &&
   √(1 - ρ34) ω √(8 - (-1 + ρ34) ω^2) < 4 + (-1 + ρ34) ω^2 && 4 + (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4 +
     √(1 - ρ12) √(1 - ρ23) √(1 - ρ34) ω^2 √(8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4) > 0 &&
   √(1 - ρ12) √(1 - ρ23) √(1 - ρ34) ω^2 √(8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4) <
    4 + (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4, {ρ23, 0, 0.5}, {ω, 1, 2}],
 {ρ12, {0, .005, .05, .5}}, {ρ34, {0, .005, .05, .5}}]
```

{{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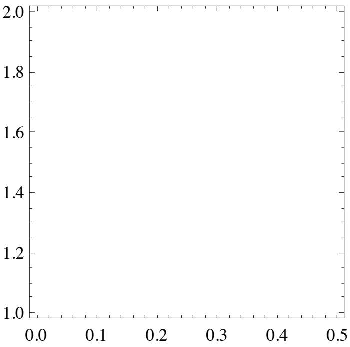
1.8
1.6
1.4
1.2
1.0
0.0
0.1
0.2
0.3
0.4
0.5

,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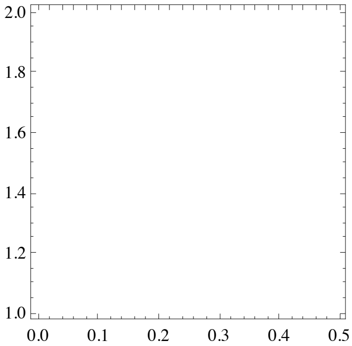
1.8
1.6
1.4
1.2
1.0
0.0
0.1
0.2
0.3
0.4
0.5

,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1.8
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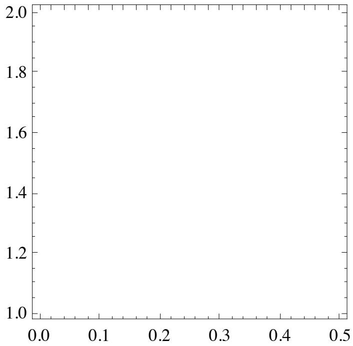
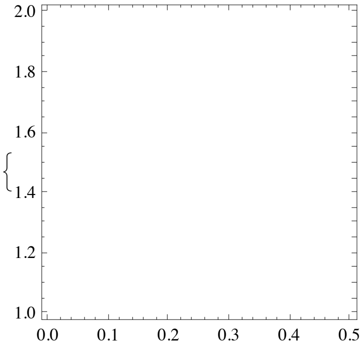
1.4
1.2
1.0
0.0
0.1
0.2
0.3
0.4
0.5

,


2.0
1.8
1.6
1.4
1.2
1.0
0.0
0.1
0.2
0.3
0.4
0.5

},

{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1.4
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1.0
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0.1
0.2
0.3
0.4
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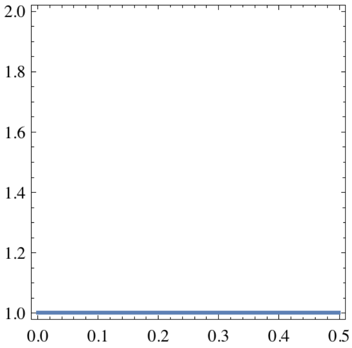
,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0.2
0.3
0.4
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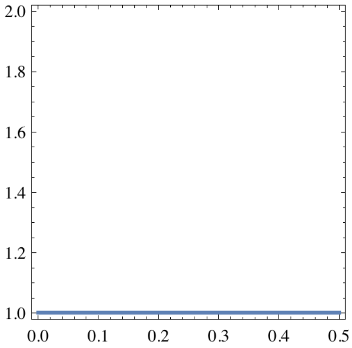
,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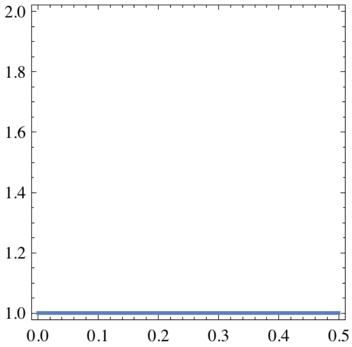
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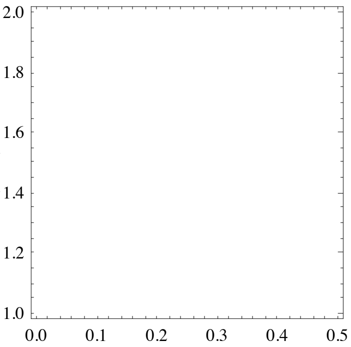
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0.0
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0.2
0.3
0.4
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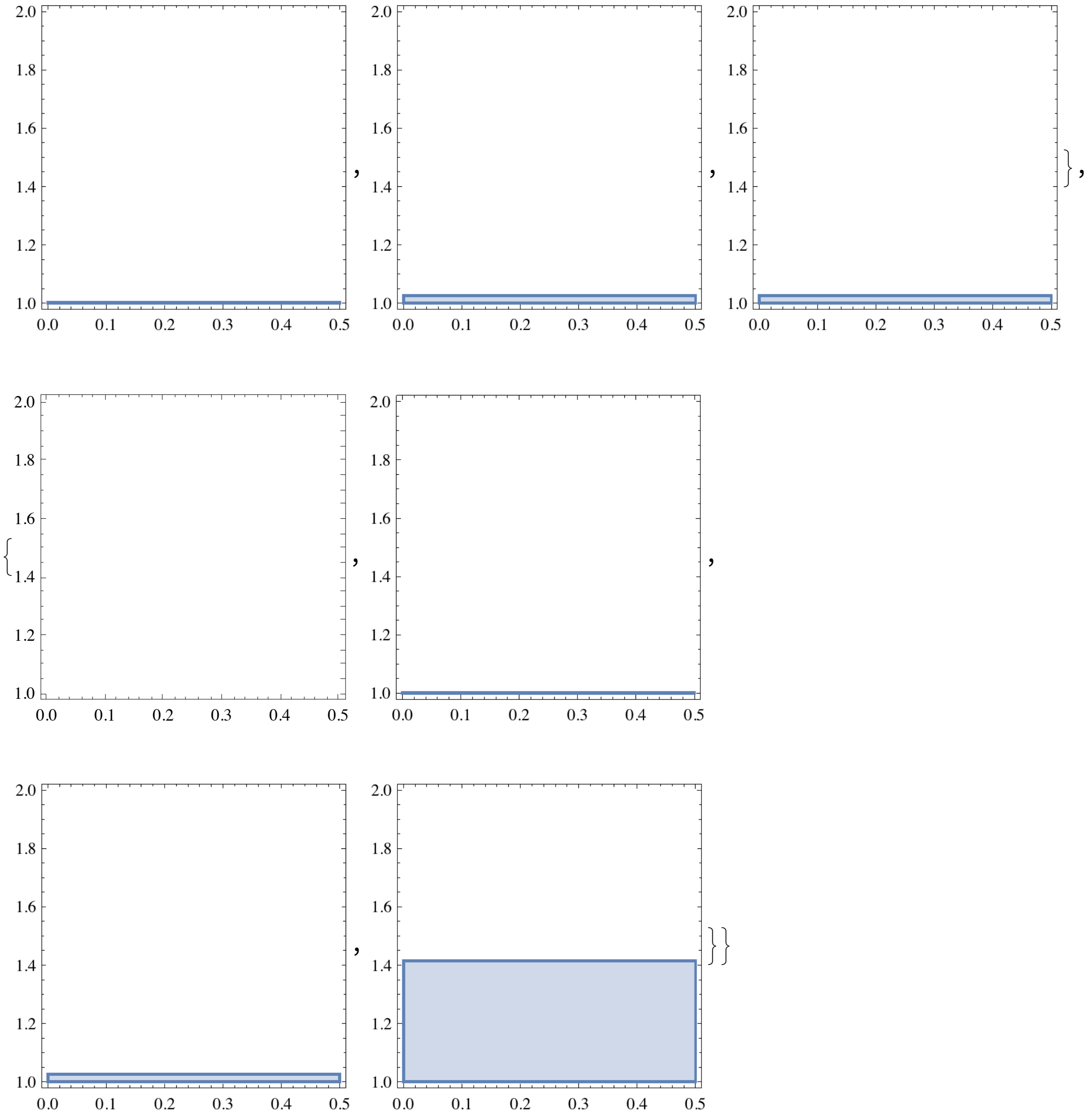
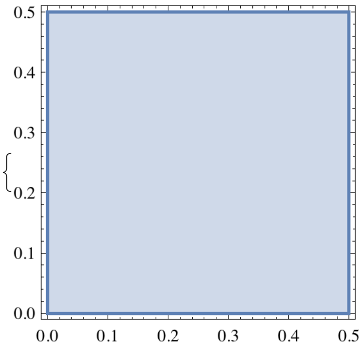


```
Table[RegionPlot[ω < 2 && 2 + ρ23 ω^2 > ω^2 &&
   (1 - ρ23 + ρ12 (-1 + 2 ρ23)) ω^2 < 2 && (1 - ρ34 + ρ23 (-1 + 2 ρ34)) ω^2 < 2 &&
   2 + (-1 + ρ23 + ρ34 - 2 ρ23 ρ34 + ρ12 (-1 + 2 ρ23) (-1 + 2 ρ34)) ω^2 > 0 &&
   (-1 + ρ12) (-1 + ρ23) ω^3 < 2 && (-1 + ρ23) (-1 + ρ34) ω^3 < 2 &&
   2 + (1 - ρ23 + ρ12 (-1 + 2 ρ23)) (-1 + ρ34) ω^3 > 0 &&
   2 + (-1 + ρ12) (1 - ρ34 + ρ23 (-1 + 2 ρ34)) ω^3 > 0 &&
   4 + ρ12 ω^2 + √(1 - ρ12) ω √(8 + ω^2 - ρ12 ω^2) > ω^2 && √(1 - ρ12) ω √(8 - (-1 + ρ12) ω^2) <
    4 + (-1 + ρ12) ω^2 && 4 + ρ34 ω^2 + √(1 - ρ34) ω √(8 + ω^2 - ρ34 ω^2) > ω^2 &&
   √(1 - ρ34) ω √(8 - (-1 + ρ34) ω^2) < 4 + (-1 + ρ34) ω^2 && 4 + (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4 +
     √(1 - ρ12) √(1 - ρ23) √(1 - ρ34) ω^2 √(8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4) > 0 &&
   √(1 - ρ12) √(1 - ρ23) √(1 - ρ34) ω^2 √(8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4) <
    4 + (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4, {ρ12, 0, 0.5}, {ρ34, 0, .5}],
 {ρ23, {0, .005, .05, .5}}, {ω, {1, 1.005, 1.2, 1.4, 1.7}}]
```

{{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0.3
0.4
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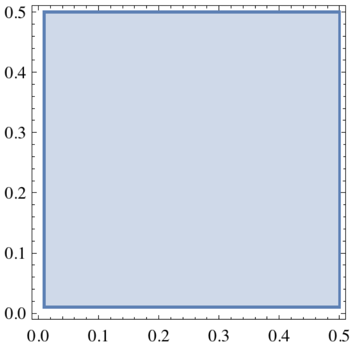
,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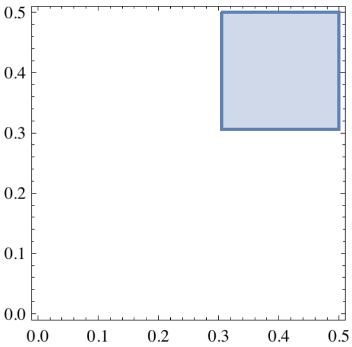
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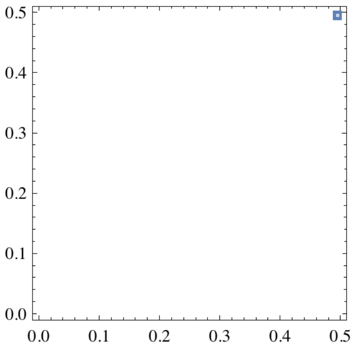
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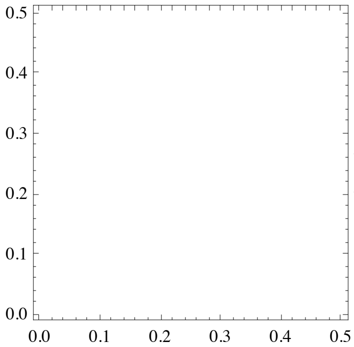
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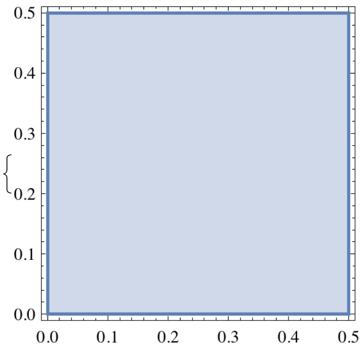
{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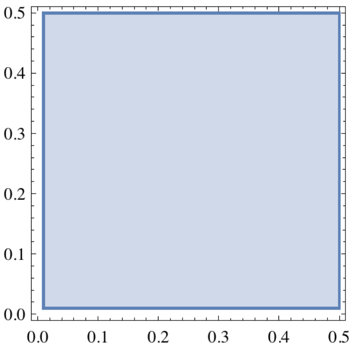
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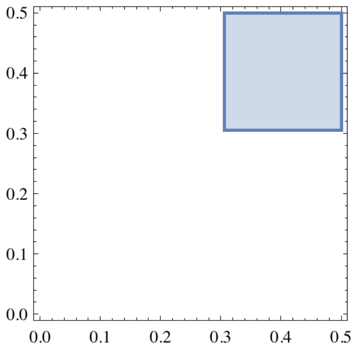
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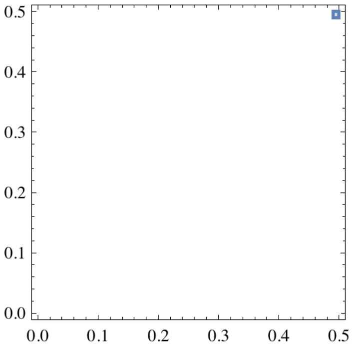
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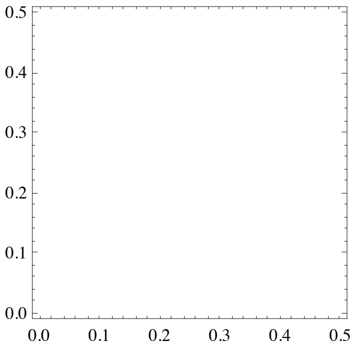
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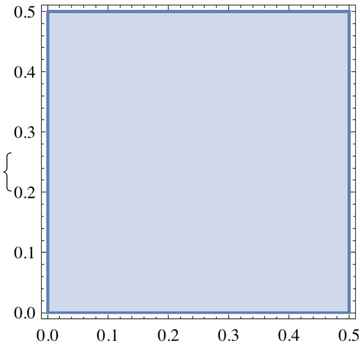
},

{



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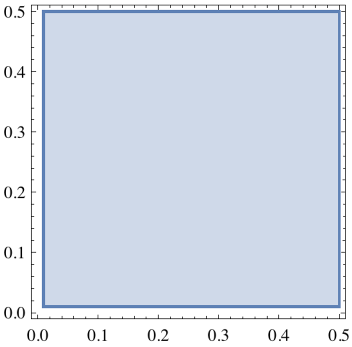

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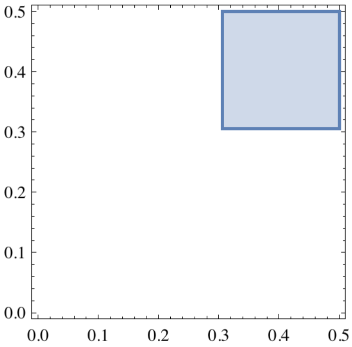

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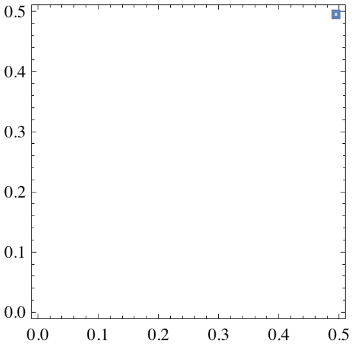

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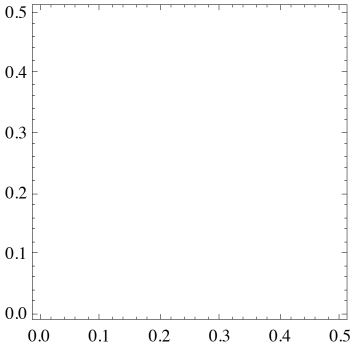

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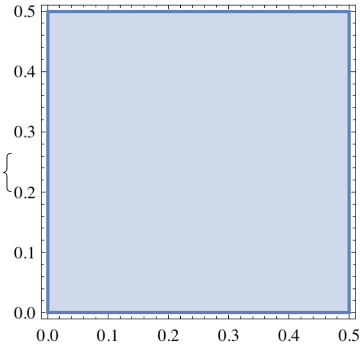

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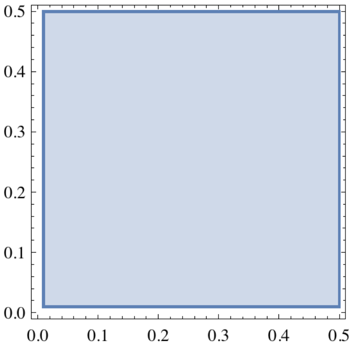

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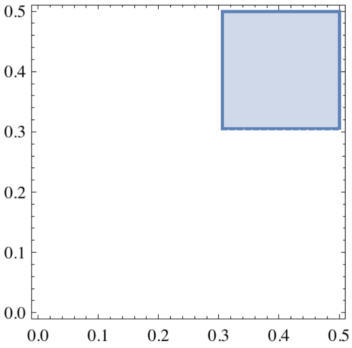

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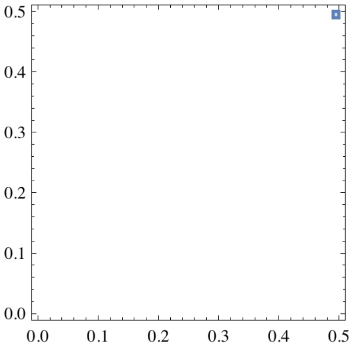

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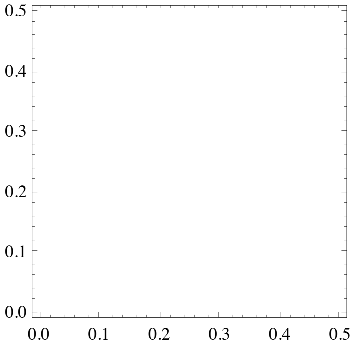


}}

Conditions for local stability of the exclusion case for arbitrary recombination rate

```
Thread[eig < 1]
```

$$
\begin{array}{l}
\{\text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True},\\
\quad \text{True}, \text{True}, \text{True}, \text{True}, \frac{\omega}{2} < 1, \frac{\omega}{2} < 1, \frac{\omega}{2} < 1, \frac{\omega}{2} < 1, -\frac{1}{2}(-1+\rho23)\,\omega^2 < 1,\\
\quad \frac{1}{2}(1-\rho23+\rho12\,(-1+2\,\rho23))\,\omega^2 < 1, \frac{1}{2}(1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^2 < 1,\\
\quad -\frac{1}{2}(-1+\rho23+\rho34-2\,\rho23\,\rho34+\rho12\,(-1+2\,\rho23)\,(-1+2\,\rho34))\,\omega^2 < 1,\\
\quad \frac{1}{2}(-1+\rho12)\,(-1+\rho23)\,\omega^3 < 1, \frac{1}{2}(-1+\rho23)\,(-1+\rho34)\,\omega^3 < 1,\\
\quad -\frac{1}{2}(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34)\,\omega^3 < 1,\\
\quad -\frac{1}{2}(-1+\rho12)\,(1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^3 < 1,\\
\quad -\frac{1}{4}\omega\left((-1+\rho12)\,\omega+\sqrt{1-\rho12}\,\sqrt{8-(-1+\rho12)\,\omega^2}\right) < 1,\\
\quad \frac{1}{4}\omega\left(\omega-\rho12\,\omega+\sqrt{1-\rho12}\,\sqrt{8-(-1+\rho12)\,\omega^2}\right) < 1,\\
\quad -\frac{1}{4}\omega\left((-1+\rho34)\,\omega+\sqrt{1-\rho34}\,\sqrt{8-(-1+\rho34)\,\omega^2}\right) < 1,\\
\quad \frac{1}{4}\omega\left(\omega-\rho34\,\omega+\sqrt{1-\rho34}\,\sqrt{8-(-1+\rho34)\,\omega^2}\right) < 1,\\
\quad \frac{1}{4}\left((1-\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4-\sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2\right.\\
\qquad \left.\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4}\right) < 1, \frac{1}{4}\left((1-\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4+\right.\\
\qquad \left.\sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4}\right) < 1\}
\end{array}
$$

