



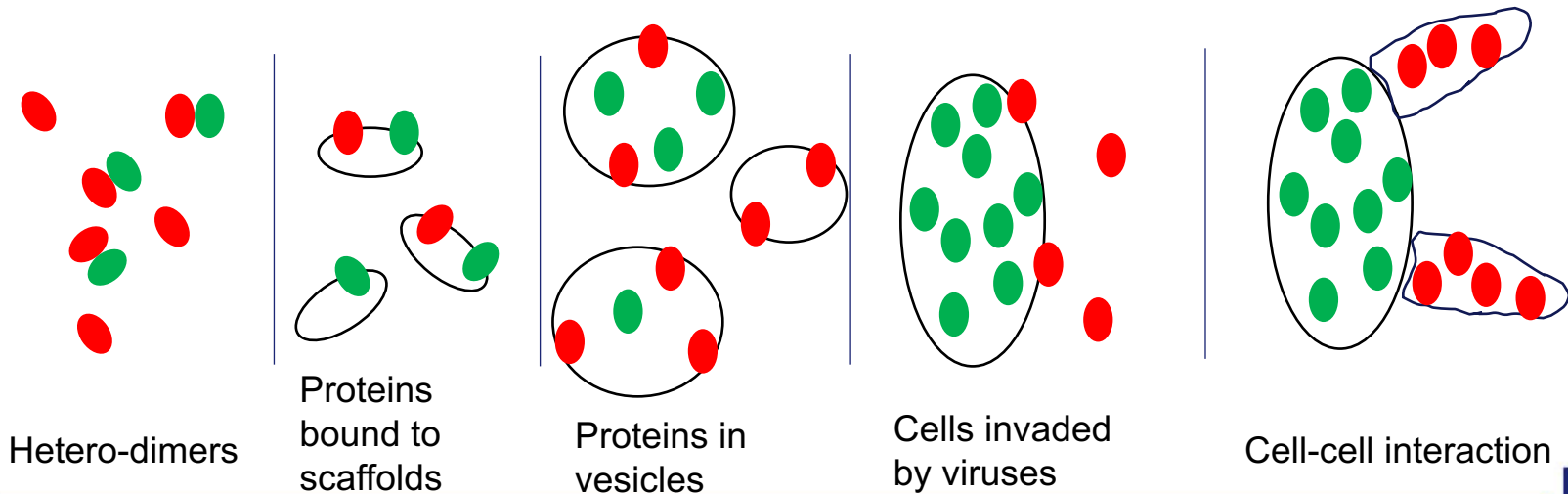
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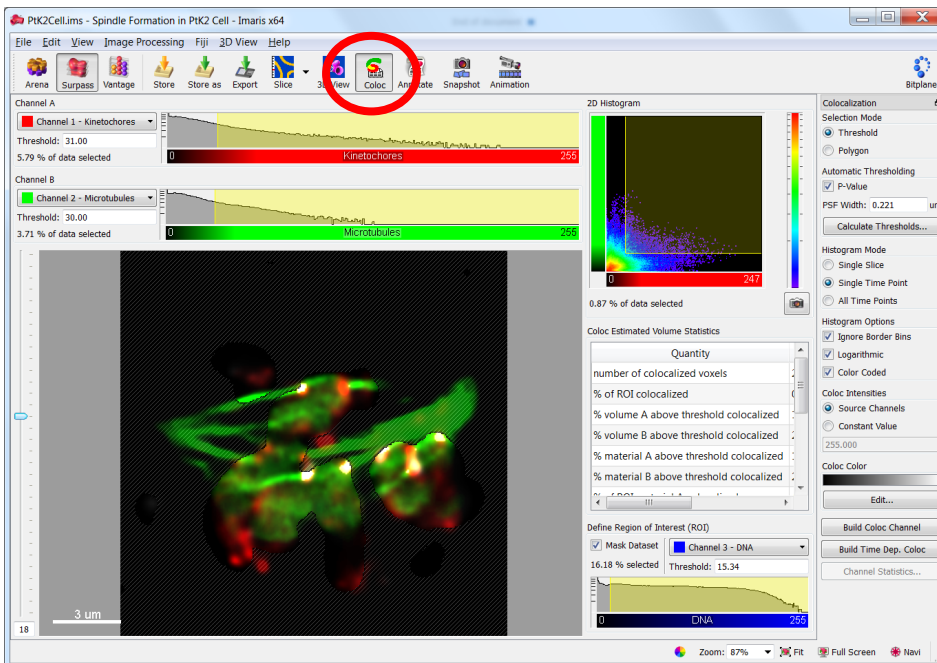
Voxel-Based Colocalization

Colocalization as a Tool for Multichannel Analysis

- Imaris has several tools to quantify and visualize colocalization:
 - Intensity/voxel-based (ImarisColoc)
 - Object-based (Spots, Surfaces, Filaments)
- Which method is right for you?
 - Fluorescent labels form distinct objects or diffused distribution?
 - What is the underlying biological hypothesis?
 - Interaction? Co-expression? Proximity? Volume overlap?
 - A practical guide to evaluating colocalization in biological microscopy. Dunn et al. 2011 *Am J Physiol Cell Physiol*



- Automated, standardized determination of colocalized voxels.
- Processes 2D, 3D, and 4D images.
- Real-time feedback on changes in selection.
- Display of co-localized voxels with original channels as defined in channel visibility editor.
- Output of co-localized voxels into new channel allows maximal flexibility with respect to display and analysis using all other Imaris functions.

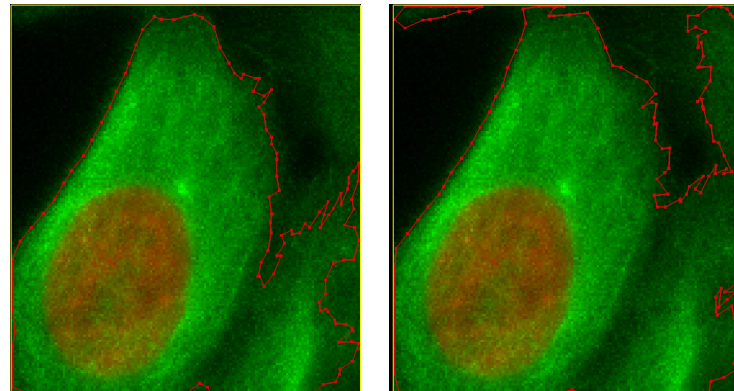


ImarisColoc: Quantitative Outputs

Base Color Mapped Color Coloc Estimated Statistics

time frame	1
threshold A	20.000
threshold B	18.000
number of colocalized voxels	449211
% of dataset colocalized	5.16
% of ROI colocalized	19.32
% of volume A above threshold colocalized	57.51
% of volume B above threshold colocalized	48.85
% of material A above threshold colocalized	63.22
% of material B above threshold colocalized	56.99
% of ROI material A colocalized	42.48
% of ROI material B colocalized	42.86
Pearson's coefficient in dataset volume	0.5808
Pearson's coefficient in ROI volume	0.3271
Pearson's coefficient in colocalized volume	-0.0990
original Mander's coefficient A	0.9694
original Mander's coefficient B	0.9351
thresholded Mander's coefficient A	0.4988
thresholded Mander's coefficient B	0.3783

- Colocalization statistics are calculated within the ROI and determined by intensity threshold.
 - ROI can be defined by any channel.
 - ImarisColoc provides both automatic and manual Threshold selection.



