

ColocZStats: A Z-Stack Signal Colocalization Extension Tool for 3D Slicer

Xiang Chen^{1,2}, Teena Thakur³, Anand D. Jeyasekharan³, Touati Benoukraf^{1,3*} and Oscar Meruvia-Pastor^{2*}

¹*Division of BioMedical Sciences, Faculty of Medicine, Memorial University of Newfoundland, St. John's, NL, Canada*

²*Department of Computer Science, Faculty of Science, Memorial University of Newfoundland, St. John's, NL, Canada*

³*Cancer Science Institute of Singapore, National University of Singapore, Singapore, Singapore*

Correspondence*:

Oscar Meruvia-Pastor

oscar@mun.ca

Touati Benoukraf

tbenoukraf@mun.ca

2 ABSTRACT

3 Confocal microscopy has evolved as a widely adopted imaging technique in molecular biology
4 and is frequently utilized to achieve accurate subcellular localization of proteins. Applying
5 colocalization analysis on image z-stacks obtained from confocal fluorescence microscopes
6 is a dependable method to reveal the association between different molecules. In addition,
7 despite the established advantages and growing adoption of 3D visualization software in various
8 microscopy research domains, there has been a scarcity of systems supporting colocalization
9 analysis within a user-specified region of interest (ROI). In this context, several broadly employed
10 biological image visualization platforms were meticulously explored in this study to comprehend
11 the current landscape. It has been observed that while these applications can generate three-
12 dimensional (3D) reconstructions for the z-stacks and in some cases transfer them into an
13 immersive Virtual Reality (VR) scene, there is still a lack of support for performing quantitative
14 colocalization analysis on such images based on a user-defined ROI and thresholding levels. To
15 address these issues, an extension called ColocZStats has been developed for 3D Slicer, a widely
16 used free and open-source software package for image analysis and scientific visualization. With
17 a custom-designed user-friendly interface, ColocZStats allows investigators to conduct intensity
18 thresholding and ROI selection on imported 3D image stacks. It can deliver several essential
19 colocalization metrics for structures of interest and produce reports in the form of diagrams and
20 spreadsheets.

21 **Keywords:** Confocal microscopy, Colocalization analysis, Confocal microscopy visualization, 3D Slicer, Virtual reality (VR), Volume
22 rendering

1 INTRODUCTION

23 Compared to conventional fluorescence microscopes, the most significant advantage of confocal
24 microscopes is that they can exclude the out-of-focus light from either above or below the current focal
25 plane (Jonkman et al., 2020). This capability facilitates precisely detecting the specific organelle in which

26 the target molecule is present. In addition, the confocal microscope's features of sharpening fluorescence
27 images and reducing haze contribute to enhancing image clarity (Collazo et al., 2005). Many of these
28 two-dimensional (2D) image slices can be continuously collected from focal planes at different depths
29 along the z-dimension and eventually assembled to produce a z-stack comprising the specimen's entire 3D
30 data (Collazo et al., 2005; Theart et al., 2017).

31 Examining interactions between different proteins or molecular structures holds significant importance
32 in biological sciences. Biologists often perform colocalization analysis on confocal image z-stacks to
33 better understand the roles and interactions of proteins (Pompey et al., 2013; Bolte and Cordelières,
34 2006). Colocalization detects the spatial overlap between distinct fluorescent labels with different emission
35 wavelengths to determine whether the fluorophores are close or within the same region (Lacoste et al.,
36 2000; Adler and Parmryd, 2013). Colocalization involves two aspects: co-occurrence and correlation.
37 Co-occurrence refers to the simple spatial intersection of different fluorophores. Correlation refers to
38 distinct fluorophores codistributed proportionally with a more apparent statistical relationship (Adler
39 and Parmryd, 2013; Dunn et al., 2011). Typical application examples of colocalization analysis include
40 confirming whether a specific protein associates with microtubules (Bassell et al., 1998; Nicolas et al.,
41 2008) or mitochondria (Lynch et al., 1996), or verifying whether different proteins associate with identical
42 plasma membrane domains (Lachmanovich et al., 2003).

43 Visualizing superimposed fluorescence micrographs is the most common method for assessing
44 colocalization. When the images of each fluorescence label are merged, their combined contribution
45 can be indicated by the color of the microstructure appearance. For instance, because of the combined
46 effects of green and red fluorescence, the colocalization of fluorescein and rhodamine can be recognized in
47 yellow structures (Dunn et al., 2011). When analyzing z-stacks, a popular visualization method involves
48 performing 3D reconstruction using techniques such as volume rendering, transforming the data into 3D
49 semi-translucent voxels to enhance the user's perception when observing samples (Theart et al., 2017;
50 Lucas et al., 1996; Liu and Chiang, 2003). Another cutting-edge visualization technology is Virtual Reality
51 (VR). VR is a digitally created immersive 3D simulated environment that closely resembles reality. While
52 being fully immersed in this environment, users can navigate through and interact with virtual objects. It
53 is noteworthy that as VR technology has developed, the characteristic it supplies that allows immersive
54 observation of biological samples has led to this technology being continuously combined with a variety of
55 visual analysis methods in recent years, enabling biologists to obtain a more realistic 3D awareness in the
56 process of scientific exploration (Patil and Batra, 2019; Sommer et al., 2018). Although the application
57 of VR in various subfields of bioinformatics has been steadily increasing, a study published in 2017
58 by Theart et al. (Theart et al., 2017) revealed that, before that time, no applications had provided the
59 capability for colocalization analysis in VR. Nevertheless, this study, along with its subsequent research
60 (Theart et al., 2018), collectively demonstrated the substantial potential and advantages of performing
61 colocalization analysis for z-stacks based on the generated volume-rendered images in an immersive VR
62 environment, namely that the efficiency of conducting such analysis and the precision of inspecting and
63 assessing biological samples can be significantly improved.

64 In consideration of the above background, several well-known applications, with a focus on 3D graphics
65 systems with VR functionalities, were investigated during the study period to gain an overview of the
66 current status of these commonly accepted bioimaging visualization and analysis platforms for visualizing
67 confocal microscopy data and evaluating its degree of colocalization.

68 ExMicroVR (Immersive Science LLC., 2024b) is a VR tool created for the immersive visualization and
69 manipulation of multi-channel confocal image stacks. Its VR environment and easy-to-use user interface

allow it to considerably expand microscopic samples so biologists can view and explore the molecules' structures in greater detail. Another software, ConfocalVR (Immersive Science LLC., 2024a), in its current form, is an upgraded version of ExMicroVR. Not only does it have more added interactive features, but it also provides a range of relatively advanced image analysis capabilities, such as adding markers in 3D scenes, counting the number of interesting objects, and measuring the distance between them, allowing researchers to further investigate the complexity of cellular structures. ChimeraX (Goddard et al., 2018; Pettersen et al., 2021) is an interactive platform for visualizing diverse types of data, including atomic structures, sequences, and 3D multi-channel microscopy data. It supplies around 100 different analysis functionalities. ChimeraX VR is the VR extension of ChimeraX, enabling users to interact with cellular protein structures with stereo depth perception. When activated, a floating panel, precisely the same as the desktop interface, is available in the VR scene to help users use controllers to perform all necessary manipulations on the images. 3D Slicer (Fedorov et al., 2024) is a broadly recognized, accessible, and open-source platform that provides multifarious biomedical image processing and visualization features (Kikinis et al., 2013). Similarly, SlicerVR is the VR extension within 3D Slicer. Thanks to the capabilities of the 3D Slicer ecosystem, SlicerVR offers seamless VR integration in this popular image computing application (Lasso et al., 2018) so that observers can quickly transfer images displayed in desktop mode to the VR scenario. Additionally, it supports multi-user collaboration, allowing images within the exact scene to be manipulated synchronously (Pinter et al., 2020).

Through this investigation, it was found that all of the platforms above are capable of reading datasets generated by fluorescence confocal microscopy and converting them into 3D semi-translucent voxels that can be delivered to VR scenes for visualization. For instance, ConfocalVR offers a 'blend function' option that allows the extraction of voxels representing the spatially intersecting regions between two channels. The 3D rendering of these voxels can aid researchers in visually assessing the level of colocalization between channels. However, for more comprehensive colocalization analysis, relying solely on subjective identification of the relative distribution of different molecules from a visual perspective is insufficient. Objective and quantitative analysis is crucial. Despite the commendable image visualization and diverse analytical capabilities inherent in these platforms, there is still room for them to improve in obtaining colocalization statistics for confocal stacks. As indicated by a published work of Stefani et al. (Stefani et al., 2018), developing a dedicated tool to gain objective colocalization measurements remains one of the goals and challenges for ConfocalVR.

To address the aforementioned limitation and take advantage of the comparatively superior high extensibility of 3D Slicer, which supports the creation of interactive and batch-processing tools for various purposes (Kapur et al., 2016), a free, open-source extension called ColocZStats has been developed for 3D Slicer. ColocZStats is currently designed as a desktop application, which enables users to visually observe the spatial relationship between different biological microstructures while performing thresholding and ROI selection on the channels' 3D volumetric representations via an easy-to-use graphical user interface (GUI) and then acquiring critical colocalization metrics with one-mouse click. The proposal of this tool contributes to supplementing the capabilities of 3D Slicer in visualizing multi-channel confocal image stacks and quantifying colocalization, thereby broadening its scope as an integrated image analysis platform.