```
Thread[-1 < eig < 1]
```

$$\Big\{\text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, -1<\frac{\omega}{2}<1, -1<\frac{\omega}{2}<1, -1<\frac{\omega}{2}<1, -1<\frac{\omega}{2}<1, -1<-\frac{1}{2}(-1+\rho23)\,\omega^2<1,$$
$$-1<\frac{1}{2}(1-\rho23+\rho12\,(-1+2\,\rho23))\,\omega^2<1, -1<\frac{1}{2}(1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^2<1,$$
$$-1<-\frac{1}{2}(-1+\rho23+\rho34-2\,\rho23\,\rho34+\rho12\,(-1+2\,\rho23)\,(-1+2\,\rho34))\,\omega^2<1,$$
$$-1<\frac{1}{2}(-1+\rho12)\,(-1+\rho23)\,\omega^3<1, -1<\frac{1}{2}(-1+\rho23)\,(-1+\rho34)\,\omega^3<1,$$
$$-1<-\frac{1}{2}(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34)\,\omega^3<1,$$
$$-1<-\frac{1}{2}(-1+\rho12)\,(1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^3<1,$$
$$-1<-\frac{1}{4}\omega\left((-1+\rho12)\,\omega+\sqrt{1-\rho12}\,\sqrt{8-(-1+\rho12)\,\omega^2}\right)<1,$$
$$-1<\frac{1}{4}\omega\left(\omega-\rho12\,\omega+\sqrt{1-\rho12}\,\sqrt{8-(-1+\rho12)\,\omega^2}\right)<1,$$
$$-1<-\frac{1}{4}\omega\left((-1+\rho34)\,\omega+\sqrt{1-\rho34}\,\sqrt{8-(-1+\rho34)\,\omega^2}\right)<1,$$
$$-1<\frac{1}{4}\omega\left(\omega-\rho34\,\omega+\sqrt{1-\rho34}\,\sqrt{8-(-1+\rho34)\,\omega^2}\right)<1,$$
$$-1<\frac{1}{4}\Big((1-\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4-\sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2$$
$$\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4}\Big)<1, -1<\frac{1}{4}\Big((1-\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4+$$
$$\sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4}\Big)<1\Big\}$$

Below we check each eigenvalues one by one and infer the boundary on ω

```
eig[[19]]
```

$$-\frac{1}{2}(-1+\rho23)\,\omega^2$$

always ≥ 0

```
eig[[19]] /. ω → 0
```

```
0
```

```
Solve[eig[[19]] == 1, ω]
```

$$\left\{\left\{\omega\to-\frac{\sqrt{2}}{\sqrt{1-\rho23}}\right\}, \left\{\omega\to\frac{\sqrt{2}}{\sqrt{1-\rho23}}\right\}\right\}$$

Therefore $\omega < \dfrac{\sqrt{2}}{\sqrt{1-\rho23}}$

```
eig[[20]]
```

$$\frac{1}{2}(1-\rho23+\rho12\,(-1+2\,\rho23))\,\omega^2$$

```
Reduce[(1 - ρ23 + ρ12 (-1 + 2 ρ23)) < 0 && 0 ≤ ρ23 ≤ .5 && 0 ≤ ρ12 ≤ .5]
```

```
Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a
  corresponding exact system and numericizing the result.
```

```
False
```

always ≥ 0

```
eig[[20]] /. ω → 0
```

```
0
```

```
Solve[eig[[20]] == 1, ω]
```

$$\left\{\left\{\omega \to -\frac{\sqrt{2}}{\sqrt{1-\rho12-\rho23+2\,\rho12\,\rho23}}\right\},\left\{\omega \to \frac{\sqrt{2}}{\sqrt{1-\rho12-\rho23+2\,\rho12\,\rho23}}\right\}\right\}$$

Therefore $\omega < \frac{\sqrt{2}}{\sqrt{1-\rho12-\rho23+2\,\rho12\,\rho23}}$

```
eig[[21]]
```

$$\frac{1}{2}\left(1-\rho34+\rho23\,(-1+2\,\rho34)\right)\omega^2$$

always ≥ 0 (symmetric with previous case)

```
eig[[21]] /. ω → 0
```

```
0
```

```
Solve[eig[[21]] == 1, ω]
```

$$\left\{\left\{\omega \to -\frac{\sqrt{2}}{\sqrt{1-\rho23-\rho34+2\,\rho23\,\rho34}}\right\},\left\{\omega \to \frac{\sqrt{2}}{\sqrt{1-\rho23-\rho34+2\,\rho23\,\rho34}}\right\}\right\}$$

Therefore $\omega < \frac{\sqrt{2}}{\sqrt{1-\rho23-\rho34+2\,\rho23\,\rho34}}$

```
eig[[22]]
```

$$-\frac{1}{2}\left(-1+\rho23+\rho34-2\,\rho23\,\rho34+\rho12\,(-1+2\,\rho23)\,(-1+2\,\rho34)\right)\omega^2$$

```
Reduce[-1/2 (-1 + ρ23 + ρ34 - 2 ρ23 ρ34 + ρ12 (-1 + 2 ρ23) (-1 + 2 ρ34)) < 0 &&
  0 ≤ ρ23 ≤ .5 && 0 ≤ ρ12 ≤ .5 && 0 ≤ ρ34 ≤ .5]
```

```
Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a
  corresponding exact system and numericizing the result.
```

```
False
```

always ≥ 0

```
eig[[22]] /. ω → 0
```

```
0
```

```
Solve[eig[[22]] == 1, ω] // FullSimplify
```

$$\left\{\left\{\omega \to -\left(\left(\sqrt{2}\right)\Big/\left(\sqrt{(1-\rho 34+\rho 23\,(-1+2\,\rho 34)+\rho 12\,(-1+\rho 23\,(2-4\,\rho 34)+2\,\rho 34))}\right)\right)\right\},\ \left\{\omega \to \left(\sqrt{2}\right)\Big/\left(\sqrt{(1-\rho 34+\rho 23\,(-1+2\,\rho 34)+\rho 12\,(-1+\rho 23\,(2-4\,\rho 34)+2\,\rho 34))}\right)\right\}\right\}$$

Therefore $\omega < \left(\sqrt{2}\right)\Big/\left(\sqrt{(1-\rho 34+\rho 23\,(-1+2\,\rho 34)+\rho 12\,(-1+\rho 23\,(2-4\,\rho 34)+2\,\rho 34))}\right)$

```
eig[[23]]
```

$$\frac{1}{2}\,(-1+\rho 12)\,(-1+\rho 23)\,\omega^3$$

always ≥ 0

```
eig[[23]] /. ω → 0
```

```
0
```

```
Solve[eig[[23]] == 1, ω] // FullSimplify
```

$$\left\{\left\{\omega \to -\frac{(-2)^{1/3}}{((-1+\rho 12)\,(-1+\rho 23))^{1/3}}\right\},\ \left\{\omega \to \frac{2^{1/3}}{((-1+\rho 12)\,(-1+\rho 23))^{1/3}}\right\},\ \left\{\omega \to \frac{(-1)^{2/3}\,2^{1/3}}{((-1+\rho 12)\,(-1+\rho 23))^{1/3}}\right\}\right\}$$

```
Out[75] /. {ρ12 → .02, ρ23 → .4}
```

```
{{ω → -0.751948 - 1.30241 i}, {ω → 1.5039}, {ω → -0.751948 + 1.30241 i}}
```

Therefore $\omega < \dfrac{2^{1/3}}{((-1+\rho 12)\,(-1+\rho 23))^{1/3}}$

```
eig[[24]]
```

$$\frac{1}{2}\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^3$$

always ≥ 0

```
eig[[24]] /. ω → 0
```

```
0
```

```
Solve[eig[[24]] == 1, ω] // FullSimplify
```

$$\left\{\left\{\omega \to -\frac{(-2)^{1/3}}{((-1+\rho 23)\,(-1+\rho 34))^{1/3}}\right\},\ \left\{\omega \to \frac{2^{1/3}}{((-1+\rho 23)\,(-1+\rho 34))^{1/3}}\right\},\ \left\{\omega \to \frac{(-1)^{2/3}\,2^{1/3}}{((-1+\rho 23)\,(-1+\rho 34))^{1/3}}\right\}\right\}$$

Therefore $\omega < \dfrac{2^{1/3}}{((-1+\rho 23)\,(-1+\rho 34))^{1/3}}$

```
eig[[25]]
```

$$-\frac{1}{2}\,(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,(-1+\rho 34)\,\omega^3$$

Reduce

$$\mathbf{Reduce}\left[-\frac{1}{2}\,(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,(-1+\rho 34)<0\;\&\&\;0\leq\rho 23\leq .5\;\&\&\;0\leq\rho 12\leq .5\;\&\&\;0\leq\rho 34\leq .5\right]$$

⋯ Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a corresponding exact system and numericizing the result.

```
False
```

always ≥ 0

```
eig[[25]] /. ω → 0
```

```
0
```

```
Solve[eig[[25]] == 1, ω] // FullSimplify
```

$$\left\{\left\{\omega\to-\frac{(-2)^{1/3}}{(-(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,(-1+\rho 34))^{1/3}}\right\},\right.$$
$$\left\{\omega\to\frac{2^{1/3}}{(-(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,(-1+\rho 34))^{1/3}}\right\},$$
$$\left.\left\{\omega\to\frac{(-1)^{2/3}\,2^{1/3}}{(-(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,(-1+\rho 34))^{1/3}}\right\}\right\}$$

Therefore $\omega<\dfrac{2^{1/3}}{(-(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,(-1+\rho 34))^{1/3}}$

```
eig[[26]]
```

$$-\frac{1}{2}\,(-1+\rho 12)\,(1-\rho 34+\rho 23\,(-1+2\,\rho 34))\,\omega^3$$

$$\mathbf{Reduce}\left[-\frac{1}{2}\,(-1+\rho 12)\,(1-\rho 34+\rho 23\,(-1+2\,\rho 34))<0\;\&\&\;0\leq\rho 23\leq .5\;\&\&\;0\leq\rho 12\leq .5\;\&\&\;0\leq\rho 34\leq .5\right]$$

⋯ Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a corresponding exact system and numericizing the result.

```
False
```

always ≥ 0

```
eig[[26]] /. ω → 0
```

```
0
```

```
Solve[eig[[26]] == 1, ω] // FullSimplify
```

$$\left\{\left\{\omega\to-\frac{(-2)^{1/3}}{(-(-1+\rho 12)\,(1-\rho 34+\rho 23\,(-1+2\,\rho 34)))^{1/3}}\right\},\right.$$
$$\left\{\omega\to\frac{2^{1/3}}{(-(-1+\rho 12)\,(1-\rho 34+\rho 23\,(-1+2\,\rho 34)))^{1/3}}\right\},$$
$$\left.\left\{\omega\to\frac{(-1)^{2/3}\,2^{1/3}}{(-(-1+\rho 12)\,(1-\rho 34+\rho 23\,(-1+2\,\rho 34)))^{1/3}}\right\}\right\}$$

Therefore $\omega<\dfrac{2^{1/3}}{(-(-1+\rho 12)\,(1-\rho 34+\rho 23\,(-1+2\,\rho 34)))^{1/3}}$

```
eig[[27]]
```

$$-\frac{1}{4}\omega\left((-1+\rho 12)\,\omega+\sqrt{1-\rho 12}\,\sqrt{8-(-1+\rho 12)\,\omega^2}\right)$$

```
Reduce[-1/4 ω ((-1 + ρ12) ω + Sqrt[1 - ρ12] Sqrt[8 - (-1 + ρ12) ω^2]) > 0 && 0 ≤ ρ12 ≤ .5 && ω > 0]
```

··· Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a corresponding exact system and numericizing the result.

```
False
```

always ≤ 0

```
Reduce[-1/4 ω ((-1 + ρ12) ω + Sqrt[1 - ρ12] Sqrt[8 - (-1 + ρ12) ω^2]) < -1 && 0 ≤ ρ12 ≤ .5 && ω > 0]
```

··· Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a corresponding exact system and numericizing the result.

```
False
```

always ≥ -1

Therefore always TRUE

```
eig[[28]]
```

$$\frac{1}{4}\omega\left(\omega-\rho 12\,\omega+\sqrt{1-\rho 12}\,\sqrt{8-(-1+\rho 12)\,\omega^2}\right)$$

```
Reduce[1/4 ω (ω - ρ12 ω + Sqrt[1 - ρ12] Sqrt[8 - (-1 + ρ12) ω^2]) < 0 && 0 ≤ ρ12 ≤ .5 && ω > 0]
```

··· Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a corresponding exact system and numericizing the result.

```
False
```

always ≥ 0

```
eig[[28]] /. ω → 0
```

```
0
```

```
Solve[eig[[28]] == 1, ω] // FullSimplify
```

$$\left\{\left\{\omega\to\frac{1}{\sqrt{1-\rho 12}}\right\}\right\}$$

Therefore $\omega < \frac{1}{\sqrt{1-\rho 12}}$

```
eig[[29]]
```

$$-\frac{1}{4}\omega\left((-1+\rho 34)\,\omega+\sqrt{1-\rho 34}\,\sqrt{8-(-1+\rho 34)\,\omega^2}\right)$$

per symmetry with eig[[27]], always ≥ -1 and always <=0

Therefore always TRUE

```
eig[[30]]
```

$$\frac{1}{4}\,\omega\left(\omega-\rho 34\,\omega+\sqrt{1-\rho 34}\,\sqrt{8-(-1+\rho 34)\,\omega^2}\right)$$

always ≥ 0

```
eig[[30]] /. ω → 0
```

0

```
Solve[eig[[30]] == 1, ω] // FullSimplify
```

$$\left\{\left\{\omega\to\frac{1}{\sqrt{1-\rho 34}}\right\}\right\}$$

Therefore $\omega < \frac{1}{\sqrt{1-\rho 34}}$

```
eig[[31]]
```

$$\frac{1}{4}\left((1-\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4-\sqrt{1-\rho 12}\,\sqrt{1-\rho 23}\,\sqrt{1-\rho 34}\,\omega^2\,\sqrt{8-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4}\right)$$

```
Reduce[1/4 ((1 - ρ12) (-1 + ρ23) (-1 + ρ34) ω^4 -
     Sqrt[1 - ρ12] Sqrt[1 - ρ23] Sqrt[1 - ρ34] ω^2 Sqrt[8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4]) > 0 &&
  0 ≤ ρ23 ≤ .5 && 0 ≤ ρ12 ≤ .5 && 0 ≤ ρ34 ≤ .5 && ω > 0]
```

Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a corresponding exact system and numericizing the result.

False

```
Reduce[1/4 ((1 - ρ12) (-1 + ρ23) (-1 + ρ34) ω^4 -
     Sqrt[1 - ρ12] Sqrt[1 - ρ23] Sqrt[1 - ρ34] ω^2 Sqrt[8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4]) < -1 &&
  0 ≤ ρ23 ≤ .5 && 0 ≤ ρ12 ≤ .5 && 0 ≤ ρ34 ≤ .5 && ω > 0]
```

Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a corresponding exact system and numericizing the result.

False

Therefore always TRUE

```
eig[[32]]
```

$$\frac{1}{4}\left((1-\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4+\sqrt{1-\rho 12}\,\sqrt{1-\rho 23}\,\sqrt{1-\rho 34}\,\omega^2\,\sqrt{8-(-1+\rho 12)\,(-1+\rho 23)\,(-1+\rho 34)\,\omega^4}\right)$$

$$\text{Reduce}\Big[\frac{1}{4}\Big((1-\rho 12)\ (-1+\rho 23)\ (-1+\rho 34)\ \omega^4 + \sqrt{1-\rho 12}\ \sqrt{1-\rho 23}\ \sqrt{1-\rho 34}\ \omega^2\ \sqrt{8-(-1+\rho 12)\ (-1+\rho 23)\ (-1+\rho 34)\ \omega^4}\Big) < 0\ \&\&\ 0 \le \rho 23 \le .5\ \&\&\ 0 \le \rho 12 \le .5\ \&\&\ 0 \le \rho 34 \le .5\ \&\&\ \omega > 0\Big]$$

··· Reduce: Reduce was unable to solve the system with inexact coefficients. The answer was obtained by solving a corresponding exact system and numericizing the result.

`False`

always ≥ 0

$$\text{eig[[32]] /. }\omega \to 0$$

`0`

$$\text{Solve}\big[\text{eig[[32]]} == 1,\ \omega\big]\ \text{// FullSimplify}$$

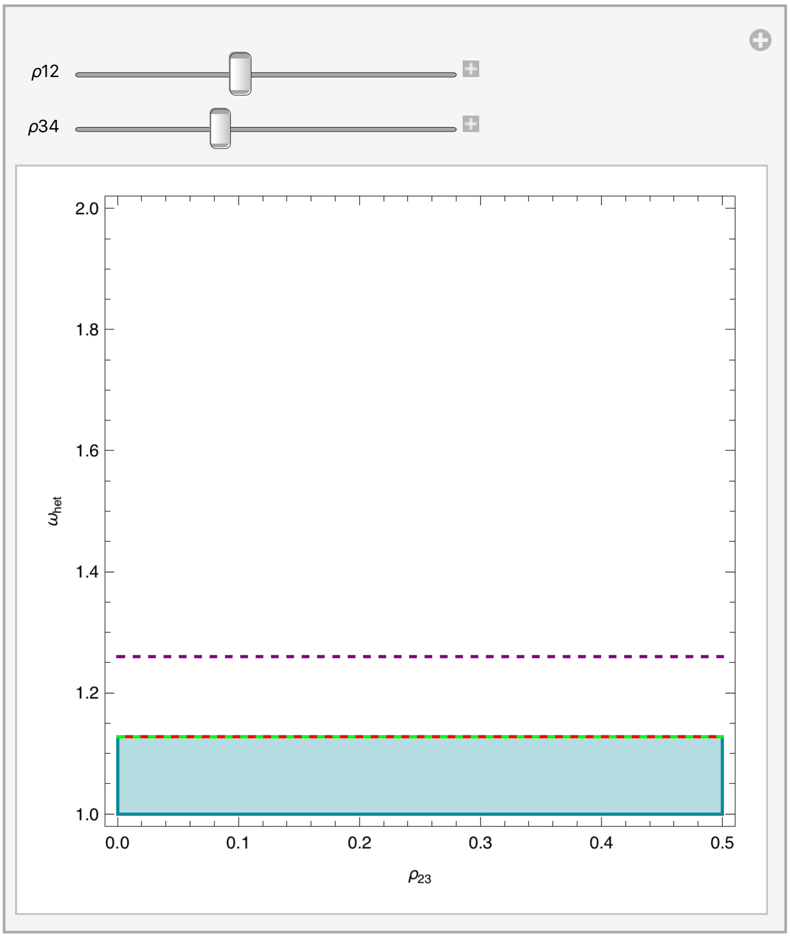
$$\Big\{\Big\{\omega \to -\frac{1}{(-(-1+\rho 12)\ (-1+\rho 23)\ (-1+\rho 34))^{1/4}}\Big\},\ \Big\{\omega \to -\frac{i}{(-(-1+\rho 12)\ (-1+\rho 23)\ (-1+\rho 34))^{1/4}}\Big\},\ \Big\{\omega \to \frac{i}{(-(-1+\rho 12)\ (-1+\rho 23)\ (-1+\rho 34))^{1/4}}\Big\},\ \Big\{\omega \to \frac{1}{(-(-1+\rho 12)\ (-1+\rho 23)\ (-1+\rho 34))^{1/4}}\Big\}\Big\}$$

Therefore $\omega < \frac{1}{(-(-1+\rho 12)\ (-1+\rho 23)\ (-1+\rho 34))^{1/4}}$

By combining each individual condition, we obtain:

$$\omega < \text{Min}\Big[\frac{\sqrt{2}}{\sqrt{1-\rho 23}},\ \frac{\sqrt{2}}{\sqrt{1-\rho 12-\rho 23+2\ \rho 12\ \rho 23}},\ \frac{\sqrt{2}}{\sqrt{1-\rho 23-\rho 34+2\ \rho 23\ \rho 34}},\ \big(\sqrt{2}\big)\Big/\big(\sqrt{(1-\rho 34+\rho 23\ (-1+2\ \rho 34)+\rho 12\ (-1+\rho 23\ (2-4\ \rho 34)+2\ \rho 34))}\big),\ \frac{2^{1/3}}{((-1+\rho 12)\ (-1+\rho 23))^{1/3}},\ \frac{2^{1/3}}{((-1+\rho 23)\ (-1+\rho 34))^{1/3}},\ \frac{2^{1/3}}{(-(1-\rho 23+\rho 12\ (-1+2\ \rho 23))\ (-1+\rho 34))^{1/3}},\ \frac{2^{1/3}}{(-(-1+\rho 12)\ (1-\rho 34+\rho 23\ (-1+2\ \rho 34)))^{1/3}},\ \frac{1}{\sqrt{1-\rho 12}},\ \frac{1}{\sqrt{1-\rho 34}},\ \frac{1}{(-(-1+\rho 12)\ (-1+\rho 23)\ (-1+\rho 34))^{1/4}}\Big]$$

```
Manipulate[Show[RegionPlot[ω < 2 && 2 + ρ23 ω^2 > ω^2 &&
    (1 - ρ23 + ρ12 (-1 + 2 ρ23)) ω^2 < 2 && (1 - ρ34 + ρ23 (-1 + 2 ρ34)) ω^2 < 2 &&
    2 + (-1 + ρ23 + ρ34 - 2 ρ23 ρ34 + ρ12 (-1 + 2 ρ23) (-1 + 2 ρ34)) ω^2 > 0 &&
    (-1 + ρ12) (-1 + ρ23) ω^3 < 2 && (-1 + ρ23) (-1 + ρ34) ω^3 < 2 &&
    2 + (1 - ρ23 + ρ12 (-1 + 2 ρ23)) (-1 + ρ34) ω^3 > 0 &&
    2 + (-1 + ρ12) (1 - ρ34 + ρ23 (-1 + 2 ρ34)) ω^3 > 0 &&
    4 + ρ12 ω^2 + √(1 - ρ12) ω √(8 + ω^2 - ρ12 ω^2) > ω^2 && √(1 - ρ12) ω √(8 - (-1 + ρ12) ω^2) <
     4 + (-1 + ρ12) ω^2 && 4 + ρ34 ω^2 + √(1 - ρ34) ω √(8 + ω^2 - ρ34 ω^2) > ω^2 &&
    √(1 - ρ34) ω √(8 - (-1 + ρ34) ω^2) < 4 + (-1 + ρ34) ω^2 && 4 + (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4 +
      √(1 - ρ12) √(1 - ρ23) √(1 - ρ34) ω^2 √(8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4) > 0 &&
    √(1 - ρ12) √(1 - ρ23) √(1 - ρ34) ω^2 √(8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4) <
     4 + (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4,
   {ρ23, 0, 0.5}, {ω, 1, 2}, FrameLabel → {ρ_23, ω_het}],