Which threshold value is right?

number of colocalized voxels

% of dataset colocalized

% of ROI colocalized

% of volume A above threshold colocalized

% of volume B above threshold colocalized

% of material A above threshold colocalized

% of material B above threshold colocalized

% of ROI material A colocalized

% of ROI material B colocalized

Pearson's coefficient in dataset volume

Pearson's coefficient in ROI volume

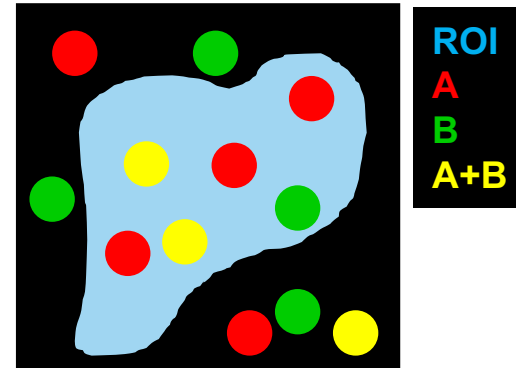
Pearson's coefficient in colocalized volume

original Mander's coefficient A

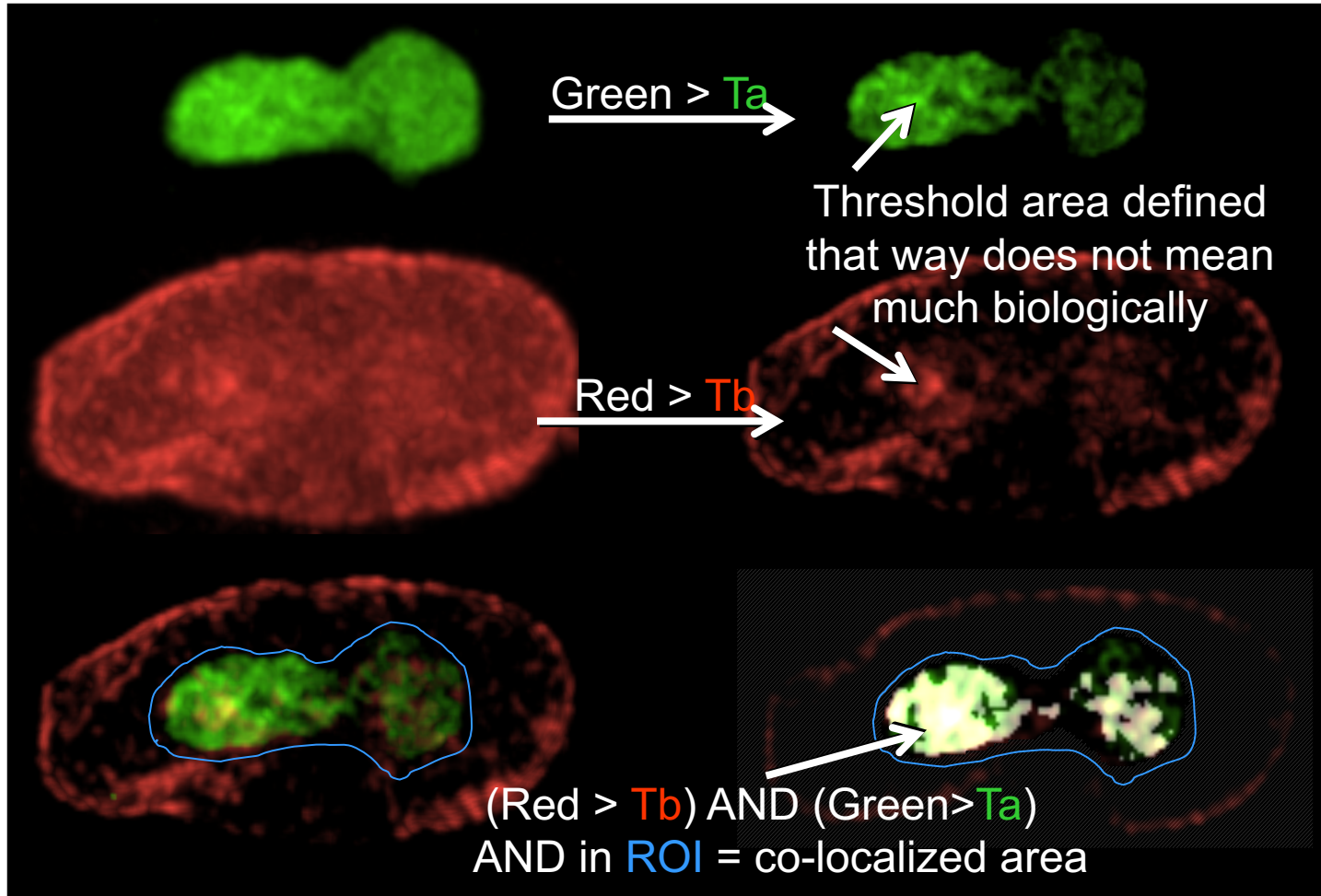
original Mander's coefficient B

thresholded Mander's coefficient A

thresholded Mander's coefficient B



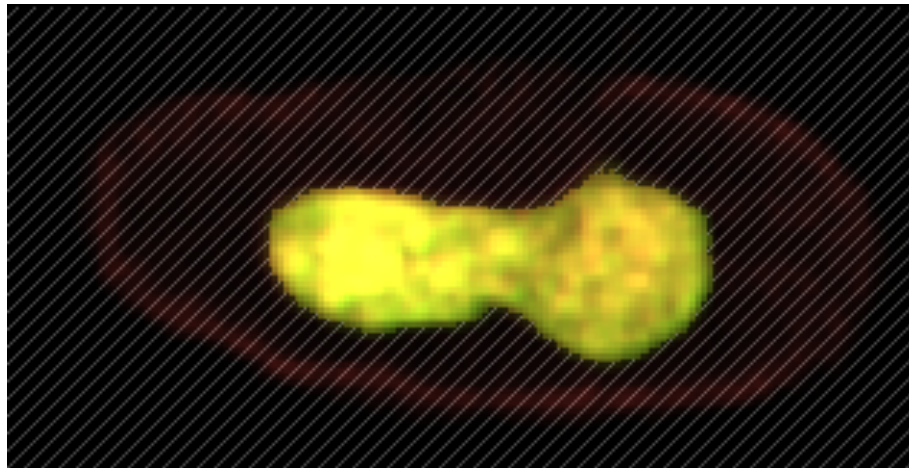
- Colocalized volume: number of voxels.
- Colocalized material: intensity sum.
- Pearson's coefficient (r):
 - Pixel-by-pixel covariance.
 - $r \sim 0 \rightarrow$ no correlation; $r \sim 1 \rightarrow$ high correlation.
- Mender's coefficient (M_A , M_B):
 - Measures co-occurrence independent of signal proportionality between 2 channels.
- ROI, thresholds, and background intensity can affect all these numbers.