2 MATERIALS AND EQUIPMENT

109 2.1 Description of Sample Data Source

110 To showcase the capabilities of ColocZStats discussed in this paper, we utilized confocal z-stack data
111 collected during a study on the colocalization of DSS1 nuclear bodies with other nuclear body types.
112 Please refer to the document/Supplementary Materials for a detailed description of the image. DSS1, also
113 known as SEM1, is a gene that encodes a protein crucial for various cellular processes, most notably the
114 function of the 26S proteasome complex in protein degradation. More specifically, a human ovarian clear
115 cell carcinoma cell line (RMG-I) was seeded at 100,000 cells per well onto a coverslip in a 6-well plate
116 and allowed to grow till 70% confluence. On the day of staining, the cells were fixed with 4% ice-cold
117 paraformaldehyde for 15 mins at room temperature (RT) and blocked with 2% Bovine Serum Albumin
118 (BSA) in 0.1% Phosphate Buffer Saline containing 0.1% Triton-X (PBSTx) for 30 mins. Following fixation
119 and blocking, the cells were incubated with a primary antibody cocktail containing anti-DSS1 (Catalogue#
120 NB100-1334, Novus Biologicals) and anti-PML (Catalogue#sc-966, SCBT) for 1h at RT. After that, the
121 cells were washed 3 times with 0.1% PBSTx for 5 mins each and incubated with a secondary antibody
122 cocktail containing anti-goat Alexa FluorTM 647 (for DSS1), anti-mouse Alexa FluorTM 488 (for PML)
123 and Hoechst 33342 (Catalogue# H3570, Invitrogen) for 1h at RT. Following this incubation, the cells were
124 subjected to 3 washes, each lasting 5 mins, with 0.1% PBSTx to ensure thorough cleansing. Subsequently,
125 z-stack imaging was performed using a Zeiss LSM800 confocal microscope with Airyscan. The above
126 process utilized three distinct dyes to specifically label DSS1 nuclear bodies (Red), promyelocytic leukemia
127 (PML) nuclear bodies (Green), and the nucleus (Blue). The data file was named ‘Sample Image Stack.tif’.

128 2.2 Description of VR Equipment

129 All screenshots of the VR environments presented in the upcoming section were captured using an HTC
130 Vive Cosmos Elite VR System. The VR system’s Head Mounted Display (HMD) provides an approximate
131 FoV of around 110° through two displays refreshed at a rate of 90 Hz.

3 METHODS

132 3.1 ColocZStats Development

133 High-quality 3D reconstruction or rendering is an essential prerequisite for accurately performing
134 colocalization analysis on confocal z-stacks, as it can reveal more detail in structures, enhance users’
135 recognition of colocalization areas, and elevate colocalization analysis sensitivity.

136 Figure 1 shows two channels of the same sample dataset and their combination displayed as colored
137 semi-transparent voxels in ChimeraX desktop, ChimeraX VR, ExMicroVR, ConfocalVR, SlicerVR, and
138 3D Slicer desktop separately. Although 3D Slicer supports volume rendering, before the development of
139 ColocZStats, it could not automatically split multi-channel confocal z-stack channels and color them, nor
140 did it provide specialized GUI widgets for separate manipulation of each channel or navigation between
141 them. Therefore, an image processing package, FIJI (Schindelin et al., 2012), was initially utilized to save
142 the channels as separate multi-page z-stack files. Subsequently, these files were selected and imported as
143 scalar volumes into the ‘Volume Rendering’ module of 3D Slicer (National Alliance for Medical Image
144 Computing, 2024) for rendering. Their colors were then manually configured to ensure consistency with
145 the others. Currently, ChimeraX desktop and ChimeraX VR do not support applying lighting to volumetric
146 renderings, but only to surfaces and meshes (Goddard, T., 2024). However, adjustable highlights or

147 shadows are necessary for showing 3D semi-translucent voxels, as this can help create refined volumetric
148 representations and allow viewers to distinguish intricate topologies and distance relationships more easily
149 (The American Society for Cell Biology., 2024). Unlike them, the remaining programs in Figure 1 possess
150 the capability of adding lighting and shadows to such renderings. For example, the ‘Volume Rendering’
151 module of 3D Slicer provides many options for calculating shading effects, which enables finer adjustments
152 to the rendered volume’s appearance. Regarding the rendering effects, it was observed that the quality
153 produced by 3D Slicer desktop or SlicerVR is not inferior to that of other visualization software programs.

154 More importantly, it has also been learned that researchers can efficiently develop, assess new methods,
155 and add more capabilities through custom modules by benefiting from the highly extendable features
156 of 3D Slicer. That is to say, in 3D Slicer, developers do not need extra time to redevelop primary data
157 import/export, visualization, or interaction functionalities. Instead, they can easily call or integrate these
158 characteristics and focus on developing new required features (Fedorov et al., 2024; Vipiana and Crocco,
159 2023). Although ChimeraX is also extensible, many of its functional Application Programming Interfaces
160 (APIs) were not documented during the tool development, and many existing APIs were experimental. In
161 contrast, 3D Slicer has provided relatively extensive API documentation and developer tutorials. Moreover,
162 the 3D Slicer community has offered a large and active forum for developers, where considerable issues
163 related to the tool development can be found, discussed, or raised for timely feedback. The other two,
164 ConfocalVR and ExMicroVR, have not provided publicly available APIs. All the above factors have
165 constituted the rationale for developing the tool for 3D Slicer.

166 ColocZStats is a scripted extension that utilizes the 3D Slicer APIs (Slicer Community., 2024)
167 and is implemented using Python. The code was written in PyCharm (JetBrains s.r.o., 2024), an
168 integrated development environment (IDE) designed explicitly for Python programming. The fundamental
169 organizational structures of ColocZStats are ‘classes,’ which represent independent code blocks containing
170 a group of functions and methods.

171 Once a multi-channel confocal z-stack is loaded into ColocZStats, in the program’s background, the
172 stack’s metadata will be parsed to extract individual Numpy arrays of each channel. Simultaneously, several
173 methods from a base module, ‘util.py’ and a core class, ‘vtkMRMLDisplayNode,’ of 3D Slicer will be
174 iteratively invoked to set up separate scalar volume nodes for each channel’s Numpy array and to assign
175 individual pseudo colors to them. Also, the rendering method from 3D Slicer’s ‘VolumeRendering’ module
176 (Fedorov et al., 2024) will be applied to all individual channels separately, eventually presenting their
177 merged visual appearance. Similar to most open-source medical imaging systems, such as MITK (Nolden
178 et al., 2013), itksNAP (Yushkevich et al., 2006), and CustusX (Askeland et al., 2016), the volume rendering
179 back-end of 3D Slicer is based on the Visualization Toolkit (VTK) (Drouin and Collins, 2018). VTK is a
180 powerful cross-platform library that supports a variety of visualization and image-processing techniques,
181 making it widely adopted in open-source and commercial visualization software (Bozorgi and Lindseth,
182 2015). The ‘Volume Rendering’ module provides three volume rendering methods: (i) VTK CPU Ray
183 Casting, (ii) VTK GPU Ray Casting, and (iii) VTK Multi-Volume. The ‘VTK GPU Ray Casting’ is the
184 default method for rendering because graphics hardware can significantly accelerate rendering (National
185 Alliance for Medical Image Computing, 2024).

186 Moreover, at the moment a stack is loaded, a set of separate GUI elements will be created for each channel
187 to achieve purposes such as adjusting channels’ threshold values or revealing any number of channels
188 in the scene by controlling their visibility. The GUIs in ColocZStats are provided by the Qt toolkit (The
189 Qt Company., 2024). Numerous modules in 3D Slicer offer a suite of reusable, modifiable GUI widgets,
190 allowing developers to integrate them seamlessly into custom user interfaces via Qt Designer. Qt Designer

191 is a tool for crafting and constructing GUIs with Qt Widgets. For instance, in ColocZStats, the widget
192 integrated for controlling each channel's threshold range is the 'qMRMLVolumeThresholdWidget,' which
193 is also a widget within 3D Slicer's 'Volumes' module (3D Slicer., 2024b).

194 By integrating and leveraging several existing classes and methods in 3D Slicer, the initial need for a
195 series of manual operations to create appropriate volumetric representations for channels has evolved into
196 the current state where all these steps can be automatically completed, with each channel equipped with
197 individually controllable GUI widgets. The above process is also an illustrative example of how the high
198 extensibility of 3D Slicer can be exploited to fulfill certain specific requirements of the tool.

199 **3.2 Statistical Analysis of Colocalization**

200 As previously mentioned in the 'Introduction' section, ColocZStats not only helps researchers identify the
201 relative distribution of different cellular molecules but can also generate effective metrics for quantifying
202 colocalization to help investigate the presence of spatial association between different channels. Next, these
203 coefficients are described in detail.

204 **3.2.1 Pearson's Correlation Coefficient**

205 In the field of colocalization analysis, Intensity Correlation Coefficient-Based (ICCB) analysis methods
206 constitute one of the primary categories of methods for assessing colocalization events. They depend on
207 the image's channel intensity information, which provides a powerful way to quantify the degree of spatial
208 overlapping of two channels (Georgieva et al., 2016). A large number of colocalization analysis tools
209 employing ICCB methods have been widely integrated into various image analysis applications (Bolte and
210 Cordelières, 2006). Pearson's correlation coefficient (PCC) is one of the most commonly employed ICCB
211 methods (Bolte and Cordelières, 2006; Dunn et al., 2011). It originated in the 19th century and has been
212 extensively used to evaluate the linear correlation between two data sets (Adler and Parmryd, 2010). When
213 analyzing colocalization, PCC is employed to quantify the linear relationship between the signal intensities
214 in one channel and the related values in another (Aaron et al., 2018). The PCC can be considered as a
215 normalized assessment of two channels' covariance (Aaron et al., 2018). The formula for PCC applied
216 in ColocZStats is defined below, with the signal intensities of two channels at each voxel included in the
217 calculation:

$$PCC = \frac{\sum_{i=1}^n (ch1_i - \bar{ch1})(ch2_i - \bar{ch2})}{\sqrt{\sum_{i=1}^n (ch1_i - \bar{ch1})^2} \sqrt{\sum_{i=1}^n (ch2_i - \bar{ch2})^2}} \quad (1)$$

218 For any pair of selected channels in the tool, the $ch1_i$ and $ch2_i$ represent the intensity values of each
219 channel at voxel i , respectively, and the $\bar{ch1}$ and $\bar{ch2}$ represent the mean intensities of each channel,
220 respectively.