  Plot[Min[√2 / √(1 - ρ23), √2 / √(1 - ρ12 - ρ23 + 2 ρ12 ρ23), √2 / √(1 - ρ23 - ρ34 + 2 ρ23 ρ34),
    (√2) / (√(1 - ρ34 + ρ23 (-1 + 2 ρ34) + ρ12 (-1 + ρ23 (2 - 4 ρ34) + 2 ρ34))),
    2^(1/3) / ((-1 + ρ12) (-1 + ρ23))^(1/3), 2^(1/3) / ((-1 + ρ23) (-1 + ρ34))^(1/3),
    2^(1/3) / (-(1 - ρ23 + ρ12 (-1 + 2 ρ23)) (-1 + ρ34))^(1/3),
    2^(1/3) / (-(-1 + ρ12) (1 - ρ34 + ρ23 (-1 + 2 ρ34)))^(1/3), 1 / √(1 - ρ12), 1 / √(1 - ρ34),
    1 / (-(-1 + ρ12) (-1 + ρ23) (-1 + ρ34))^(1/4), 1 / (-(-1 + ρ12) (-1 + ρ23) (-1 + ρ34))^(1/4)],
   {ρ23, 0, .5}, PlotStyle → Red], Plot[{1 / √(1 - ρ12), 1 / √(1 - ρ34)}, {ρ23, 0, .5},
   PlotStyle → {{Dashed, Green}, {Dashed, Purple}}]], {ρ12, 0, .5}, {ρ34, 0, 1}]
```



$$\texttt{ListExpression} = \texttt{Min}\Big[\frac{\sqrt{2}}{\sqrt{1-\rho23}}, \frac{\sqrt{2}}{\sqrt{1-\rho12-\rho23+2\,\rho12\,\rho23}}, \frac{\sqrt{2}}{\sqrt{1-\rho23-\rho34+2\,\rho23\,\rho34}},$$

$$\left(\sqrt{2}\right)\Big/\left(\sqrt{(1-\rho34+\rho23\,(-1+2\,\rho34)+\rho12\,(-1+\rho23\,(2-4\,\rho34)+2\,\rho34))}\right),$$

$$\frac{2^{1/3}}{((-1+\rho12)\,(-1+\rho23))^{1/3}}, \frac{2^{1/3}}{((-1+\rho23)\,(-1+\rho34))^{1/3}},$$

$$\frac{2^{1/3}}{(-(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34))^{1/3}}, \frac{2^{1/3}}{(-(-1+\rho12)\,(1-\rho34+\rho23\,(-1+2\,\rho34)))^{1/3}},$$

$$\frac{1}{\sqrt{1-\rho12}}, \frac{1}{\sqrt{1-\rho34}}, \frac{1}{(-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34))^{1/4}}\Big];$$

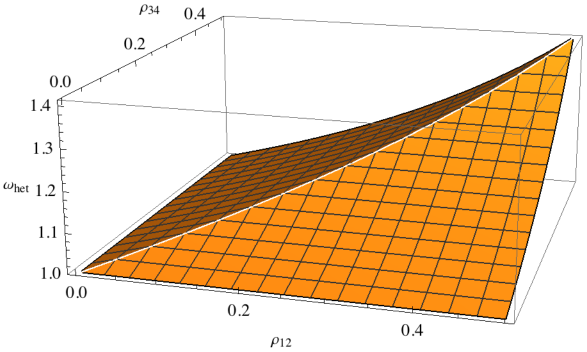
The previous expression can be reduce to two elements:

$$\texttt{Table}\Big[\texttt{Reduce}\Big[\frac{1}{\sqrt{1-\rho12}} > \texttt{ListExpression}[[\texttt{i}]]\ \&\&\ \frac{1}{\sqrt{1-\rho34}} > \texttt{ListExpression}[[\texttt{i}]]\ \&\&$$

$$0<\rho12\le 1/2\ \&\&\ 0<\rho23\le 1/2\ \&\&\ 0<\rho34\le 1/2,\ \texttt{Reals}\Big],\ \{\texttt{i}, 1, \texttt{Length}[\texttt{ListExpression}]\}\Big]$$

```
{False, False, False, False, False, False, False, False, False, False, False}
```

```
Plot3D[Min[1/√(1 - ρ34), 1/√(1 - ρ12)], {ρ12, 0, .5},
 {ρ34, 0, .5}, PlotRange → {1, √2}, AxesLabel → {"ρ12", "ρ34", "ωhet"}]
```



The network case: all loci interacts with each other (epistasis is here lethal)

Define the male fitness table

```
selectionMatrixMales4Lallϵ = Table[0 + Boole[i1 == i2 == i3 == i4],
   {i1, 0, 1}, {i2, 0, 1}, {i3, 0, 1}, {i4, 0, 1}] // Flatten
```

```
{1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1}
```

Define the female fitness table

```
selectionMatrixFemales4Lallϵ = Table[0, 256];
Do[
 indicem = 8 * i1m + 4 * i2m + 2 * i3m + i4m;
 indicef = 8 * i1f + 4 * i2f + 2 * i3f + i4f;
 indice = 16 * indicem + indicef;
 i1 = i1m + i1f;
 i2 = i2m + i2f;
 i3 = i3m + i3f;
 i4 = i4m + i4f;
 selectionMatrixFemales4Lallϵ[[indice + 1]] =
  1 * (1 + s) ^ (Boole[i1 == 1] + Boole[i2 == 1] + Boole[i3 == 1] + Boole[i4 == 1]) *
   (1 - Boole[Abs[i2 - i1] == 2 || Abs[i3 - i1] == 2 || Abs[i4 - i1] == 2 || Abs[i3 - i2] == 2 ||
       Abs[i4 - i2] == 2 || Abs[i4 - i3] == 2]), {i1m, 0, 1}, {i2m, 0, 1},
 {i3m, 0, 1}, {i4m, 0, 1}, {i1f, 0, 1}, {i2f, 0, 1}, {i3f, 0, 1}, {i4f, 0, 1}]
```

```
Table[selectionMatrixFemales4Lalle[[16 * (j - 1) + i]], {j, 1, 16}, {i, 1, 16}] // MatrixForm
```

```
 1         1+s       1+s       (1+s)^2   1+s       (1+s)^2   (1+s)^2   (1+s)^3   1+s       (1+s)^2   (1+s)^2
 1+s       0         (1+s)^2   0         (1+s)^2   0         (1+s)^3   0         (1+s)^2   0         (1+s)^3
 1+s       (1+s)^2   0         0         (1+s)^2   (1+s)^3   0         0         (1+s)^2   (1+s)^3   0
 (1+s)^2   0         0         0         (1+s)^3   0         0         0         (1+s)^3   0         0
 1+s       (1+s)^2   (1+s)^2   (1+s)^3   0         0         0         0         (1+s)^2   (1+s)^3   (1+s)^3
 (1+s)^2   0         (1+s)^3   0         0         0         0         0         (1+s)^3   0         (1+s)^4
 (1+s)^2   (1+s)^3   0         0         0         0         0         0         (1+s)^3   (1+s)^4   0
 (1+s)^3   0         0         0         0         0         0         0         (1+s)^4   (1+s)^3   (1+s)^3
 1+s       (1+s)^2   (1+s)^2   (1+s)^3   (1+s)^2   (1+s)^3   (1+s)^3   (1+s)^4   0         0         0
 (1+s)^2   0         (1+s)^3   0         (1+s)^3   0         (1+s)^4   (1+s)^3   0         0         0
 (1+s)^2   (1+s)^3   0         0         (1+s)^3   (1+s)^4   0         (1+s)^3   0         0         0
 (1+s)^3   0         0         0         (1+s)^4   (1+s)^3   (1+s)^3   (1+s)^2   0         0         0
 (1+s)^2   (1+s)^3   (1+s)^3   (1+s)^4   0         0         0         (1+s)^3   0         0         0
 (1+s)^3   0         (1+s)^4   (1+s)^3   0         0         (1+s)^3   (1+s)^2   0         0         (1+s)^3
 (1+s)^3   (1+s)^4   0         (1+s)^3   0         (1+s)^3   0         (1+s)^2   0         (1+s)^3   0
 (1+s)^4   (1+s)^3   (1+s)^3   (1+s)^2   (1+s)^3   (1+s)^2   (1+s)^2   1+s       (1+s)^3   (1+s)^2   (1+s)^2
```

```
Dynamic4LGenalle = Dynamics4L[gamF4L, hapM4L, ρ12, ρ23, ρ34, ρ21,
   ρ32, ρ43, selectionMatrixMales4Lalle, selectionMatrixFemales4Lalle];

Dynamic4LGenalle
```

```
{{h1/(h1+h16), 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, h16/(h1+h16)}, {⋯ 1 ⋯}}

large output    show less    show more    show all    set size limit...
```

Define the Jacobian matrix

```
Jac4LGenalle =
  D[Flatten[Dynamic4LGenalle], {{g1, g2, g3, g4, g5, g6, g7, g8, g9, g10, g11, g12, g13,
     g14, g15, g16, h1, h2, h3, h4, h5, h6, h7, h8, h9, h10, h11, h12, h13, h14, h15, h16}}];

Jac4LGenalle /. exclusion
```

```
{{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
  0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, -1},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
 {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1},
```

$$\{0,\ -1-s+\frac{1+s}{2},\ -1-s+\frac{1+s}{2},\ -(1+s)^2+\frac{1}{2}(1+s)^2\rho43,$$

$$-1-s+\frac{1+s}{2},\ -(1+s)^2+\frac{1}{2}(1+s)^2\rho23\,\rho34+\frac{1}{2}(1+s)^2\rho32\,\rho43,$$

$$-(1+s)^2+\frac{1}{2}(1+s)^2\rho32,\ -(1+s)^3+\frac{1}{2}(1+s)^3\rho32\,\rho43,\ -1-s+\frac{1+s}{2},$$

$$-(1+s)^2+\frac{1}{2}(1+s)^2\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^2\rho12\,\rho32\,\rho34+\frac{1}{2}(1+s)^2\rho12\,\rho23\,\rho43+$$

$$\frac{1}{2}(1+s)^2\rho21\,\rho32\,\rho43,\ -(1+s)^2+\frac{1}{2}(1+s)^2\rho12\,\rho23+\frac{1}{2}(1+s)^2\rho21\,\rho32,$$

$$-(1+s)^3+\frac{1}{2}(1+s)^3\rho12\,\rho23\,\rho43+\frac{1}{2}(1+s)^3\rho21\,\rho32\,\rho43,\ -(1+s)^2+\frac{1}{2}(1+s)^2\rho21,$$

$$-(1+s)^3+\frac{1}{2}(1+s)^3\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\rho21\,\rho32\,\rho43,\ -(1+s)^3+\frac{1}{2}(1+s)^3\rho21\,\rho32,$$

$$-(1+s)^4+\frac{1}{2}(1+s)^4\rho21\,\rho32\,\rho43,\ 0,\ -1-s+\frac{1+s}{2},\ -1-s+\frac{1+s}{2},$$

$$-(1+s)^2+\frac{1}{2}(1+s)^2\rho43,\ -1-s+\frac{1+s}{2},\ -(1+s)^2+\frac{1}{2}(1+s)^2\rho23\,\rho34+\frac{1}{2}(1+s)^2\rho32\,\rho43,$$

$$-(1+s)^2+\frac{1}{2}(1+s)^2\rho32,\ -(1+s)^3+\frac{1}{2}(1+s)^3\rho32\,\rho43,\ -1-s+\frac{1+s}{2},$$

$$-(1+s)^2+\frac{1}{2}(1+s)^2\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^2\rho12\,\rho32\,\rho34+\frac{1}{2}(1+s)^2\rho12\,\rho23\,\rho43+$$

$$\frac{1}{2}(1+s)^2\rho21\,\rho32\,\rho43,\ -(1+s)^2+\frac{1}{2}(1+s)^2\rho12\,\rho23+\frac{1}{2}(1+s)^2\rho21\,\rho32,$$

$$-(1+s)^3+\frac{1}{2}(1+s)^3\rho12\,\rho23\,\rho43+\frac{1}{2}(1+s)^3\rho21\,\rho32\,\rho43,\ -(1+s)^2+\frac{1}{2}(1+s)^2\rho21,$$

$$-(1+s)^3+\frac{1}{2}(1+s)^3\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\rho21\,\rho32\,\rho43,$$

$$-(1+s)^3+\frac{1}{2}(1+s)^3\rho21\,\rho32,\ -(1+s)^4+\frac{1}{2}(1+s)^4\rho21\,\rho32\,\rho43\},$$

$$\{0,\ \frac{1+s}{2},\ 0,\ \frac{1}{2}(1+s)^2\rho34,\ 0,\ \frac{1}{2}(1+s)^2\rho32\,\rho34+\frac{1}{2}(1+s)^2\rho23\,\rho43,\ 0,\ \frac{1}{2}(1+s)^3\rho32\,\rho34,\ 0,$$

$$\frac{1}{2}(1+s)^2\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^2\rho21\,\rho32\,\rho34+\frac{1}{2}(1+s)^2\rho21\,\rho23\,\rho43+\frac{1}{2}(1+s)^2\rho12\,\rho32\,\rho43,$$

$$0,\ \frac{1}{2}(1+s)^3\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\rho21\,\rho32\,\rho34,\ 0,$$

$$\frac{1}{2}(1+s)^3\rho21\,\rho32\,\rho34+\frac{1}{2}(1+s)^3\rho21\,\rho23\,\rho43,\ 0,\ \frac{1}{2}(1+s)^4\rho21\,\rho32\,\rho34,\ 0,\ \frac{1+s}{2},$$

$$0,\ \frac{1}{2}(1+s)^2\rho34,\ 0,\ \frac{1}{2}(1+s)^2\rho32\,\rho34+\frac{1}{2}(1+s)^2\rho23\,\rho43,\ 0,\ \frac{1}{2}(1+s)^3\rho32\,\rho34,\ 0,$$

$$\frac{1}{2}(1+s)^2\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^2\rho21\,\rho32\,\rho34+\frac{1}{2}(1+s)^2\rho21\,\rho23\,\rho43+\frac{1}{2}(1+s)^2\rho12\,\rho32\,\rho43,$$

$$0,\ \frac{1}{2}(1+s)^3\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\rho21\,\rho32\,\rho34,\ 0,$$

$$\frac{1}{2}(1+s)^3\rho21\,\rho32\,\rho34+\frac{1}{2}(1+s)^3\rho21\,\rho23\,\rho43,\ 0,\ \frac{1}{2}(1+s)^4\rho21\,\rho32\,\rho34\},$$

$$\{0,\ 0,\ \frac{1+s}{2},\ \frac{1}{2}(1+s)^2\rho34,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho23,\ \frac{1}{2}(1+s)^3\rho23\,\rho34,\ 0,\ 0,$$

$$\frac{1}{2}(1+s)^2\rho21\,\rho23+\frac{1}{2}(1+s)^2\rho12\,\rho32,\ \frac{1}{2}(1+s)^3\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\rho12\,\rho32\,\rho34,$$

$$0,\ 0,\ \frac{1}{2}(1+s)^3\rho21\,\rho23,\ \frac{1}{2}(1+s)^4\rho21\,\rho23\,\rho34,\ 0,\ 0,\ \frac{1+s}{2},\ \frac{1}{2}(1+s)^2\rho34,\ 0,\ 0,$$

$$\frac{1}{2}(1+s)^2\rho23,\ \frac{1}{2}(1+s)^3\rho23\,\rho34,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho21\,\rho23+\frac{1}{2}(1+s)^2\rho12\,\rho32,$$

$$\frac{1}{2}(1+s)^3\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\rho12\,\rho32\,\rho34,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\rho21\,\rho23,$$

$$\frac{1}{2}(1+s)^4\rho21\,\rho23\,\rho34\Big\},\ \Big\{0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho43,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\rho23\,\rho43,$$

$$0,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\rho21\,\rho23\,\rho43+\frac{1}{2}(1+s)^3\rho12\,\rho32\,\rho43,\ 0,\ 0,\ 0,$$

$$\frac{1}{2}(1+s)^4\rho21\,\rho23\,\rho43,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho43,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\rho23\,\rho43,\ 0,\ 0,$$

$$0,\ \frac{1}{2}(1+s)^3\rho21\,\rho23\,\rho43+\frac{1}{2}(1+s)^3\rho12\,\rho32\,\rho43,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^4\rho21\,\rho23\,\rho43\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ \frac{1+s}{2},\ \frac{1}{2}(1+s)^2\rho32\,\rho34+\frac{1}{2}(1+s)^2\rho23\,\rho43,\ \frac{1}{2}(1+s)^2\rho23,\ \frac{1}{2}(1+s)^3\rho23\,\rho43,$$

$$0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho12,\ \frac{1}{2}(1+s)^3\rho12\,\rho32\,\rho34+\frac{1}{2}(1+s)^3\rho12\,\rho23\,\rho43,\ \frac{1}{2}(1+s)^3\rho12\,\rho23,$$

$$\frac{1}{2}(1+s)^4\rho12\,\rho23\,\rho43,\ 0,\ 0,\ 0,\ 0,\ \frac{1+s}{2},\ \frac{1}{2}(1+s)^2\rho32\,\rho34+\frac{1}{2}(1+s)^2\rho23\,\rho43,$$

$$\frac{1}{2}(1+s)^2\rho23,\ \frac{1}{2}(1+s)^3\rho23\,\rho43,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho12,$$

$$\frac{1}{2}(1+s)^3\rho12\,\rho32\,\rho34+\frac{1}{2}(1+s)^3\rho12\,\rho23\,\rho43,\ \frac{1}{2}(1+s)^3\rho12\,\rho23,\ \frac{1}{2}(1+s)^4\rho12\,\rho23\,\rho43\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho23\,\rho34+\frac{1}{2}(1+s)^2\rho32\,\rho43,\ 0,\ \frac{1}{2}(1+s)^3\rho23\,\rho34,\ 0,\ 0,$$

$$0,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\rho12\,\rho32\,\rho43,\ 0,\ \frac{1}{2}(1+s)^4\rho12\,\rho23\,\rho34,$$

$$0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho23\,\rho34+\frac{1}{2}(1+s)^2\rho32\,\rho43,\ 0,\ \frac{1}{2}(1+s)^3\rho23\,\rho34,\ 0,\ 0,$$

$$0,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\rho12\,\rho32\,\rho43,\ 0,\ \frac{1}{2}(1+s)^4\rho12\,\rho23\,\rho34\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho32,\ \frac{1}{2}(1+s)^3\rho32\,\rho34,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,$$

$$\frac{1}{2}(1+s)^3\rho12\,\rho32,\ \frac{1}{2}(1+s)^4\rho12\,\rho32\,\rho34,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\rho32,$$

$$\frac{1}{2}(1+s)^3\rho32\,\rho34,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\rho12\,\rho32,\ \frac{1}{2}(1+s)^4\rho12\,\rho32\,\rho34\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\rho32\,\rho43,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,$$

$$\frac{1}{2}(1+s)^4\rho12\,\rho32\,\rho43,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\rho32\,\rho43,\ 0,\ 0,$$

$$0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^4\rho12\,\rho32\,\rho43\Big\},\ \Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1+s}{2},$$

$$\frac{1}{2}(1+s)^2\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^2\rho21\,\rho32\,\rho34+\frac{1}{2}(1+s)^2\rho21\,\rho23\,\rho43+\frac{1}{2}(1+s)^2\rho12\,\rho32\,\rho43,$$

$$\frac{1}{2}(1+s)^2\,\rho21\,\rho23+\frac{1}{2}(1+s)^2\,\rho12\,\rho32,\ \frac{1}{2}(1+s)^3\,\rho21\,\rho23\,\rho43+\frac{1}{2}(1+s)^3\,\rho12\,\rho32\,\rho43,$$

$$\frac{1}{2}(1+s)^2\,\rho12,\ \frac{1}{2}(1+s)^3\,\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\,\rho12\,\rho32\,\rho43,$$

$$\frac{1}{2}(1+s)^3\,\rho12\,\rho32,\ \frac{1}{2}(1+s)^4\,\rho12\,\rho32\,\rho43,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1+s}{2},$$

$$\frac{1}{2}(1+s)^2\,\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^2\,\rho21\,\rho32\,\rho34+\frac{1}{2}(1+s)^2\,\rho21\,\rho23\,\rho43+\frac{1}{2}(1+s)^2\,\rho12\,\rho32\,\rho43,$$

$$\frac{1}{2}(1+s)^2\,\rho21\,\rho23+\frac{1}{2}(1+s)^2\,\rho12\,\rho32,\ \frac{1}{2}(1+s)^3\,\rho21\,\rho23\,\rho43+\frac{1}{2}(1+s)^3\,\rho12\,\rho32\,\rho43,$$

$$\frac{1}{2}(1+s)^2\,\rho12,\ \frac{1}{2}(1+s)^3\,\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\,\rho12\,\rho32\,\rho43,$$

$$\frac{1}{2}(1+s)^3\,\rho12\,\rho32,\ \frac{1}{2}(1+s)^4\,\rho12\,\rho32\,\rho43\Big\},\ \Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,$$

$$\frac{1}{2}(1+s)^2\,\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^2\,\rho12\,\rho32\,\rho34+\frac{1}{2}(1+s)^2\,\rho12\,\rho23\,\rho43+\frac{1}{2}(1+s)^2\,\rho21\,\rho32\,\rho43,$$

$$0,\ \frac{1}{2}(1+s)^3\,\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\,\rho12\,\rho32\,\rho34,\ 0,$$

$$\frac{1}{2}(1+s)^3\,\rho12\,\rho32\,\rho34+\frac{1}{2}(1+s)^3\,\rho12\,\rho23\,\rho43,\ 0,\ \frac{1}{2}(1+s)^4\,\rho12\,\rho32\,\rho34,\ 0,\ 0,\ 0,\ 0,$$

$$0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\,\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^2\,\rho12\,\rho32\,\rho34+\frac{1}{2}(1+s)^2\,\rho12\,\rho23\,\rho43+$$

$$\frac{1}{2}(1+s)^2\,\rho21\,\rho32\,\rho43,\ 0,\ \frac{1}{2}(1+s)^3\,\rho21\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\,\rho12\,\rho32\,\rho34,$$

$$0,\ \frac{1}{2}(1+s)^3\,\rho12\,\rho32\,\rho34+\frac{1}{2}(1+s)^3\,\rho12\,\rho23\,\rho43,\ 0,\ \frac{1}{2}(1+s)^4\,\rho12\,\rho32\,\rho34\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\,\rho12\,\rho23+\frac{1}{2}(1+s)^2\,\rho21\,\rho32,$$

$$\frac{1}{2}(1+s)^3\,\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\,\rho21\,\rho32\,\rho34,\ 0,\ 0,$$

$$\frac{1}{2}(1+s)^3\,\rho12\,\rho23,\ \frac{1}{2}(1+s)^4\,\rho12\,\rho23\,\rho34,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,$$

$$\frac{1}{2}(1+s)^2\,\rho12\,\rho23+\frac{1}{2}(1+s)^2\,\rho21\,\rho32,\ \frac{1}{2}(1+s)^3\,\rho12\,\rho23\,\rho34+\frac{1}{2}(1+s)^3\,\rho21\,\rho32\,\rho34,$$

$$0,\ 0,\ \frac{1}{2}(1+s)^3\,\rho12\,\rho23,\ \frac{1}{2}(1+s)^4\,\rho12\,\rho23\,\rho34\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^3\,\rho12\,\rho23\,\rho43+\frac{1}{2}(1+s)^3\,\rho21\,\rho32\,\rho43,$$

$$0,\ 0,\ 0,\ \frac{1}{2}(1+s)^4\,\rho12\,\rho23\,\rho43,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,$$

$$\frac{1}{2}(1+s)^3\,\rho12\,\rho23\,\rho43+\frac{1}{2}(1+s)^3\,\rho21\,\rho32\,\rho43,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^4\,\rho12\,\rho23\,\rho43\Big\},$$

$$\Big\{0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\,\rho21,$$

$$\frac{1}{2}(1+s)^3\,\rho21\,\rho32\,\rho34+\frac{1}{2}(1+s)^3\,\rho21\,\rho23\,\rho43,\ \frac{1}{2}(1+s)^3\,\rho21\,\rho23,$$

$$\frac{1}{2}(1+s)^4\,\rho21\,\rho23\,\rho43,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{1}{2}(1+s)^2\,\rho21,$$

$$
\begin{aligned}
&\tfrac{1}{2}(1+s)^3\,\rho21\,\rho32\,\rho34+\tfrac{1}{2}(1+s)^3\,\rho21\,\rho23\,\rho43,\ \tfrac{1}{2}(1+s)^3\,\rho21\,\rho23,\ \tfrac{1}{2}(1+s)^4\,\rho21\,\rho23\,\rho43\Big\},\\
&\Big\{0,0,0,0,0,0,0,0,0,0,0,0,0,\ \tfrac{1}{2}(1+s)^3\,\rho21\,\rho23\,\rho34+\tfrac{1}{2}(1+s)^3\,\rho21\,\rho32\,\rho43,\\
&\ 0,\ \tfrac{1}{2}(1+s)^4\,\rho21\,\rho23\,\rho34,\ 0,0,0,0,0,0,0,0,0,0,0,0,0,\\
&\ \tfrac{1}{2}(1+s)^3\,\rho21\,\rho23\,\rho34+\tfrac{1}{2}(1+s)^3\,\rho21\,\rho32\,\rho43,\ 0,\ \tfrac{1}{2}(1+s)^4\,\rho21\,\rho23\,\rho34\Big\},\\
&\Big\{0,0,0,0,0,0,0,0,0,0,0,0,0,0,\ \tfrac{1}{2}(1+s)^3\,\rho21\,\rho32,\ \tfrac{1}{2}(1+s)^4\,\rho21\,\rho32\,\rho34,\\
&\ 0,0,0,0,0,0,0,0,0,0,0,0,0,0,\ \tfrac{1}{2}(1+s)^3\,\rho21\,\rho32,\ \tfrac{1}{2}(1+s)^4\,\rho21\,\rho32\,\rho34\Big\},\\
&\Big\{0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,\ \tfrac{1}{2}(1+s)^4\,\rho21\,\rho32\,\rho43,\ 0,\\
&\ 0,0,0,0,0,0,0,0,0,0,0,0,0,0,\ \tfrac{1}{2}(1+s)^4\,\rho21\,\rho32\,\rho43\Big\}\Big\}
\end{aligned}
$$

Define the Eigenvalues, with using again ρ21=1-ρ12 to avoid unwanted simplification by Mathematica

