# COLOCALISATION

**Alexia Loynton-Ferrand** 

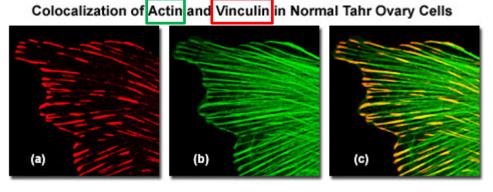
Imaging Core Facility Biozentrum Basel



• Colocalisation: What does that really mean?

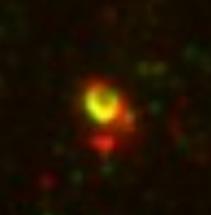
Adapted from Fabrice Cordelières

- Colocalisation = Presence of two (or more) structures on the same location
- Colocalisation in fluorescence microscopy at subcellular level = the distance between signal is below the resolution of the imaging system



http://www.olympusconfocal.com/ applications/colocalization.html

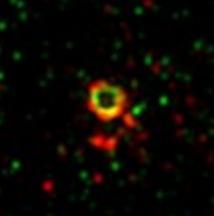
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Deltavision Widefield+Deconvolution

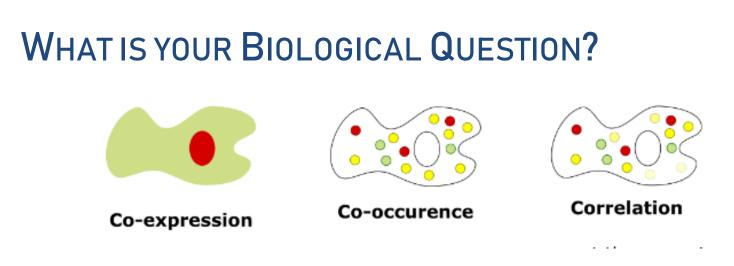
 Limitation (best case scenario): optical resolution of the microscope → XYZ 200 x 200 x 400 nm

- Colocalisation = Presence of two (or more) structures on the same location
- Colocalisation in fluorescence microscopy at subcellular level = the distance between signal is below the resolution of the imaging system



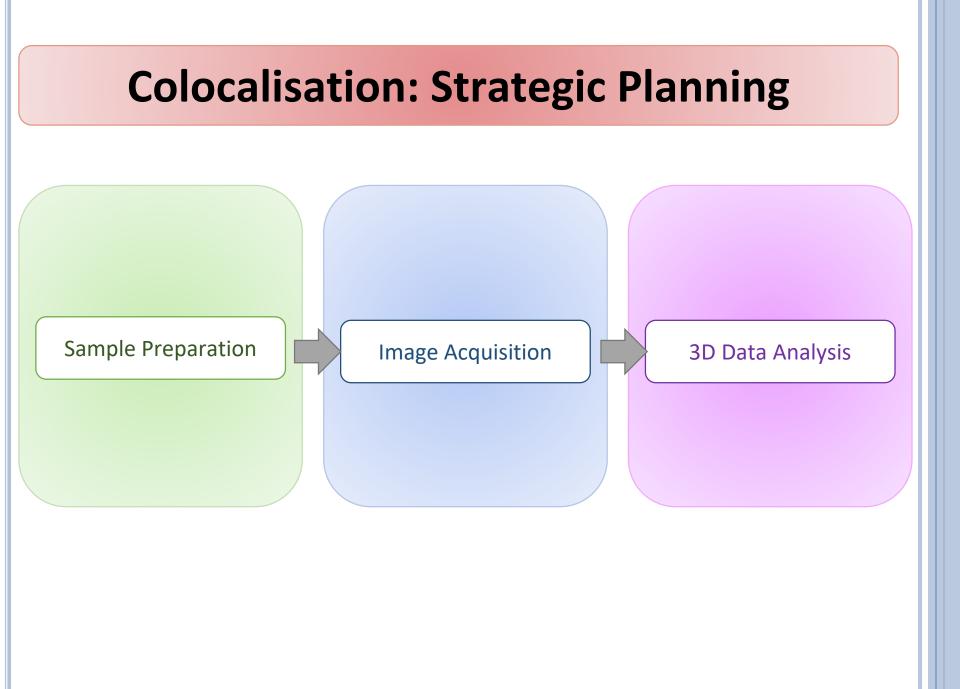
OMX Blaze Super-resolution

- Limitation (3D SIM method): optical resolution of the microscope
  → XYZ 120 x 120 x 250 nm
- Colocalisation <u>never</u> measures interaction, it states that 2 dyes are in a close proximity in a defined volume.



- Are you looking for Co-Compartmentalisation?
- Are your looking for exclusion / anti-correlation?
- Are you looking for interacting molecules?
  - Then you also need some biochemistry experiments (co-IP, FCS...)
  - FRET / FLIM might be very informative!





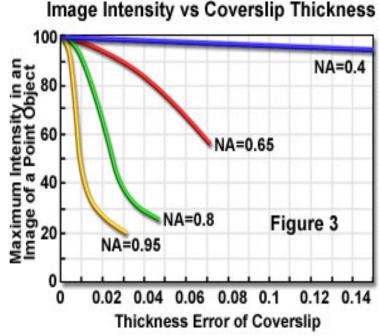
# HOW TO BEST PREPARE YOUR SAMPLES FOR COLOCALISATION

- It all starts with your experimental design!
- Select stable fluorescent dyes
  - Alexa dyes (Invitrogen/Molecular Probes)
  - Atto dyes
  - Avoid Cyanine dyes, especially Cy2