221 The range of PCC is between +1 and -1. +1 indicates that the two channels are entirely linearly correlated,
222 and -1 means that the two channels are perfectly but inversely correlated. The value of zero means that the
223 distributions of the two channels are uncorrelated (Dunn et al., 2011). Although PCC is theoretically not
224 influenced by thresholds, they are incorporated into the tool's computation to handle specified threshold
225 settings uniformly across all coefficients computed by ColocZStats. The specific approach of setting
226 thresholds for calculating PCC is similar to that of the 'Colocalization Analyzer' in the Huygens Essential
227 software (Scientific Volume Imaging B.V., 2024a). The Huygens Essential software (Scientific Volume
228 Imaging B.V., 2024b) is a widely acknowledged desktop software for the visualization and analysis of

229 microscopic images (Pennington et al., 2022; Davis et al., 2023; Volk et al., 2022). The distinction between
230 the two is that, in ColocZStats, not only the value of the lower threshold but also that of the upper threshold
231 can be specified for each channel. The purpose of allowing the setting for channels' upper threshold values
232 is analogous to the design of ConfocalVR's previous 'Cut Range Max' widget or its latest 'Max Threshold'
233 widget, which is used to filter out oversaturated voxels that may be occasionally observed by observers in
234 some particular circumstances (Stefani et al., 2018). During the calculation process, if a particular channel
235 is set with lower and upper thresholds, voxel intensities greater than the upper threshold will be set to zero.
236 Based on that, the lower threshold will be subtracted from the remaining voxel intensities. If any negative
237 voxel values occur after the subtraction, they will be set to zero.

238 3.2.2 Intersection coefficients

239 In distinction from the PCC, which is calculated based on actual voxel intensities, more straightforward
240 coefficients can be calculated based only on the presence or absence of signals in a voxel, regardless of
241 its actual intensity value. All intersection coefficients calculated by ColocZStats are examples of such
242 coefficients, and the computation methods were borrowed from the Huygens Colocalization Analyzer
243 (Scientific Volume Imaging B.V., 2024a). Similarly, the difference is that the upper threshold value for
244 each selected channel is included in ColocZStats's calculation. To be more specific, once a voxel's intensity
245 value is within a specific intensity range bounded by upper and lower thresholds, it can be regarded as
246 having some meaningful signal. If so, its value could be considered as 1, regardless of its actual intensity,
247 and 0 otherwise. This indicates that a binary image $ch1_{weight}$ with intensity $ch1_{weight,i}$ at voxel i can be
248 created based on the voxel's actual intensity $ch1_i$ and the channel's intensity range. This explanation is
249 illustrated by taking the first channel, $ch1$, of all selected channels as an example (the same applies to all
250 the other channels):

$$ch1_{weight,i} = \begin{cases} 0 & \text{if } ch1_i \leq ch1_{lower} \text{ or } ch1_i > ch1_{upper} \\ 1 & \text{if } ch1_{lower} < ch1_i \leq ch1_{upper} \end{cases} \quad (2)$$

251 Based on the definition of $ch1_{weight,i}$, another metric called the global intersection coefficient (I) can
252 be calculated. It is defined as the ratio of the total volume of voxels where all channels intersect to the
253 total volume of all channels. In other words, it calculates the proportion of voxels having valid intensity
254 values in all thresholded channels. Multiplying this figure by 100 is interpreted as the intersection's volume
255 percentage. For any two specified channels in ColocZStats, the formula of I is defined as follows:

$$I = \frac{\sum_{i=1}^n (ch1_{weight,i} \ ch2_{weight,i})}{\sum_{i=1}^n ch1_{weight,i} + \sum_{i=1}^n ch2_{weight,i} - \sum_{i=1}^n (ch1_{weight,i} \ ch2_{weight,i})} \quad (3)$$

256 The numerator refers to the intersecting voxels' total volume. For each voxel, the overlapping contribution
257 is defined as the product of $ch1_{weight,i}$ and $ch2_{weight,i}$. The denominator represents the total volume of
258 the two channels, which is defined as the sum of the volume of the first channel and the volume of the
259 second channel minus their intersection's total volume (to prevent double counting). Another two individual
260 intersection coefficients are derived from I , which describes what proportion of the first and second
261 channels are intersecting:

$$i_1 = \frac{\sum_{i=1}^n (ch1_{weight,i} \ ch2_{weight,i})}{\sum_{i=1}^n ch1_{weight,i}} \quad (4)$$

$$i_2 = \frac{\sum_{i=1}^n (ch1_{weight,i} ch2_{weight,i})}{\sum_{i=1}^n ch2_{weight,i}} \quad (5)$$

262 Another contribution of ColocZStats is that it allows researchers to choose up to three channels in a
263 z-stack for statistical analysis. Extending from the above-mentioned formulas, the intersection coefficients'
264 formulas tailored to this scenario have also been proposed. In this case, the formula for I is given as:

$$I = \frac{\sum_{i=1}^n (ch1_{weight,i} ch2_{weight,i} ch3_{weight,i})}{\sum_{i=1}^n ch1_{weight,i} + \sum_{i=1}^n ch2_{weight,i} + \sum_{i=1}^n ch3_{weight,i} - \sum_{i=1}^n (ch1_{weight,i} ch2_{weight,i}) - \sum_{i=1}^n (ch1_{weight,i} ch3_{weight,i}) - \sum_{i=1}^n (ch2_{weight,i} ch3_{weight,i}) + \sum_{i=1}^n (ch1_{weight,i} ch2_{weight,i} ch3_{weight,i})} \quad (6)$$

265 Likewise, the three channels' intersecting volume of a given voxel i is defined as the product of $ch1_{weight,i}$,
266 $ch2_{weight,i}$, $ch3_{weight,i}$, while the sum acts as the numerator. The denominator is the total volume of the
267 three channels, determined by the inclusion-exclusion principle for three sets (Chen, 2014). Also, three
268 respective intersection coefficients can be obtained to exhibit the proportion of the intersection in each
269 channel:

$$i_1 = \frac{\sum_{i=1}^n (ch1_{weight,i} ch2_{weight,i} ch3_{weight,i})}{\sum_{i=1}^n ch1_{weight,i}} \quad (7)$$

$$i_2 = \frac{\sum_{i=1}^n (ch1_{weight,i} ch2_{weight,i} ch3_{weight,i})}{\sum_{i=1}^n ch2_{weight,i}} \quad (8)$$

$$i_3 = \frac{\sum_{i=1}^n (ch1_{weight,i} ch2_{weight,i} ch3_{weight,i})}{\sum_{i=1}^n ch3_{weight,i}} \quad (9)$$

4 RESULTS

270 4.1 Availability of ColocZStats

271 ColocZStats is freely available under an MIT license and requires the stable version of 3D Slicer
272 (3D Slicer., 2024a) for compatibility. The Slicer community maintains a website called the 'Slicer
273 Extensions Catalog' for finding and downloading extensions, and ColocZStats is available there (3D
274 Slicer., 2024c). The 'Extensions Manager' in 3D Slicer provides direct access to the website, facilitating
275 easy installation, updating, or uninstallation of extensions with a few clicks in the application. As
276 shown in Figure 2, ColocZStats can be found within the 'Quantification' category in the catalog. After
277 installing the ColocZStats, it will be presented to users as a built-in extension. More information
278 about installing and using ColocZStats can be found on the homepage of its repository on GitHub
279 (<https://github.com/ChenXiang96/SlicerColoc-Z-Stats>).

280 4.2 Input Image File

281 For compatibility with ColocZStats, each input image file must be a 3D multi-channel confocal image
282 z-stack in TIFF format that maintains the original intensity values, with each channel in grayscale. Each
283 channel must possess the same dimensions, image order, and magnification. Even though ColocZStats

284 supports loading z-stacks containing up to fifteen channels, only up to three channels can be specified
285 for each colocalization computation because the statistical analysis and the possible interactions between
286 channels become more complex with each additional channel.

287 **4.3 User Interface**

288 Figure 3 shows an example of ColocZStats's user interface, which consists of two separate areas: a control
289 panel on the left side that provides a series of interactive widgets, and a 3D view on the right side that
290 displays the volumetric rendering of the loaded sample image stack. Users can adjust these volume-rendered
291 images and calculate the corresponding colocalization metrics by manipulating the widgets on the control
292 panel. To display the details of these widgets clearly, a close-up of the control panel is shown in Figure 3.
293 The following subsection describes a typical workflow for ColocZStats.

294 **4.4 The Workflow of ColocZStats**

295 A typical workflow of ColocZStats is shown in Figure 4A, which is divided into five steps: (i) 'Inputs';
296 (ii) 'Visualization'; (iii) 'Channel Selection & Thresholding'; (iv) 'ROI Selection'; and (v) 'Analysis.'
297 The sequence of certain steps in this workflow can be slightly adjusted based on particular conditions
298 or personal preferences. In 3D Slicer, a file browser can be opened by clicking the 'DATA' button at
299 the upper-left corner to load a multi-channel confocal z-stack file into the scene. All channels' colored
300 volume-rendered images will immediately appear in the 3D view by default when the stack is loaded into
301 ColocZStats, and they can be moved and rotated arbitrarily with mouse clicks and movements.

302 The widgets in the 'Channels' sub-panel will also be displayed concurrently upon loading the input
303 file. The checkbox in front of each channel's name label is not only used for managing the visibility
304 of the channel's rendered volume but also for determining whether the channel will be included in the
305 colocalization analysis. Figure 4B,C represents an example where all three channels of the sample data
306 are selected. After the channel selection, threshold segmentation is often necessary because it is a helpful
307 approach for extracting interesting voxels from the image. For individual channels, as any slider for
308 controlling the thresholds is adjusted, the display range of the channel's volumetric representation will be
309 changed synchronously, facilitating users' observation and the decision-making for the following analysis.
310 By default, when a confocal z-stack is imported, the checkboxes of all its channels are turned on, and the
311 threshold ranges for all channels are displayed as their original ranges, respectively.