```
eigall∈ = Eigenvalues[Out[74]] /.
   {s → ω - 1, ρ21 → 1 - ρ12, ρ32 → 1 - ρ23, ρ43 → 1 - ρ34} // FullSimplify
```

$$
\begin{aligned}
&\Big\{0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,\ \tfrac{\omega}{2},\ \tfrac{\omega}{2},\ \tfrac{\omega}{2},\ \tfrac{\omega}{2},\ -\tfrac{1}{2}(-1+\rho12)\,\omega^2,\\
&\ -\tfrac{1}{2}(-1+\rho23)\,\omega^2,\ \tfrac{1}{2}(-1+\rho12)(-1+\rho23)\,\omega^3,\ \tfrac{1}{2}(1-\rho23+\rho12\,(-1+2\,\rho23))\,\omega^2,\\
&\ -\tfrac{1}{2}(-1+\rho34)\,\omega^2,\ \tfrac{1}{2}(-1+\rho23)(-1+\rho34)\,\omega^3,\ \tfrac{1}{2}(1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^2,\\
&\ -\tfrac{1}{2}(-1+\rho23+\rho34-2\,\rho23\,\rho34+\rho12\,(-1+2\,\rho23)(-1+2\,\rho34))\,\omega^2,\\
&\ -\tfrac{1}{2}(-1+\rho12)(1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^3,\ -\tfrac{1}{2}(1-\rho23+\rho12\,(-1+2\,\rho23))(-1+\rho34)\,\omega^3,\\
&\ \tfrac{1}{4}\Big(-(-1+\rho12)(-1+\rho23)(-1+\rho34)\,\omega^4-\sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2\\
&\qquad\sqrt{8-(-1+\rho12)(-1+\rho23)(-1+\rho34)\,\omega^4}\Big),\ \tfrac{1}{4}\Big(-(-1+\rho12)(-1+\rho23)(-1+\rho34)\,\omega^4+\\
&\qquad\sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{8-(-1+\rho12)(-1+\rho23)(-1+\rho34)\,\omega^4}\Big)\Big\}
\end{aligned}
$$

$$\text{eigalle} = \Big\{0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, \frac{\omega}{2}, \frac{\omega}{2}, \frac{\omega}{2}, \frac{\omega}{2}, -\frac{1}{2}(-1+\rho 12)\,\omega^2,$$
$$-\frac{1}{2}(-1+\rho 23)\,\omega^2, \frac{1}{2}(-1+\rho 12)(-1+\rho 23)\,\omega^3, \frac{1}{2}(1-\rho 23+\rho 12(-1+2\rho 23))\,\omega^2,$$
$$-\frac{1}{2}(-1+\rho 34)\,\omega^2, \frac{1}{2}(-1+\rho 23)(-1+\rho 34)\,\omega^3, \frac{1}{2}(1-\rho 34+\rho 23(-1+2\rho 34))\,\omega^2,$$
$$-\frac{1}{2}(-1+\rho 23+\rho 34-2\rho 23\,\rho 34+\rho 12(-1+2\rho 23)(-1+2\rho 34))\,\omega^2,$$
$$-\frac{1}{2}(-1+\rho 12)(1-\rho 34+\rho 23(-1+2\rho 34))\,\omega^3, -\frac{1}{2}(1-\rho 23+\rho 12(-1+2\rho 23))(-1+\rho 34)\,\omega^3,$$
$$\frac{1}{4}\Big(-(-1+\rho 12)(-1+\rho 23)(-1+\rho 34)\,\omega^4-\sqrt{1-\rho 12}\,\sqrt{1-\rho 23}\,\sqrt{1-\rho 34}\,\omega^2$$
$$\sqrt{8-(-1+\rho 12)(-1+\rho 23)(-1+\rho 34)\,\omega^4}\Big), \frac{1}{4}\Big(-(-1+\rho 12)(-1+\rho 23)(-1+\rho 34)\,\omega^4+$$
$$\sqrt{1-\rho 12}\,\sqrt{1-\rho 23}\,\sqrt{1-\rho 34}\,\omega^2\,\sqrt{8-(-1+\rho 12)(-1+\rho 23)(-1+\rho 34)\,\omega^4}\Big)\Big\};$$

Case 1 Equidistant loci

For free recombination

```
Apply[And, Thread[eigalle < 1]] /. {ρ12 → 1 / 2, ρ23 -> 1 / 2, ρ34 → 1 / 2} // Simplify
```

$$-2<\omega<2\;\&\&\;32+\omega^2\sqrt{64+\omega^4}>\omega^4\;\&\&\;\omega^4+\omega^2\sqrt{64+\omega^4}<32$$

```
Reduce[
  -2 < ω < 2 && 32 + ω^2 Sqrt[64 + ω^4] > ω^4 && ω^4 + ω^2 Sqrt[64 + ω^4] < 32 && ω > 1 && 0 ≤ r ≤ 1 / 2, Reals] // N
```

$$1.<\omega<1.68179\;\&\&\;0.\le r\le 0.5$$

```
Solve [x ^ 4 == 8]
```

$$\{\{x\to -2^{3/4}\}, \{x\to -i\,2^{3/4}\}, \{x\to i\,2^{3/4}\}, \{x\to 2^{3/4}\}\}$$

```
Apply[And, Thread[eigalle > -1]] /. {ρ12 → 1 / 2, ρ23 -> 1 / 2, ρ34 → 1 / 2} // Simplify
```

$$2+\omega>0\;\&\&\;\omega^2\sqrt{64+\omega^4}<32+\omega^4\;\&\&\;32+\omega^4+\omega^2\sqrt{64+\omega^4}>0$$

```
Reduce[
  2 + ω > 0 && ω^2 Sqrt[64 + ω^4] < 32 + ω^4 && 32 + ω^4 + ω^2 Sqrt[64 + ω^4] > 0 && ω > 1 && 0 ≤ r ≤ 1 / 2, Reals] // N
```

$$\omega>1.\;\&\&\;0.\le r\le 0.5$$

For arbitrary recombination

```
Apply[And, Thread[eigalle < 1]] /. {ρ12 → r, ρ23 → r, ρ34 → r} // Simplify
```

$$\omega<2\;\&\&\;2+r\,\omega^2>\omega^2\;\&\&\;(1-2r+2r^2)\,\omega^2<2\;\&\&\;(1-3r+6r^2-4r^3)\,\omega^2<2\;\&\&\;(-1+r)^2\omega^3<2\;\&\&$$
$$(1-3r+4r^2-2r^3)\,\omega^3<2\;\&\&\;4+(-1+r)^3\omega^4+(1-r)^{3/2}\omega^2\sqrt{8-(-1+r)^3\omega^4}>0\;\&\&$$
$$\frac{1}{4}\left(-(-1+r)^3\omega^4+(1-r)^{3/2}\omega^2\sqrt{8-(-1+r)^3\omega^4}\right)<1$$

$$\begin{aligned}&\textbf{Reduce}\Big[\omega < 2 \,\&\&\, 2 + r\,\omega^2 > \omega^2 \,\&\&\, \left(1 - 2\,r + 2\,r^2\right)\omega^2 < 2 \,\&\&\\ &\quad \left(1 - 3\,r + 6\,r^2 - 4\,r^3\right)\omega^2 < 2 \,\&\&\, (-1 + r)^2\,\omega^3 < 2 \,\&\&\, \left(1 - 3\,r + 4\,r^2 - 2\,r^3\right)\omega^3 < 2 \,\&\&\\ &\quad 4 + (-1 + r)^3\,\omega^4 + (1 - r)^{3/2}\,\omega^2\,\sqrt{8 - (-1 + r)^3\,\omega^4} > 0 \,\&\&\\ &\quad \frac{1}{4}\left(-(-1 + r)^3\,\omega^4 + (1 - r)^{3/2}\,\omega^2\,\sqrt{8 - (-1 + r)^3\,\omega^4}\right) < 1 \,\&\&\, \omega > 1 \,\&\&\, 0 \le r \le 1/2,\ \omega,\ \textbf{Reals}\Big]\end{aligned}$$

$$0 < r \le \frac{1}{2} \,\&\&\, 1 < \omega < \text{Root}\left[1 + \left(-1 + 3\,r - 3\,r^2 + r^3\right)\#1^4\,\&,\ 2\right]$$

$$0 < r \le \frac{1}{2} \,\&\&\, 1 < \omega < \textbf{Root}\left[1 + \left(-1 + 3\,r - 3\,r^2 + r^3\right)\#1^4\,\&,\ 2\right] \ //\ \textbf{N}$$

$$0. < r \le 0.5 \,\&\&\, 1. < \omega < \text{Root}\left[1 + \left(-1 + 3\,r - 3\,r^2 + r^3\right)\#1^4\,\&,\ 2\right]$$

$$\textbf{Reduce}\left[\left(-1 + 3\,r - 3\,r^2 + r^3\right) < 0\right]$$

$$r < 1$$

```
Solve[1 - a x^4 == 0, x]
```

$$\left\{\left\{x \to -\frac{1}{a^{1/4}}\right\},\ \left\{x \to -\frac{i}{a^{1/4}}\right\},\ \left\{x \to \frac{i}{a^{1/4}}\right\},\ \left\{x \to \frac{1}{a^{1/4}}\right\}\right\}$$

$$\omega < 1 \Big/ \left(-1 + 3\,r - 3\,r^2 + r^3\right)\,\texttt{^}\,(1/4)$$

$$\omega < \frac{1}{\left(-1 + 3\,r - 3\,r^2 + r^3\right)^{1/4}}$$

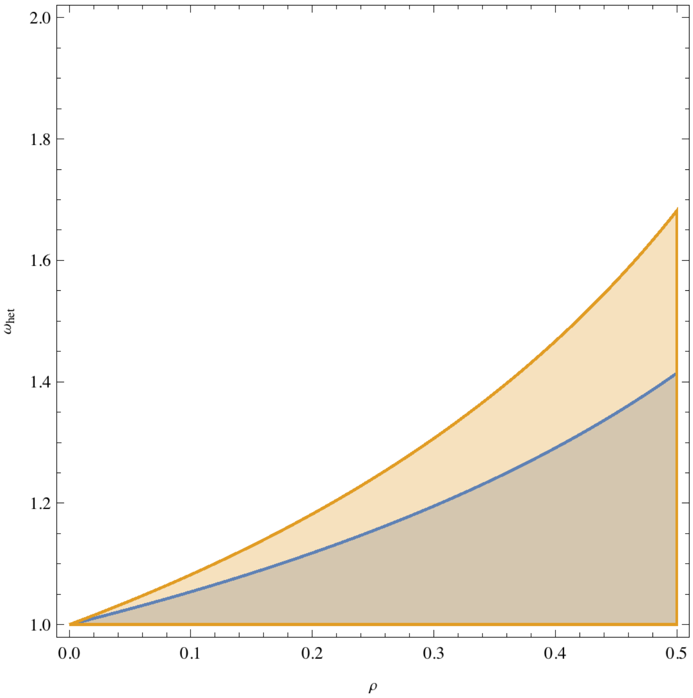
$$\textbf{Apply}\left[\textbf{And},\ \textbf{Thread}\left[\textbf{eigalle} > -1\right]\right]\ /.\ \{\rho12 \to r,\ \rho23 \to r,\ \rho34 \to r\}\ //\ \textbf{Simplify}$$

$$\begin{aligned}&2 + \omega > 0 \,\&\&\, (-1 + r)\,\omega^2 < 2 \,\&\&\, 2 + \left(1 - 2\,r + 2\,r^2\right)\omega^2 > 0 \,\&\&\\ &\quad \left(-1 + 3\,r - 6\,r^2 + 4\,r^3\right)\omega^2 < 2 \,\&\&\, 2 + (-1 + r)^2\,\omega^3 > 0 \,\&\&\, \left(-1 + 3\,r - 4\,r^2 + 2\,r^3\right)\omega^3 < 2 \,\&\&\\ &\quad (-1 + r)^3\,\omega^4 + (1 - r)^{3/2}\,\omega^2\,\sqrt{8 - (-1 + r)^3\,\omega^4} < 4 \,\&\&\, (-1 + r)^3\,\omega^4 < 4 + (1 - r)^{3/2}\,\omega^2\,\sqrt{8 - (-1 + r)^3\,\omega^4}\end{aligned}$$

$$\begin{aligned}&\textbf{Reduce}\Big[2 + \omega > 0 \,\&\&\, (-1 + r)\,\omega^2 < 2 \,\&\&\\ &\quad 2 + \left(1 - 2\,r + 2\,r^2\right)\omega^2 > 0 \,\&\&\, \left(-1 + 3\,r - 6\,r^2 + 4\,r^3\right)\omega^2 < 2 \,\&\&\, 2 + (-1 + r)^2\,\omega^3 > 0 \,\&\&\\ &\quad \left(-1 + 3\,r - 4\,r^2 + 2\,r^3\right)\omega^3 < 2 \,\&\&\, (-1 + r)^3\,\omega^4 + (1 - r)^{3/2}\,\omega^2\,\sqrt{8 - (-1 + r)^3\,\omega^4} < 4 \,\&\&\\ &\quad (-1 + r)^3\,\omega^4 < 4 + (1 - r)^{3/2}\,\omega^2\,\sqrt{8 - (-1 + r)^3\,\omega^4} \,\&\&\, \omega > 1 \,\&\&\, 0 \le r \le 1/2,\ \omega,\ \textbf{Reals}\Big]\end{aligned}$$

$$0 \le r \le \frac{1}{2} \,\&\&\, \omega > 1$$

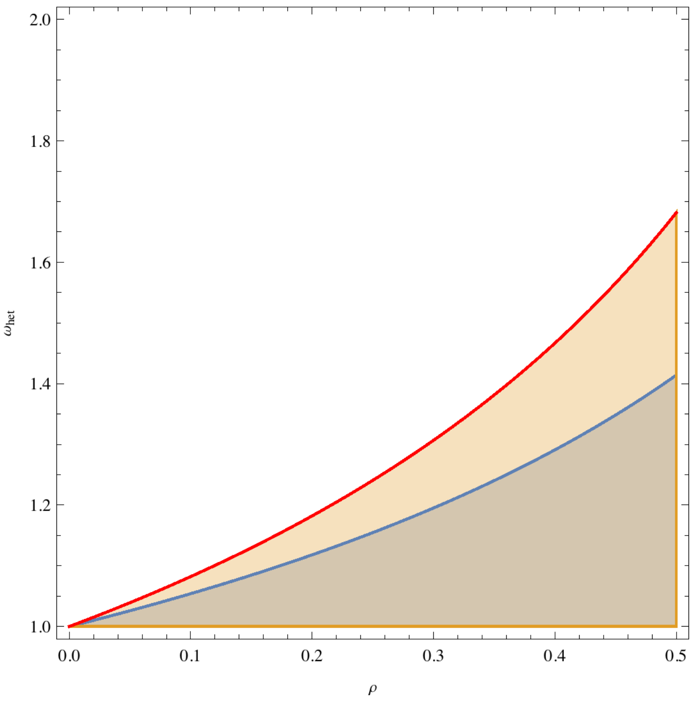
```
RegionPlot[
 {0 < r ≤ 1/2 && 1 < ω < √(1/(1 - r)), 0 < r ≤ 1/2 && 1 < ω < Root[1 + (-1 + 3 r - 3 r^2 + r^3) #1^4 &, 2]},
 {r, 0, .5}, {ω, 1, 2}, FrameLabel → {ρ, ω_het}]
 (* 2 independent inc. versus a 4 locus inc.*)
```



$$\texttt{Show}\Big[\texttt{RegionPlot}\Big[\Big\{0 < r \le \frac{1}{2}\ \&\&\ 1 < \omega < \sqrt{\frac{1}{1-r}},\ 0 < r \le \frac{1}{2}\ \&\&\ 1 < \omega < \texttt{Root}\big[1 + \left(-1 + 3\,r - 3\,r^2 + r^3\right)\#1^4\ \&,\ 2\big]\Big\},$$

$$\{r,\ 0,\ .5\},\ \{\omega,\ 1,\ 2\},\ \texttt{FrameLabel} \to \{\rho,\ \omega_{\text{het}}\}\Big],$$

$$\texttt{Plot}\Big[\frac{1}{\left(1 - 3\,r + 3\,r^2 - r^3\right)^{1/4}},\ \{r,\ 0,\ .5\},\ \texttt{PlotStyle} \to \texttt{Red}\Big]\Big]$$



Case 2: 2 Loci per choromosome

$$\texttt{Apply}\big[\texttt{And},\ \texttt{Thread}\big[\texttt{eigalle} < 1\big]\big]\ \texttt{/.}\ \{\rho 23 \to 1/2\}\ \texttt{//}\ \texttt{Simplify}$$

$$\omega < 2\ \&\&\ \omega^2 < 4\ \&\&$$
$$(-1+\rho 12)\,(-1+\rho 34)\,\omega^4 < 8 + \sqrt{1-\rho 12}\,\sqrt{1-\rho 34}\,\omega^2\,\sqrt{16+(-1+\rho 12)\,(-1+\rho 34)\,\omega^4}\ \&\&$$
$$(-1+\rho 12)\,(-1+\rho 34)\,\omega^4 + \sqrt{1-\rho 12}\,\sqrt{1-\rho 34}\,\omega^2\,\sqrt{16+(-1+\rho 12)\,(-1+\rho 34)\,\omega^4} < 8\ \&\&$$
$$2+\rho 12\,\omega^2 > \omega^2\ \&\&\ 2+\rho 34\,\omega^2 > \omega^2\ \&\&\ 4+\rho 12\,\omega^3 > \omega^3\ \&\&\ 4+\rho 34\,\omega^3 > \omega^3$$

$$\texttt{Reduce}\big[\omega < 2\ \&\&\ \omega^2 < 4\ \&\&$$
$$(-1+\rho 12)\,(-1+\rho 34)\,\omega^4 < 8 + \sqrt{1-\rho 12}\,\sqrt{1-\rho 34}\,\omega^2\,\sqrt{16+(-1+\rho 12)\,(-1+\rho 34)\,\omega^4}\ \&\&$$
$$(-1+\rho 12)\,(-1+\rho 34)\,\omega^4 + \sqrt{1-\rho 12}\,\sqrt{1-\rho 34}\,\omega^2\,\sqrt{16+(-1+\rho 12)\,(-1+\rho 34)\,\omega^4} < 8\ \&\&$$
$$2+\rho 12\,\omega^2 > \omega^2\ \&\&\ 2+\rho 34\,\omega^2 > \omega^2\ \&\&\ 4+\rho 12\,\omega^3 > \omega^3\ \&\&\ 4+\rho 34\,\omega^3 > \omega^3\ \&\&$$
$$\omega > 1\ \&\&\ 0 \le \rho 12 \le 1/2\ \&\&\ 0 \le \rho 34 \le 1/2,\ \omega,\ \texttt{Reals}\big]\ \texttt{//}\ \texttt{N}$$

$$0. \le \rho 34 \le 0.5\ \&\&\ 0. \le \rho 12 \le 0.5\ \&\&\ 1. < \omega < \texttt{Root}\big[-2 + (1 - \rho 12 - \rho 34 + \rho 12\,\rho 34)\,\#1^4\ \&,\ 2\big]$$

$$\texttt{Reduce}[(1 - \rho 12 - \rho 34 + \rho 12\,\rho 34) > 0\ \&\&\ 0 \le \rho 12 \le 1/2\ \&\&\ 0 \le \rho 34 \le 1/2]$$

$$0 \le \rho 34 \le \frac{1}{2}\ \&\&\ 0 \le \rho 12 \le \frac{1}{2}$$