# HOW TO BEST PREPARE YOUR SAMPLES FOR COLOCALISATION

# • The last 500 µm are important

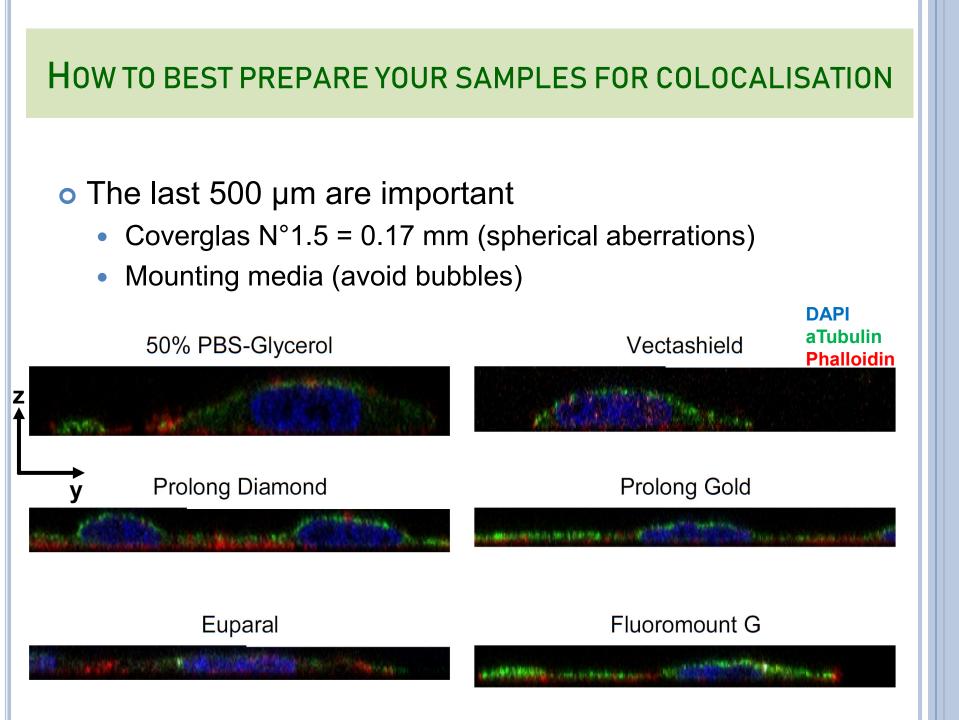
Coverglas N°1.5 = 0.17 mm (spherical aberrations)



NumericalAperture	0.01 mm Deviation	0.02 mm Deviation
0.30	none	none
0.45	none	none
0.70	2 percent	8 percent
0.85	19 percent	57 percent
0.95	55 percent	71 percent
		, , , , , , , , , , , , , , , , , , , ,

Performance Reduction with Coverslip Thickness Variation

http://www.olympusmicro.com



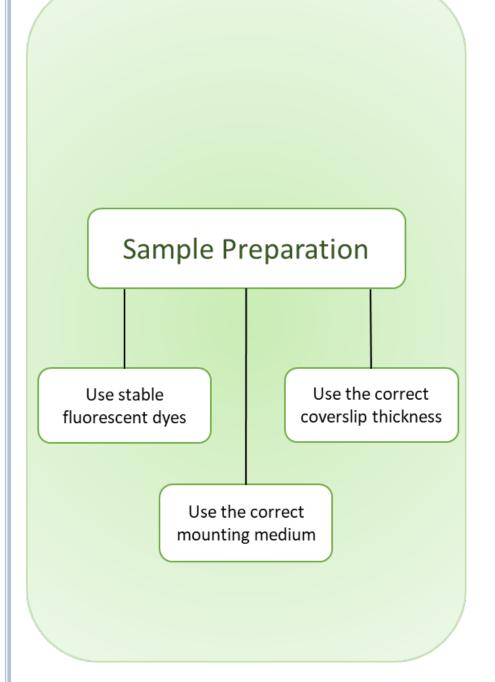
# HOW TO BEST PREPARE YOUR SAMPLES FOR COLOCALISATION

# • The last 500 µm are important

- Coverglas N°1.5 = 0.17 mm (spherical aberrations)
- Mounting media (avoid bubbles)
- Match in the refractive indexes (spherical aberrations)



A refractive index mismatch gives rise to geometrical aberrations.

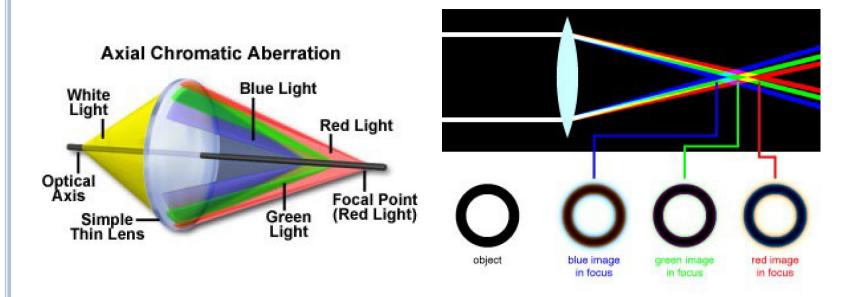


# TAKE HOME MESSAGE PART1

- Carefully select stable dyes
- Make sure that your last "500  $\mu m$  " are optimal
- Don't forget to prepare positive and negative controls

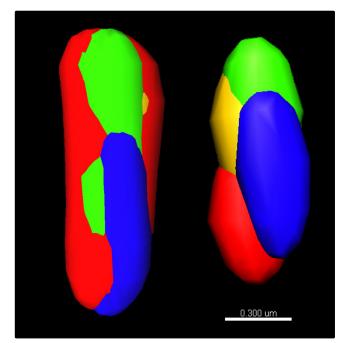
## Use the correct lens

- Remember, the higher the NA, the better the resolution
  →Aim for a 1.40 NA or above
- Apochromat lens (λ corrected)



# Use the correct lens

- Remember, the higher the NA, the better the resolution  $\rightarrow$  Aim for a 1.40 NA or above
- Apochromat lens (λ corrected)
- Check the PSF (Point Spread Function with multicolored beads)

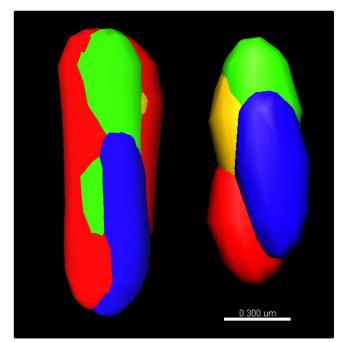


Even the best lenses are not perfect!

Left: LSM700 – Confocal, non-deconvolved Right: DeltaVision – Widefield, deconvolved

# Use the correct lens

- Remember, the higher the NA, the better the resolution
  →Aim for a 1.40 NA or above
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- Check the PSF (Point Spread Function with multicolored beads)



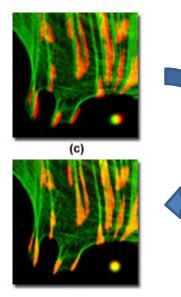
Even the best lenses are not perfect!

→ Better results in colocalisation if you compare green and red fluorophores...