312 The ROI box integrated into ColocZStats facilitates researchers' analysis of any parts of the loaded
313 stack. By default, there is no ROI box for the imported stack in the scene. Upon the first click on the eye
314 icon beside the 'Display ROI', an ROI box will be created, and after that, its visibility can be customized
315 to be toggled on or off. While the ROI box is displayed, depth peeling will automatically be applied to
316 the volumetric rendering to produce a better translucent appearance. The handle points on the ROI box
317 can be dragged to crop the rendered visualization with six planes. As any handle point is dragged, the
318 volumetric rendering outside the box will disappear synchronously. The final analysis will only include
319 the voxels inside the ROI box. When there is a need to analyze the entire stack, the ROI box should be
320 adjusted to enclose it completely. The functionality to extract the voxels inside the ROI is enabled by
321 the 'Crop Volume' module, and the related methods will be called in the back-end when a calculation is
322 executed. The 'Crop Volume' module is a built-in loadable module of 3D Slicer that allows the extraction
323 of a rectangular sub-volume from a scalar volume. With the above control options, users can conveniently
324 configure voxel intensity thresholds and ROI for all channels to be analyzed while intuitively focusing on
325 the critical structures to obtain the final colocalization metrics.

326 The ‘Analysis’ step is performed when clicking the ‘Compute Colocalization’ button; all the thresholded
327 channels and overlapping areas inside the ROI will be identified in the program’s background process.
328 Subsequently, the colocalization coefficients described previously will be computed. Meanwhile, a series of
329 graphical representations will pop up on the screen, such as a Venn diagram illustrating volume percentages
330 and 2D histograms showing the combinations of intensities for all possible pairs of selected channels.
331 The following subsection provides detailed descriptions of these generated graphical representations. In
332 addition, users can add a custom annotation for the associated image stack at any step after it is loaded to
333 record any necessary information.

334 4.5 Produced Graphical Representations

335 4.5.1 Venn Diagrams

336 ColocZStats allows two or three channels to be selected simultaneously to perform colocalization
337 measurements. The Venn diagrams generated from the above two scenarios allow researchers to quickly
338 recognize the volume percentages of overlapping regions along with that of the remaining parts. A popular
339 Python package, ‘matplotlib-venn,’ was utilized to implement this functionality while leveraging its
340 ‘venn2_unweighted’ and ‘venn3_unweighted’ functions for the creation of the two kinds of Venn diagrams
341 consisting of two or three circles without area-weighting, respectively.

342 In the Venn diagrams generated, the colors in these circles match the colors in the volume-rendered
343 images, and the area where all circles intersect signifies the part where all specified channels intersect,
344 with the displayed percentage corresponding to the result obtained by multiplying the global intersection
345 coefficient by 100 and retaining four decimal places. Based on this, the percentages of the remaining
346 parts of these channels can be derived and displayed in the other areas of the Venn diagrams. Besides, the
347 Venn diagram’s title matches the specified name on the GUI’s combo box, and the channel names shown
348 correspond to the channel name labels defined on the interface.

349 The examples shown in Figure 5 demonstrate a typical scenario of setting lower thresholds for each
350 channel and configuring their upper thresholds to their maximum values. Figures 5E, F are also components
351 of the result illustrations composed together with the two Venn diagrams, respectively, and for clarity, they
352 were extracted as two separate figures.

353 4.5.2 2D Histograms

354 The 2D histograms produced by ColocZStats serve as a supplementary tool for visually assessing
355 colocalization, providing a qualitative indication. The feature of generating 2D histograms has become a
356 basic functionality of most colocalization analysis software. One specific application of 2D histograms
357 is that they can be employed to identify populations within different compartments (Brown et al., 2000;
358 Wang et al., 2001). For any two channels, a 2D histogram illustrates the connection of intensities between
359 them, where the x-axis corresponds to the intensities of the first channel, and the y-axis corresponds to the
360 intensities of the second channel. The histogram’s points can be observed closely gathering along a straight
361 line if the two channels are highly correlated. The line’s slope indicates the two channels’ fluorescence
362 ratio. Following the method introduced in Caltech’s ‘Introduction to Data Analysis in the Biological
363 Sciences’ course in 2019, in ColocZStats, a Python library, called ‘Holoviews,’ (Stevens et al., 2015) was
364 applied to plot the 2D histograms. With the scenario corresponding to Figure 5A, Figure 6 demonstrates
365 the generation of a 2D histogram. For any precise position within the channels, the related intensities of
366 both channels are combined to define a coordinate in the 2D histogram. Simultaneously, the count of points
367 at this coordinate is incremented by one. As shown in Figure 6C, the blank area in the lower-left corner

368 represents the background. For any background's voxel, the intensity values of its two channels are both
369 outside the respective valid channel threshold ranges, so such voxels will not be plotted as points in the 2D
370 histogram. The definition of the valid threshold ranges mentioned in this context is consistent with those
371 applied when calculating the intersection coefficients. The color bar on the histogram's right side indicates
372 the number of points with the same intensity combinations. The 2D histograms generated by ColocZStats
373 will be saved as static images and interactive HTML files that can be viewed in more detail.

374 The correspondence between the example 2D histogram in Figure 6 and its related Venn diagram is
375 depicted in Figure 7. The defined threshold value boundaries for the channels delineate four regions in
376 Figure 7A. In this 2D histogram, three colored regions, and their outlines aligned with the boundaries, are
377 used to highlight all possible distribution positions of points. All points within the yellow region and along
378 its yellow outlines represent all the voxels that contain valid signals in both channels, and the percentage
379 of all these points aligns with the percentage displayed in the yellow area of Figure 7B. Likewise, the
380 points distributed in the red or green parts represent the voxels with exclusively valid signals in channel 1
381 or channel 2, respectively, and the percentage of points in the two regions are consistent with the values
382 shown in the Venn diagram's red and green areas, respectively. Also, no points are plotted on coordinates
383 corresponding to 'b,' 'c,' and 'd' or the boundaries formed between them, as they lie outside the defined
384 threshold ranges.

385 4.6 Results Spreadsheet

386 After clicking the 'Compute Colocalization' button, a comprehensive results spreadsheet will be
387 automatically saved for researchers' further reference or sharing. It contains all graphical representations,
388 coefficient results, and the ROI-related information generated from each calculation. Please refer to the
389 document/Supplementary Materials for a detailed description of the spreadsheet.

390 4.7 Case Study

391 This subsection provides an example demonstrating a specific scenario of applying ColocZStats to
392 perform a colocalization analysis task. It primarily focuses on how changes in the threshold range of
393 an individual channel influence the objective quantitative colocalization indicators and the variations in
394 colocalization degree that can be revealed during this process. The ROI box remains unchanged throughout
395 the four cases shown in Figure 8, and the red channel is individually assigned four distinct lower threshold
396 values. In contrast, the threshold ranges for the other channels remain constant. By observing the 3D
397 rendering appearance of the data provided by this tool, a continuous change can be found; that is, as the
398 red channel's lower threshold gradually increases, the volume of its overlap with other channels shows an
399 evident decreasing trend. Combining a series of objective quantifications generated by ColocZStats for
400 each case aids in validating this subjective visual impression and obtaining a more reliable assessment.

401 Through Figure 8C, a noticeable phenomenon regarding the variation of colocalization coefficients is
402 exposed: as the lower threshold value of channel 1 increases, the PCCs between channel 1 and the other
403 two channels gradually approach 0, indicating a diminishing linear correlation between channel 1 and the
404 other two channels. Meanwhile, as demonstrated by the additional histograms created based on the Venn
405 diagrams, with the reduction in the threshold range of channel 1, the proportions of overlapping regions
406 between channel 1 and the other two channels also decrease. Integrating the above observations effectively
407 validates a biological fact: the reduction of channel 1 leads to a decline in its colocalization with the other
408 two channels. In addition, the values of the global intersection coefficient and its three derived coefficients
409 also gradually decrease, implying a decline in the overall colocalization degree of the three channels. This

410 example also exhibits how the visual representations and coefficients produced by this tool can provide
411 multiple perspectives for assisting colocalization analysis.

412 **4.8 Comprehensive Comparison of Visualization Tools**

413 The related features of the programs mentioned in the ‘Introduction’ section, including ColocZStats, for
414 visualizing confocal z-stacks and measuring their colocalization are summarized in Table 1. This table
415 divides these features into four categories, encompassing the most meaningful comparable features for
416 the execution of colocalization analysis. Consequently, although certain programs may have many other
417 functionalities, they are not included in this table. Regarding the choice of programs, ChimeraX VR and
418 SlicerVR are VR extensions of ChimeraX and 3D Slicer correspondingly, and their image processing and
419 analysis capabilities almost entirely depend on the specifics of each platform. As a result, only ChimeraX
420 and 3D Slicer are listed in this table for comparison. For each feature in the table, if the programs
421 themselves or any plugins or modules they incorporate offer matching functionality, the corresponding cell
422 is marked with a check. For instance, in the case of 3D Slicer, its ‘Volume Rendering’ module supports
423 loading multi-page Z-stack files; thus, the corresponding cell is checked. Another module in 3D Slicer,
424 ‘ImageStacks,’ allows loading the image sequence of z-stack slices, resulting in the respective cell being
425 checked as well. It is worth noting that because the ‘ImageStacks’ module is designed specifically for
426 working with image stacks, all the listed image formats in the ‘Supported image format’ for 3D Slicer are
427 consistent with those supported by the ‘ImageStacks’ module.

428 The category ‘Confocal Image Z-stack Observation’ summarizes the general practical features for
429 meticulously observing the channels in confocal z-stacks. Most of them are common to several tools
430 in this comparison. Among these, as for ‘ExMicroVR’ or ‘ConfocalVR,’ if one intends to manipulate
431 individual channels separately, a necessary step is to extract each channel of the original z-stack as a single
432 multi-page z-stack file using FIJI and save all of them into a designated directory for loading. Therefore,
433 while both tools support users in manipulating channels individually, they do not have the functionality
434 to automatically separate all channels of the z-stack to enable this operation. Before the completion of
435 ColocZStats development, as indicated by the information from the 3D Slicer community, 3D Slicer
436 still needed specialized tools for properly visualizing multi-channel confocal z-stacks and manipulating
437 channels separately. Therefore, in the table, no features related to operating z-stack channels corresponding
438 to 3D Slicer have been checked. On a side note, in the context of the third and seventh items within this
439 category, ‘Delete’ refers to removing channels’ rendering and matching GUI widgets from the scene rather
440 than deleting any associated files from the file system.