```
Solve[-2 + a x^4 == 0, x]
```

$$\left\{\left\{x \to -\frac{2^{1/4}}{a^{1/4}}\right\}, \left\{x \to -\frac{i\, 2^{1/4}}{a^{1/4}}\right\}, \left\{x \to \frac{i\, 2^{1/4}}{a^{1/4}}\right\}, \left\{x \to \frac{2^{1/4}}{a^{1/4}}\right\}\right\}$$

```
ω < 2^(1/4) / (1 - ρ12 - ρ34 + ρ12 ρ34) ^(1/4)
```

$$\omega < \frac{2^{1/4}}{(1-\rho12-\rho34+\rho12\,\rho34)^{1/4}}$$

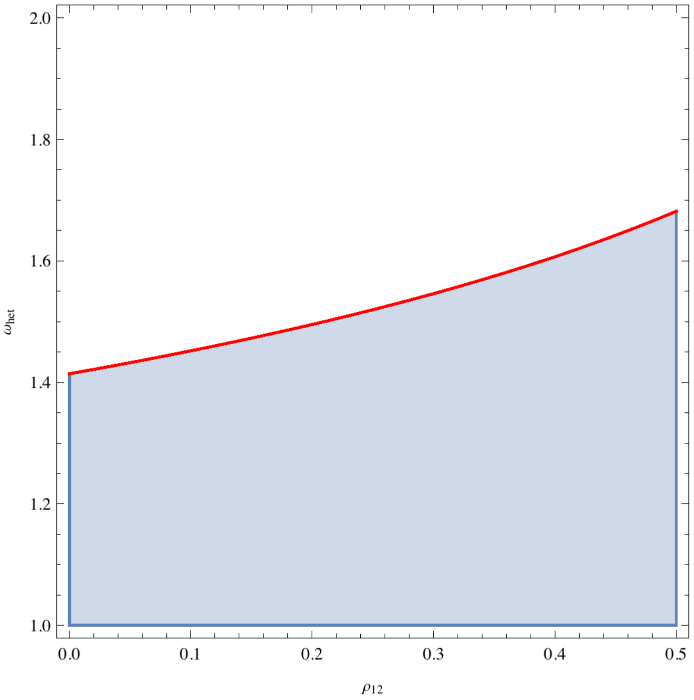
```
Apply[And, Thread[eigallε > -1]] /. {ρ23 -> 1/2} // Simplify
```

$$(-1+\rho12)\,\omega^2 < 2 \,\&\&\, (-1+\rho34)\,\omega^2 < 2 \,\&\&\, (-1+\rho12)\,\omega^3 < 4 \,\&\&\, (-1+\rho34)\,\omega^3 < 4 \,\&\&\, 2+\omega > 0 \,\&\&\, 4+\omega^2 > 0 \,\&\&\, 8+(-1+\rho12)\,(-1+\rho34)\,\omega^4 > \sqrt{1-\rho12}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{16+(-1+\rho12)\,(-1+\rho34)\,\omega^4} \,\&\&\, 8+(-1+\rho12)\,(-1+\rho34)\,\omega^4+\sqrt{1-\rho12}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{16+(-1+\rho12)\,(-1+\rho34)\,\omega^4} > 0$$

$$\text{Reduce}\Big[(-1+\rho12)\,\omega^2 < 2 \,\&\&\, (-1+\rho34)\,\omega^2 < 2 \,\&\&\, (-1+\rho12)\,\omega^3 < 4 \,\&\&\, (-1+\rho34)\,\omega^3 < 4 \,\&\&\, 2+\omega > 0 \,\&\&\, 4+\omega^2 > 0 \,\&\&\, 8+(-1+\rho12)\,(-1+\rho34)\,\omega^4 > \sqrt{1-\rho12}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{16+(-1+\rho12)\,(-1+\rho34)\,\omega^4} \,\&\&\, 8+(-1+\rho12)\,(-1+\rho34)\,\omega^4+\sqrt{1-\rho12}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{16+(-1+\rho12)\,(-1+\rho34)\,\omega^4} > 0 \,\&\&\, \omega > 1 \,\&\&\, 0 \le \rho12 \le 1/2 \,\&\&\, 0 \le \rho34 \le 1/2,\ \omega,\ \text{Reals}\Big]\ //\ \text{N}$$

$$0. \le \rho34 \le 0.5 \,\&\&\, 0. \le \rho12 \le 0.5 \,\&\&\, \omega > 1.$$

$$\text{With}\Big[\{\rho34 = .5\},\ \text{Show}\Big[\text{RegionPlot}\Big[\Big\{\omega < 2 \,\&\&\, \omega^2 < 4 \,\&\&\, (-1+\rho12)\,(-1+\rho34)\,\omega^4 < 8+\sqrt{1-\rho12}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{16+(-1+\rho12)\,(-1+\rho34)\,\omega^4} \,\&\&\, (-1+\rho12)\,(-1+\rho34)\,\omega^4+\sqrt{1-\rho12}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{16+(-1+\rho12)\,(-1+\rho34)\,\omega^4} < 8 \,\&\&\, 2+\rho12\,\omega^2 > \omega^2 \,\&\&\, 2+\rho34\,\omega^2 > \omega^2 \,\&\&\, 4+\rho12\,\omega^3 > \omega^3 \,\&\&\, 4+\rho34\,\omega^3 > \omega^3 \,\&\&\, \omega > 1 \,\&\&\, 0 \le \rho12 \le 1/2 \,\&\&\, 0 \le \rho34 \le 1/2\Big\},\ \{\rho12, 0, .5\},\ \{\omega, 1, 2\},\ \text{FrameLabel} \to \{\rho_{12}, \omega_{\text{het}}\}\Big],\ \text{Plot}\Big[\frac{2^{1/4}}{(1-\rho12-\rho34+\rho12\,\rho34)^{1/4}},\ \{\rho12, 0, .5\},\ \text{PlotStyle} \to \text{Red}\Big]\Big]\Big]$$



Case 3: Arbitrary recombination rate

```
Apply[And, Thread[eigallε < 1]] // Simplify
```

$$\omega < 2 \,\&\&\, 2 + \rho12\,\omega^2 > \omega^2 \,\&\&\, 2 + \rho23\,\omega^2 > \omega^2 \,\&\&\, (-1+\rho12)\,(-1+\rho23)\,\omega^3 < 2 \,\&\&\, (1-\rho23+\rho12\,(-1+2\,\rho23))\,\omega^2 < 2 \,\&\&\, 2+\rho34\,\omega^2 > \omega^2 \,\&\&\, (-1+\rho23)\,(-1+\rho34)\,\omega^3 < 2 \,\&\&\, (1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^2 < 2 \,\&\&\, 2+(-1+\rho23+\rho34-2\,\rho23\,\rho34+\rho12\,(-1+2\,\rho23)\,(-1+2\,\rho34))\,\omega^2 > 0 \,\&\&\, 2+(-1+\rho12)\,(1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^3 > 0 \,\&\&\, 2+(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34)\,\omega^3 > 0 \,\&\&\, 4+(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4 + \sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4} > 0 \,\&\&\, \sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4} < 4+(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4$$

```
Thread[eigallε < 1] // Simplify
```

$$\{\text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \text{True}, \omega < 2, \omega < 2, \omega < 2, \omega < 2, 2+\rho12\,\omega^2 > \omega^2, 2+\rho23\,\omega^2 > \omega^2, (-1+\rho12)\,(-1+\rho23)\,\omega^3 < 2, (1-\rho23+\rho12\,(-1+2\,\rho23))\,\omega^2 < 2, 2+\rho34\,\omega^2 > \omega^2, (-1+\rho23)\,(-1+\rho34)\,\omega^3 < 2, (1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^2 < 2, 2+(-1+\rho23+\rho34-2\,\rho23\,\rho34+\rho12\,(-1+2\,\rho23)\,(-1+2\,\rho34))\,\omega^2 > 0, 2+(-1+\rho12)\,(1-\rho34+\rho23\,(-1+2\,\rho34))\,\omega^3 > 0, 2+(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34)\,\omega^3 > 0, 4+(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4 + \sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4} > 0, \sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^2\,\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4} < 4+(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^4\}$$

Define the conditions for every single eigenvalues for the stability of the exclusion case

```
eigallε[[21]]
```

$$-\frac{1}{2}\,(-1+\rho12)\,\omega^2$$

$$\text{Reduce}\left[-\frac{1}{2}\,(-1+\rho12)\,\omega^2 < 0 \,\&\&\, \omega > 0 \,\&\&\, 0 \le \rho12 \le 1/2\right]$$

```
False
```

Always ≥ 0

```
eigallε[[21]] /. ω → 0
```

```
0
```

```
Solve[eigallε[[21]] == 1, ω]
```

$$\left\{\left\{\omega \to -\frac{\sqrt{2}}{\sqrt{1-\rho12}}\right\}, \left\{\omega \to \frac{\sqrt{2}}{\sqrt{1-\rho12}}\right\}\right\}$$

Therefore $\omega < \frac{\sqrt{2}}{\sqrt{1-\rho12}}$

```
eigallε[[22]]
```

$$-\frac{1}{2}\,(-1+\rho23)\,\omega^2$$

Always ≥ 0

```
eigallϵ[[22]] /. ω → 0
```

```
0
```

```
Solve[eigallϵ[[22]] == 1, ω]
```

$$\left\{\left\{\omega \to -\frac{\sqrt{2}}{\sqrt{1-\rho 23}}\right\}, \left\{\omega \to \frac{\sqrt{2}}{\sqrt{1-\rho 23}}\right\}\right\}$$

Therefore $\omega < \dfrac{\sqrt{2}}{\sqrt{1-\rho 23}}$

```
eigallϵ[[23]]
```

$$\frac{1}{2}\,(-1+\rho 12)\,(-1+\rho 23)\,\omega^3$$

Always ≥ 0

```
eigallϵ[[23]] /. ω → 0
```

```
0
```

```
Solve[eigallϵ[[23]] == 1, ω]
```

$$\left\{\left\{\omega \to -\frac{(-2)^{1/3}}{(1-\rho 12-\rho 23+\rho 12\,\rho 23)^{1/3}}\right\}, \left\{\omega \to \frac{2^{1/3}}{(1-\rho 12-\rho 23+\rho 12\,\rho 23)^{1/3}}\right\}, \left\{\omega \to \frac{(-1)^{2/3}\,2^{1/3}}{(1-\rho 12-\rho 23+\rho 12\,\rho 23)^{1/3}}\right\}\right\}$$

Therefore $\omega < \dfrac{2^{1/3}}{(1-\rho 12-\rho 23+\rho 12\,\rho 23)^{1/3}}$

```
eigallϵ[[24]]
```

$$\frac{1}{2}\,(1-\rho 23+\rho 12\,(-1+2\,\rho 23))\,\omega^2$$

```
Reduce[1/2 (1 - ρ23 + ρ12 (-1 + 2 ρ23)) ω^2 < 0 && ω > 0 && 0 ≤ ρ12 ≤ 1/2 && 0 ≤ ρ23 ≤ 1/2]
```

```
False
```

Always ≥ 0

```
eigallϵ[[24]] /. ω → 0
```

```
0
```

```
Solve[eigallϵ[[24]] == 1, ω]
```

$$\left\{\left\{\omega \to -\frac{\sqrt{2}}{\sqrt{1-\rho 12-\rho 23+2\,\rho 12\,\rho 23}}\right\}, \left\{\omega \to \frac{\sqrt{2}}{\sqrt{1-\rho 12-\rho 23+2\,\rho 12\,\rho 23}}\right\}\right\}$$

Therefore $\omega < \dfrac{\sqrt{2}}{\sqrt{1-\rho 12-\rho 23+2\,\rho 12\,\rho 23}}$

eigallϵ[[25]]

$$-\frac{1}{2}(-1+\rho34)\,\omega^2$$

Always ≥ 0

eigallϵ[[25]] /. ω → 0

0

Solve[eigallϵ[[25]] == 1, ω]

$$\left\{\left\{\omega\to-\frac{\sqrt{2}}{\sqrt{1-\rho34}}\right\},\left\{\omega\to\frac{\sqrt{2}}{\sqrt{1-\rho34}}\right\}\right\}$$

Therefore $\omega<\dfrac{\sqrt{2}}{\sqrt{1-\rho34}}$

eigallϵ[[26]]

$$\frac{1}{2}(-1+\rho23)(-1+\rho34)\,\omega^3$$

Always ≥ 0

eigallϵ[[26]] /. ω → 0

0

Solve[eigallϵ[[26]] == 1, ω]

$$\left\{\left\{\omega\to-\frac{(-2)^{1/3}}{(1-\rho23-\rho34+\rho23\,\rho34)^{1/3}}\right\},\left\{\omega\to\frac{2^{1/3}}{(1-\rho23-\rho34+\rho23\,\rho34)^{1/3}}\right\},\left\{\omega\to\frac{(-1)^{2/3}\,2^{1/3}}{(1-\rho23-\rho34+\rho23\,\rho34)^{1/3}}\right\}\right\}$$

Therefore $\omega<\dfrac{2^{1/3}}{(1-\rho23-\rho34+\rho23\,\rho34)^{1/3}}$

eigallϵ[[27]]

$$\frac{1}{2}(1-\rho34+\rho23(-1+2\,\rho34))\,\omega^2$$

$$\mathbf{Reduce}\left[\frac{1}{2}(1-\rho34+\rho23(-1+2\,\rho34))\,\omega^2<0\,\&\&\,\omega>0\,\&\&\,0\le\rho34\le1/2\,\&\&\,0\le\rho23\le1/2\right]$$

False

Always ≥ 0

eigallϵ[[27]] /. ω → 0

0

Solve[eigallϵ[[27]] == 1, ω]

$$\left\{\left\{\omega\to-\frac{\sqrt{2}}{\sqrt{1-\rho23-\rho34+2\,\rho23\,\rho34}}\right\},\left\{\omega\to\frac{\sqrt{2}}{\sqrt{1-\rho23-\rho34+2\,\rho23\,\rho34}}\right\}\right\}$$

Therefore $\omega < \dfrac{\sqrt{2}}{\sqrt{1 - \rho 23 - \rho 34 + 2\,\rho 23\,\rho 34}}$

```
eigalleϵ[[28]]
```

$$-\frac{1}{2}\,(-1 + \rho 23 + \rho 34 - 2\,\rho 23\,\rho 34 + \rho 12\,(-1 + 2\,\rho 23)\,(-1 + 2\,\rho 34))\,\omega^2$$

$$\text{Reduce}\Big[-\frac{1}{2}\,(-1 + \rho 23 + \rho 34 - 2\,\rho 23\,\rho 34 + \rho 12\,(-1 + 2\,\rho 23)\,(-1 + 2\,\rho 34))\,\omega^2 < 0\ \&\&\ \omega > 0\ \&\&\ 0 \le \rho 34 \le 1/2\ \&\&\ 0 \le \rho 23 \le 1/2\ \&\&\ 0 \le \rho 12 \le 1/2\Big]$$

```
False
```

Always ≥ 0

```
eigalleϵ[[28]] /. ω → 0
```

```
0
```

```
Solve[eigalleϵ[[28]] == 1, ω] // FullSimplify
```

$$\Big\{\Big\{\omega \to -\Big(\big(\sqrt{2}\big)\Big/\Big(\sqrt{(1 - \rho 34 + \rho 23\,(-1 + 2\,\rho 34) + \rho 12\,(-1 + \rho 23\,(2 - 4\,\rho 34) + 2\,\rho 34))}\Big)\Big)\Big\},$$
$$\Big\{\omega \to \big(\sqrt{2}\big)\Big/\Big(\sqrt{(1 - \rho 34 + \rho 23\,(-1 + 2\,\rho 34) + \rho 12\,(-1 + \rho 23\,(2 - 4\,\rho 34) + 2\,\rho 34))}\Big)\Big\}\Big\}$$

Therefore $\omega < \big(\sqrt{2}\big)\Big/\Big(\sqrt{(1 - \rho 34 + \rho 23\,(-1 + 2\,\rho 34) + \rho 12\,(-1 + \rho 23\,(2 - 4\,\rho 34) + 2\,\rho 34))}\Big)$

```
eigalleϵ[[29]]
```

$$-\frac{1}{2}\,(-1 + \rho 12)\,(1 - \rho 34 + \rho 23\,(-1 + 2\,\rho 34))\,\omega^3$$

$$\text{Reduce}\Big[-\frac{1}{2}\,(-1 + \rho 12)\,(1 - \rho 34 + \rho 23\,(-1 + 2\,\rho 34))\,\omega^3 < 0\ \&\&\ \omega > 0\ \&\&\ 0 \le \rho 34 \le 1/2\ \&\&\ 0 \le \rho 23 \le 1/2\ \&\&\ 0 \le \rho 12 \le 1/2\Big]$$

```
False
```

Always ≥ 0

```
eigalleϵ[[29]] /. ω → 0
```

```
0
```

```
Solve[eigalleϵ[[29]] == 1, ω] // FullSimplify
```

$$\Big\{\Big\{\omega \to -\frac{(-2)^{1/3}}{(-(-1 + \rho 12)\,(1 - \rho 34 + \rho 23\,(-1 + 2\,\rho 34)))^{1/3}}\Big\},$$
$$\Big\{\omega \to \frac{2^{1/3}}{(-(-1 + \rho 12)\,(1 - \rho 34 + \rho 23\,(-1 + 2\,\rho 34)))^{1/3}}\Big\},$$
$$\Big\{\omega \to \frac{(-1)^{2/3}\,2^{1/3}}{(-(-1 + \rho 12)\,(1 - \rho 34 + \rho 23\,(-1 + 2\,\rho 34)))^{1/3}}\Big\}\Big\}$$

Therefore $\omega < \dfrac{2^{1/3}}{(-(-1 + \rho 12)\,(1 - \rho 34 + \rho 23\,(-1 + 2\,\rho 34)))^{1/3}}$

```
eigallϵ[[30]]
```

$$-\frac{1}{2}\,(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34)\,\omega^{3}$$

Always ≥ 0 per symmetry with the previous case

