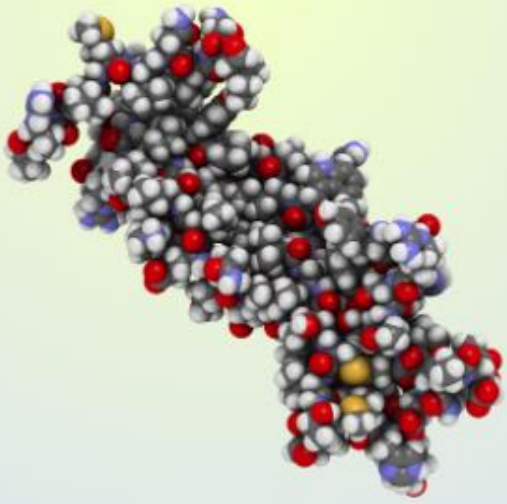
Cosimo

BiohackerDAO

BIOHACK YOUR INFLAMMATION

A SCIENTIFIC STUDY



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1. Introduction

This report presents the analysis of baseline blood tests conducted in Edge City. The study follows a two-phase design (pre- and post-treatment) to quantitatively measure the impact of lifestyle changes adopted by participants during the program.

This preliminary analysis focuses on exploration, with two main objectives: first, understanding relationships between key biomarkers and identifying potential patterns; second, establishing a standardized framework for blood test analysis.

We aim to evaluate various data analytics, modeling, and visualization techniques to determine the most effective approaches for our purposes. In alignment with BioHacker DAO's collaborative philosophy, we encourage and welcome feedback and suggestions to refine, expand and generalize our analytical methodology.

2. Data Collection and Sample Characteristics

The data was collected through participant surveys that incorporated their blood test results. The dataset encompasses both quantitative and qualitative elements, including demographic information (gender and age), key biomarkers (CRP, cortisol, testosterone/DHEA, glucose, LDL, HDL), and qualitative responses regarding treatment intentions and lifestyle changes.

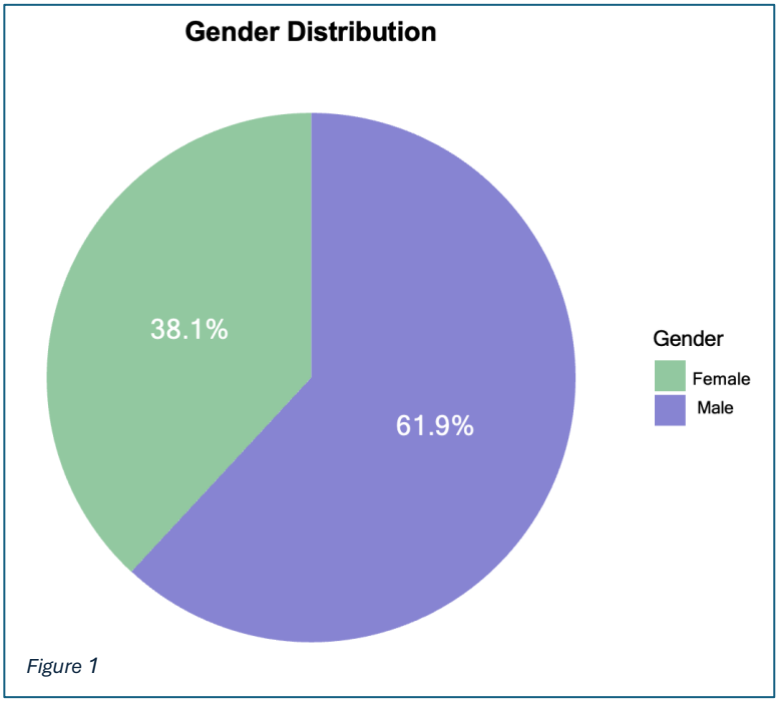

Figure 1

The study sample consists of 21 individuals, with a gender distribution of 13 males (61.9%) and 8 females (38.1%), as illustrated in Figure 1.

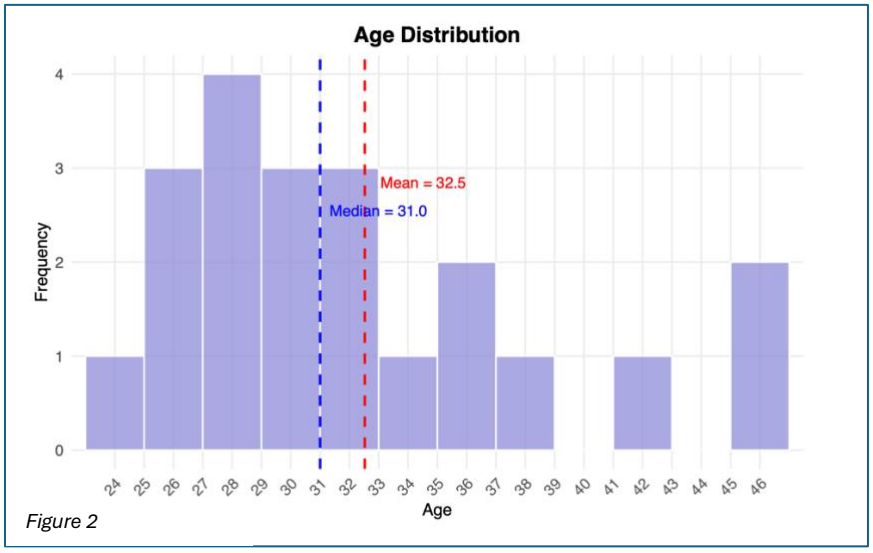

Figure 2

The age profile of participants spans from 24 to 46 years, with a mean age of 32.5 years and a median of 31.0 years. The overall age distribution exhibits a right-skewed pattern, with the highest concentration of participants falling within the 27-29 age range, as shown in Figure 2.