# HOW TO ACQUIRE THE IMAGES FOR COLOCALISATION

# Use the correct lens

- Remember, the higher the NA, the better the resolution  $\rightarrow$  Aim for a 1.40 NA or above
- Apochromat lens (λ corrected)
- Check the PSF (Point Spread Function with multicolored beads)

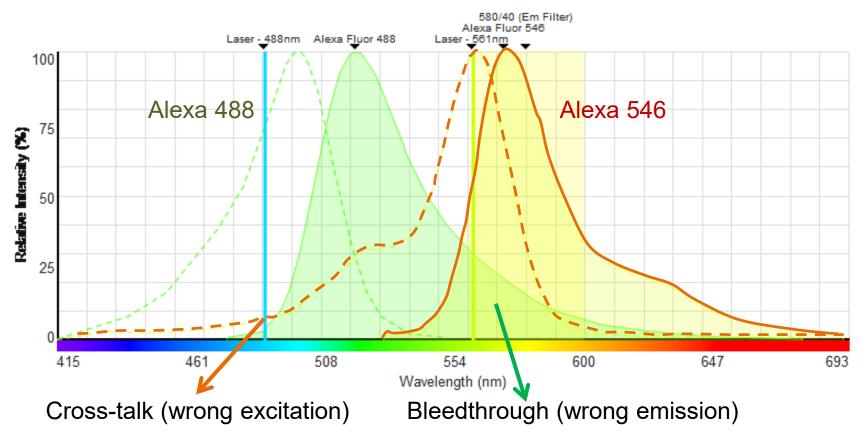


Mis-registration can be corrected afterwards (Post acquisition image processing to restore the image registration)

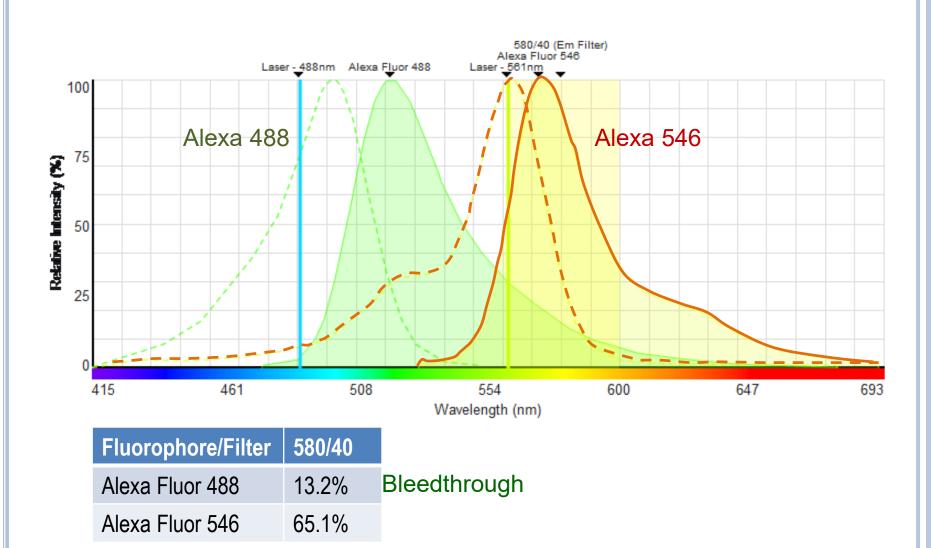
- $\rightarrow$  needs a reference
- $\rightarrow$  Mix beads with your samples

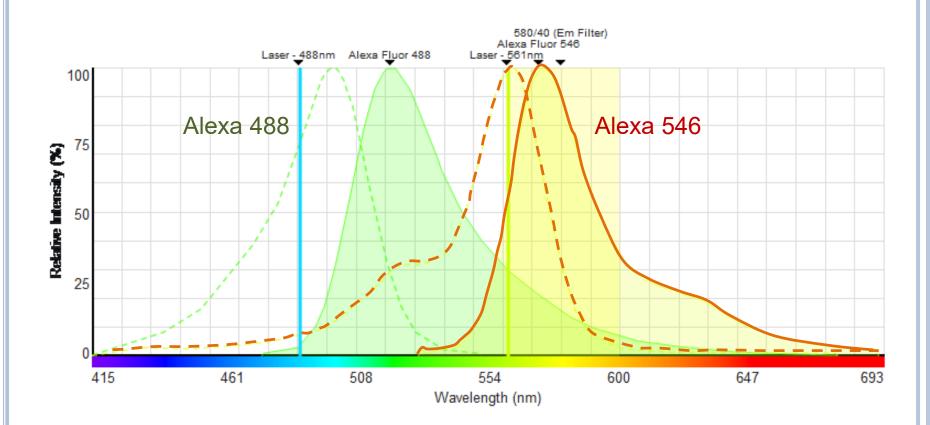
http://www.olympusconfocal.com/ applications/colocalization.html

# Avoid Cross-talk and Bleedthrough



SpectraViewer on <a href="https://www.biozentrum.unibas.ch/IMCF-links">https://www.biozentrum.unibas.ch/IMCF-links</a>





 $\rightarrow$  Scan with the sequential mode

# Avoid bleaching

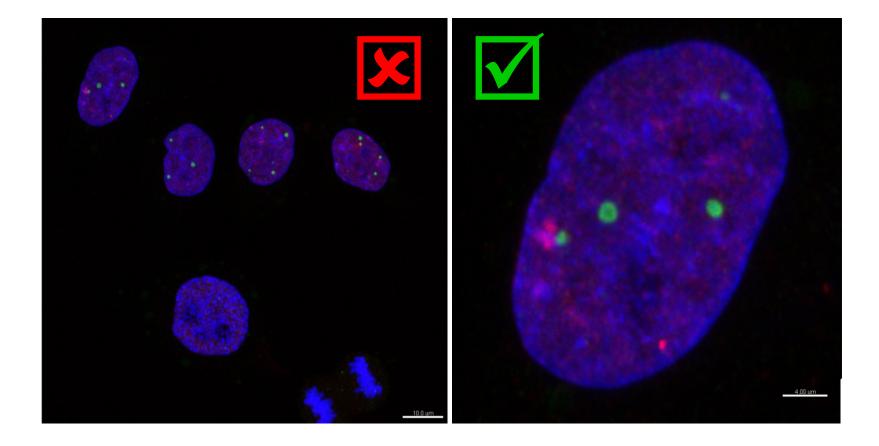
Don't bleach the area before imaging it!
 When possible, use brightfield to find you cells

# Avoid Noise

- Bleached samples  $\rightarrow$  lower signal/higher noise
- Avoid saturation (use the whole dynamic range)

# HOW TO ACQUIRE THE IMAGES FOR COLOCALISATION

# • One cell per field of view (pre or post acquisition)



# HOW TO ACQUIRE THE IMAGES FOR COLOCALISATION

• Match the pixel size – Oversampling XY

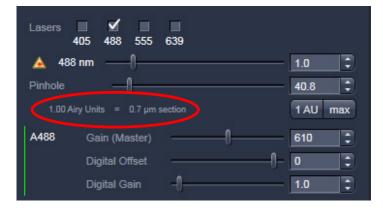
LSM700/LSM880

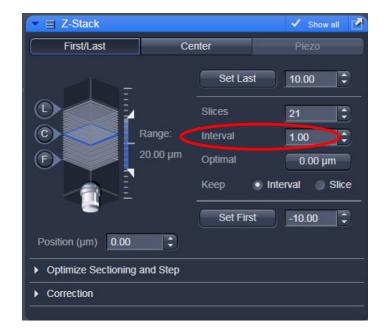
Show All 🛃
)
1
‡ 0 Scan Area
Scan Area
: 0.04 µm
Presets •
Optimal
0.44 µs
Max
1
2
16x
TOX
n