```
eigallϵ[[30]] /. ω → 0
```

0

```
Solve[eigallϵ[[30]] == 1, ω] // FullSimplify
```

$$\left\{\left\{\omega\to-\frac{(-2)^{1/3}}{(-(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34))^{1/3}}\right\},\right.$$
$$\left\{\omega\to\frac{2^{1/3}}{(-(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34))^{1/3}}\right\},$$
$$\left.\left\{\omega\to\frac{(-1)^{2/3}\,2^{1/3}}{(-(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34))^{1/3}}\right\}\right\}$$

Therefore $\omega<\dfrac{2^{1/3}}{(-(1-\rho23+\rho12\,(-1+2\,\rho23))\,(-1+\rho34))^{1/3}}$

```
eigallϵ[[31]]
```

$$\frac{1}{4}\left((1-\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^{4}-\sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^{2}\,\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^{4}}\right)$$

```
Reduce[1/4 ((1 - ρ12) (-1 + ρ23) (-1 + ρ34) ω^4 -
      Sqrt[1 - ρ12] Sqrt[1 - ρ23] Sqrt[1 - ρ34] ω^2 Sqrt[8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4]) > 0 &&
  ω > 0 && 0 ≤ ρ34 ≤ 1/2 && 0 ≤ ρ23 ≤ 1/2 && 0 ≤ ρ12 ≤ 1/2]
```

False

```
Reduce[1/4 ((1 - ρ12) (-1 + ρ23) (-1 + ρ34) ω^4 -
      Sqrt[1 - ρ12] Sqrt[1 - ρ23] Sqrt[1 - ρ34] ω^2 Sqrt[8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4]) < -1 &&
  ω > 0 && 0 ≤ ρ34 ≤ 1/2 && 0 ≤ ρ23 ≤ 1/2 && 0 ≤ ρ12 ≤ 1/2]
```

False

Therefore always True

```
eigallϵ[[32]]
```

$$\frac{1}{4}\left((1-\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^{4}+\sqrt{1-\rho12}\,\sqrt{1-\rho23}\,\sqrt{1-\rho34}\,\omega^{2}\,\sqrt{8-(-1+\rho12)\,(-1+\rho23)\,(-1+\rho34)\,\omega^{4}}\right)$$

$$\mathbf{Reduce}\Big[\frac{1}{4}\Big((1-\rho12)\ (-1+\rho23)\ (-1+\rho34)\ \omega^4+\sqrt{1-\rho12}\ \sqrt{1-\rho23}\ \sqrt{1-\rho34}\ \omega^2\ \sqrt{8-(-1+\rho12)\ (-1+\rho23)\ (-1+\rho34)\ \omega^4}\Big)<0\ \&\&\ \omega>0\ \&\&\ 0\le\rho34\le1/2\ \&\&\ 0\le\rho23\le1/2\ \&\&\ 0\le\rho12\le1/2\Big]$$

```
False
```

Always ≥ 0

```
eigalle[[32]] /. ω → 0
```

```
0
```

```
Solve[eigalle[[32]] == 1, ω] // FullSimplify
```

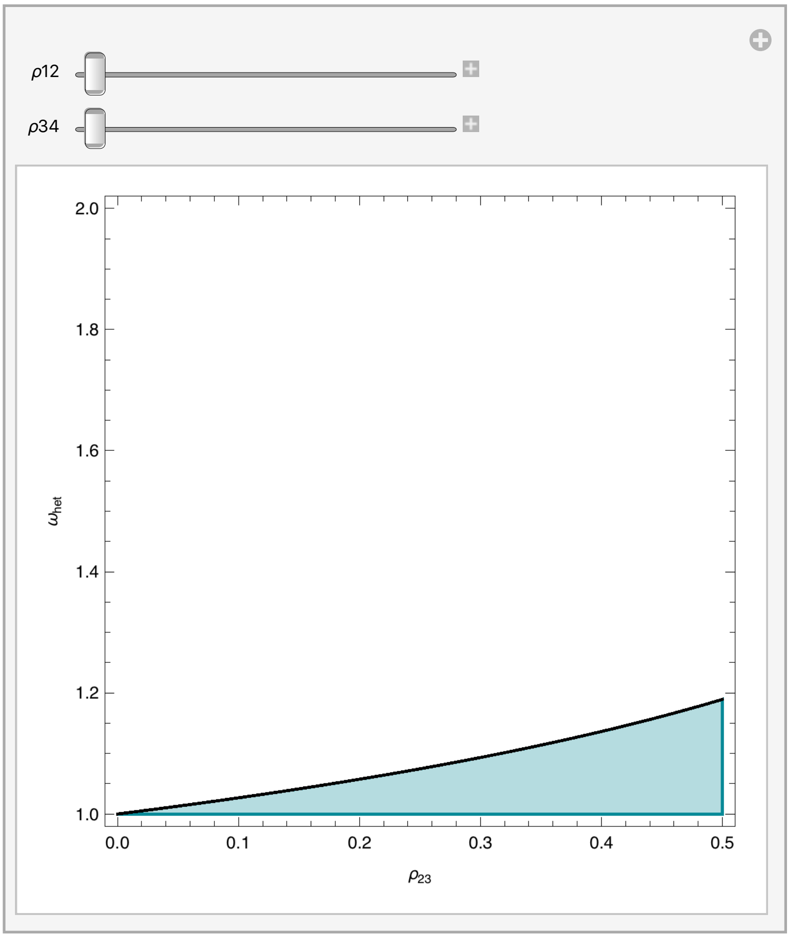
$$\Big\{\Big\{\omega\to-\frac{1}{(-(-1+\rho12)\ (-1+\rho23)\ (-1+\rho34))^{1/4}}\Big\},\ \Big\{\omega\to-\frac{i}{(-(-1+\rho12)\ (-1+\rho23)\ (-1+\rho34))^{1/4}}\Big\},\ \Big\{\omega\to\frac{i}{(-(-1+\rho12)\ (-1+\rho23)\ (-1+\rho34))^{1/4}}\Big\},\ \Big\{\omega\to\frac{1}{(-(-1+\rho12)\ (-1+\rho23)\ (-1+\rho34))^{1/4}}\Big\}\Big\}$$

$$\text{Therefore }\omega<\frac{1}{(-(-1+\rho12)\ (-1+\rho23)\ (-1+\rho34))^{1/4}}$$

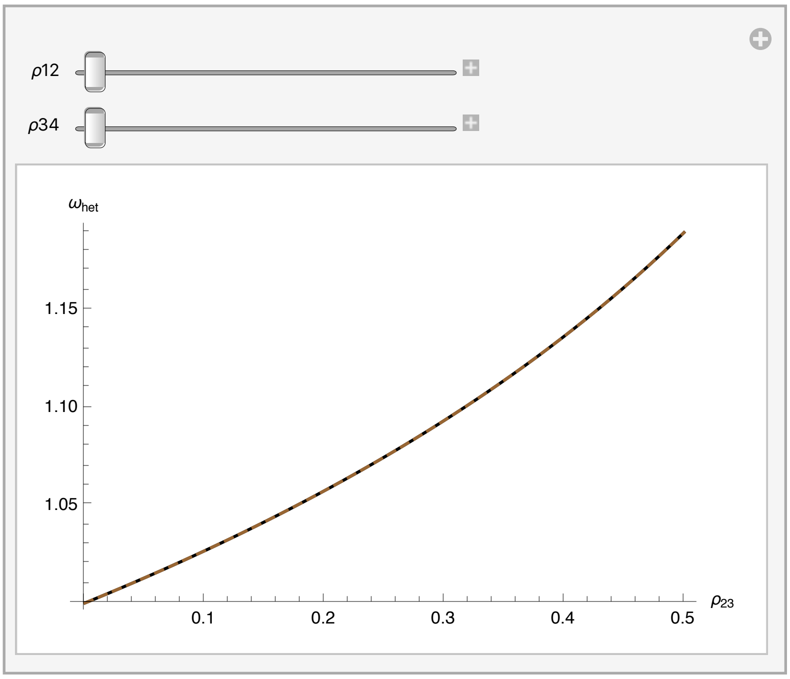
Put all the conditions together

$$\mathbf{List\omega}=\Big\{\frac{\sqrt{2}}{\sqrt{1-\rho12}},\ \frac{\sqrt{2}}{\sqrt{1-\rho23}},\ \frac{2^{1/3}}{(1-\rho12-\rho23+\rho12\ \rho23)^{1/3}},\ \frac{\sqrt{2}}{\sqrt{1-\rho12-\rho23+2\ \rho12\ \rho23}},\ \frac{\sqrt{2}}{\sqrt{1-\rho34}},\ \frac{2^{1/3}}{(1-\rho23-\rho34+\rho23\ \rho34)^{1/3}},\ \frac{\sqrt{2}}{\sqrt{1-\rho23-\rho34+2\ \rho23\ \rho34}},$$
$$\big(\sqrt{2}\big)\Big/\big(\sqrt{(1-\rho34+\rho23\ (-1+2\ \rho34)+\rho12\ (-1+\rho23\ (2-4\ \rho34)+2\ \rho34))}\big),$$
$$\frac{2^{1/3}}{(-(-1+\rho12)\ (1-\rho34+\rho23\ (-1+2\ \rho34)))^{1/3}},$$
$$\frac{2^{1/3}}{(-(1-\rho23+\rho12\ (-1+2\ \rho23))\ (-1+\rho34))^{1/3}},\ \frac{1}{(-(-1+\rho12)\ (-1+\rho23)\ (-1+\rho34))^{1/4}}\Big\};$$

```
Manipulate[Show[RegionPlot[ω < 2 && 2 + ρ12 ω^2 > ω^2 && 2 + ρ23 ω^2 > ω^2 &&
    (-1 + ρ12) (-1 + ρ23) ω^3 < 2 && (1 - ρ23 + ρ12 (-1 + 2 ρ23)) ω^2 < 2 &&
    2 + ρ34 ω^2 > ω^2 && (-1 + ρ23) (-1 + ρ34) ω^3 < 2 && (1 - ρ34 + ρ23 (-1 + 2 ρ34)) ω^2 < 2 &&
    2 + (-1 + ρ23 + ρ34 - 2 ρ23 ρ34 + ρ12 (-1 + 2 ρ23) (-1 + 2 ρ34)) ω^2 > 0 &&
    2 + (-1 + ρ12) (1 - ρ34 + ρ23 (-1 + 2 ρ34)) ω^3 > 0 &&
    2 + (1 - ρ23 + ρ12 (-1 + 2 ρ23)) (-1 + ρ34) ω^3 > 0 && 4 + (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4 +
      √(1 - ρ12) √(1 - ρ23) √(1 - ρ34) ω^2 √(8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4) > 0 &&
    √(1 - ρ12) √(1 - ρ23) √(1 - ρ34) ω^2 √(8 - (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4) <
     4 + (-1 + ρ12) (-1 + ρ23) (-1 + ρ34) ω^4,
   {ρ23, 0, .5}, {ω, 1, 2}, FrameLabel → {"ρ23", "ωhet"}],
  Plot[Min[√2/√(1 - ρ12), √2/√(1 - ρ23), 2^(1/3)/(1 - ρ12 - ρ23 + ρ12 ρ23)^(1/3), √2/√(1 - ρ12 - ρ23 + 2 ρ12 ρ23),
     √2/√(1 - ρ34), 2^(1/3)/(1 - ρ23 - ρ34 + ρ23 ρ34)^(1/3), √2/√(1 - ρ23 - ρ34 + 2 ρ23 ρ34),
     (√2) / (√(1 - ρ34 + ρ23 (-1 + 2 ρ34) + ρ12 (-1 + ρ23 (2 - 4 ρ34) + 2 ρ34))),
     2^(1/3)/(-(-1 + ρ12) (1 - ρ34 + ρ23 (-1 + 2 ρ34)))^(1/3),
     2^(1/3)/(-(1 - ρ23 + ρ12 (-1 + 2 ρ23)) (-1 + ρ34))^(1/3), 1/(-(-1 + ρ12) (-1 + ρ23) (-1 + ρ34))^(1/4)],
   {ρ23, 0, .5}, PlotStyle → Black]], {ρ12, 0, .5}, {ρ34, 0, .5}]
```


ρ12
ρ34
2.0
1.8
1.6
1.4
1.2
1.0
ω_{het}
0.0
0.1
0.2
0.3
0.4
0.5
ρ_{23}

```
Manipulate[
 Show[Plot[Min[√2/√(1 - ρ12), √2/√(1 - ρ23), 2^(1/3)/(1 - ρ12 - ρ23 + ρ12 ρ23)^(1/3), √2/√(1 - ρ12 - ρ23 + 2 ρ12 ρ23),
     √2/√(1 - ρ34), 2^(1/3)/(1 - ρ23 - ρ34 + ρ23 ρ34)^(1/3), √2/√(1 - ρ23 - ρ34 + 2 ρ23 ρ34),
     (√2) / (√(1 - ρ34 + ρ23 (-1 + 2 ρ34) + ρ12 (-1 + ρ23 (2 - 4 ρ34) + 2 ρ34))),
     2^(1/3)/(-(-1 + ρ12) (1 - ρ34 + ρ23 (-1 + 2 ρ34)))^(1/3), 2^(1/3)/(-(1 - ρ23 + ρ12 (-1 + 2 ρ23)) (-1 + ρ34))^(1/3),
     1/(-(-1 + ρ12) (-1 + ρ23) (-1 + ρ34))^(1/4), 1/(-(-1 + ρ12) (-1 + ρ23) (-1 + ρ34))^(1/4)],
    {ρ23, 0, .5}, PlotStyle → Black, AxesLabel → {ρ23, ωhet}],
  Plot[{√2/√(1 - ρ12), √2/√(1 - ρ23), 2^(1/3)/(1 - ρ12 - ρ23 + ρ12 ρ23)^(1/3), √2/√(1 - ρ12 - ρ23 + 2 ρ12 ρ23),
     √2/√(1 - ρ34), 2^(1/3)/(1 - ρ23 - ρ34 + ρ23 ρ34)^(1/3), √2/√(1 - ρ23 - ρ34 + 2 ρ23 ρ34),
     (√2) / (√(1 - ρ34 + ρ23 (-1 + 2 ρ34) + ρ12 (-1 + ρ23 (2 - 4 ρ34) + 2 ρ34))),
     2^(1/3)/(-(-1 + ρ12) (1 - ρ34 + ρ23 (-1 + 2 ρ34)))^(1/3), 2^(1/3)/(-(1 - ρ23 + ρ12 (-1 + 2 ρ23)) (-1 + ρ34))^(1/3),
     1/(-(-1 + ρ12) (-1 + ρ23) (-1 + ρ34))^(1/4)}, {ρ23, 0, .5},
   PlotStyle → {{Dashed, Gray}, {Dashed, Purple}, {Dashed, Blue}, {Dashed, Cyan},
     {Dashed, Green}, {Dashed, Yellow}, {Dashed, Orange}, {Dashed, Red},
     {Dashed, Magenta}, {Dashed, Pink}, {Dashed, Brown}}]], {ρ12, 0, .5}, {ρ34, 0, .5}]
```



Simplify the conditions:

```
Table[Reduce[1/(-(-1 + ρ12) (-1 + ρ23) (-1 + ρ34))^(1/4) > Listω[[i]] &&
    0 < ρ12 ≤ 1 / 2 && 0 < ρ23 ≤ 1 / 2 && 0 < ρ34 ≤ 1 / 2, Reals], {i, 1, Length[Listω]}]
```

```
{False, False, False, False, False, False, False, False, False, False, False, False}
```

Extrapolate for n loci and shows that for n from to 2 to 10 that the more loci that more stable exclusion is

```
1 / ((1 - r) ^ (n - 1)) ^ (1 / n)
```

```
((1 - r)^(-1+n))^(-1/n)
```

```
Limit[((1 - r)^(-1+n))^(-1/n), r → 1 / 2]
```

```
(2^(1-n))^(-1/n)
```

```
With[{n = 3}, Reduce[Apply[And, Thread[Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}][[n - 1]] <
      Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}]]] && 0 ≤ r ≤ 0.5]]
```

```
False
```

```
With[{n = 4}, Reduce[Apply[And, Thread[Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}][[n - 1]] <
      Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}]]] && 0 ≤ r ≤ 0.5]]
```

```
False
```

```
With[{n = 5}, Reduce[Apply[And, Thread[Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}][[n - 1]] <
      Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}]]] && 0 ≤ r ≤ 0.5]]
```

```
False
```

```
With[{n = 6}, Reduce[Apply[And, Thread[Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}][[n - 1]] <
      Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}]]] && 0 ≤ r ≤ 0.5]]
```

```
False
```

```
With[{n = 7}, Reduce[Apply[And, Thread[Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}][[n - 1]] <
      Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}]]] && 0 ≤ r ≤ 0.5]]
```

```
False
```

```
With[{n = 8}, Reduce[Apply[And, Thread[Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}][[n - 1]] <
      Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}]]] && 0 ≤ r ≤ 0.5]]
```

```
False
```

```
With[{n = 9}, Reduce[Apply[And, Thread[Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}][[n - 1]] <
      Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}]]] && 0 ≤ r ≤ 0.5]]
```

```
False
```

```
With[{n = 10}, Reduce[Apply[And, Thread[Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}][[n - 1]] <
      Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}]]] && 0 ≤ r ≤ 0.5]]
```

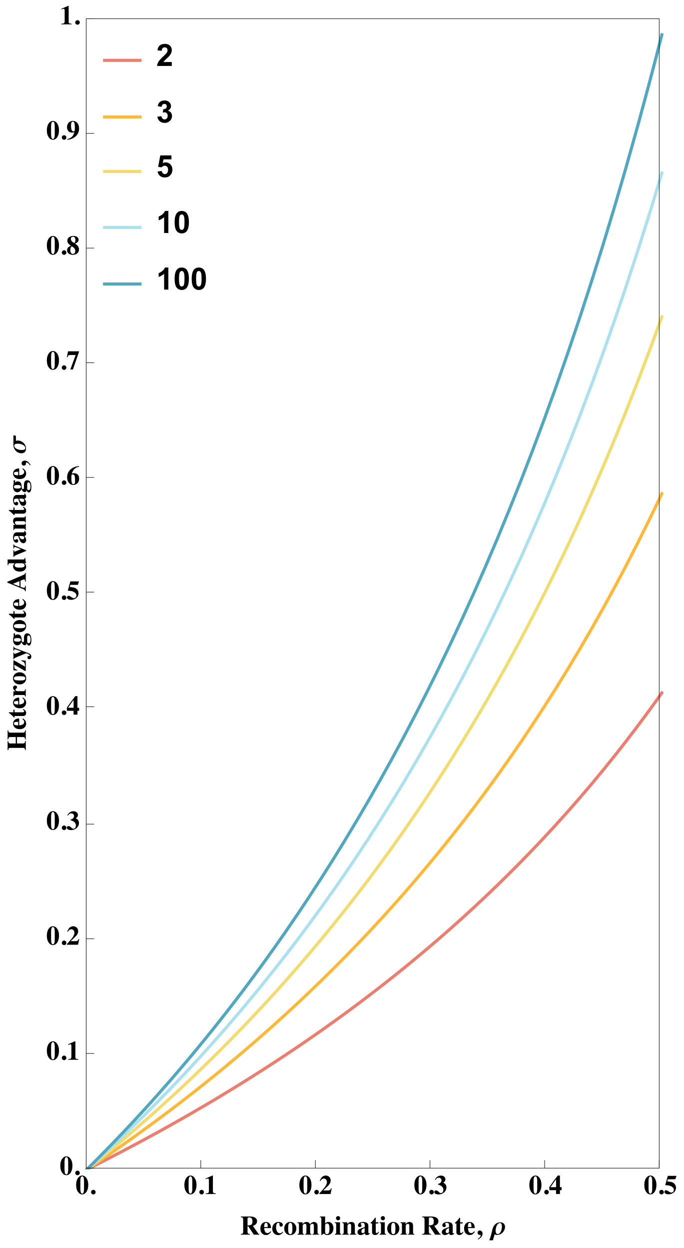
```
False
```

```
Table[((1 - r)^(-1+i))^(-1/i), {i, 2, n}][[n - 1]]
```

$$\frac{1}{\left((1-r)^{4}\right)^{1/5}}$$

Plot of solution for multiple loci

```
(*PLOT42 HERE*)
xx = Plot[Evaluate[Table[1 / (1 - r)^((n-1)/n) - 1, {n, {2, 3, 5, 10, 100}}]],
  {r, 0, 0.5}, Frame → True, PlotRange → {{0, 0.5}, {0, 1}},
  FrameLabel → {"Recombination Rate, ρ", "Heterozygote Advantage, σ"},
  AspectRatio → Automatic, FrameTicks →
   {{Range[0, 1, 0.1], None}, {Range[0, 1, 0.1], None}}, PlotStyle → ColorData[24],
  PlotLegends → Placed[LineLegend[Automatic, {2, 3, 5, 10, 100}]
    , {Left, Top}], ImageSize → 350, BaseStyle → {FontSize → 14, FontWeight → Bold}]
```



```
Export[ToString[NotebookDirectory[]] <>
  "analytic-limit-lethal-haplodiploid-many-loci.pdf", xx]
```

```
/Users/nando/Documents/finnish_hybrid_ants/results/analytic-limit-lethal-haplodiploid
  -many-loci.pdf
```

Chapter 5: Simulations with (and without) preference

Code to run the simulations

For convenience in tracking convergence trajectories (but incredible annoyance in LD calculations), I summarized the 16 female genotypes into 7 classes in this order:

purebred –	introgressed –	heterozygous hybrids	homozygous hybrid γ1	homozygous hybrid γ2	introgresse
$A_- B_- / A_- B_-$	$A_- B_- / A_- B_+$ $A_- B_- / A_+ B_-$ $A_- B_+ / A_- B_-$ $A_+ B_- / A_- B_-$	$A_- B_- / A_+ B_+$ $A_- B_+ / A_+ B_-$ $A_+ B_- / A_- B_+$ $A_+ B_+ / A_- B_-$	$A_- B_+ / A_- B_+$	$A_+ B_- / A_+ B_-$	$A_+ B_+ / A_+ B_-$ $A_+ B_+ / A_- B_+$ $A_+ B_- / A_+ B_+$ $A_- B_+ / A_+ B_+$

Each class has either a different fitness but cannot be assigned to one of the two parental subpopulations (e.g. homozygous hybrids) or has the same fitness as another class but is assigned to a different parental subpopulation (e.g. introgressed types).