- Blue shows ROI
- Top row: Green pixels before and after T_a .
- Middle row: Red pixels before and after T_b
- Bottom row left: Red and green pixels after thresholds
- Bottom row right: White = overlap pixels from left that are above thresholds and also in the ROI

- **Signal consistency:**
 - Consistent microscope settings (laser power, PMT/camera gain, exposure time, etc.).
 - Adequate signal to noise ratio.
 - Avoid saturated pixels.
 - Enough intensity dynamic range with higher bit depth (12/16 bit).
- **Multi-channel acquisition:**
 - No channel bleed through (check single labeled probes).
 - Similar Point Spread function for each color (check PSF of the channels with multicolor beads).
 - No registration errors between channels.
 - Minimize chromatic aberration.

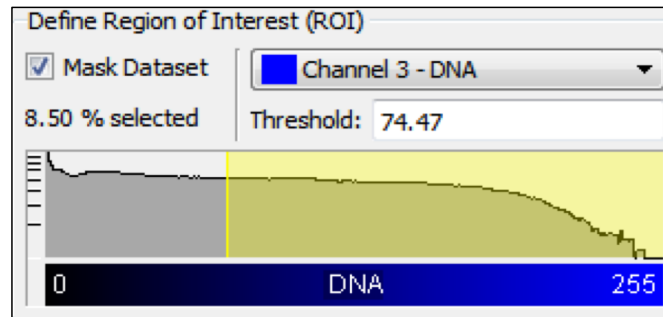
- The automated colocalization analysis takes into account the whole image.
- For accurate results, a region of interest should be defined in order to ignore the background and to focus on biologically meaningful region for analysis.



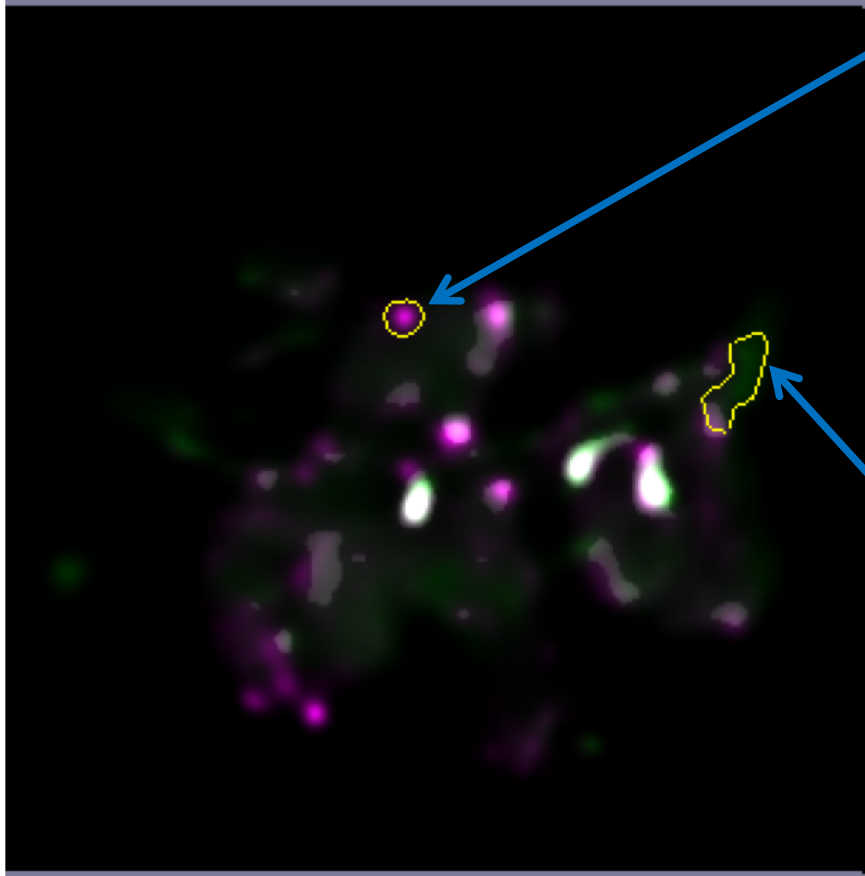
Step 1: Region of Interest

- Options:
 - Acquire a 3rd channel in which the labelling represents the ROI.
 - Use Surface > Mask to generate an ROI channel.
 - Draw a manual Contour Surface, or
 - Use existing channel to create Surface.
 - For masking, set outside to 0, inside to any mid-range value.
 - Use Image Processing > Channel Arithmetics to merge the two channels into one mask channel.

The resulting channels from above can be used to create an ROI in Coloc:

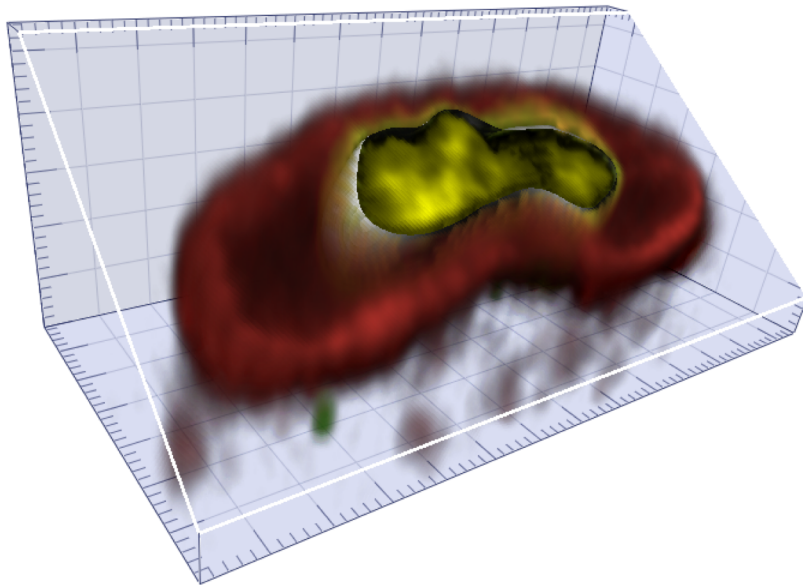
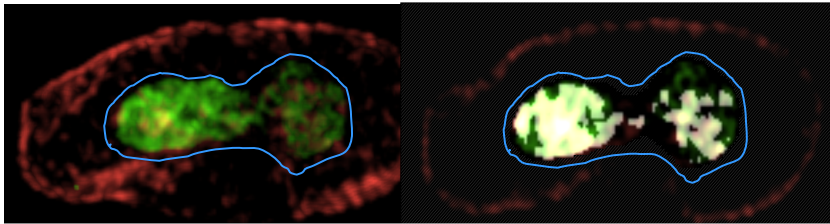