When examining the intersection of age and gender, several distinctive patterns emerge. Female participants tend to cluster more tightly within the younger age brackets, creating a more concentrated distribution. In contrast, male participants display a broader age spread, with representation distributed more evenly across all age groups. This pattern is particularly evident in Figure 3, where the density plot reveals that female participants show a pronounced peak in the late 20s, while male participants demonstrate a more uniform distribution characterized by multiple smaller peaks across different age ranges.

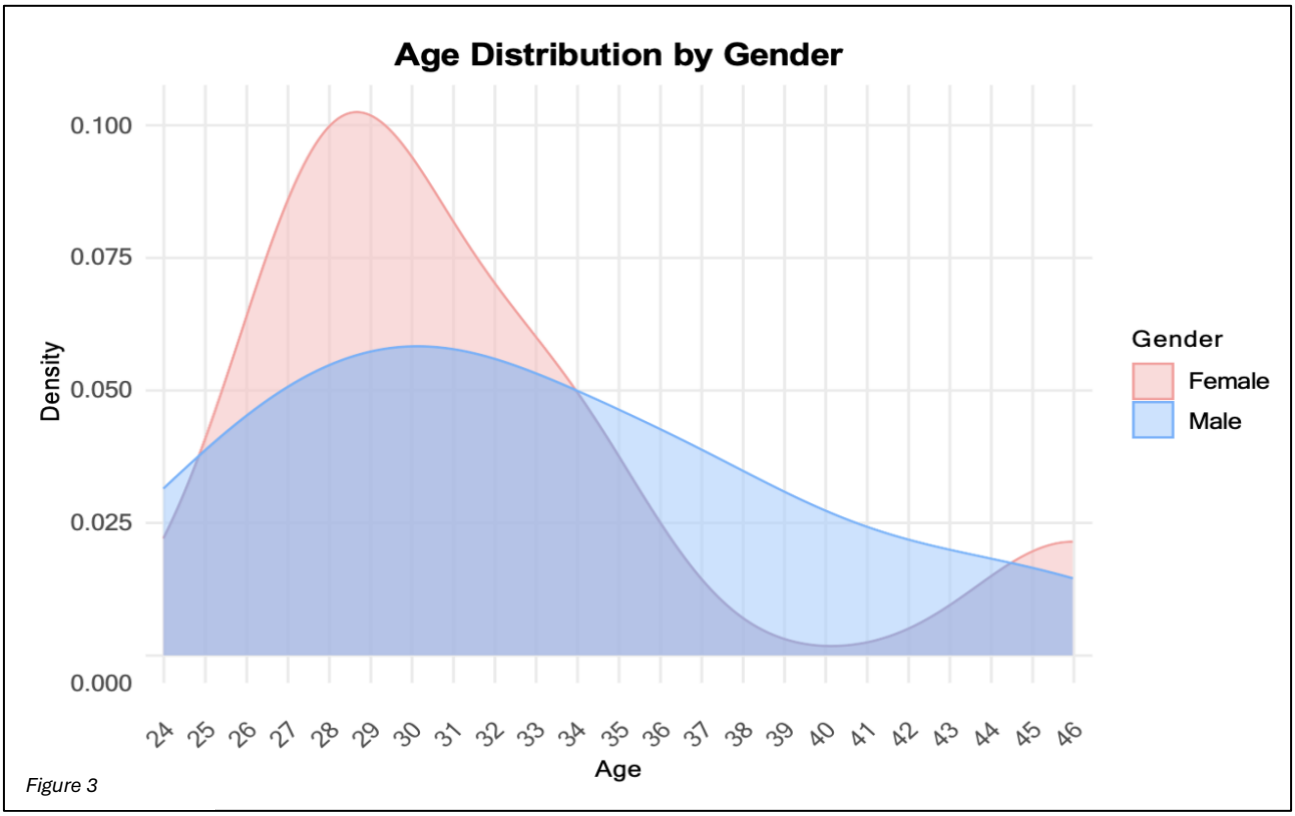

Figure 3

While the sample provides representation across different age and gender groups to support preliminary analysis, it's important to acknowledge the limitations imposed by its small size (n=21). This limited sample size constrains our ability to draw statistically robust conclusions and may not fully capture the broader population characteristics. Furthermore, the uneven gender distribution and age clustering could introduce bias in our analyses. These limitations should be considered when interpreting the biomarker relationships and patterns in subsequent analyses, and findings should be viewed as exploratory rather than definitive.