LSM880 (FAST mode)

LSM800 II

# • Match the pixel size – Oversampling Z





### LSM700/800/880

# Match the optical thickness - pinholes



- Fig. 77 Optimize Sectioning and Step: Optimal Interval is set starting with one Airy unit for all channels
- Example with the LSM700 Zeiss



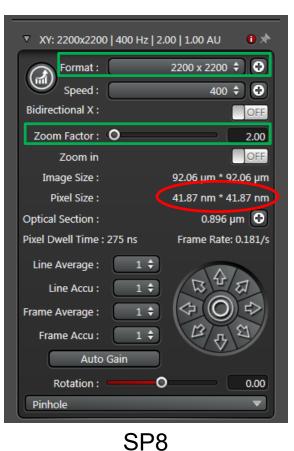
Fig. 78 Optimize Sectioning and Step: Match Pinhole to Step resulting in equal optical sections for all channels

# HOW TO ACQUIRE THE IMAGES FOR COLOCALISATION



# • Match the pixel size – Oversampling XY

Experiments	Acquisition
Acquisition Mode: xyz	00
XY: 512 x 512   400 Hz   1   387.5	50 μm * 387.50 μm 🛛 🕗 🕥
Format: 512 x 512	Pinhole
Speed : 400 Hz 🗢	Bidirectional X
Zoom factor :	1
Zoom in Image Size : 387.56 pm - 337. Pixel Size : 758.32 nm * 758.	
Section Thickness: 0.969 µm	
Line Average : 1	Accu:
Frame Average : 1 Auto Ga	Accu:
Rotation:	
Pinhole:	67.92 µm
Unit : \mu m 🗢	Airy 1



SP5 Matrix

#### θ 2200 x 2200 🗘 Format : Experiments Acquisition **(\_\_\_\_\_** 400 🗘 🕀 Speed : 00 Acquisition Mode: xyz Bidirectional X : OFF P ≌ | <del>\$</del> Zoom Factor : O 2.00 XY: 512 x 512 | 400 Hz | 1 | 387.50 um \* 387.50 um 00 SP5 Matrix OFF SP8 Zoom in 512 x 512 10 $\checkmark$ Pinhole Format: Image Size : 92.06 µm \* 92.06 µm Speed 400 Hz 00 Z-Stack: 0 µm | 62 steps Pixel Size : 41.87 nm \* 41.87 nm Z-Stack : 5.34µm | 42 Steps 0.896 µm 🕀 Optical Section : Zoom factor z - Galvo \$ Set Plane Go to Zoom in Pixel Dwell Time : 275 ns Frame Rate: 0.181/s Begin End Image Size : 387.50 µm \* 387.50 µm Begin : [µn 1 🗘 <u>ش</u> Line Average : Pixel Size : 758.32 nm \* 758.32 nm 6.00 1 🗘 Line Accu : Section Thickness: 0.969 µm End : [um 1 🛊 0.66 Frame Average : Line Average ⊨ 31.18 1 \$ Frame Average : 1 🗢 Z-Position [ Frame Accu : Begin [µm] -81.17 Auto Gain 0.65 Auto Gain End [um] Rotation: Z-Size [µm 0 Rotation : 0.00 5.34 Pinhole $\mathbf{\nabla}$ Pinhole: Re-Cente Unit: 1 0 z-Position [µm] 31.18 Plane: 30.63 µm Stack Direction (Z): z - Galvo 🗘 0 Nr. of steps 62 Q. 0 z-step size 0 um 0 µm Z-Volume No. of Steps **Travel Range** 500 µm 0.13 Z-Step Size System optimized Compensation 0 System Optimized

# • Match the pixel size – Oversampling Z



eice

# SETTINGS FOR DECONVOLUTION: CONFOCALS

Microscope and Objective	Required XY	Required Z	Example: Settings to use
SP5 II Matrix; 63x 1.4 Oil	43 nm	131 nm	ZOOM 2XY: 2800*2800Z: 0.13 nmZOOM 4XY: 1500*1500Z: 0.13 nm
SP8; 63x 1.4 Oil	43 nm	131 nm	ZOOM 2XY: 2200*2200Z: 0.13 nmZOOM 4XY: 1080*1080Z: 0.13 nm
LSM700 Up; 63x 1.4 Oil	43 nm	131 nm	ZOOM 1XY: 2048*2048Z: 0.13 nmZOOM 2XY: 1200*1200Z: 0.13 nm
LSM800; 63x 1.4 Oil	43 nm	131 nm	ZOOM 1XY: 2400*2400Z: 0.13 nmZOOM 2XY: 1200*1200Z: 0.13 nm
LSM880; 63x 1.4 Oil	43 nm	131 nm	CONFOCAL - <b>ZOOM 1.5</b> XY: 2048*2048 Z: 0.13 nm CONFOCAL - <b>ZOOM 2.6</b> XY: 1200*1200 Z: 0.13 nm FAST: Use the SR sampling (2x Nyquist)

- Required values are calculated for a 488-568 nm colocalisation
- Any Zoom/XY frame size is possible, as long as you match the XYZ pixel requirements
- **O** For more information, check <u>https://svi.nl/NyquistCalculator</u>

# SETTINGS FOR DECONVOLUTION: <u>SPINNING DISK</u>

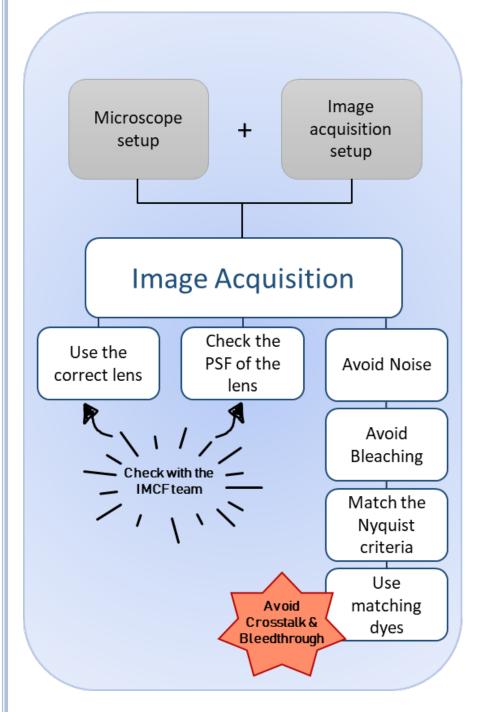
Microscope and Objective	Required XY	Required Z	Example: Settings to use
SpinSR; 60x 1.5 Oil	40 nm	93 nm	Check the camera installed on the system*
SpinSR; 100x 1.5 Oil	40 nm	93 nm	Check the camera installed on the system*