Step 2.1: Manual Thresholding



- 1) Click on a bright area and drag toward a dark region to set Channel A threshold.
 - 2) An **IsoLine** tool is used to visualize the area above the threshold next to the mouse.
 - 3) Hold Shift Key and do same to set Channel B threshold.
- For 3D image, the optimal slice to perform manual thresholding for each channel may not be the same.
 - For complex images, manual thresholding can be subjective.

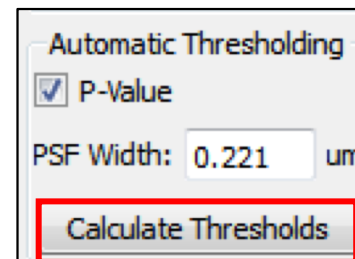
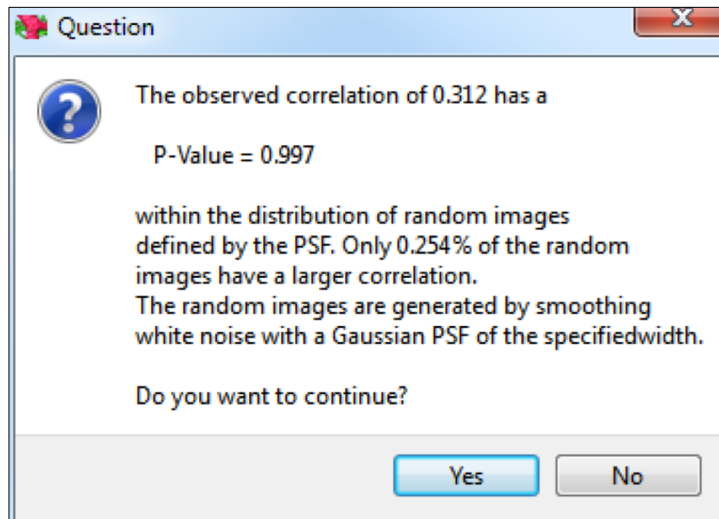
Step 2.2: Automatic Thresholding



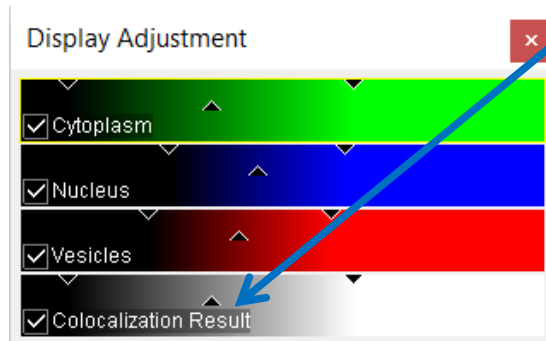
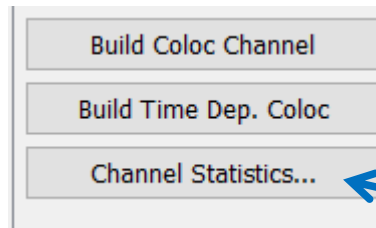
- ImarisColoc – especially the implementation of the automated thresholding – was developed together with Dr. Sylvain Costes, today working at the Lawrence Berkeley National Laboratory.
- Publication: Costes, S. V., Daelemans, D., Cho, E. H., Dobbin, Z., Pavlakis, G., and Lockett, S. (2004). Automatic and Quantitative Measurement of Protein-Protein Colocalization in Live Cells. *Biophys J* 86, 3993-4003.

Step 2.2: Automatic Thresholding

- P-value depends on **PSF Width**.
 - Default PSF width = longest diagonal of 1 voxel.
 - This calculation does NOT affect the automatic thresholding values, and is only used to check if colocalization is significant.
- Specific, non-random colocalization depends on resolution (both PSF size and voxel size), and signal to noise ratio.
- Deconvolution may help.



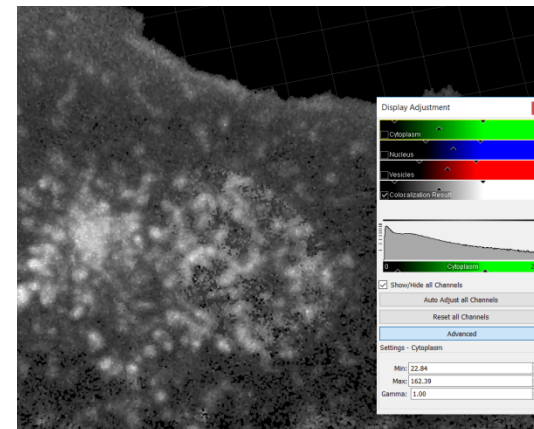
Step 3: Quantification and Visualization



- Colocalization result is saved as a channel
- Click 'Channel Statistics' or the coloc channel to access final statistical values.
- Don't use the preview statistics in Coloc viewer.
- Coloc channel can be visualized and measured just like any other data channel.

Base Color	Mapped Color	Coloc Statistics
time frame	1	
threshold A	10.000	
threshold B	7.000	
number of colocalized voxels	77990	
% of dataset colocalized	3.72	
% of ROI colocalized	25.00	
% of volume A above threshold colocalized	60.96	
% of volume B above threshold colocalized	58.55	
% of material A above threshold colocalized	64.96	
% of material B above threshold colocalized	60.05	

Export...



Special Case: Time Dependent Auto-Threshold

- Build time-dependent Coloc channel.
- The relationship between correlation and intensity could change over time.
- For automatic thresholding, scatterplot histogram is analyzed separately for each time-point.
- Different threshold result is possible at each time-point, for both image and statistics output.

Build Coloc Channel

Build Time Dep. Coloc

Channel Statistics...