3. Exploratory Analysis

This chapter presents a comprehensive examination of the blood test results, focusing on two main aspects. First, we analyze the distribution of individual biomarkers (CRP, cortisol, testosterone/DHEA, glucose, LDL, and HDL), examining their spread and relationship to standard reference ranges. We also investigate how these distributions vary across gender and age groups, providing insights into demographic-specific patterns. Second, we explore the interconnections among these biomarkers through correlation analysis, both at the overall sample level and within gender-specific subgroups. This dual approach allows us to understand both the individual behavior of each biomarker and their complex interactions, laying the groundwork for more targeted analyses in future studies.

3.1. Biomarker Distribution and Reference Ranges

General Distribution Analysis

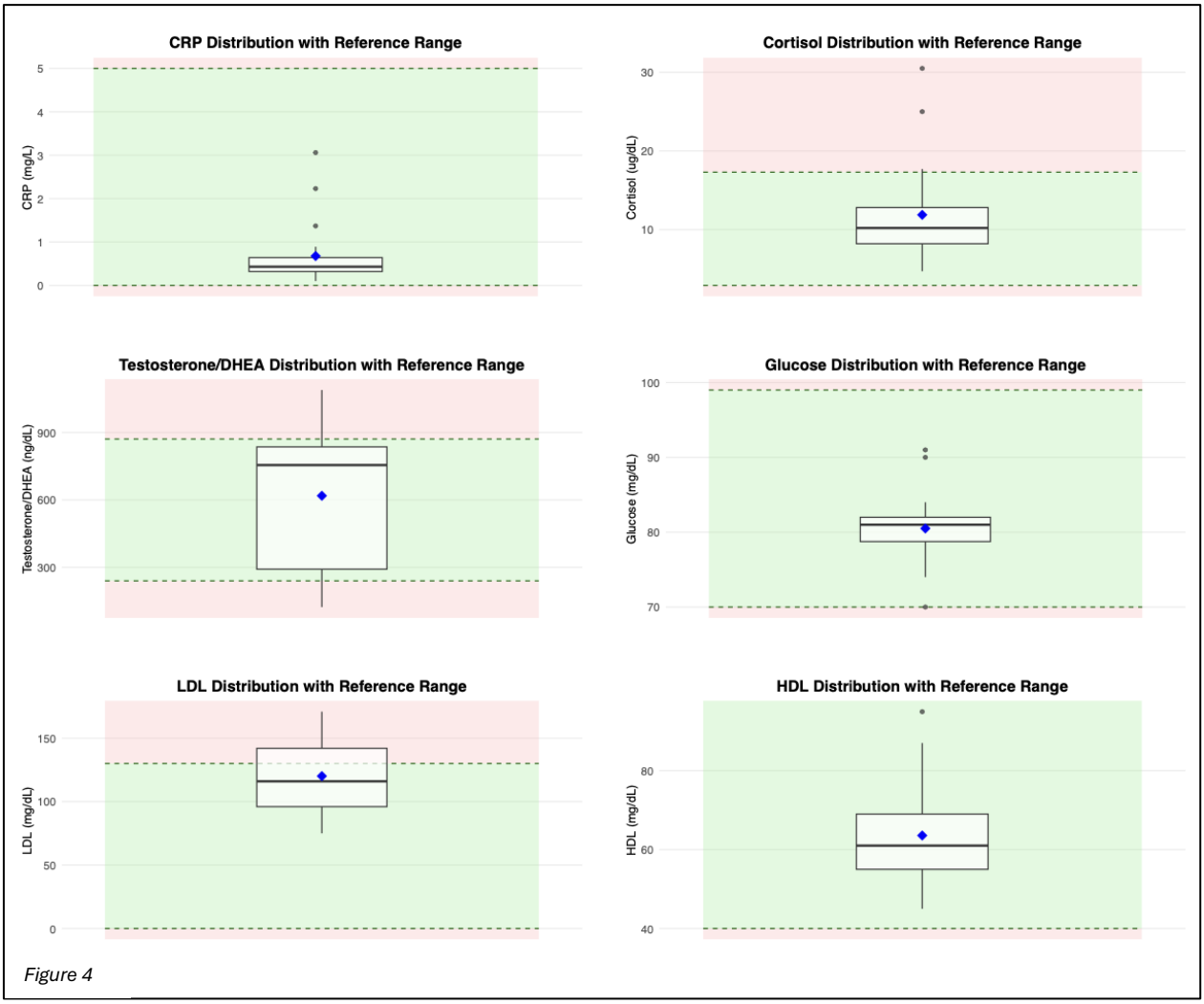

Figure 4

The first set of boxplots displays the overall distribution of each biomarker against their reference ranges, indicated by the green (within range) and red (out of range) backgrounds. The data reveals varying levels of deviation from reference ranges across biomarkers. CRP values cluster entirely within the reference range (0% out of range). Cortisol shows notable variability, with 14.29% of values (3 out of 21) exceeding the reference limits. For testosterone/DHEA - measured only in male participants due to reference range availability - 30.77% of values (4 out of 13) fall outside the expected range. Glucose levels demonstrate perfect compliance with reference ranges (0% out of range). The lipid profile shows interesting patterns: LDL has the highest proportion of out-of-range values at 38.10% (8 out of 21), while HDL maintains optimal levels across all participants (0% out of range for both genders).