```
fem7CategoriesPosition =
  {{1}, {2, 3, 5, 9}, {4, 7, 10, 13}, {6}, {11}, {8, 12, 14, 15}, {16}};
(* I determined the category of each position in the genotypes vector by hand...
 Yeah, this is rather dirty. *)
fem7Catfreq[gen_] :=
 Table[Total[gen[[1]][[fem7CategoriesPosition[[k]]]]], {k, 1, 7}] // N
```

This is the workhorse function for the simulations.
Parameter combinations are inputted first as a list in this order: $\{\alpha, \sigma, \gamma 1, \gamma 2, \rho\}$
Then the starting genotype frequencies are given as a list of two lists, female genotype frequencies (16 values [0,1] summing to 1) followed by male genotype frequencies (16 values [0,1] summing to 1). Here is an example input: {{0.4,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0.6},{0.4,0,0,0.6}}

The output is to several global variables:
convergence returns 1 if simulation successfully converged after 100000 generations and 0 otherwise;
finalfrequencies and **finalfrequenciesAfterSelection** return a list of 11 genotype frequencies (first 7 correspond to female categories listed above and last 4 correspond to male haplotype frequencies) either before or after selection, respectively;
results and **resultsAfterSelection** return a table of genotype frequencies for every 10th generation either before selection or after selection, respectively (it is used to track trajectories to convergence);
generation returns the generation when convergence was reached (or 100000 if simulation failed to converge).

```
ConvergeTOEQ[pars_, femaleMaleInitial_] :=
 Module[{NextGen, femalesPostSel, malesPostSel, freqAfterSel},
  (* create the appropriate function for updating each generation: *)
  NextGen[freqs_] := dynamicsHaplodiploidWithMatching[pars // N][freqs];

  (* if α=0, get the stable equilibria from the numerical solution.
     This prevents spurious convergence to
    an unstable equilibrium but is only possible for α=0 *)
  If[pars[[1]] == 0.,
   youngMaleEquil = stableEquilibriaHaplotype[1][pars[[2 ;; 5]], True][[3, All, 1]];
   youngMaleEquil =
    Transpose[Append[Transpose@youngMaleEquil, 1 - Total[#] & /@ youngMaleEquil]];
```

```
    ];

    (* create functions for calculating freq just after selection *)
    femalesPostSel = femaleGenotypesAfterSelection /. epistasisRecessiveAsymmetric /.
      Thread[{s, γ01, γ10} → pars[[2 ;; 4]]];
    malesPostSel = malesAfterSelection /. epistasisRecessiveAsymmetric /.
      Thread[{γ01, γ10} → pars[[3 ;; 4]]];

    (* initialize variables: *)
    results = {{"f-pure0", "f-most0", "f-hybBEST", "f-hybHOM01",
        "f-hybHOM10", "f-most1", "f-pure1", "m-00", "m-01", "m-10", "m-11"}};
    resultsAfterSelection = {{"f-pure0", "f-most0", "f-hybBEST", "f-hybHOM01",
        "f-hybHOM10", "f-most1", "f-pure1", "m-00", "m-01", "m-10", "m-11"}};
AppendTo[results, Join[fem7Catfreq[femaleMaleInitial], femaleMaleInitial[[2]] ]];
    freqAfterSel  = {femalesPostSel /. Thread[genotypeFemale → femaleMaleInitial[[1]] ],
      malesPostSel /. Thread[genotypeMale → femaleMaleInitial[[2]] ]};
    AppendTo[resultsAfterSelection, Join[fem7Catfreq[freqAfterSel],
      freqAfterSel[[2]] ]];

    frequencies  = femaleMaleInitial // N;

(* Run iteration *)
    k = 1;
convergence = 0; (* default value of convergence:false *)
generation = 100 000;  (* Max generation if no stop because of convergence.*)

    While[k < 100 000 && convergence == 0,
(* next generation: *)
     frequenciesPrevious  =  frequencies;
frequencies = NextGen[frequencies ] // Chop;

If[IntegerQ[k / 10],
      AppendTo[results, Join[fem7Catfreq[frequencies], frequencies[[2]] ]];
      freqAfterSel  =  {femalesPostSel /. Thread[genotypeFemale → frequencies[[1]] ],
        malesPostSel /. Thread[genotypeMale → frequencies[[2]] ]};
      AppendTo[resultsAfterSelection, Join[fem7Catfreq[freqAfterSel],
        freqAfterSel[[2]] ]];
     ] (* Write frequencies into lists, every 10 generations *)

If [(k > 2 && (Max[Abs[frequencies - frequenciesPrevious]]) <= 10 ^ - 8) ,
(* Testing convergence for each genotype by
       comparing the differences of frequencies between the previous
       generation and the actual generation, with a 10^-8 tolerance.*)
      If[pars[[1]] == 0., (* if pref is set to zero,
        we can ensure the stable equilibrium has been reached *)
        (* now we check if frequencies is sufficiently close
         to any of the stable equilibria *)
        If[AnyTrue[Chop[frequencies[[2]] - #, 10 ^ - 6] & /@ youngMaleEquil,
```

```
                 TrueQ[# == ConstantArray[0, 4]] &],
                convergence = 1; (* Changing convergence in true value to
                 stop the loop when populations are converging. *)
                  generation = k; (* Generation number when
                 populations start converging*)
                  (* Keeping in memory frequencies of last generation*)
                  finalfrequencies = Join[fem7Catfreq[frequencies], frequencies[[2]] ];
                freqAfterSel = {femalesPostSel /. Thread[genotypeFemale → frequencies[[
                     1]] ], malesPostSel /. Thread[genotypeMale → frequencies[[2]] ]};
                finalfrequenciesAfterSelection = Join[fem7Catfreq[freqAfterSel],
                  freqAfterSel[[2]] ];
                (* do nothing if frequencies does NOT match any of the stable equil. This
                 will continue searching without triggering the converge flag. *)
                (*,Print@"I wanna converge but I'm all wrong :'(";*)
               ];


              ,
              (* if pref is NOT set to zero,
              let's just assume this is the right equilibrium... *)
              convergence = 1; (* Changing convergence in true value to
               stop the loop when populations are converging. *)
               generation = k; (* Generation number when populations start converging*)
               (* Keeping in memory frequencies of last generation*)
               finalfrequencies = Join[fem7Catfreq[frequencies], frequencies[[2]] ];
              freqAfterSel = {femalesPostSel /. Thread[genotypeFemale → frequencies[[1]] ],
                malesPostSel /. Thread[genotypeMale → frequencies[[2]] ]};
              finalfrequenciesAfterSelection = Join[fem7Catfreq[freqAfterSel],
                freqAfterSel[[2]] ];
             ];
           ];
       (* Run next iteration *)
       k++];

        ]
```

And here is the function to run simulations of the diploid model.
In this case the initial genotype frequencies are specified as just one list (16 values [0,1] summing to 1); here is an example: {0.4,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0.6}

?

Here are two functions that allow you to analyze the output from simulations with preference:

```
(* a function to get allele frequencies (A+ then B+) and LD from male haplotypes *)
GetMaleAlleleFreqsLD[gen11_] := Module[{gens},
  gens = Chop[gen11, 5 * 10 ^ -6];
  Return@{Total[gens[[{10, 11}]]],
    Total[gens[[{9, 11}]]], gens[[8]] * gens[[11]] - gens[[9]] * gens[[10]]};
 ]

(* a function to identify the evolutionary scenario from the final
 frequencies before selection (variable called finalfrequencies) *)
IdentifySimulatedCase[gen11_] := Module[{},
  gens = Chop[gen11, 5 * 10 ^ -6];
  case = Null;
  Which[
   (gens[[{1, 8}]] == {0, 0}) && (gens[[{5, 10}]] == {0, 0}), case = "M"(* purebreds of
    only W type are present but no A_wB_r homozygous hybrids or hybrid males *),
   (gens[[{1, 8}]] == {0, 0}), case = "C"(* purebreds of only W type are
    present AND A_wB_r homozygous hybrids or hybrid males are present *),
   (gens[[{7, 11}]] == {0, 0}) && (gens[[{5, 10}]] == {0, 0}),
   case = "M"(* purebreds of only R type are present but no
    (lower cost) A_wB_r homozygous hybrids or hybrid males *),
   (gens[[{7, 11}]] == {0, 0}), case = "C"(* purebreds of only R type are
    present AND A_rB_w homozygous hybrids or hybrid males are present *),
   Chop[{gens[[1]] - gens[[7]], gens[[8]] - gens[[11]]}, 5 * 10 ^ -6] == {0, 0},
   case = "F" (* purebreds of W and R type are present at equal frequencies *),
   AllTrue[Join[gens[[1 ;; 3]], gens[[6 ;; 11]]], # > 0 &],
   case = "A" (* heterozygous hybrid females and hybrid males are present,
   both purebred types are present but unequal freq *),
   True, case = "weird"
  ];
  Return@case;
 ]
```

Note that you need to multiply the output from **IdentifySimulatedCase** with the boolean output from **ConvergeTOEQ** that indicates whether convergence was reached for the simulation.

Basin of attraction

The phase plane diagrams given in the manuscript show the basin of attraction. See Chapter 2 above for plotting the phase plane diagrams. The basin of attraction was done by simulation below.

This function finds the index of the stable equilibrium (from **stableEquilibriaHaplotype**) that is converged to for a transect along the secondary contact line:

```
SecContactBasin[pars_, pqVals_ (* a list from (0,1) avoiding 0.5 *)] :=
 Module[{init},
  convergeOUT = {};
  genOUT = {};
  eqIndexOUT = {};
  (* pick initial conditions along y=x secondary contact *)
  Do[
   (* get initial genotypes *)
   init = GetGenotypesfromHaps[GetHapsfromAlleles[pq, pq]];
   (* run simulation *)
   ConvergeTOEQ[Join[{0.}, pars], init];
   (*
   TimeConstrained[ConvergeTOEQ[Join[{0.},pars], init],1,"Fail!"] (* increase the
    time if the function gives errors about "Part 1 of {} does not exist. " *)
   *)
   (* keep info on whether convergence happened *)
   AppendTo[convergeOUT , convergence];
   AppendTo[genOUT, k];
   (* keep index of converged equilibrium *)
   AppendTo[eqIndexOUT,
    Position[Chop[finalfrequencies[[8 ;; 11]] - #, 10^-6] & /@ youngMaleEquil,
      ConstantArray[0, 4]][[1, 1]] ];
   , {pq, pqVals}];
 ]

(* here is the complete list of pqVals I used for analysis: *)
pqRange = Subdivide[0.01, 0.98, 11] (* first 2 values picked to avoid symmetry *)
```

Grid plots of different parameter combinations

Create grid plots without preference:

```
(* initialize parameter combos such that s≠γ1≠γ2 for any possible combinations *)
recomb = Join[Range[10^-1, 0.5, 1 / 7], {0.5}] // N;
sel = Join[{0.}, 10^Subdivide[-3.999, Log10@0.251, 18]] // N;
gama1 = 10^{-5, -3, -2, 0} // N;
gama2scaled = 3^Subdivide[-4.9, -.0001, 20] // N;
(* gama2 = k * gama1 such that gama2 < gama 1 always *)

(* For haplodiploids, store the LD and the evolutionary scenario *)
LDtemp1 = {};
LDtemp2 = {};
LD = {};

casetemp1 = {};
casetemp2 = {};
case = {};
Do[
 out = IdentifyCase[{SIGMA, G1, kay * G1, REC}];
 AppendTo[casetemp1, out];
```

```
 AppendTo[LDtemp1, equilOutput[[4]]];

 If[kay == Max@gama2scaled ,
  Print["got γ1=" <> ToString@G1 <> " σ=" <>
     ToString@SIGMA <> " r=" <> ToString@REC <> " for all γ2 scale values"] ×
   AppendTo[casetemp2, casetemp1];
  AppendTo[LDtemp2, LDtemp1];
  casetemp1 = {};
  LDtemp1 = {};

  If[ G1 == Max@gama1,
   AppendTo[case, casetemp2];
   AppendTo[LD, LDtemp2];
   casetemp2 = {};
   LDtemp2 = {};

   If[ SIGMA == Max@sel,
    Save["LD_no_preference-r_" <> ToString[REC],
     { sel, gama1, gama2scaled, LD, case}];
    LD = {};
    case = {};
   ]
  ];
 ];
 , {REC, recomb}, {SIGMA, sel}, {G1, gama1}, {kay, gama2scaled }]

(* do the same thing for diploids *)
LDtemp1 = {};
LDtemp2 = {};
LD = {};

casetemp1 = {};
casetemp2 = {};
case = {};
Do[
 out = IdentifyCaseDIPLOID[{SIGMA, G1, kay * G1, REC}];
 AppendTo[casetemp1, out];
 AppendTo[LDtemp1, equilOutput[[4]]];

 If[kay == Max@gama2scaled ,
  Print["got γ1=" <> ToString@G1 <> " σ=" <>
     ToString@SIGMA <> " r=" <> ToString@REC <> " for all γ2 scale values"] ×
   AppendTo[casetemp2, casetemp1];
  AppendTo[LDtemp2, LDtemp1];
  casetemp1 = {};
  LDtemp1 = {};

  If[ G1 == Max@gama1,
   AppendTo[case, casetemp2];
```

```
            AppendTo[LD, LDtemp2];
            casetemp2 = {};
            LDtemp2 = {};

            If[ SIGMA == Max@sel,
             Save["DIPLOID_LD_no_preference-r_" <> ToString[REC],
              { sel, gama1, gama2scaled, LD, case}];
             LD = {};
             case = {};
            ]
          ];
        ];
       , {REC, recomb}, {SIGMA, sel}, {G1, gama1}, {kay, gama2scaled }]
```

Here is a function to get LD/Dmax from the list of 3 values that I stored for all of the LD's: {freq of allele w at locus A, freq of allele w at locus B, LD}

```
LDoverDmax[vals_] :=
 Quiet[vals[[3]] / (Min[1 - vals[[1]], 1 - vals[[2]]] * Min[vals[[1]], vals[[2]]])]
```

Chapter 6: Data fitting

First, here are the estimated values for the male frequencies in the observed data and the purebred female frequencies:

```
(*male frequencies before selection: *)
maleRpureBS = 0.0412;
maleRhybridBS = 0.0618;
maleWhybridBS = 0.26013;
maleWpureBS = 0.63687;

(*male frequencies after selection: *)
maleRpureAS = 0.1022;
maleRhybridAS = 0.0008110;
maleWhybridAS = 0.06928;
maleWpureAS = 0.8277;

(*female frequencies before selection:
    "intro" refers to females inferred to be purebred
   based on having NO loci heterozygous for introgressed alleles
    "diag" refers to females inferred to be purebred based on having
   MORE THAN ZERO loci homozygous for diagnostic alleles *)
femaleRintroBS = 0.02163;
femaleWintroBS = 0.51129;
femaleRdiagBS = 0.08343;
femaleWdiagBS = 0.31395;

(*female frequencies after selection: *)
femaleRintroAS = 0.;
femaleWintroAS = 0.4238;
femaleRdiagAS = 0.002142;
femaleWdiagAS = 0.1889;
```

Data fitting to the model without preference

Two functions to calculate the sum of squared differences (SSD) between the model and data. The input is a list of two lists, first before selection and second after selection. Each of the two lists gives the 11 genotype frequencies (first 7 correspond to female categories listed above and last 4 correspond to male haplotype frequencies).

```
(* Functions to calculate sum of square
 differences between model and observations: *)
(* Calculates sum of squares differences using females inferred to be
 purebred based on having NO loci heterozygous for introgressed alleles *)
SSDintro[freq_] := Total[Power[
                    Flatten[
                     {Flatten@{freq[[1, 1]], Total@freq[[1, 2 ;; 6]],
           freq[[1, 7 ;; 8]], Total@freq[[1, 9 ;; 10]], freq[[1, 11]]} -
                           {femaleRintroBS, 1 - (femaleRintroBS + femaleWintroBS),
         femaleWintroBS, maleRpureBS, maleRhybridBS + maleWhybridBS, maleWpureBS},
                       Flatten@{freq[[2, 1]], Total@freq[[2, 2 ;; 6]],
           freq[[2, 7 ;; 8]], Total@freq[[2, 9 ;; 10]], freq[[2, 11]]} -
                           {femaleRintroAS, 1 - (femaleRintroAS + femaleWintroAS),
         femaleWintroAS, maleRpureAS, maleRhybridAS + maleWhybridAS, maleWpureAS}}
                     ], 2]];

(* Calculates sum of squares differences using females inferred to be purebred
 based on having MORE THAN ZERO loci homozygous for diagnostic alleles *)
SSDdiag[freq_] := Total[Power[
                        Flatten[
                         {Flatten@{freq[[1, 1]], Total@freq[[1, 2 ;; 6]],
           freq[[1, 7 ;; 8]], Total@freq[[1, 9 ;; 10]], freq[[1, 11]]} -
                           {femaleRdiagBS, 1 - (femaleRdiagBS + femaleWdiagBS),
         femaleWdiagBS, maleRpureBS, maleRhybridBS + maleWhybridBS, maleWpureBS},
                           Flatten@{freq[[2, 1]], Total@freq[[2, 2 ;; 6]],
           freq[[2, 7 ;; 8]], Total@freq[[2, 9 ;; 10]], freq[[2, 11]]} -
                           {femaleRdiagAS, 1 - (femaleRdiagAS + femaleWdiagAS),
         femaleWdiagAS, maleRpureAS, maleRhybridAS + maleWhybridAS, maleWpureAS}}
                         ], 2]];
```

Calculate the SSD for a lot of parameter values and save the results to output:

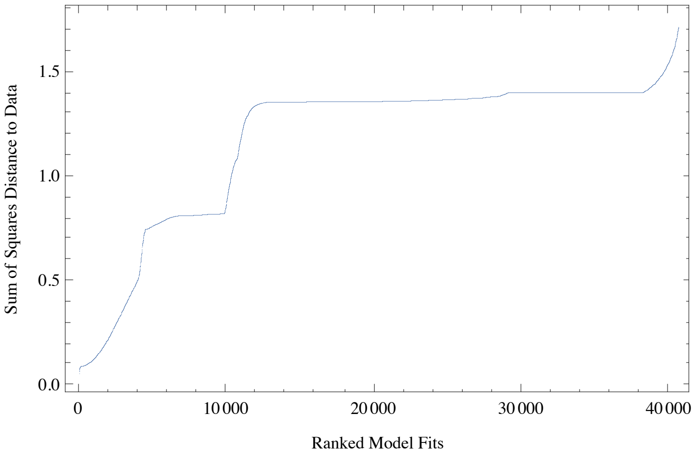
```
(* initialize parameter combos such that s≠γ1≠γ2 for any possible combinations *)
recomb = Join[Range[10^-5, 0.5, 1/11], {0.5}] // N;
sel = Join[{0.}, 10^Subdivide[-3.999, Log10@0.251, 27]] // N;
gama1 = 5^Range[-7, 0] // N;
k = 3^Subdivide[-4.9, -.0001, 24] // N;
(* gama2 = k * gama1 such that gama2 < gama 1 always *)

Save["ssd_no_preference-params", {recomb, sel, gama1, k}]

(* initialize variables for storage *)
typeEquilibria = {};
LDEquilibria = {};
introgressDist = {};
diagnosticDist = {};
(* Here are some temp variables *)
vecTypeEquil = {};
mat1TypeEquil = {};
```

```
vecLD = {};
mat1LD = {};
vecIntroD = {};
mat1IntroD = {};
vecDiagD = {};
mat1DiagD = {};
(* and just in case, *)
Clear@equilfreq;

(* Loop through different parameter values *)
Do[
    testpars = {σ, γ1, kay * γ1, r} // N;
    (* Get the equilibrium frequencies numerically *)
    equilfreq = noPrefEquilGenotypes[testpars, True];
     (* Store the category of equilibria found at this parameter combo *)
    AppendTo[vecTypeEquil, equilfreq[[2]] ];
    AppendTo[vecLD, equilfreq[[3]] ];
    equilfreq = equilfreq[[1]];

    tempIntroD = 999;
    tempDiagD = 999;
    (* Loop through all the equilibria to find minimum distances *)
    Do[
        testfreq = equilfreq[[j]];
        (* For the data based on introgressed alleles,
   calculate the distance from each equilibrium frequency to the data. *)
        tempD = SSDintro@testfreq;
        If[tempD < tempIntroD,
            tempIntroD = tempD];
        (* For the data based on diagnostic alleles,
   calculate the distance from each equilibrium frequency to the data. *)
        tempD = SSDdiag@testfreq;
        If[tempD < tempDiagD,
            tempDiagD = tempD];
    , {j, Length@equilfreq}]

        AppendTo[vecIntroD, tempIntroD];
        AppendTo[vecDiagD, tempDiagD];

    (* Store the minimum distances in a giant freakin matrix!!! *)
    If[kay == Max@k,
          AppendTo[mat1TypeEquil, vecTypeEquil];
        AppendTo[mat1LD, vecLD];
        AppendTo[mat1IntroD, vecIntroD];
        AppendTo[mat1DiagD, vecDiagD];
          vecTypeEquil = {};
        vecLD = {};
        vecIntroD = {};
        vecDiagD = {};
```