Base Color	Mapped Color	Coloc Estimated Statistics				
time frame		1	2	3	4	5
threshold A		1.000	3.000	2.000	2.000	2.000
threshold B		3.000	2.000	3.000	3.000	2.000
number of colocalized voxels		321267	336929	323047	338339	334260
% of dataset colocalized		11.02	11.55	11.08	11.60	11.46
% of ROI colocalized		11.02	11.55	11.08	11.60	11.46
% of volume A above threshold colocalized		66.25	39.15	55.68	48.54	53.72
% of volume B above threshold colocalized		78.85	95.54	87.34	90.06	90.41



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Object-Based Colocalization

2018 Stanford UGM

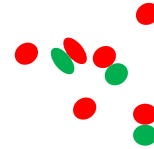
Possible methods

- XTensions (Built-in):
 - Distance transform
 - Colocalize spots
 - Split spots into surfaces
 - Spots close to surface
 - Spots close to filament

- Imaris Open (not officially supported):
 - Surface-surface coloc
 - Surface contact area
 - Triple spots coloc
 - Kiss and run (tracking)

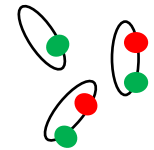
- Other Less Conventional Methods:
 - ImarisCell module
 - Intensity filtering

Hetero-
dimers

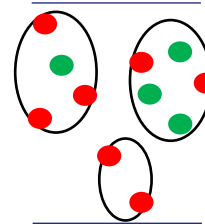


ImarisColoc
Colocalize spots
FCS, super-res

Proteins
bound to
scaffolds

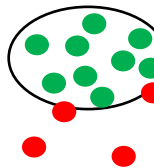


Proteins
in
vesicles



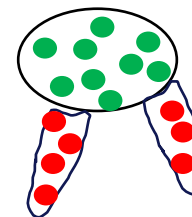
Split spots into surfaces
ImarisCell

Cells
invaded by
viruses



Spots close to surface
Spots close to filament

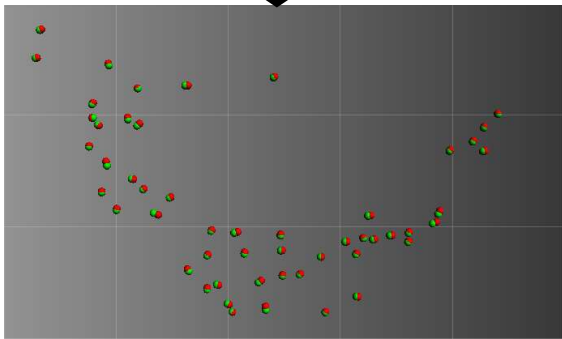
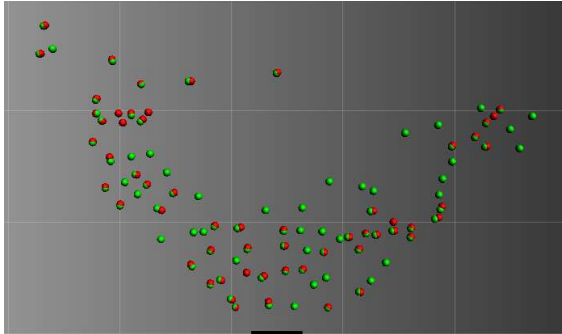
Cell-cell
interaction



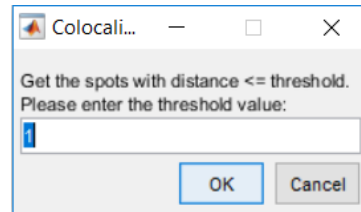
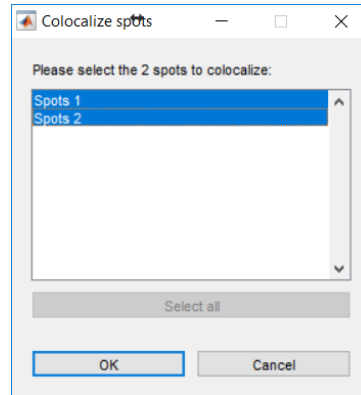
Surface-surface coloc
Surface contact area

XTension: Colocalize Spots

All red and green spots

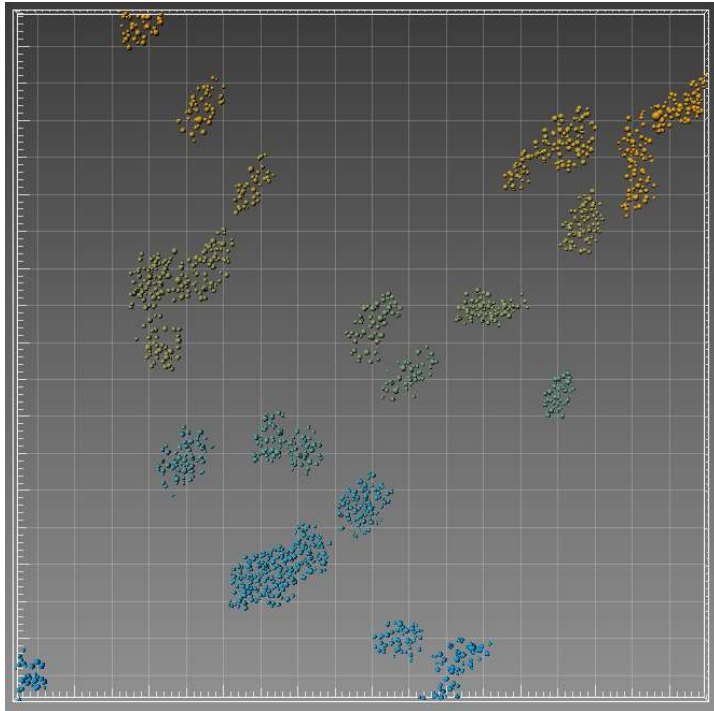


Colocalized spots



- 1) Create Spots using channel 1.
- 2) Create Spots using channel 2.
- 3) Run Colocalize Spots XT, select the two Spots objects.
- 4) Define distance threshold.
- 5) New Spots objects are generated based on colocalization for further analysis.