Gender-Specific Patterns

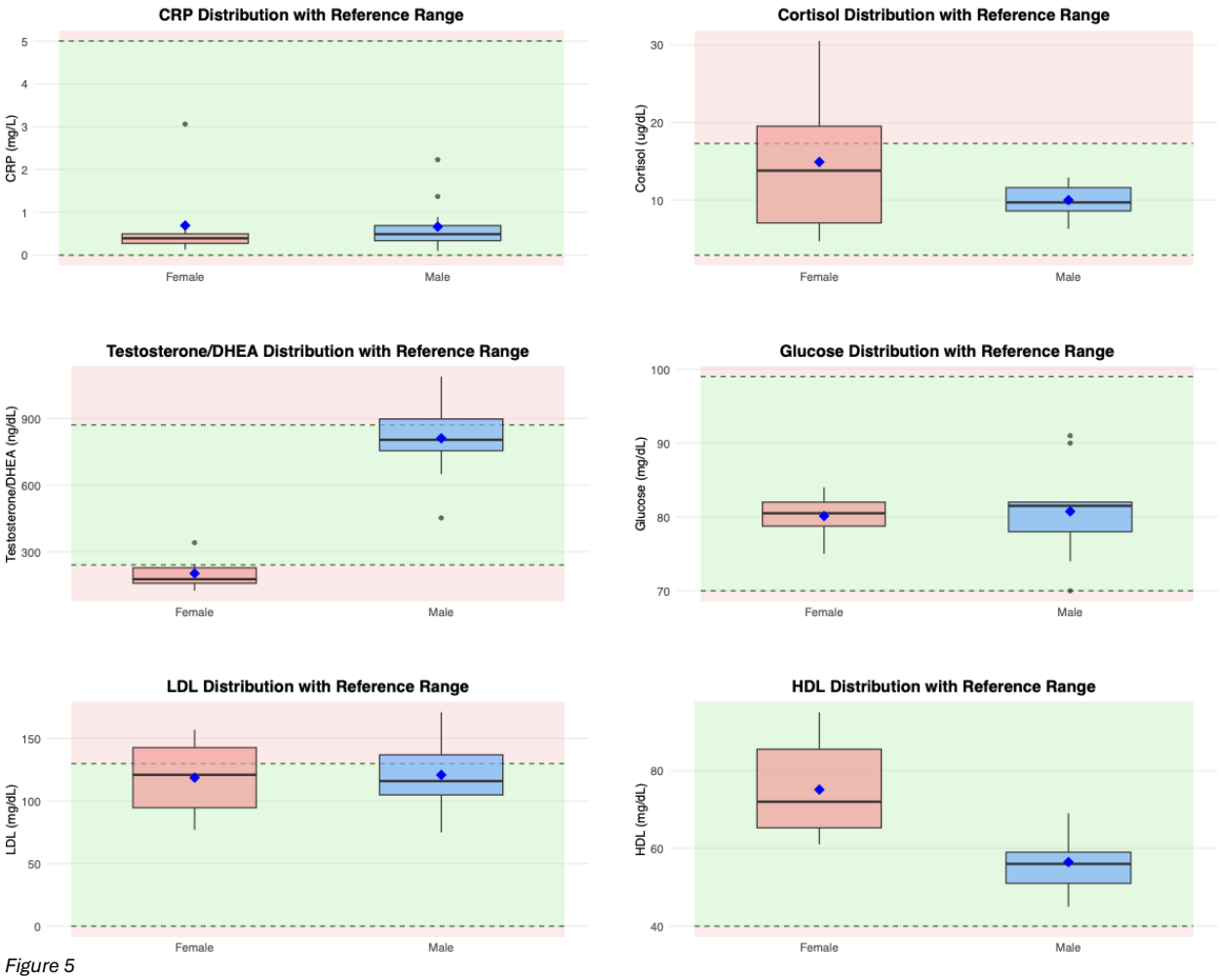

Figure 5

When examining biomarker distributions by gender, several distinct patterns emerge. Female participants show significantly higher cortisol variability, with 37.50% (3 out of 8) exceeding reference ranges, while males show no out-of-range values (0 out of 13). Male participants show concerning testosterone levels, with 30.77% (4 out of 13) outside reference ranges. LDL levels are similarly elevated in both genders: 37.50% of females (3 out of 8) and 38.46% of

males (5 out of 13) exceed reference ranges. Notably, both CRP and HDL maintain perfect compliance with reference ranges across genders, and glucose shows no deviations in either group.