- Required values are calculated for a 488-568 nm colocalisation
- XY pixel size is determined by the camera and the use or not of an extra auxiliary lens
- **O** \* the final camera choice is under testing at the IMCF
- Any Zoom/XY frame size is possible, as long as you match the XYZ pixel requirements
- For more information, check <u>https://svi.nl/NyquistCalculator</u>

# SETTINGS FOR DECONVOLUTION: WIDEFIELDS

Microscope and Objective	Required XY	Required Z	Example: Settings to use
Deltavision; 100x 1.40 Oil CCD camera	92 nm	279 nm	XY – no Aux Mag: 65 nm Z: 0.2nm
Deltavision; 60x 1.42 Oil CCD camera	91 nm	264 nm	XY – no Aux Mag: 107 nm Z: 0.2nm XY – with Aux Mag: 65 nm Z: 0.2nm
Nikon Ti2; 100x 1.45 Oil sCMOS camera	89 nm	243 nm	XY - no Aux Mag: 110 nm Z: 0.2 nm XY - with Aux Mag: 73 nm Z: 0.2 nm
Nikon Ti2; 60x 1.40 Oil sCMOS camera	92 nm	279 nm	XY - no Aux Mag: 180 nm Z: 0.2 nm XY - with Aux Mag: 120 nm Z: 0.2 nm
MORE; 100x 1.4 Oil sCMOS camera	92 nm	279 nm	XY: 65 nm Z: 0.2nm
MORE; 60x 1.49 Oil sCMOS camera	87 nm	211 nm	XY 109 nm Z: 0.2nm

- Required values are calculated for a 488-568 nm colocalisation
- XY pixel size is determined by the camera and the use or not of the extra auxiliary lens (1.5x for Nikon Ti2, 1.6x for Deltavision)
- Changing the XY px size with the extra lens does NOT change the acquisition time
- Changing the frame size can speed up the acquisition (MORE and Nikon Ti2)



# TAKE HOME MESSAGE PART 2

- Make sure that you are aware of the PSF of the lens (beads)

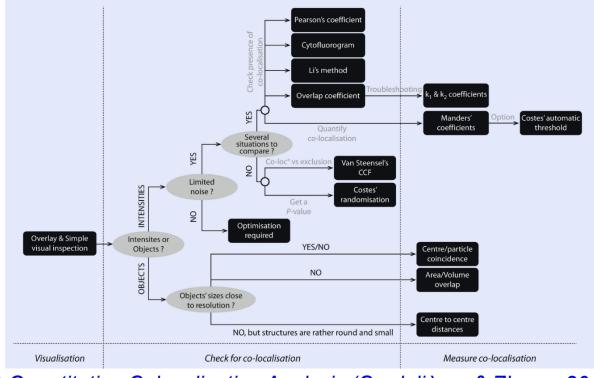
- Avoid noise/ bleaching/ saturation when you acquire your images (good SNR)

 Make sure you match pinholes and the oversampling (Nyquist)

- Make sure that you use sequential acquisition if you suspect crosstalk and/or bleedthrough

# How to analyse your Colocalisation Data

- Colocalisation is 3D
- Colocalisation should be more thought in terms of correlation
- Colocalisation needs Quantification & Statistics



3D Quantitative Colocalisation Analysis (Cordelières & Zhang, 2019)

# How to analyse your Colocalisation Data

#### (1) Intensity/pixel-based

Correlation of the strength of linear relation between two channels  $\rightarrow$  no spatial exploration of the colocalisation signal

#### (2) Object-based

Structure identification and determination of overlap of objects (for discrete structures) → Segmentation

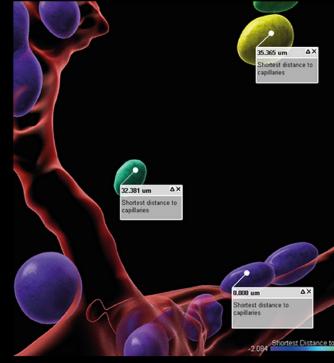
- Many tools available
  See Bioimage Informatics Search Engine (BISE) <u>colocalisation</u>
- Object-based analysis: Please contact our IMCF Image Analysis experts (Wednesday Workshops)

# HOW TO ANALYSE YOUR DATA: PROXIMITY - IMARIS

# Native Distance Measurements

For every Surfaces and Spots object Imaris 9.5 **natively calculates** the **shortest distance** to any other Surfaces or Spots. The edge of surfaces and the center of spots are used for these calculations. The computation is fast and capable of running on **large images**. Calculations can also be performed on multiple datasets at once in **Batch mode** 

- Color code Spots or Surfaces by Distance from Surfaces (view movie).
- Filter Spots inside or outside of Surfaces (view movie)
- Count Spots inside the ROI (view movie)
- Filter Spots in a specific distance band outside or inside Surfaces. (view movie)
- Filter tracks of objects that "go inside" Surfaces (view movie)
- Calculate Shortest Distance for multiple datasets at once in the Batch mode view movie

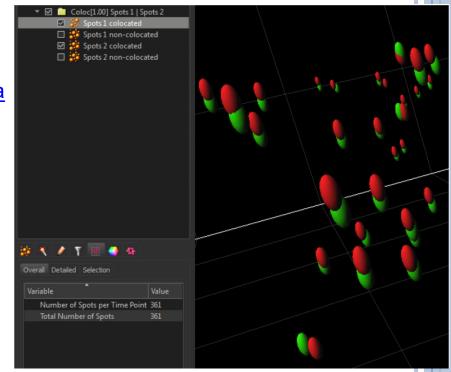


### Caution! No statistics, this is NOT real colocalisation!!!

# HOW TO ANALYSE YOUR DATA: PROXIMITY - IMARIS

# Matlab extension for Imaris

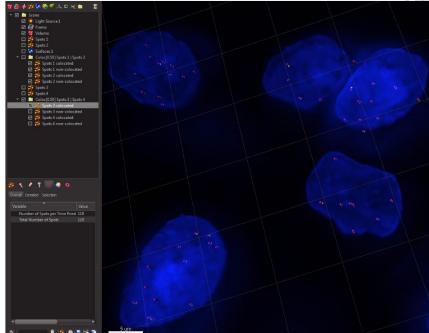
• See dedicated wiki page : <u>https://wiki.biozentrum.unibas.ch/pages/viewpa</u> <u>ge.action?spaceKey=IMCF&title=Imaris+-</u> +colocalize+spots



Caution! No statistics, this is NOT real colocalisation!!!