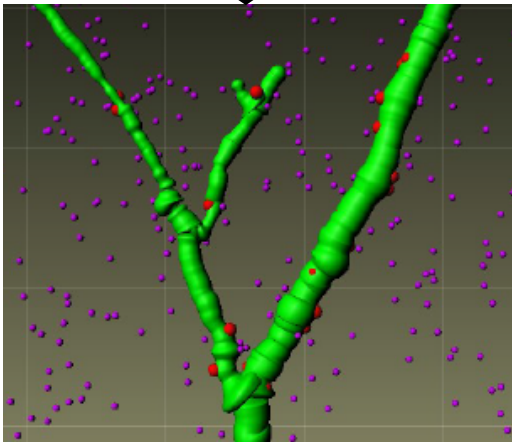
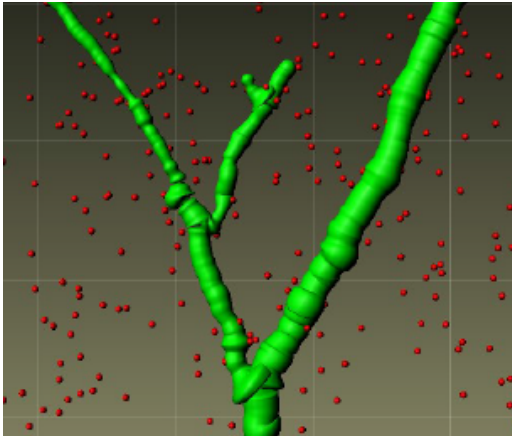
- ✓ ☒ Coloc[3.00] Spots 1 | Spots 2
 - ✓ ☒ Spots 1 colocated
 - ✓ ☒ Spots 1 non-colocated
 - ✓ ☒ Spots 2 colocated
 - ✓ ☒ Spots 2 non-colocated



- This tool is able to segment spots that lie within a surface volume.
 - It generates a new spots object for each surface.
 - Quantification of #spots/cell.
- If a Spot object lies outside one of the isosurface volumes, it will not be counted.
- Cell module (Surfaces = Cells, Spots = Vesicles) would provide a better solution.
 - More statistical options.
 - Automatic and batchable.
 - All information within one Cell object.

XTension: Find Spots Close to Filaments/Surface

Total Spots & Filament





Spots **close** and **far** from
the Filament

- 1) Generate Filaments and Spots.
- 2) Run Find Spots Close to Filaments XT.
- 3) Spots closer and further than X μm of Filament are separated into 2 new groups.

☒  Filaments 1

☐  Spots 1

☒  Spots 1 closer than 1.0 μm to Filaments 1 edge

☒  Spots 1 farther than 1.0 μm to Filaments 1 edge

- Similar workflow for Find Spots Close to Surface

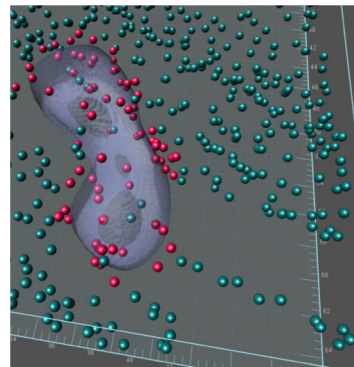


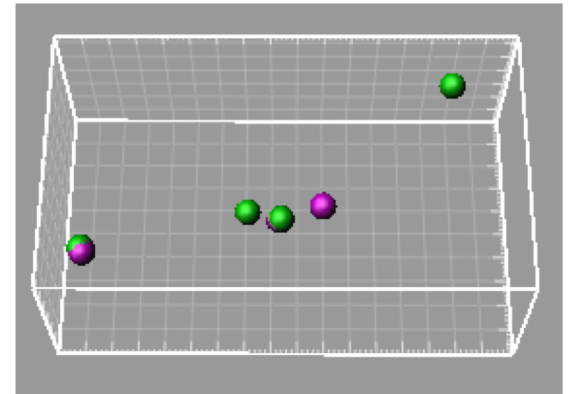
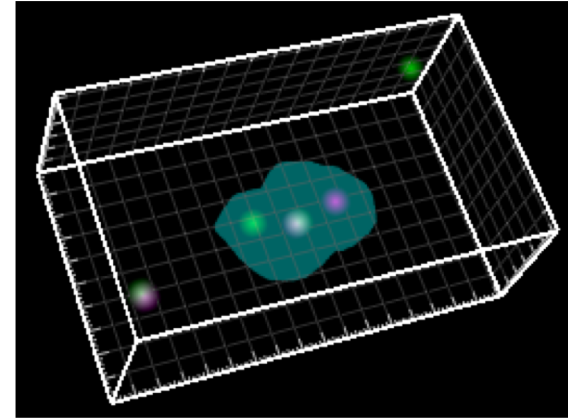
Image courtesy of Dr.
Marc Landry, Bordeaux

Exercise 1: Synthetic Spots Coloc

- Load SyntheticColoc_new.ims.
 - Analyze as if you are looking for overlap between Ch1 and Ch2 within the Ch3 region.
 - Set the threshold in an appropriate manner for this dataset.
 - Hint: Are these better described as well-defined “objects” or diffuse “patterns”?
 - Export Coloc Statistics.

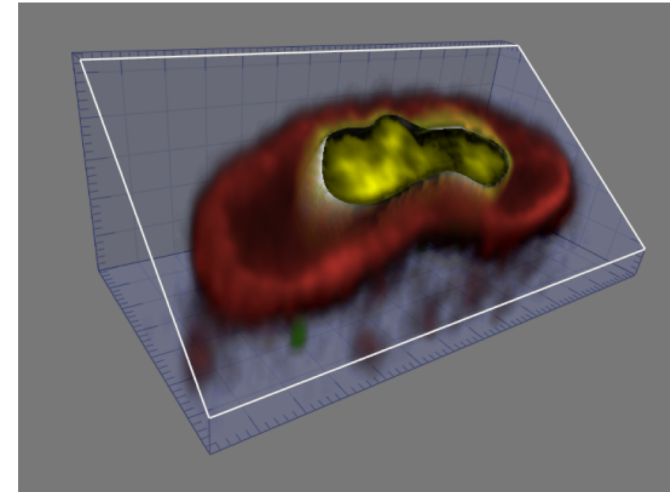
- Next, Create Spots objects from Ch1, Ch2, and Colocalization Result Channel.
 - Color each Spots object differently.
 - Save the Surpass Scene file.

- BONUS: Ch4 is a noisy version of Ch1 with background offset = 1. Use Ch4 instead of Ch1 and repeat the analysis. Which statistical value is the most/least robust?