Age-Related Patterns

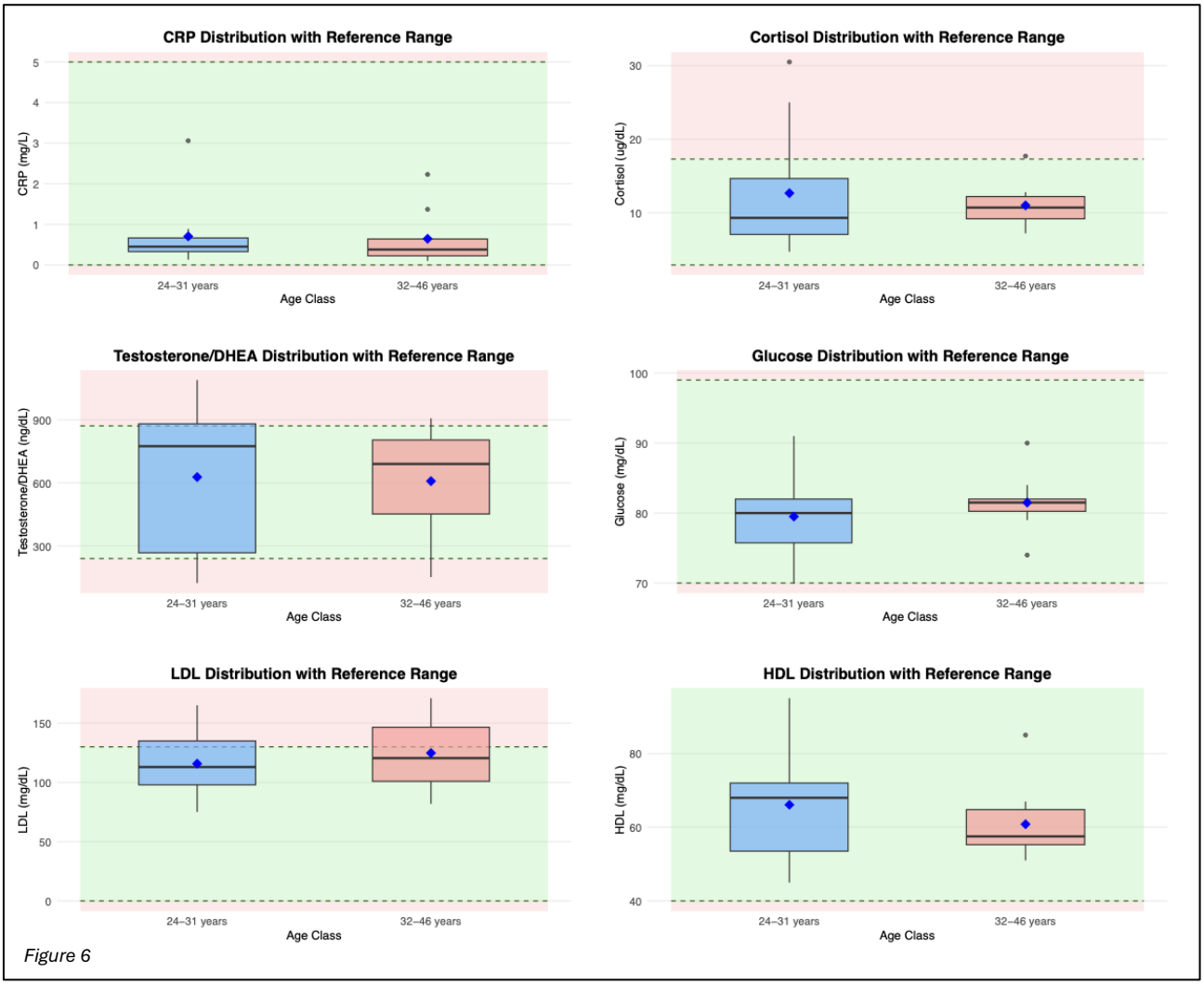

Figure 6

Dividing the sample into two age groups (24-31 years and 32-46 years) reveals additional insights. This binary division was chosen deliberately: given our limited sample size, attempting finer age groupings would result in statistically unreliable subgroups. Using the median age (31) as the splitting point ensures balanced representation in both classes while capturing maximum variability in our data. In the younger group (24-31), testosterone shows the highest deviation at 50% (3 out of 6), followed by LDL at 36.36% (4 out of 11), and cortisol at 18.18% (2 out of 11). The older group (32-46) shows a different pattern: LDL remains problematic at 40% (4 out of 10), but testosterone deviations decrease to 14.29% (1 out of 7), and cortisol drops to 10% (1 out of 10). CRP, glucose, and HDL maintain perfect compliance across both age groups. This age-based analysis suggests that hormonal imbalances might be more prevalent in younger participants, while lipid profile issues persist across age groups.

3.2. Correlation Analysis and Pattern Detection

The analysis of biomarker relationships comprises three layers of increasing specificity: overall correlations across the entire sample, gender-specific patterns, and partial correlations that account for potential confounding effects.