441 From the information presented in Table 1, it is indicated that in contrast to other platforms, ColocZStats
442 not only retains several necessary control options for channels of confocal z-stacks, but can also objectively
443 analyze the colocalization in such stacks. Significantly, this comparison also reveals some limitations in
444 the current functionalities of ColocZStats. The current prominent limitations of ColocZStats and potential
445 directions for future enhancements are discussed in detail in the ‘Discussion’ section.

5 DISCUSSION

446 Through a comprehensive examination of several widely recognized biological image visualization
447 applications, all with VR functionalities and some of which already own extensive analytical features, it has
448 been identified that these tools lack dedicated built-in options and user interfaces for 3D graphics to perform
449 the quantitative colocalization analysis for multi-channel z-stacks generated by confocal microscopes. The
450 development of an open-source 3D Slicer extension named ColocZStats has contributed to expanding

451 potential solutions for addressing this challenge. Certain functionalities from multiple modules within
452 3D Slicer were reasonably utilized and integrated by ColocZStats, enabling the effective presentation of
453 confocal microscopy images' merged multi-channel volumetric appearances. This endeavor aims to support
454 researchers in quickly discerning spatial relationships between molecular structures within organisms.
455 On top of that, ColocZStats can generate colocalization metrics for thresholded channels within ROIs
456 of samples, which has positive significance for biologists who now avail of a tool to gain detailed and
457 objective insights into biological processes.

458 More specifically, ColocZStats allows users to select up to three channels of each Z-stack concurrently
459 for analysis. It permits customized control over channels' lower or upper threshold limits according
460 to researchers' specific needs and obtaining metrics such as PCCs for all possible channel pairwise
461 combinations and intersection coefficients. The above distinctive characteristics distinguish ColocZStats
462 from most tools, which typically restrict users from performing colocalization analysis between two
463 channels at a time and only allow setting the lower threshold for each channel. Via the Venn diagram it
464 generates, the ratios of all parts, including the part where all channels intersect, can be clearly displayed.
465 Moreover, users can further enhance their understanding of the intensity relationship between different
466 channels through the generated 2D histograms. For each calculation, all the results and diagrams are
467 conveyed to researchers through a supplementary spreadsheet, making it easy for them to share or compare
468 data. In summary, with the ultimate goal of merging with SlicerVR, ColocZStats is presently functioning as
469 a desktop extension for 3D Slicer, incorporating an intuitive GUI that allows users to customize ROIs and
470 define the threshold ranges for all stack channels while supporting the one-click generation and saving of
471 colocalization analysis results. More importantly, the development of the ColocZStats extension has further
472 enhanced the comprehensiveness of 3D Slicer, which means that the extensive audience of 3D Slicer can
473 now seamlessly perform colocalization analysis for confocal stacks without frequently switching between
474 different tools.

475 At present, as a purpose-built tool for colocalization analysis, ColocZStats requires prioritized
476 improvements in the following aspects. Firstly, there is a need to expand the variety of colocalization
477 metrics. In addition to the existing PCC, other coefficients belonging to the ICCB methodology that
478 are also extensively employed, such as Manders' coefficients, Spearman's coefficient, and the overlap
479 coefficient, could be integrated into the extension to further enhance its analytical capabilities. As more
480 colocalization coefficients become incorporated into ColocZStats in the future, enhancing the capability
481 of image pre-processing becomes increasingly essential. The need for this enhancement arises from the
482 potential impact of excessive noise in microscopic images, which affects the correlation between distinct
483 signals and leads to an underestimation of colocalization analysis results (Adler et al., 2008). Deconvolution
484 is a well-established method for image filtering and restoration (Landmann and Marbet, 2004). Integrating
485 this technique into the tool could significantly help eliminate image noise, improve image quality (Wu
486 et al., 2012), and consequently improve the accuracy of subsequent analysis.

487 Meanwhile, to further increase the coverage of ColocZStats for a wider range of input images and the
488 efficiency of analyzing multi-channel image stacks, it is anticipated that features allowing compatibility
489 with stacks containing more channels and permitting the simultaneous selection of more channels in a
490 single computation will be implemented.

491 Moreover, as elucidated in the aforementioned 'User Interface' subsection, ColocZStats supports changing
492 channels' thresholds by manually adjusting the sliders or entering values in the input fields to help
493 biologists customize structures of interest. Nonetheless, relying on visual inspection of images to estimate
494 suitable thresholds can be challenging and may result in inconsistent outcomes. Figure 3(k), as one of

495 the components of the ‘qMRMLVolumeThresholdWidget’ provided by 3D Slicer, although it includes an
496 ‘Auto’ option that can be used to assign a threshold range for any channel automatically, incorporating
497 more reliable, robust, and objective automated threshold methods will undoubtedly further enhance the
498 functionality of ColocZStats. The method developed by Costes et al (Costes et al., 2004), to determine the
499 appropriate threshold value for background identification is expected to be appropriately integrated into
500 ColocZStats. The Costes method is founded on the linear fitting of channels’ 2D histograms (Costes et al.,
501 2004; Pike et al., 2017) and has been proven to be a robust and reproducible approach that can be readily
502 automated (Dunn et al., 2011).

503 Enabling users to utilize ColocZStats within an immersive VR environment is a primary objective for
504 future work. At the time of writing, integrating arbitrary interactive Qt widgets into the VR environment is
505 an ongoing development effort by the SlicerVR development team. Once this feature is fully implemented,
506 this would imply that any functionality in 3D Slicer and its extensions could be easily accessed in VR
507 through these virtual widgets (NA-MIC Project Weeks., 2024; Pinter et al., 2020). This work illuminates the
508 significant potential for extending ColocZStats into the immersive scene offered by Slicer VR, which will
509 provide valuable assets and support for this forthcoming endeavor. Through these and other improvements
510 along these lines, ColocZStats will be continually enhanced to become a more efficient and flexible software
511 tool.

AUTHOR CONTRIBUTIONS

512 T.B. and O.M. conceived and designed the study, obtained funding, supervised the study, and revised
513 the manuscript; X.C. implemented the program, distributed the program to 3D Slicer, analyzed the data,
514 prepared figures, and wrote the manuscript; T.T and A.D.J provided the confocal microscopy data. All
515 authors have read and approved the submitted version of the manuscript.

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SUPPLEMENTARY MATERIALS

522 The supplementary materials can be found along with this manuscript in the same site.
523 Z-stack image and scenario files can be obtained from the Zenodo repository (10.5281/zenodo.11372183).

DATA AVAILABILITY STATEMENT

524 The confocal microscopy data presented in this study are included in the document/Supplementary
525 Materials.

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FIGURE CAPTIONS

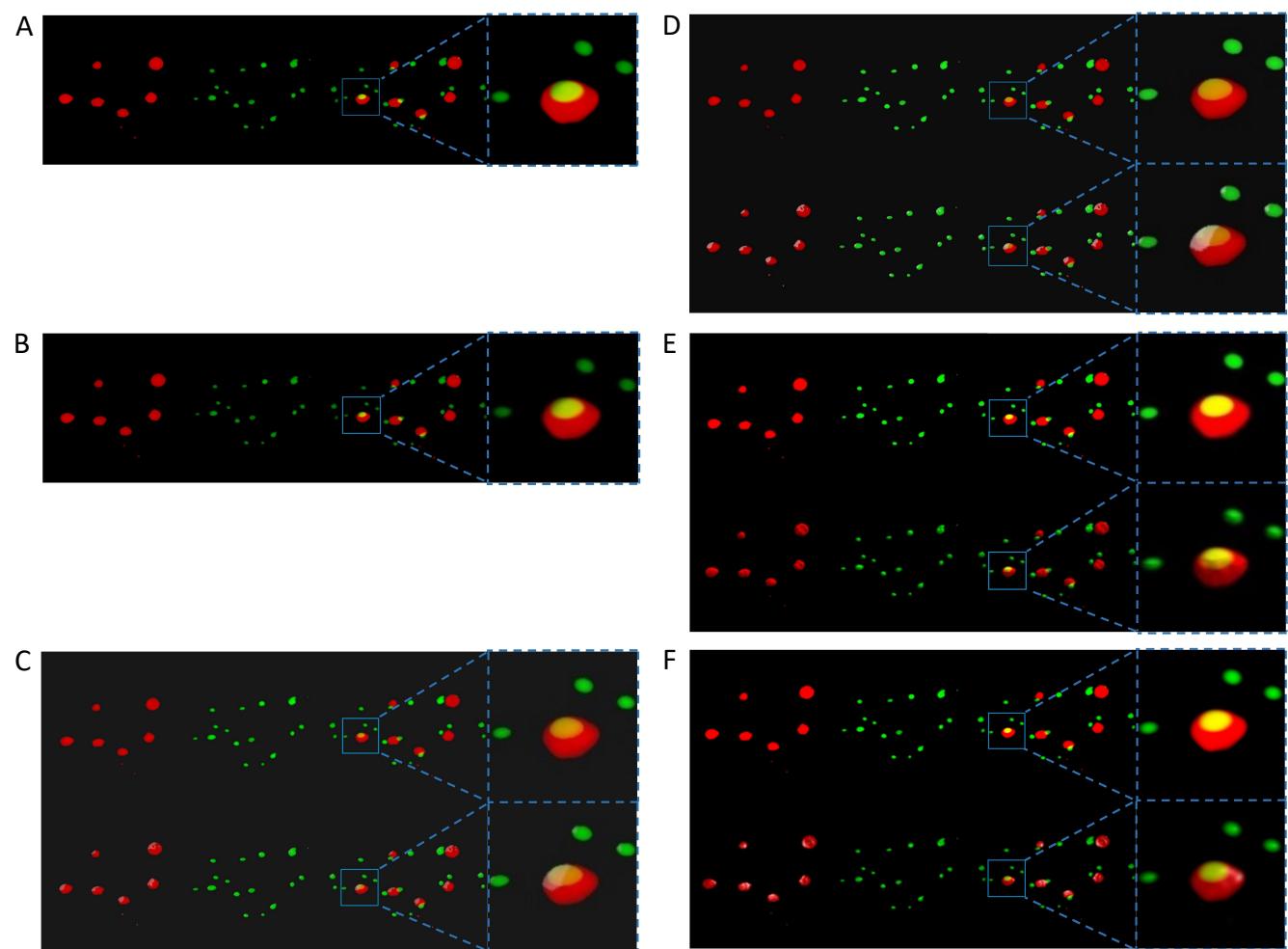


Figure 1. A series of screenshots displaying the visualization of the same specimen's channels from an identical perspective across all the mentioned programs. For each sub-figure, from left to right, two separate channels of the sample stack, their superposition, and a magnification of a specific region in the superposition are shown. (A) The volumetric rendering of the two channels in ChimeraX's desktop version. (B) The same series of scenes as (A). They were captured from a VR environment created by ChimeraX VR. The first rows in (C), (D), (E), and (F), respectively, show the scenes without external lighting in the ExMicroVR, ConfocalVR, SlicerVR, and the desktop viewport of 3D Slicer. The second row of (C) to (F) shows the scenes with external lighting turned on.