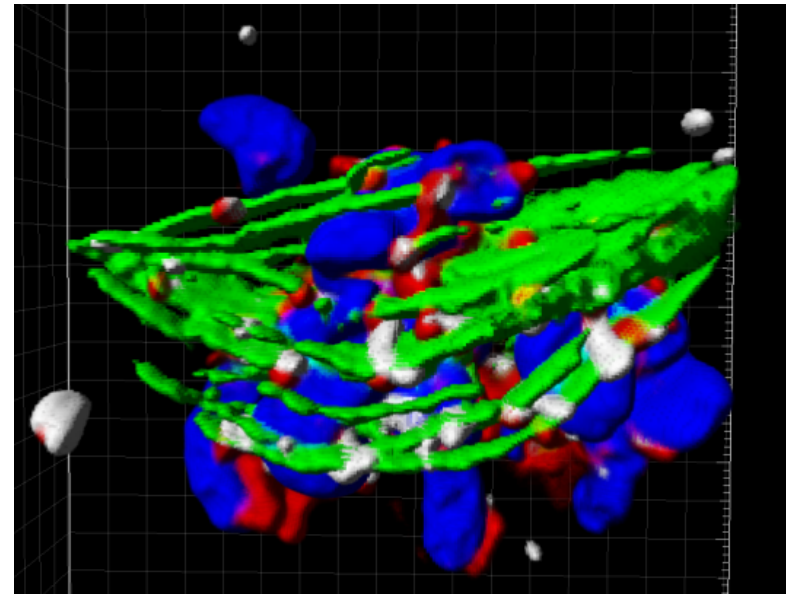
Exercise 2: Intensity-Based Coloc Exercise

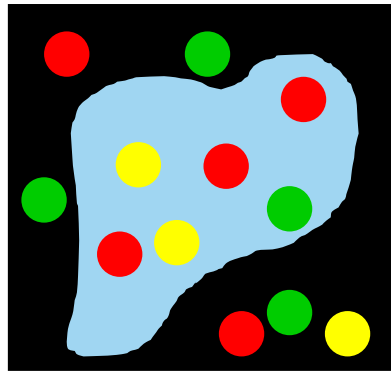
- Load EX1_Costes-Crop-12T.ims.
 - Create Surface based on the green channel. Use that surface to make a Coloc ROI (be careful to exclude any bright green signal outside that central object by filtering in Surfaces by number of voxel).
 - Mask new surface (edit tab of Surfaces) setting voxels outside Surface to zero & inside Surface to 255.
 - Set the thresholds A & B in an appropriate manner for this image, using the surface mask as ROI.
 - Create 3D Coloc Surface, highlighting the new results.
 - Modify Surfaces, transparency, clipping plane.



Exercise 3: Object-based Coloc Exercise

- Load PtK2Cell.ims in Arena (Imaris demo images).
 - Build Spots group on Kinetochores (Ch1) and a 2nd Spots group on dynactin (Ch4).
 - Click on cogwheel icon of one of the Spots groups and choose 'Colocalize Spots'.
 - Enter a distance threshold in microns (0.2um = 200nm, etc).
 - BONUS: Create Surface of DNA channel (Ch3) & run 'Split Spots into Surfaces on both the 'Colocalized Kinetochore Spots' and 'Colocalized Dynactin Spots'.
 - BONUS: Also create Surface of Microtubules channel (Ch2), and use 'Surface-Surface coloc' to estimate the overlapping volume of DNA and Microtubules.





ROI
A
B
A+B

- Overall image = 200 voxels, ROI = 100 voxels
- Each circle = 6 voxels
- Intensity inside red circle = 3
- Intensity inside green circle = 4
- Intensity outside circles = 1 for both A and B
- Set threshold A = 2, threshold B = 2

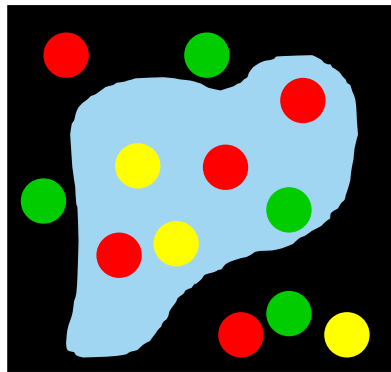
- Volume = # of voxels
- Material = Sum of intensity value
- Number of colocalized voxels = $2 \times 6 = 12$
- % of dataset colocalized = $(2 \times 6) / 200 = 6\%$
- % of ROI colocalized = $(2 \times 6) / 100 = 12\%$
- % of Volume A above threshold colocalized = $(2 \times 6) / (5 \times 6) = 40\%$
- % of Volume B above threshold colocalized = $(2 \times 6) / (3 \times 6) = 67\%$
- % of Material A above threshold colocalized = $(2 \times 6 \times 3) / (5 \times 6 \times 3) = 40\%$
- % of Material B above threshold colocalized = $(2 \times 6 \times 4) / (3 \times 6 \times 4) = 67\%$
- % of ROI material A colocalized = $(2 \times 6 \times 3) / ((100 - 5 \times 6) \times 1 + 5 \times 6 \times 3) = 23\%$
- % of ROI material B colocalized = $(2 \times 6 \times 4) / ((100 - 3 \times 6) \times 1 + 3 \times 6 \times 4) = 31\%$

$$r = \frac{\sum_i (A_i - \bar{A})(B_i - \bar{B})}{\sqrt{\sum_i (A_i - \bar{A})^2 \sum_i (B_i - \bar{B})^2}}$$

- Measures the pixel-by-pixel covariance in the signal levels of two images; assume linear relationship
- $r \sim 0 \rightarrow$ no correlation; $r \sim 1 \rightarrow$ high correlation
- Advantages:
 - Simplicity, widely available
 - Independent of signal levels and signal offset
- Disadvantages:
 - Hard to interpret intermediate values
 - Meaningful only if A and B have comparable quantity, or only analyze in colocalized volume
 - Unlabeled region can artificially inflate r as both A and B are simultaneously low

Mander's coefficient

$$M_A = \frac{\sum_i (A_i * Coloc)}{\sum_i A_i} \quad M_B = \frac{\sum_i (B_i * Coloc)}{\sum_i B_i}$$