Pairwise Correlations

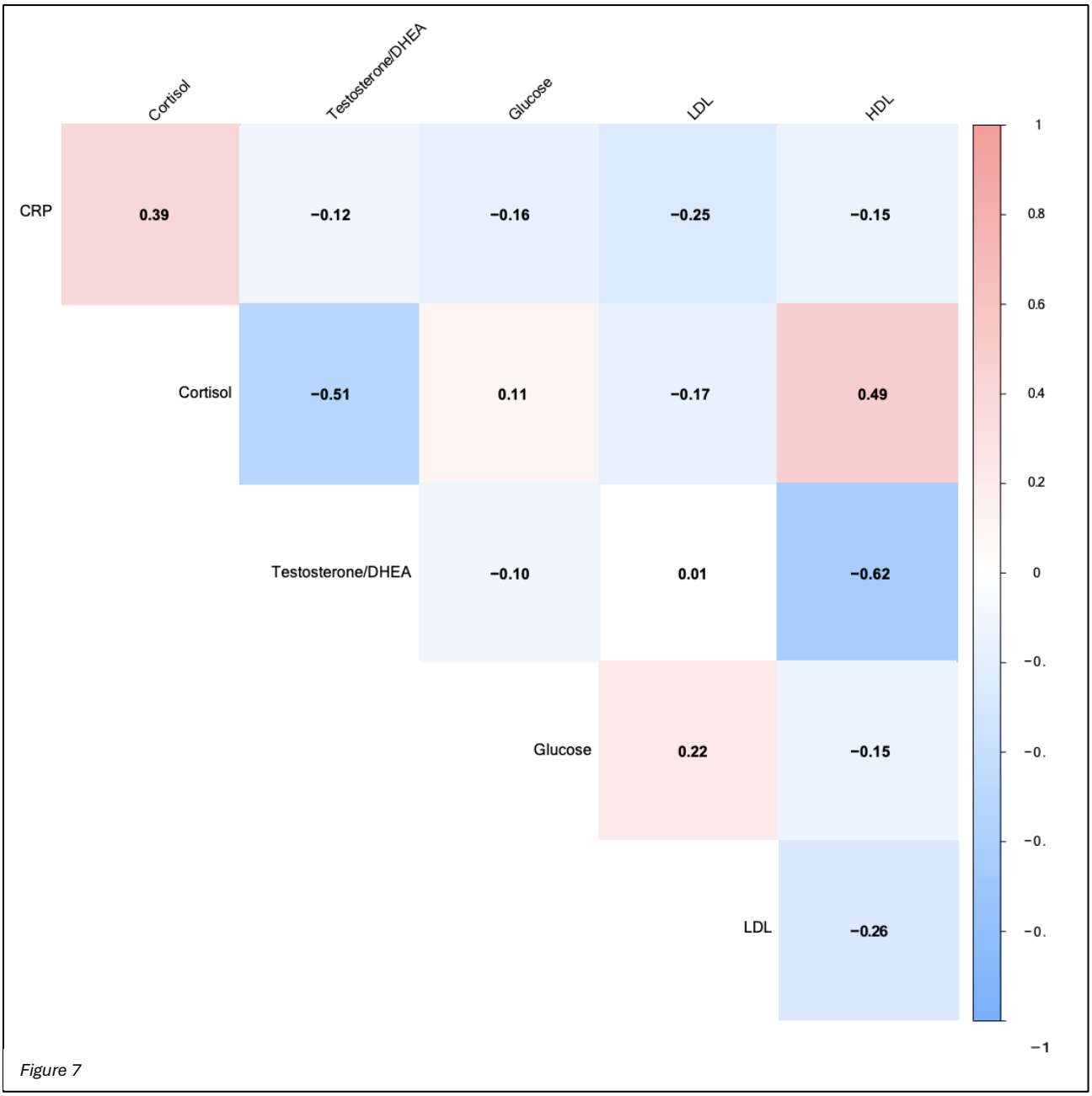

Figure 7

In the overall sample, several notable relationships emerge (Figure 7). The strongest positive correlation appears between CRP and cortisol (0.39), suggesting a potential link between inflammatory and stress responses. Testosterone/DHEA shows a strong negative correlation with HDL (-0.62), indicating an inverse relationship between these hormones and "good"

cholesterol. Glucose demonstrates moderate positive correlation with LDL (0.22), though interestingly, shows negative correlations with most other biomarkers.