```
             If[ γ1 == Max@gama1,
                  AppendTo[typeEquilibria, mat1TypeEquil];
               AppendTo[LDEquilibria, mat1LD];
               AppendTo[introgressDist, mat1IntroD];
               AppendTo[diagnosticDist, mat1DiagD];
                  mat1TypeEquil = {};
               mat1LD = {};
               mat1IntroD = {};
               mat1DiagD = {};
                  If[ σ == Max@sel,
                       Save["ssd_no_preference-r_" <> ToString[r],
       {typeEquilibria, LDEquilibria, introgressDist, diagnosticDist}];
                       typeEquilibria = {};
                   LDEquilibria = {};
                   introgressDist = {};
                   diagnosticDist = {};
                   ]
              ]
        ]

   , {r, recomb}, {σ, sel}, {γ1, gama1}, {kay, k}]
```

Finally pick the top fitting models using the following (rather arbitrary) method:

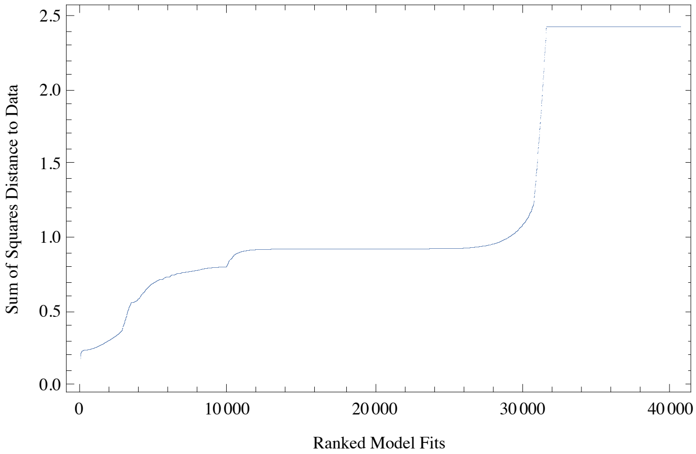
```
(* read in the data from multiple files *)
Get[ToString[NotebookDirectory[]] <> "ssd_no_preference-params"];

typeEquilibriaTEMP = {};
LDEquilibriaTEMP = {};
introgressDistTEMP = {};
diagnosticDistTEMP = {};
Do[
 Get[ToString[NotebookDirectory[]] <> "ssd_no_preference-r_" <> ToString[r]];
 AppendTo[typeEquilibriaTEMP, typeEquilibria];
 AppendTo[LDEquilibriaTEMP, LDEquilibria];
 AppendTo[introgressDistTEMP, introgressDist];
 AppendTo[diagnosticDistTEMP, diagnosticDist];
 , {r, recomb}]

typeEquilibria = typeEquilibriaTEMP;
LDEquilibria = LDEquilibriaTEMP;
introgressDist = introgressDistTEMP;
diagnosticDist = diagnosticDistTEMP;
Remove[typeEquilibriaTEMP , LDEquilibriaTEMP ,
 introgressDistTEMP , diagnosticDistTEMP ]

(* visualize the ranked model fits. The steps you
 see on the plot correspond to scenarios like exclusion and
 symmetric coexistence which have exactly equal (and bad) SSD *)
ListPlot[Sort@Flatten[introgressDist],
 FrameLabel → {"Ranked Model Fits", "Sum of Squares Distance to Data"}, Frame → True]
Length@Select[Flatten[introgressDist], # < 0.095 &]
Length@Select[Flatten[introgressDist], # < 0.094 &]
(* I'm totally eyeballing this,
so take what look like the top values. These correspond
  to the best values as per my entirely arbitrary cut-off :D *)
topIntro = DeleteDuplicates@Flatten[
    Position[introgressDist, #] & /@ Sort[Flatten[introgressDist]][[1 ;; 124]], 1];
(* need to delete duplicates because position gets ALL indices
 that have exactly the same SSD *)

(* Throw out the values that converge to CF because I found out below that the
    single locus polymorphism is that one that is being preferred and we already know
    that for this tristable param combo the SLP can only be reached under secondary
    contact when p and q are very very small/large.We think that it's more likely
    for the secondary contact to have been closer to 50-50 for some reason... *)
topIntro = Delete[topIntro, Position[Map[EquilType, topIntro], "CF"]];
outcomesIntro = Map[EquilType, topIntro]
Length@topIntro
```



```
218

124

{A, A, C, A, C, C, C, A, A, A, A, A, A, A, A, A, A, A, A, C, C, C, C, C, C, C, C, C, C, C, C,
 C, C, C, C, C, C, C, A, A, A, C, A, A, A, C, C, C, A, C, C, C, C, C, A, A, A, A, A, C, C,
 C, C, C, C, A, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, A,
 A, A, A, A, A, C, C, C, C, C, C, A, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C}

122
```

Repeat the same method as above for the diagnostic data (you need to load the data by running the cells above first).

```
ListPlot[Sort@Flatten[diagnosticDist],
 FrameLabel → {"Ranked Model Fits", "Sum of Squares Distance to Data"}, Frame → True]
Length@Select[Flatten[diagnosticDist], # < 0.24 &]
Length@Select[Flatten[diagnosticDist], # < 0.25 &]
topDiag = DeleteDuplicates@Flatten[
    Position[diagnosticDist, #] & /@ Sort[Flatten[diagnosticDist]][[1 ;; 167]], 1];

(* Throw out the values that converge to CF because I found out below that
 the single locus polymorphism is that one that is being preferred and we
 already know that for this tristable param combo the SLP can only be reached
 under secondary contact when p and q are very very small/large.We think
 that it's more likely for p and q to have some intermediate value. *)
topDiag = Delete[topDiag, Position[Map[EquilType, topDiag], "CF"]];
outcomesDiag = Map[EquilType, topDiag]
Length@topDiag
```



```
167

691

{A, A, A, A, A, A, A, A, C, A, A, A, A, A, A, C, C, A, A, A, A, C, C, A, A, C, C, C, C, A, A, A, A,
 A, C, C, C, A, C, C, C, A, A, A, C, C, C, C, A, A, A, A, A, C, C, C, C, A, C, C, C, C, C, A, C,
 C, C, C, C, A, A, A, A, A, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C,
 C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, C, A, A, C, C, C, C, C, C, C, C, C, C, C, C,
 C, A, A, A, A, A, C, C, C, C, C, C, C, C, C, C, A, A, A, C, C, C, C, C, C, C, C, C, C, C, C}

158
```

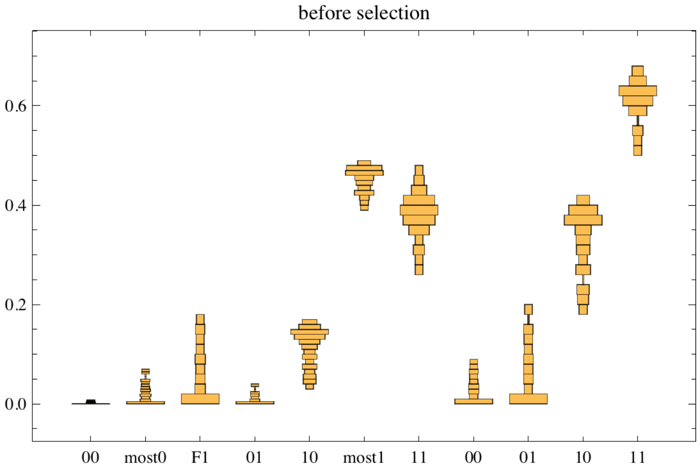
All of the analysis is straightforward from here...

However, maybe it’s helpful if I provide an example of how I got the model predictions. I’m showing the method just for the data with diagnostic alleles but the same thing was done exactly for introgressed alleles.

```
(* classify the outcomes  *)
Tally@outcomesDiag

(* all top models have 2 equilibria. Figure
 out the index of the preferred equilibrium *)
cfEqIndex = {};
bestFitFreq = {};
Do[
 equilfreq = noPrefEquilGenotypes[GetParamVals@topDiag[[i]] ];
 indexPref = Position[SSDdiag[#] & /@ equilfreq, Min[SSDdiag[#] & /@ equilfreq]];
 AppendTo[cfEqIndex, indexPref];
 AppendTo[bestFitFreq, Flatten[equilfreq[[Flatten@indexPref]], 1] ]
 , {i, Length@topDiag}]
Flatten@cfEqIndex

(* Given the indices above,it is ALWAYS the 1st equilibrium that is being preferred.
  Plot the predicted values: *)
DistributionChart[Transpose@bestFitFreq[[All, 1]],
 ChartLabels -> {"00", "most0", "F1", "01", "10", "most1", "11", "00", "01", "10", "11"},
 PlotLabel → "before selection", ChartElementFunction → "HistogramDensity"]
```

```
{{A, 51}, {C, 107}}
```

```
{1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1}
```



Data fitting to the model with preference

The data fitting to the model with preference was done by analogous methodology as above. See below.

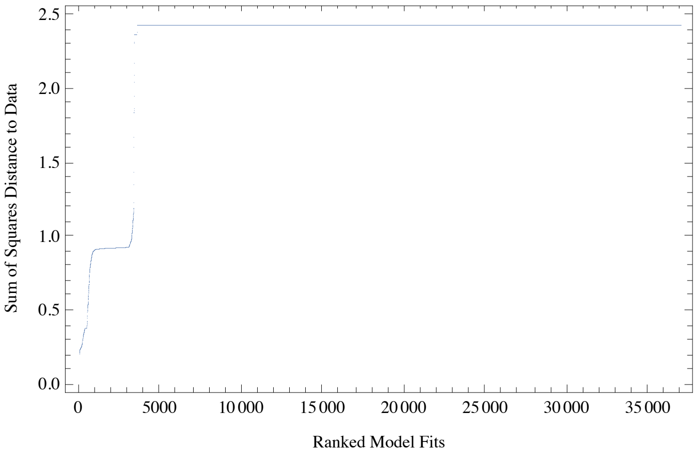
Please note that these simulations took about *TWO WEEKS* to run...

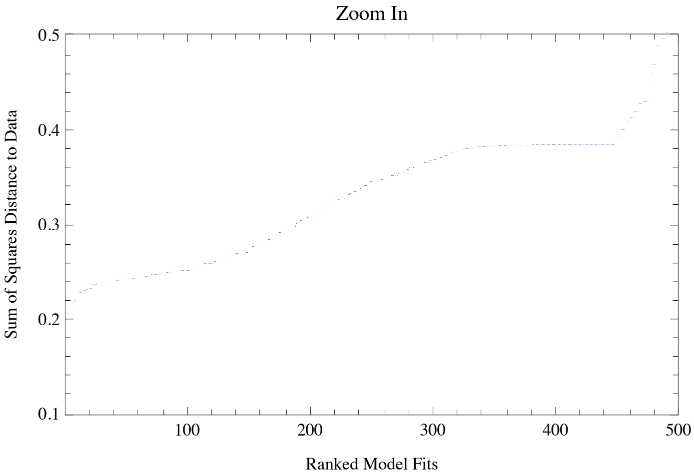
```
(* start from some random intial conditions under secondary contact *)
SeedRandom[1 342 798];
q = RandomReal[];
p = 1 - q;
init2aryContact = {Join[{p}, ConstantArray[0., 14], {q}], {p, 0., 0., q}};
```

```
(* initialize parameter combos such that s≠γ1≠γ2 for any possible combinations *)
(*recomb =  Join[Range[10^-1, 0.5, 1/7], {0.5}]//N;*)
(*pref = Subdivide[0.02,0.93,6]//N;*)
recomb = Reverse@{0.0011, 0.011, 0.11, 0.5} // N;
sel = Join[{0.}, 10^Subdivide[-3.999, Log10@0.251, 18]] // N;
gama1 = 10^{-3, -1, -5, 0, -2, -4} // N;
gama2scaled = 3^Subdivide[-4.9, -.0001, 10] // N;
(* gama2 = k * gama1 such that gama2 < gama 1 always *)
pref = -{0.0021, 0.021, 0.099, 0.19} // N;


recomb = {0.5}
sel = {0.25, 0.31}
gama1 = {1., 0.99}
gama2scaled = {0.99}
pref = {0., 0.0001}

CreateDirectory["sim_results"];
Save["sim_results/freqs_sims_preference-params",
  {recomb, sel, gama1, gama2scaled , pref}];

(* initialize variables for storage *)
freqOut = {};
freqAfterSelOut = {};
ConvOut = {};
GenOut = {};
(* Here are some temp variables *)
mat1freqOut = {};
mat2freqOut = {};
mat1freqAfterSelOut = {};
mat2freqAfterSelOut = {};
mat1ConvOut = {};
mat2ConvOut = {};
mat1GenOut = {};
mat2GenOut = {};

(* Loop through different parameter values *)
Do[
    testpars = Join[{pref[[αIndex]]}, {SIGMA}, {G1}, {kay * G1}, {REC}];
     (* Get the equilibrium frequencies by simulation *)
    (*check things are
   working: TimeConstrained[ConvergeTOEQ[testpars,init2aryContact,False],10];     *)
     ConvergeTOEQ[testpars, init2aryContact, False];
     (* Store the before and after selection frequencies,
 whether convergence happened, and generations to converge *)
    AppendTo[mat1freqOut, finalfrequencies ];
     AppendTo[mat1freqAfterSelOut, finalfrequenciesAfterSelection ];
     AppendTo[mat1ConvOut, convergence ];
     AppendTo[mat1GenOut, generation ];
```

```
      (* Store the values in a giant freakin matrix!!! *)
      If[kay == Max@gama2scaled ,
           Print["got γ1=" <> ToString@G1 <> " σ=" <> ToString@SIGMA <> " r=" <>
      ToString@REC <> " α=" <> ToString@pref[[αIndex]] <> "for all γ2 scale values"] ×
            AppendTo[freqOut, mat1freqOut ];
           AppendTo[freqAfterSelOut, mat1freqAfterSelOut ];
           AppendTo[ConvOut, mat1ConvOut];
           AppendTo[GenOut, mat1GenOut];
             mat1freqOut = {};
           mat1freqAfterSelOut = {};
           mat1ConvOut = {};
           mat1GenOut = {};
       If[ SIGMA == Max@sel,
                Save["sim_results/ssd_with_preference-r_" <> ToString[REC] <>
      "_pref_" <> ToString[ pref[[αIndex]] ] <> "_gam_" <> ToString[G1],
                     {freqOut, freqAfterSelOut, ConvOut, GenOut}];
                freqOut = {};
                freqAfterSelOut = {};
                ConvOut = {};
                GenOut = {};
            ]
     ]

 , {G1, gama1}, {REC, recomb},
  {αIndex, 1, Length@pref}, {SIGMA, sel}, {kay, gama2scaled }]


 (* read the data from file *)
 (* get the parameter values *)
 Get[ToString[NotebookDirectory[]] <>
    "haplodiploid_preference_sim_results/freqs_sims_preference-params"];
 (* create a giant array of some of the sim results: *)
 freqBsAsAll = {};
 freqRectemp = {};
 convAll = {};
 convRectemp = {};
 Do[
   Do[
    Get[ToString[NotebookDirectory[]] <> "haplodiploid_preference_sim_results/pref_" <>
      ToString@p <> "/freqs_with_preference-r_" <> ToString@r];
    freqtemp = ConstantArray[NA, Dimensions[ConvOut]];
    Do[
     freqtemp[[s, g, k]] = Chop[{freqOut[[s, g, k]], freqAfterSelOut[[s, g, k]]},
         5 * 10 ^ -6] * ConvOut[[s, g, k]] ;
       (* this means values that didn't converge will be just 0's *)
     , {s, Length@sel}, {g, Length@gama1}, {k, Length@gama2scaled}
    ];

    AppendTo[freqRectemp , freqtemp];
```

```
     AppendTo[convRectemp, ConvOut];
     , {r, recomb}
    ];
    AppendTo[freqBsAsAll, freqRectemp];
    AppendTo[convAll, convRectemp];
    freqRectemp = {};
    convRectemp = {};
    , {p, pref}
  ];

(* Now calculate the distances for diagnostic and introgressed: *)
diagDistAll = ConstantArray[NA, Dimensions[convAll]];
introDistAll = ConstantArray[NA, Dimensions[convAll]];
Do[
   diagDistAll[[p, r, s, g]] = Map[SSDdiag, freqBsAsAll[[p, r, s, g]]];
   introDistAll[[p, r, s, g]] = Map[SSDintro, freqBsAsAll[[p, r, s, g]]];
   , {p, Length@pref}, {r, Length@recomb}, {s, Length@sel}, {g, Length@gama1}
  ];

(* some useful little functions *)
GetParamVals[coord_] := {pref[[ coord[[1]] ]], sel[[ coord[[3]] ]],
   gama1[[ coord[[4]] ]], gama2scaled[[ coord[[5]] ]], recomb[[ coord[[2]] ]] }
GetFreq[val5_] := freqBsAsAll[[val5[[1]], val5[[2]], val5[[3]], val5[[4]], val5[[5]] ]];

(* Get the top model fits for diagnostic data *)
ListPlot[Sort@Flatten[diagDistAll],
  FrameLabel → {"Ranked Model Fits", "Sum of Squares Distance to Data"},
  Frame → True, PlotRange → All]
ListPlot[Sort@Flatten[diagDistAll],
  FrameLabel → {"Ranked Model Fits", "Sum of Squares Distance to Data"},
  Frame → True, PlotLabel → "Zoom In", PlotRange → {{1, 500}, {0.1, 0.5}}]
Length@Select[Flatten[diagDistAll], # < 0.25 &]
Length@Select[Flatten[diagDistAll], # < 0.26 &]
Length@Select[Flatten[diagDistAll], # < 0.27 &]
Length@Select[Flatten[diagDistAll], # < 0.28 &]
Length@Select[Flatten[diagDistAll], # < 0.29 &]
Length@Select[Flatten[diagDistAll], # < 0.3 &]
topDiag = DeleteDuplicates@
    Flatten[Position[diagDistAll, #] & /@ Sort[Flatten[diagDistAll]][[1 ;; 167]], 1];
outcomesDiag = IdentifySimulatedCase[GetFreq[#][[1]]] & /@ topDiag
```





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81

112

137

155

167

187

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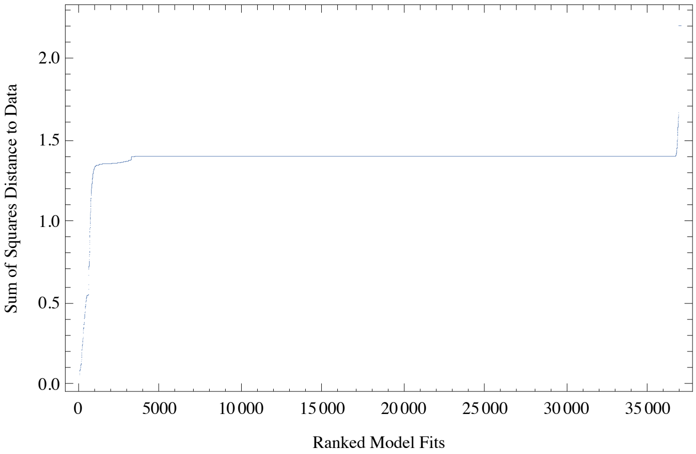
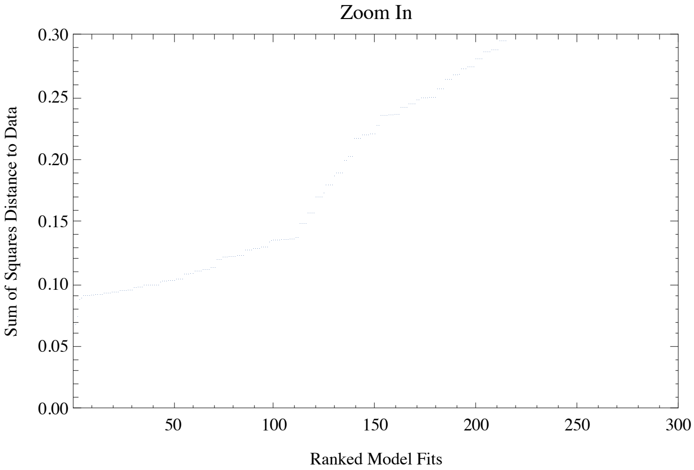
```

Repeat the same method as above for the diagnostic data (you need to load the data by running the cells above first).

```
ListPlot[Sort@Flatten[introDistAll],
 FrameLabel → {"Ranked Model Fits", "Sum of Squares Distance to Data"},
 Frame → True, PlotRange → All]
ListPlot[Sort@Flatten[introDistAll],
 FrameLabel → {"Ranked Model Fits", "Sum of Squares Distance to Data"},
 Frame → True, PlotLabel → "Zoom In", PlotRange → {{1, 300}, {0., 0.3}}]
Length@Select[Flatten[introDistAll], # < 0.14 &]
Length@Select[Flatten[introDistAll], # < 0.15 &]
Length@Select[Flatten[introDistAll], # < 0.16 &]
Length@Select[Flatten[introDistAll], # < 0.17 &]
topIntro = DeleteDuplicates@
   Flatten[Position[introDistAll, #] & /@ Sort[Flatten[introDistAll]][[1 ;; 115]], 1];
IdentifySimulatedCase[GetFreq[#][[1]]] & /@ topIntro
(* get rid of the weird one *)
topIntro = Delete[topIntro ,
   Position[IdentifySimulatedCase[GetFreq[#][[1]]] & /@ topIntro , "weird"]];
outcomesIntro = IdentifySimulatedCase[GetFreq[#][[1]]] & /@ topIntro
```





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111

115

119

119
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```