# HOW TO ANALYSE YOUR DATA: PROXIMITY - IMARIS

- Matlab extension for Imaris
- See dedicated wiki page : <u>https://wiki.biozentrum.unibas.ch/pages/viewpa</u> <u>ge.action?spaceKey=IMCF&title=Imaris+-</u> <u>+colocalize+spots</u>
- Can be limited to spots within a certain region (ie. DAPI here)



# Caution! No statistics, this is NOT real colocalisation!!!

# JACOP JUST ANOTHER COLOCALISATION PLUGIN

Journal of Microscopy, Vol. 224, Pt 3 December 2006, pp. 213–232 Received 13 April 2006; accepted 28 June 2006

#### TUTORIAL REVIEW

# A guided tour into subcellular colocalization analysis in light microscopy

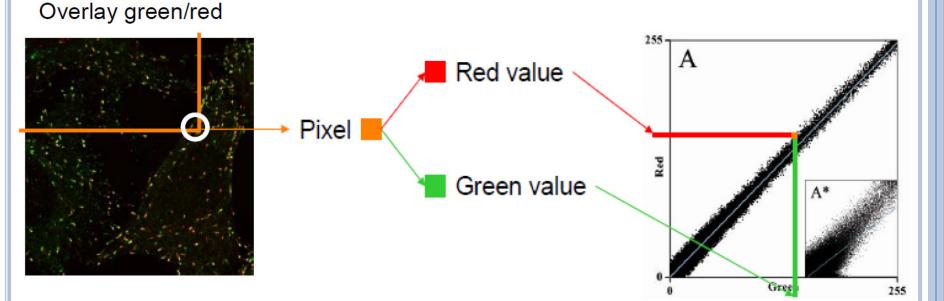
#### S. BOLTE\* & F. P. CORDELIÈRES†

\*Plateforme d'Imagerie et de Biologie Cellulaire, IFR 87 'la Plante et son Environnement', Institut des Sciences du Végétal, Avenue de la Terrasse, 91198 Gif-sur-Yvette Cedex, France †Institut Curie, CNRS UMR 146, Plateforme d'Imagerie Cellulaire et Tissulaire, Bâtiment 112, Centre Universitaire, 91405 Orsay Cedex, France

Key words. Colocalization, confocal microscopy, fluorescence microscopy, image analysis, wide-field microscopy.

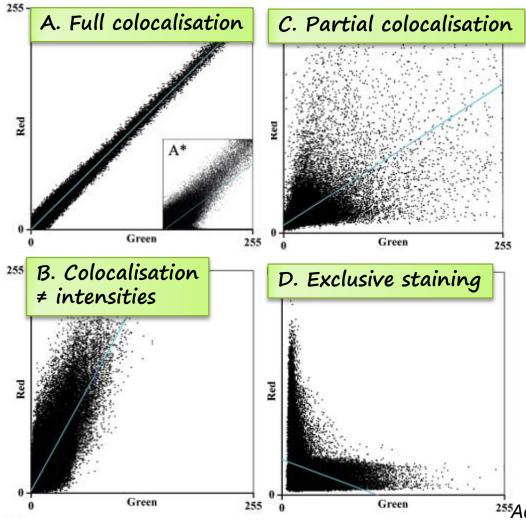
#### Must Read <u>https://doi.org/10.1111/j.1365-2818.2006.01706.x</u>

# JACOP: SCATTER PLOT/CYTOFLUOROGRAM



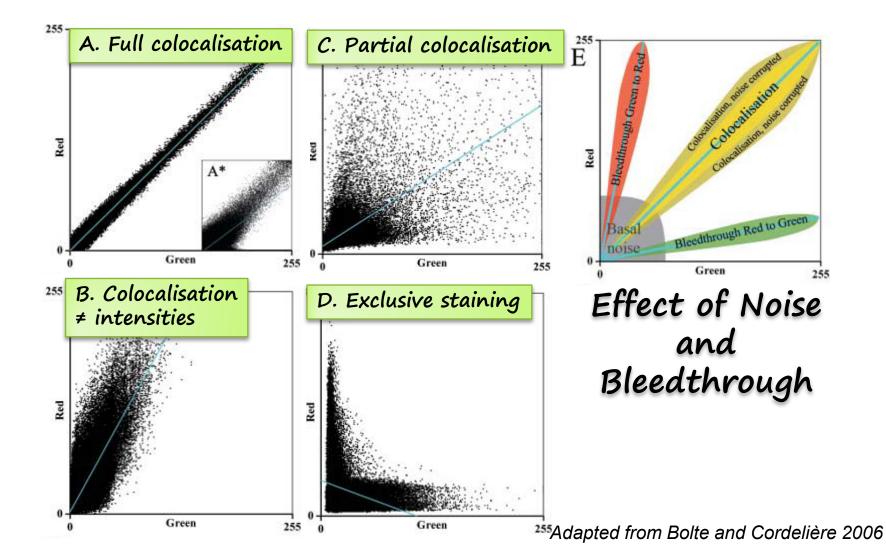
Good first visual estimate of colocalisation
 Information about the image quality
 Only qualitative correlation