Gender-Specific Correlations

Females

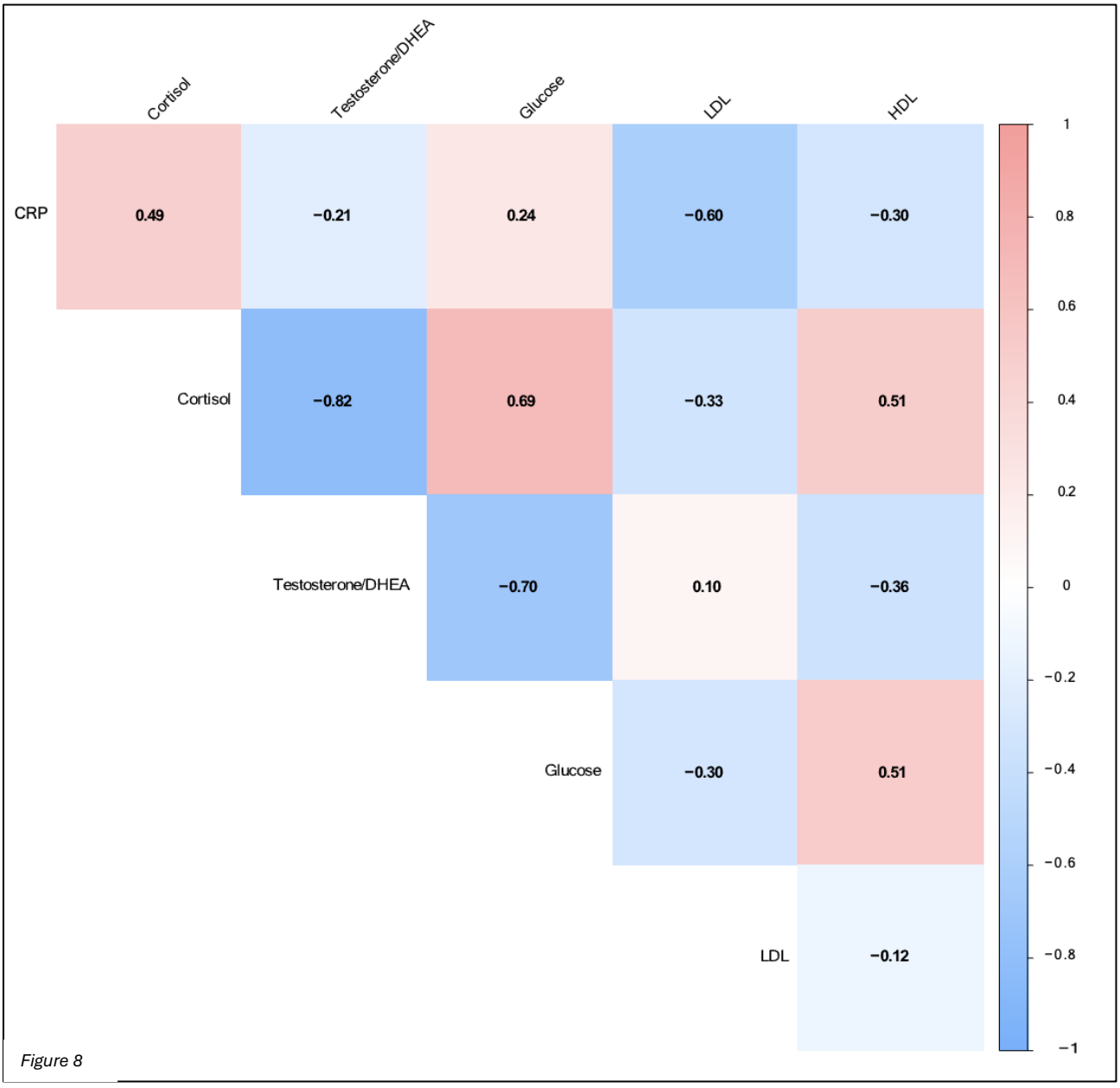

Figure 8

The relationship patterns differ markedly between genders (Figure 8/9). Female participants exhibit generally stronger correlations, particularly in the hormonal markers. The cortisol-testosterone/DHEA relationship is notably stronger in females (-0.82) compared to males (-0.17). Similarly, the correlation between cortisol and glucose is substantially higher in females (0.69) than in males (-0.33). The lipid profiles also show gender-specific patterns: the LDL-HDL relationship is weaker in females (-0.12) compared to males (-0.55).