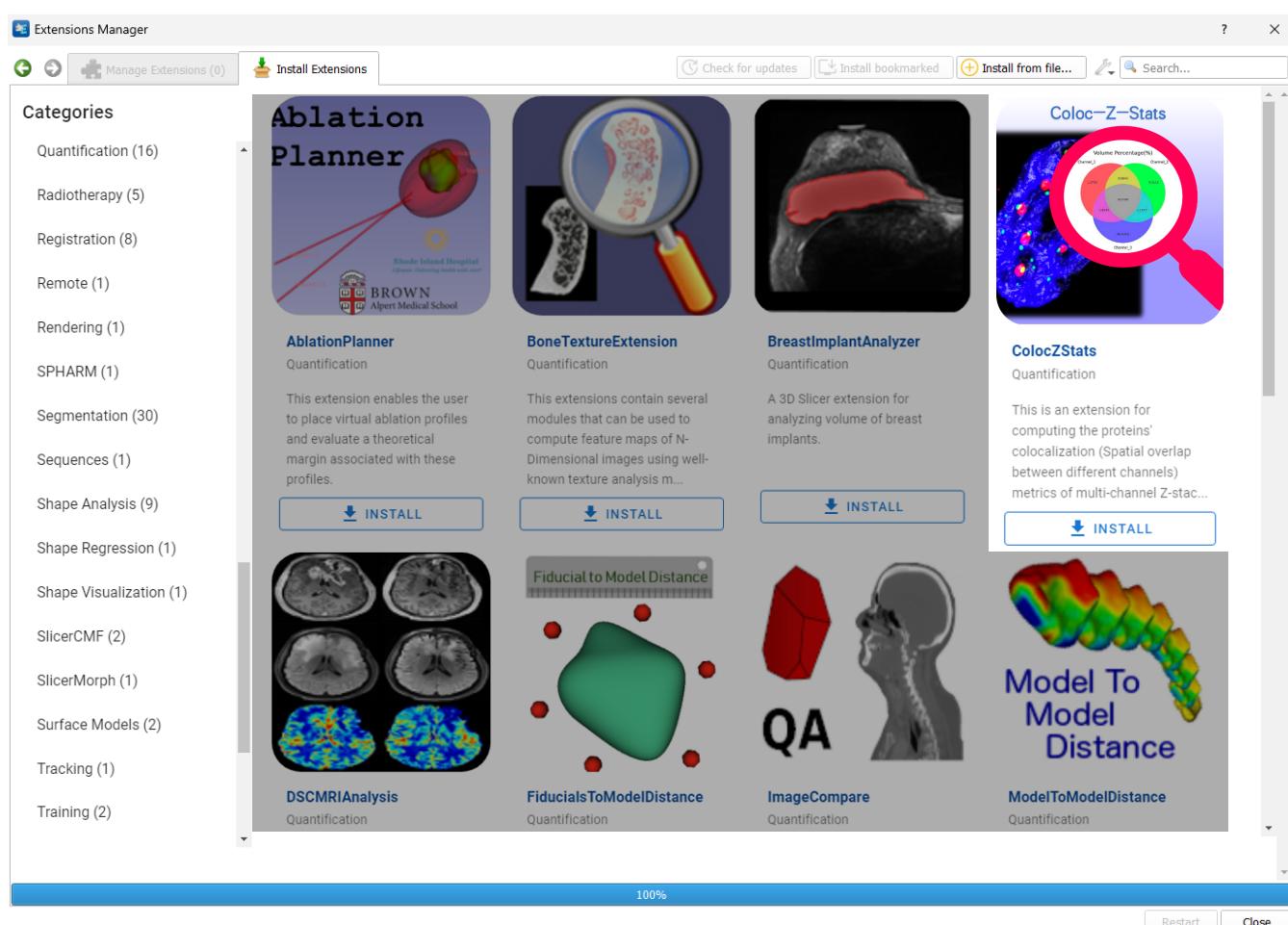


Figure 2. A screenshot showing the ‘Slicer Extensions Catalog’ via the ‘Extensions Manager’ in 3D Slicer. ColocZStats is offered within the ‘Quantification’ category.

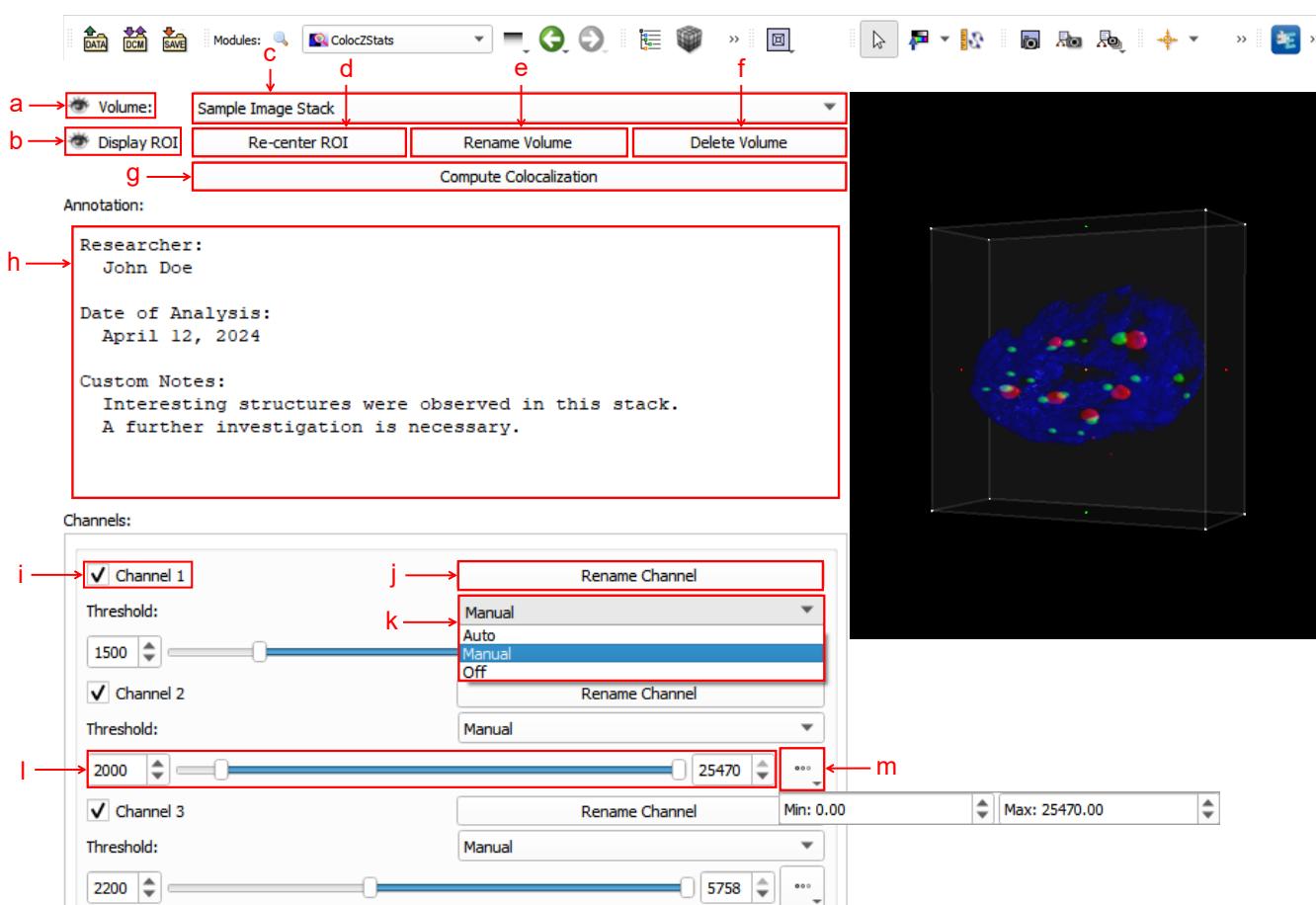


Figure 3. The Graphical User Interface (GUI) of ColocZStats. **(a)** A clickable eye icon for managing the visibility of the entire image stack's rendering. **(b)** A clickable eye icon for managing the visibility of the adjustable box for selecting ROI regions. **(c)** A combo box for switching between multiple loaded image stacks, displaying the stack's filename without extensions by default. **(d)** A button for repositioning the rendering within the ROI box to the 3D view's center. **(e)** A button for triggering a pop-up text box for customizing the displayed name on the combo box. **(f)** A button for deleting the current stack from the scene, along with its associated annotation and GUI widgets. **(g)** A button for performing colocalization analysis. **(h)** A text field for adding a customized annotation for the current stack. **(i)** A checkbox for managing the visibility of each channel. The indices in these default channel name labels start from 1. **(j)** A button for triggering a pop-up text box for customizing the corresponding channel's name label. **(k)** A drop-down list for selecting the channel threshold control mode. It comprises three options: 'Auto,' 'Manual,' and 'Off'. **(l)** Adjustable sliders for setting lower and upper thresholds. Both values can also be specified in the two input fields. **(m)** A drop-down box for displaying the initial threshold boundaries of the associated channel.