## JACOP: SCATTER PLOT/CYTOFLUOROGRAM

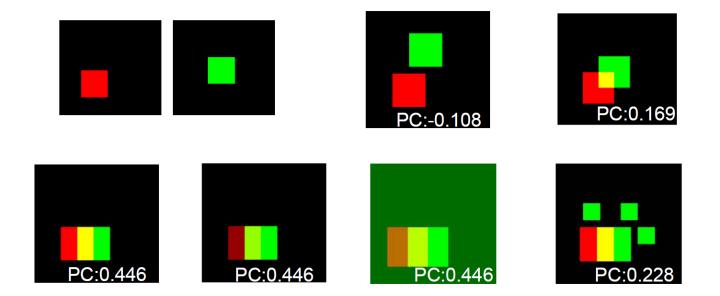


<sup>255</sup>Adapted from Bolte and Cordelière 2006

## JACOP: SCATTER PLOT/CYTOFLUOROGRAM



#### **PEARSON'S COEFFICIENT**

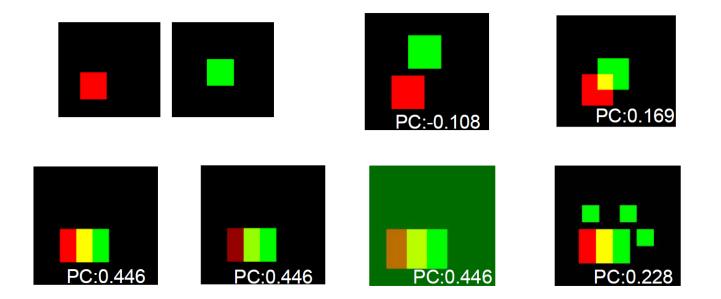


#### • PCC or « r »

Estimate of the association strength between 2 proteins

http://www.svi.nl/ColocalizationCoefficients

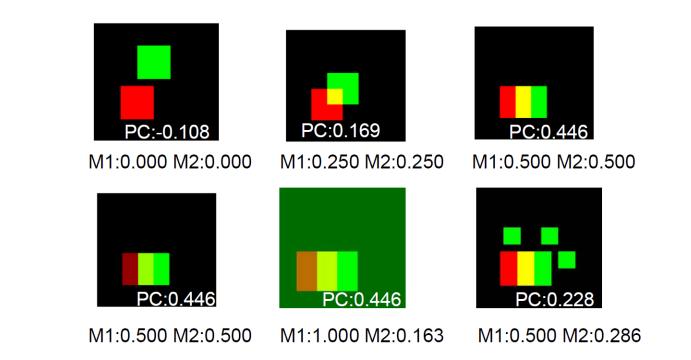
## **PEARSON'S COEFFICIENT**



- $\bigcirc$  Not sensitive on  $\neq$  intensity of the overlapping pixels
- ☺ Not sensitive on background intensity
- ⊗ Not easy to interpret
- $\ensuremath{\mathfrak{S}}$  Affected by noise
- ⊗ No perspective of both channels

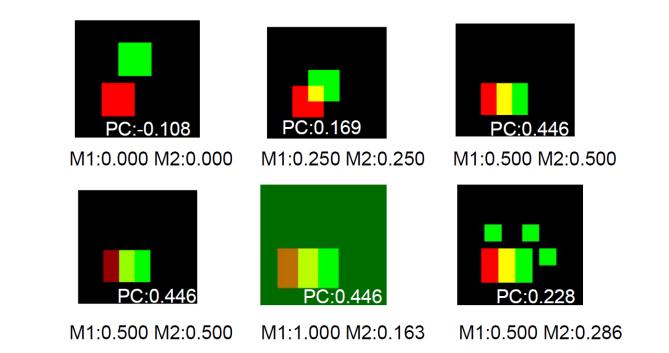
http://www.svi.nl/ColocalizationCoefficients

#### MANDERS COEFFICIENTS



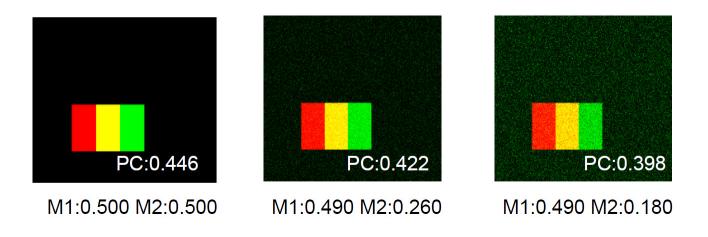
• M1 and M2 Gives the proportion of each protein colocalising with the other

## How to analyse your Colocalisation Data



- ☺ Easier to interpret that PCC
- Not sensitive to the intensity of the overlapping pixels
- ☺ Sensitive to background intensity Threshold needed!
- $\ensuremath{\mathfrak{S}}$  Affected by noise

#### INFLUENCE OF NOISE



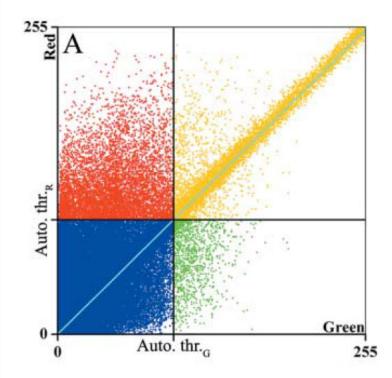


These coefficients are influenced by noise Minimize noise during the acquisition, and deconvolve your datasets prior analysis

Deconvolution improves colocalization analysis of multiple fluorochromes in 3D confocal data sets more than filtering techniques. L. Landmann. Journal of Microscopy **208**:2, 134 (2002).

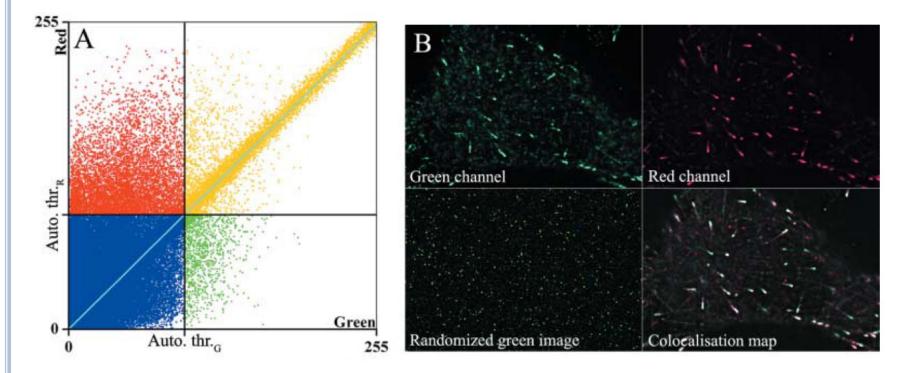
## **C**OSTES' **A**PPROACH

- Estimation of an automatic threshold
- Test of the statistical significance (Costes' P-value)



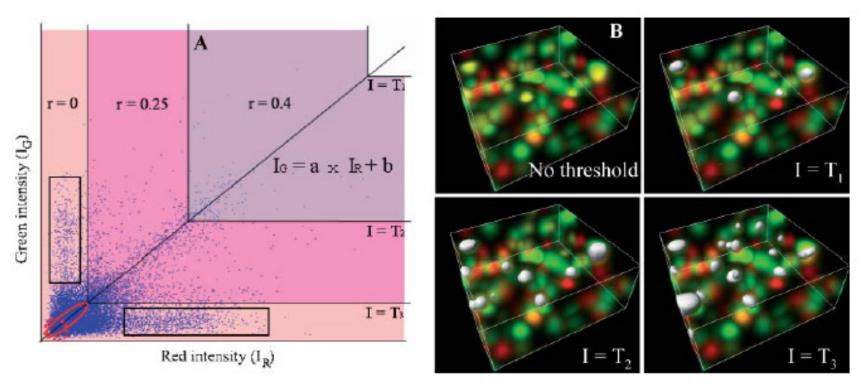
## **COSTES' APPROACH**

- Estimation of an automatic threshold
- Test of the statistical significance (Costes' P-value)



If > 95% of the random images correlate (PCC) worse than the real image, then you can trust the correlation coefficient