Males

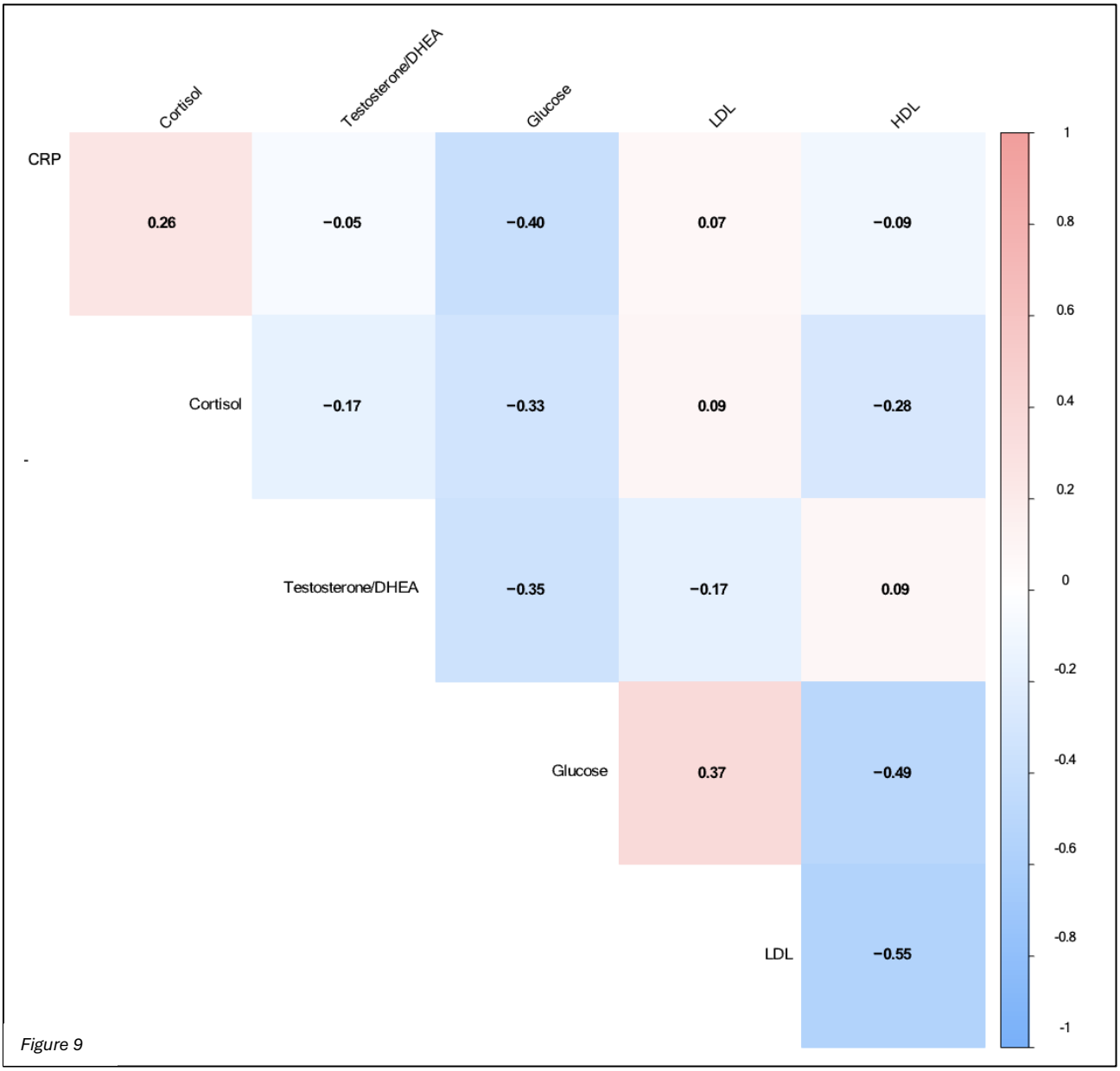

Figure 9

Partial Correlation Analysis

To better understand the true strength of these relationships while controlling for potential confounding effects, partial correlations were calculated based on 18 complete cases. The analysis reveals several tiers of relationships:

Strong Correlations ($|r| > 0.5$):

- Testosterone/DHEA and HDL (-0.575): The strongest inverse relationship
- CRP and Cortisol (0.568): A robust positive association
- CRP and HDL (-0.548): A notable negative relationship
- Cortisol and HDL (0.496): A moderately strong positive correlation

Moderate Correlations ($0.3 < |r| < 0.5$):

- Glucose and HDL (-0.425): Inverse relationship
- CRP and Glucose (-0.350): Negative association
- CRP and LDL (-0.337): Inverse relationship
- Cortisol and Glucose (0.310): Positive correlation
- LDL and HDL (-0.310): Expected inverse relationship

Weak Correlations ($|r| < 0.3$):

- Testosterone/DHEA and Glucose (-0.273)
- CRP and Testosterone/DHEA (-0.252)
- Testosterone/DHEA and LDL (-0.197)
- Cortisol and LDL (0.140)
- Glucose and LDL (0.072)
- Cortisol and Testosterone/DHEA (-0.066)

This hierarchical organization of correlations helps identify the most significant relationships while controlling for other variables, providing a clearer picture of the direct associations between biomarkers.

4. Conclusion

Our exploratory analysis has revealed several significant insights into the relationships between key biomarkers in our study population. Gender emerges as a crucial differentiating factor, with female participants exhibiting notably stronger hormonal correlations and distinct lipid profiles compared to their male counterparts. Of particular concern are the substantial proportions of out-of-range values observed in testosterone and LDL cholesterol, affecting approximately one-third of the relevant populations. The age-based analysis suggests a higher prevalence of hormonal imbalances in younger participants, while lipid profile irregularities appear consistent across age groups.

The correlation analysis, particularly through partial correlations, has illuminated strong interconnections between various biomarker categories. The relationship between hormonal markers and lipid profiles, especially the Testosterone/DHEA-HDL interaction, stands out as particularly significant. Similarly robust associations were observed between inflammatory and stress responses (CRP-Cortisol) and between metabolic and lipid parameters (Glucose-HDL), suggesting complex systemic interactions.

However, several important limitations constrain the interpretation of these results. The modest sample size of 21 participants inherently limits statistical power and generalizability. The presence of multicollinearity among biomarkers complicates the interpretation of their relationships, while the cross-sectional nature of our data precludes causal inference. Additionally, unmeasured variables such as diet, exercise, and sleep patterns might serve as important confounding factors, and the non-random sampling method may introduce selection bias.

Looking forward, several analytical approaches could deepen our understanding of these relationships. Principal Component Analysis would be valuable in identifying underlying patterns and addressing multicollinearity issues by reducing dimensionality. This could reveal hidden biomarker clusters that aren't apparent in traditional pairwise correlations. Complementary to this, cluster analysis could identify distinct participant subgroups based on their biomarker profiles, potentially informing more targeted intervention strategies.

The development of a longitudinal study framework would allow us to track biomarker changes over time, particularly in response to interventions. This would enable more robust causal inference and assessment of correlation stability. Furthermore, expanding data collection to include lifestyle factors and increasing measurement frequency would provide a more comprehensive understanding of the complex interactions between biomarkers and their relationship to health outcomes.

These suggested analytical approaches and expanded data collection efforts would significantly enhance our ability to understand and interpret the complex interplay between these important health indicators, ultimately leading to more effective personalized health interventions.