ROI
A
B
A+B

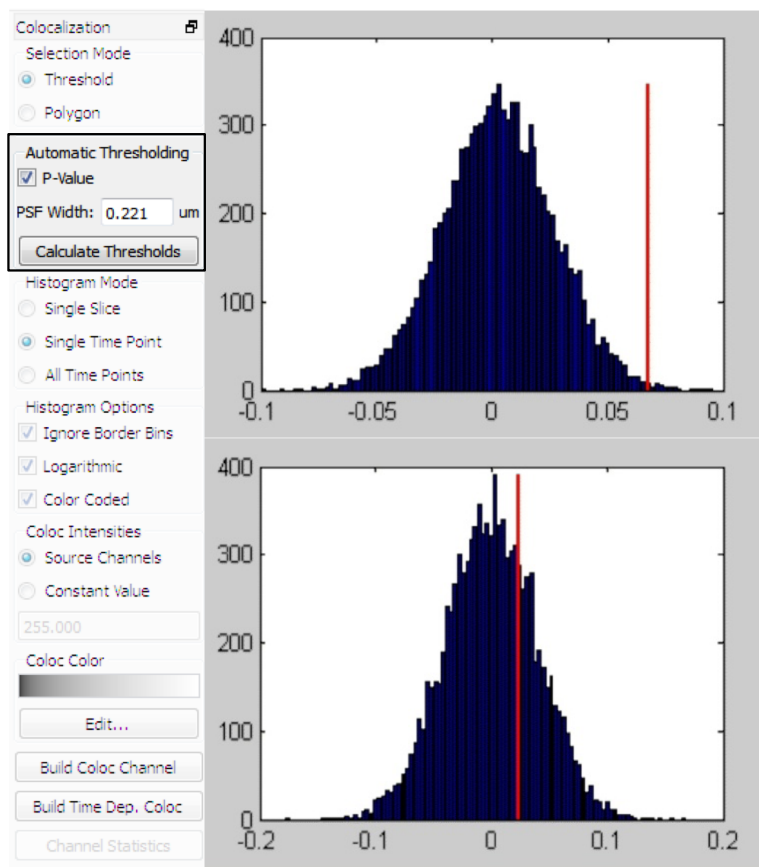
- ROI = 100 voxels
- Each circle = 6 voxels
- Intensity inside red circle = 3
- Intensity inside green circle = 4
- Intensity outside circles = 1 for both A and B
- Set threshold A = 2, threshold B = 2

For M_A :

- Original Mander's:
 - Coloc = 1 if $B_i > 0$
 - Otherwise Coloc = 0
- Thresholded Mander's:
 - Coloc = 1 if $B_i > \text{threshold B}$
 - Otherwise Coloc = 0

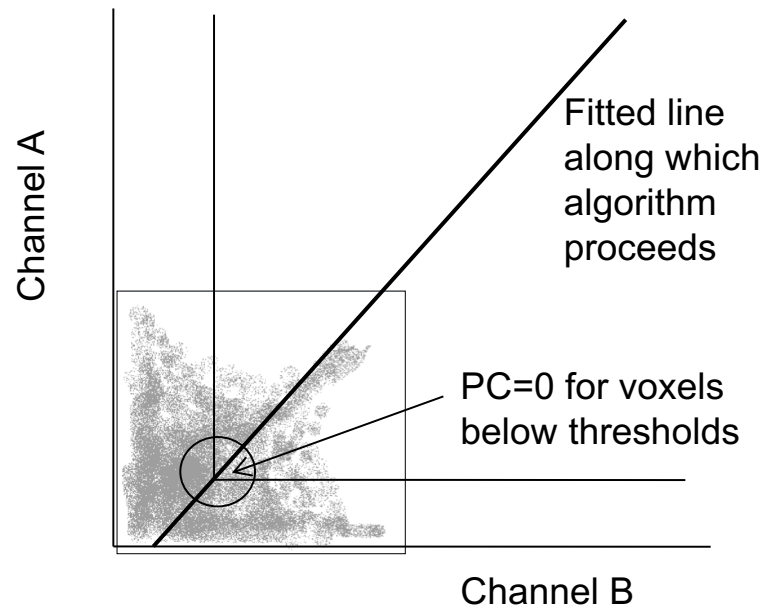
- Original $M_A = M_B = 100\%$, *due to all pixel intensity > 0!*
- Thresholded $M_A = (2 * 6 * 3) / ((100 - 5 * 6) * 1 + 5 * 6 * 3) = 23\%$
- Thresholded $M_B = (2 * 6 * 4) / ((100 - 3 * 6) * 1 + 3 * 6 * 4) = 31\%$
- Strictly measures co-occurrence independent of signal proportionality
- How to define threshold?
 - Manual threshold may introduce biases.
 - Costes et al.'s automatic thresholding method is available.

Automatic Thresholding Detail (1)

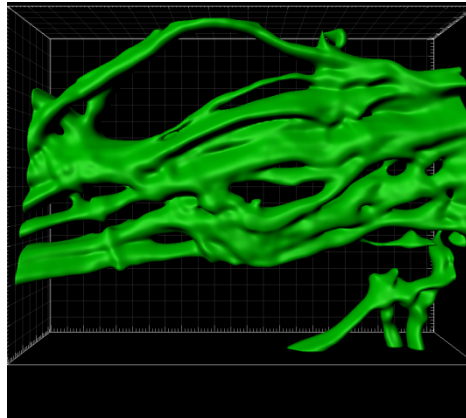


- Before the thresholds for the channels are computed, ImarisColoc performs a separate analysis which determines the probability of having non-random colocalization.
- The Pearson correlation coefficient (PCC) is computed for the acquired (masked) channels (red line) and compared to the PCC obtained with randomized images (blue histogram) which are smoothed with a PSF similar to the acquired data.
- Each blue line shows the PCC for one randomized version. The collection of blue lines shows the distribution of PCC for all randomizations.
- If the PCC of the acquired (masked) channels is not larger than the PCC for 95% of the randomized images, then it can be concluded that too much of the overlap is random, and it is recommended not to proceed (lower image).

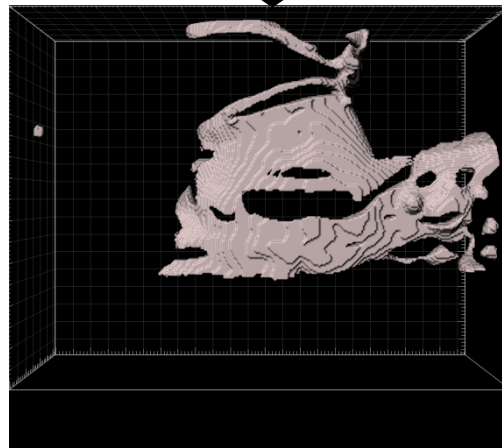
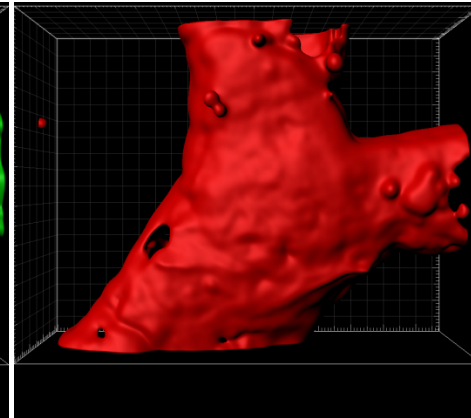
- The algorithm developed by Costes et al. is based on the exclusion of intensity pairs that exhibit no correlation (Pearson's correlation below zero).
- Starting with the highest intensity value, the algorithm reduces the threshold value step by step along a line shown below and computes the correlation coefficient of the image using only voxels with intensities above the threshold.
- The algorithm continues reducing the thresholds until the correlation reaches 0, thus defining the automatic threshold.



Surface 1



Surface 2



New Surface representing Surface 1& 2
colocalization