#### **COSTES' APPROACH**



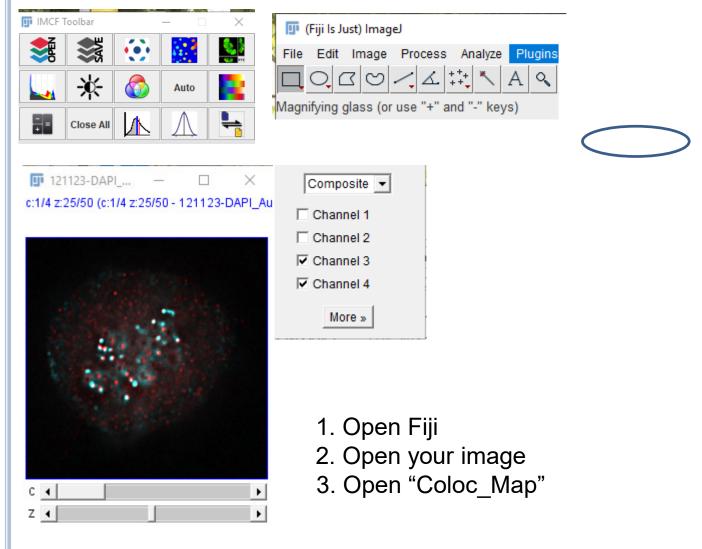
Costes et al., 2004

Statistical approach
 Minimises the influence of noise
 Long calculations (3D)

## HOW TO UNDERSTAND YOUR DATA

	Value range	Colocalisation if…	Notes
Pearson's coef r	+1 → coloc 0 → random -1 → exclusion	tends to 1	Insensitive ≠ intensities Insensitive intensity offset Affected by noise Not robust for Bioimages
Manders' coef M1 (or M2)	$0 \rightarrow 0\%$ of Ch1 colocalize with Ch2 $1 \rightarrow 100\%$ of Ch1 colocalize with Ch2	tends to 1	Insensitive ≠ intensities Sensitive intensity offset Affected by noise Biologically meaningful
Costes (P-value)	P<95% → no coloc P≥95% → coloc	≥95%	Automated thresholds Statistical approach Minimises influence of noise

#### **COLOCALISATION MAP**



Kai Schleicher, script upon request

Map is generated
p ×
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File Edit Font
now working on Image: 121123-DAPI_AurBfitc_Hec568_A(found the following calibration in x,y,z: 0.10689999908208 Channel settings: 3, 4 PCC: 0.695291980357662

#### **ANALYSIS PIPELINE**

1- Deconvolution (better resolution, lesser noise)

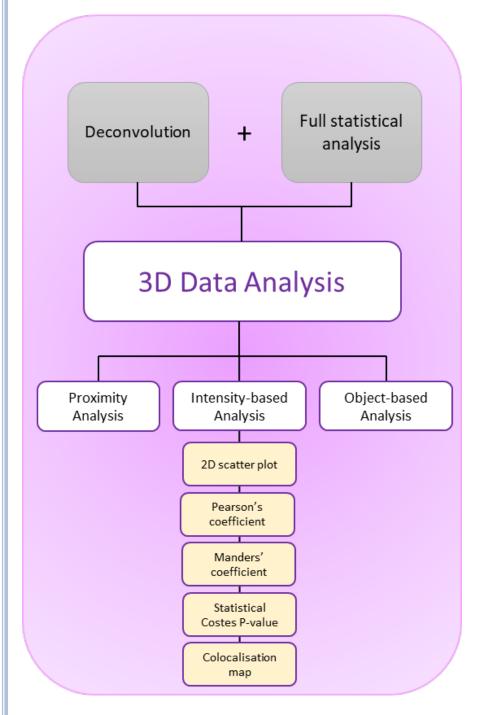
- Softworx (DeltaVision widefield images)
- Huygens (Confocals + Widefield)

2a- Colocalisation analysis (method 1, intensity-based)

- JACoP
- Colocalisation map

2b- Colocalisation analysis (method 2, object-based)

• Check the IMCF team to find the best solution



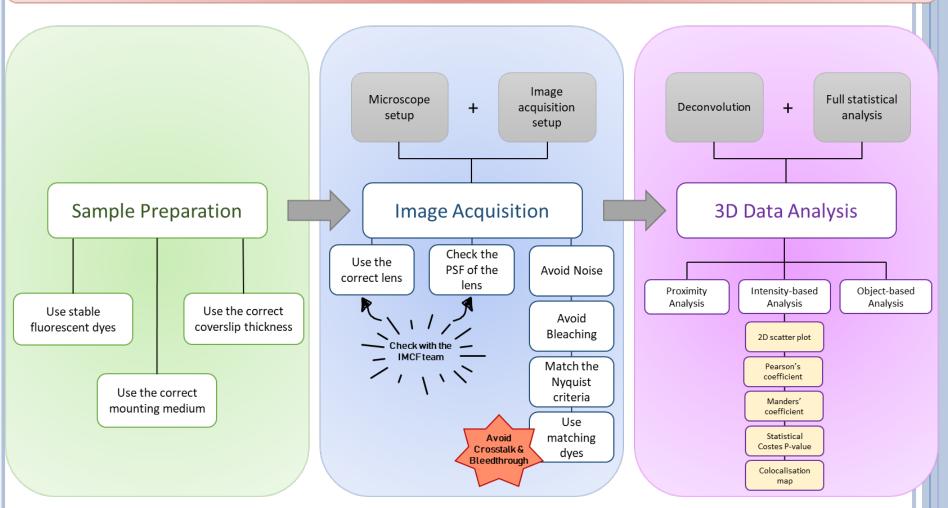
#### TAKE HOME MESSAGE PART 3

- Work on deconvolved images

 Perform a full colocalisation analysis

- Intensity-based (no defined structure)
- **Object-based** (defined structure)
- For publications, indicate:
- Pearson's coefficient
- thresholded Manders' coefficients
- colocalisation map

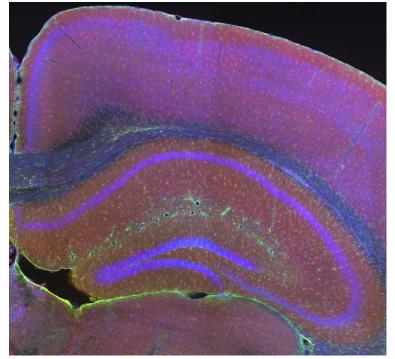
#### **Colocalisation: Strategic Planning**



Colocalisation is always relative to the resolution!

## THANKS FOR YOUR ATTENTION!





Imaging Core Facility Biozentrum University of Basel imcf@unibas.ch <u>www.biozentrum.unibas.ch/imcf</u>



#### BIOZENTRUM

Universität Basel The Center for Molecular Life Sciences