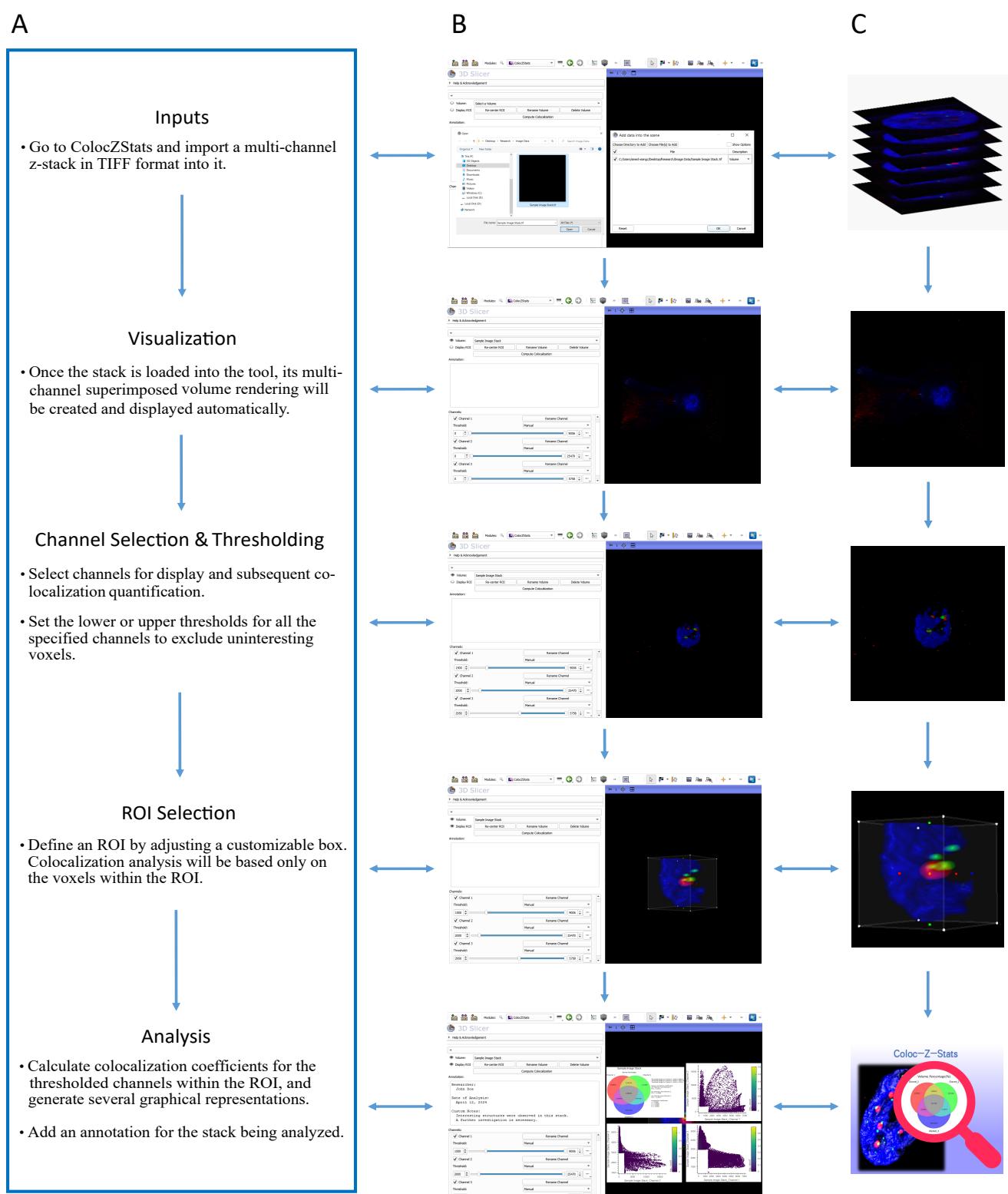


Figure 4. (A) Typical workflow of ColocZStats. (B) Example operation scenarios in ColocZStats that correspond to the steps in the workflow. (C) Visual abstractions that correspond to the steps in the workflow.

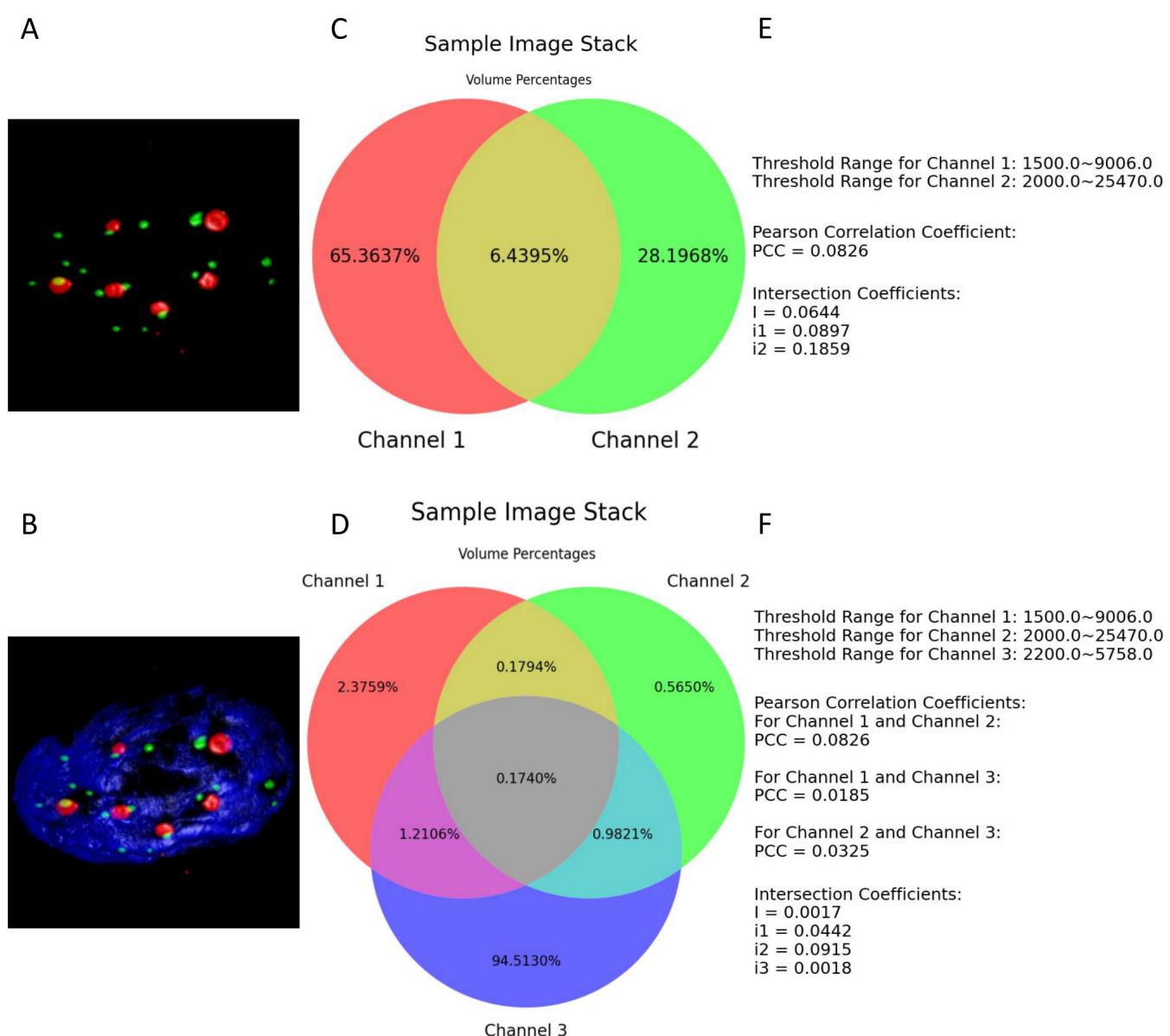


Figure 5. (A) and (B) present the thresholded volume renderings when two or three channels of the entire sample image stack were selected. (C) and (D) depict the respective resulting Venn diagrams. (E) and (F) illustrate all the defined thresholds and the colocalization metrics results are retained to four decimal places.

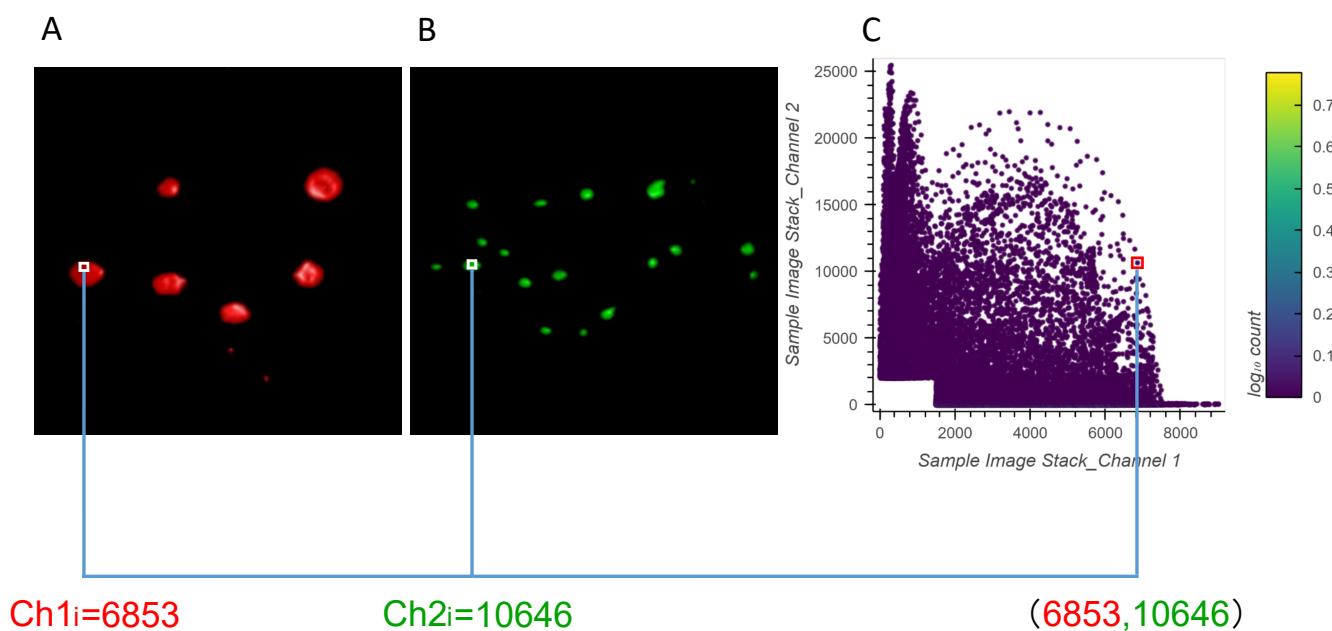


Figure 6. A visual explanation of a 2D histogram's generation process. Adapted from 'Scientific Volume Imaging-2D histograms,' 2024, Scientific Volume Imaging B.V., <https://svi.nl/TwoChannelHistogram>, Copyright 1995-2024 by Scientific Volume Imaging B.V.. **(A)** The volume rendering of channel 1 and an example intensity at a specific position. **(B)** The volume rendering of channel 2 and an example intensity at the same position. **(C)** The coordinates in the 2D histogram are generated by the combination of those intensities.

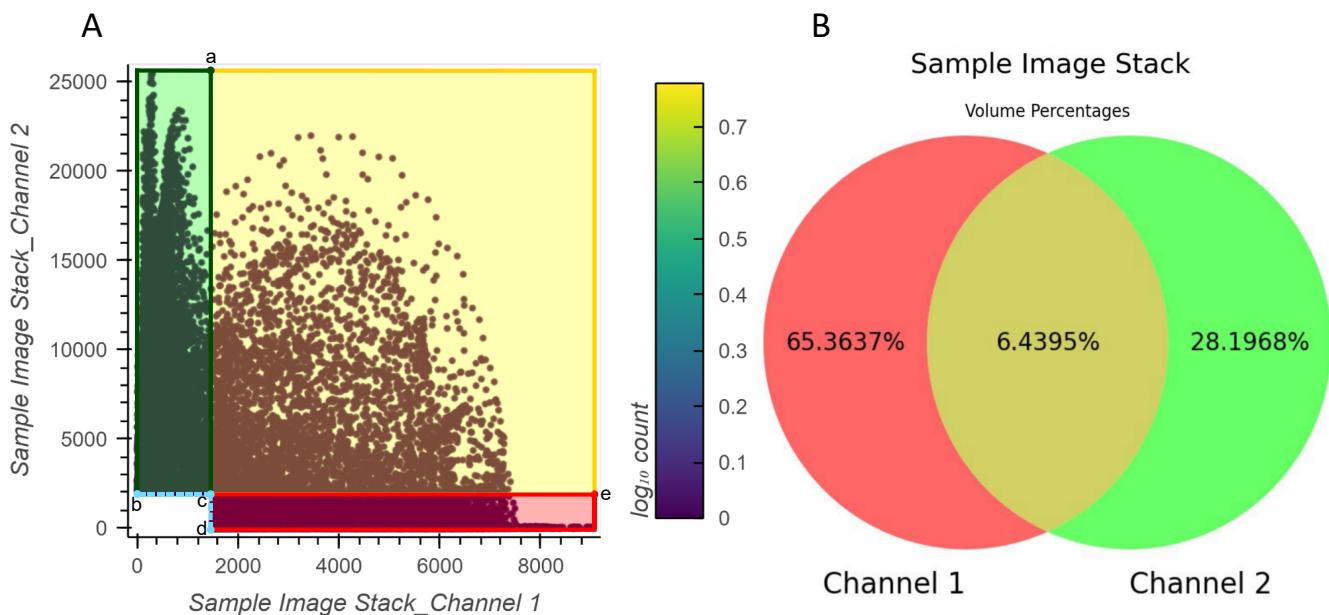


Figure 7. An illustration depicting the relationship between the example 2D histogram (A) and its corresponding Venn diagram (B). Coordinate of point **(a)**: (1500,25470); Coordinate of point **(b)**: (0,2000); Coordinate of point **(c)**: (1500,2000); Coordinate of point **(d)**: (1500,0); Coordinate of point **(e)**: (9006,2000).

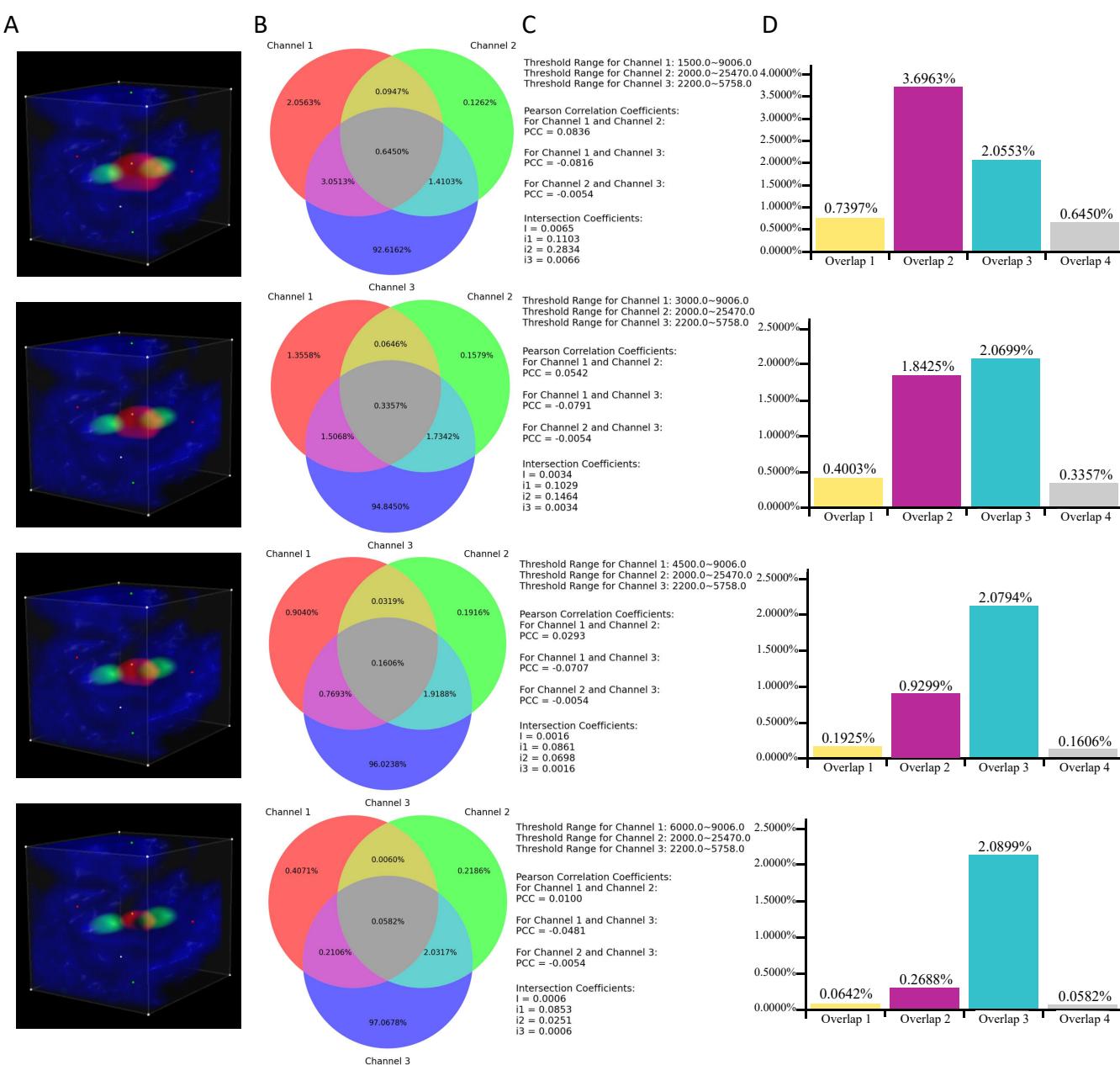


Figure 8. Illustration of Case Study. **(A)** Volume rendering of all channels within the same ROI box. **(B)** Venn diagrams corresponding to all the cases. **(C)** All the associated thresholds and colocalization metrics' results. **(D)** Additional histograms illustrating the proportions of overlaps. They were created based on the data derived directly from the Venn diagrams. 'Overlap 1': The overlap between Channel 1 and Channel 2. 'Overlap 2': The overlap between Channel 1 and Channel 3. 'Overlap 3': The overlap between Channel 2 and Channel 3. 'Overlap 4': The overlap of all three channels.

Table 1. Programs Features Overview.

Features	Programs	ExMicroVR	ConfocalVR	ChimeraX	3D Slicer	ColocZStats
Confocal Image Z-stack Loading						
Load multi-page (multi-image) z-stack files	✓	✓	✓	✓	✓	✓
Load image sequence of z-stack slices			✓	✓		
Supported image format	NIFTI	NIFTI	TIFF/PNG/PGM	TIFF/PNG/JPG/BMP		TIFF
Confocal Image Z-stack Observation						
Automatically split all channels of each z-stack for independent manipulation			✓			✓
Switch among multiple multi-channel z-stacks			✓	✓		✓
Delete all channels of any z-stack simultaneously			✓			✓
Turn on/off individual channel's visibility	✓	✓	✓			✓
Adjust lower threshold for each channel	✓	✓	✓			✓
Adjust upper threshold for each channel	✓	✓	✓			✓
Delete each channel individually		✓	✓			
Define ROI	✓	✓	✓	✓		✓
Center ROI in the visual field	✓	✓	✓			✓
Extract overlapping voxels of any 2 channels		✓				
Image Measurement and Analysis						
Quantify colocalization of confocal z-stacks						✓
Save quantified image analysis results		✓	✓	✓		✓
Create a 2D histogram for each channel pair						✓
Edit and save annotations			✓	✓		✓
Operating Environment						
Desktop			✓	✓		✓
VR (HMD)	✓	✓	✓	✓		
Multi-user VR session	✓	✓	✓	✓		