A non-parametric procedure for co-localization studies in fluorescence microscopy

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Outline

Motivation

Previous work

Our approach

Evaluation

Conclusion

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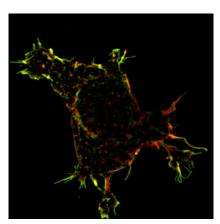
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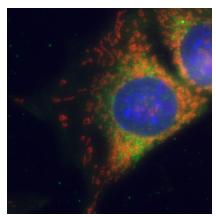
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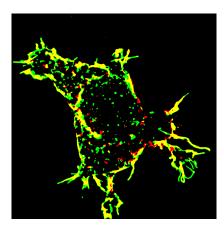
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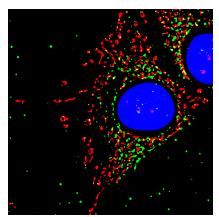
c-Src tyrosine kinase serotonin receptor



H1B mitochondria
EB1 (microtubules plus ends)
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Common co-localization approaches

- Ω : image domain
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- \overline{I}_c : mean intensity for channel c

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- Pearson's correlation coefficient:

$$PCC = \frac{\displaystyle\sum_{x \in \Omega} (I_1(x) - \overline{I}_1)(I_2(x) - \overline{I}_2)}{\sqrt{\displaystyle\sum_{x \in \Omega} (I_1(x) - \overline{I}_1)^2 (I_2(x) - \overline{I}_2)^2}}$$

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Manders' co-localization coefficients:

$$MCC_1 = \frac{\displaystyle\sum_{x \in \Omega} I_1(x) \mathbf{1}_{I_2(x) > 0}}{\displaystyle\sum_{x \in \Omega} I_1(x)}, \quad MCC_2 = \frac{\displaystyle\sum_{x \in \Omega} I_2(x) \mathbf{1}_{I_1(x) > 0}}{\displaystyle\sum_{x \in \Omega} I_2(x)}$$

Permutation test applied to the **Pearson's** correlation coefficient (PCC)

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- As neighbor pixels are correlated, blocks are preferred to pixels for permutations

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- Asymmetric Ripley's K function

$$K_{12}(r) = \frac{|\Omega|}{n_1 n_2} \sum_{x \in A_1} \sum_{y \in A_2} \mathbf{1}_{d_{xy} < r} b(x, y, r)$$

where
$$d_{xy}$$

$$b(x,y,r) = \frac{|c(x,d_{xy})|}{|c(x,d_{xy})| \cap \Omega}$$

$$c(x,d_{xy})$$

Euclidean distance between x and y boundary correction term disk (sphere) centered at xwith radius d_{xu}

Reduced statistics

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• The **null hypothesis** of A_2 uniform distribution with a confidence level of $1-\gamma$ is rejected if:

$$\tilde{K}_{12}(r) > z_{\gamma}$$

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- Γ_1 : random set in \mathbb{R}^d
- Γ_2 : random set in \mathbb{R}^d

$$p_1 = P(o \in \Gamma_1), \ p_2 = P(o \in \Gamma_2), \ p_{12} = P(o \in \Gamma_1 \cap \Gamma_2), \ \forall o \in \mathbb{R}^d$$

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Pearson correlation:

$$\hat{\rho} = \frac{\hat{p}_{12} - \hat{p}_1 \hat{p}_2}{\sqrt{\hat{p}_1 (1 - \hat{p}_1) \hat{p}_2 (1 - \hat{p}_2)}}$$

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• Let $D = \hat{p}_{12} - \hat{p}_1 \hat{p}_2$

$$E(D) = 0$$

$$Var(D) = |\Omega|^{-2} E \left(\sum_{x \in \Omega} \mathbf{1}_{\Gamma_1}(x) \mathbf{1}_{\Gamma_2}(x) - |\Omega|^{-1} \sum_{x \in \Omega} \mathbf{1}_{\Gamma_1}(x) \sum_{x \in \Omega} \mathbf{1}_{\Gamma_2}(x) \right)^2$$
$$= S1 + S2 + S3$$

where

$$S_1 = |\Omega|^{-2} \sum_{x \in \Omega} \sum_{y \in \Omega} C_1(x - y) C_2(x - y)$$

$$S_2 = -2|\Omega|^{-3} \sum_{x \in \Omega} \left(\sum_{y \in \Omega} C_1(x - y) \right) \left(\sum_{y \in \Omega} C_2(x - y) \right)$$

$$S_3 = |\Omega|^{-4} \sum_{x \in \Omega} \sum_{y \in \Omega} C_1(x - y) \sum_{x \in \Omega} \sum_{y \in \Omega} C_2(x - y)$$

and C_1 and C_2 are **auto-covariance** functions

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$$Var(D) \sim S_1 \text{ if } |\Omega| \to \infty$$

Hypothesis testing

• Following [1], it can be proved that:

$$\frac{D}{\sqrt{S_1}} \to \mathcal{N}(0,1) \text{ as } |\Omega| \to \infty$$

^[1] Shigeru Mase. Asymptotic properties of stereological estimators of volume fraction for stationary random sets. *Journal of Applied Probability*May 26th, 2016

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$$T := \sqrt{rac{\hat{p}_1(1-\hat{p}_1)\hat{p}_2(1-\hat{p}_2)}{\hat{S}_1}}\hat{
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• The **null hypothesis** of independence is **rejected** at the asymptotic level $\alpha \in (0,1)$ if $T>q(\alpha)$ corresponding to

$$p$$
-value = $1 - \Phi(T)$

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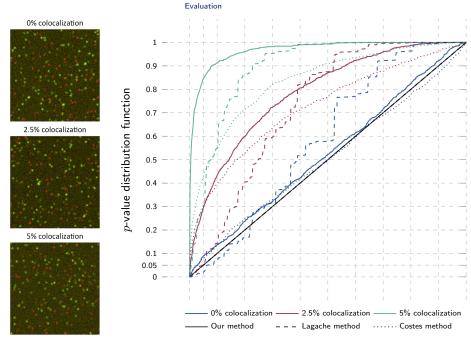
Our approach

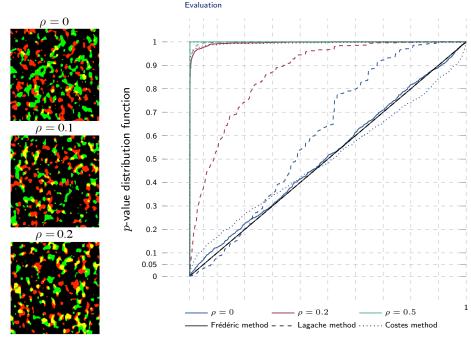
Evaluation

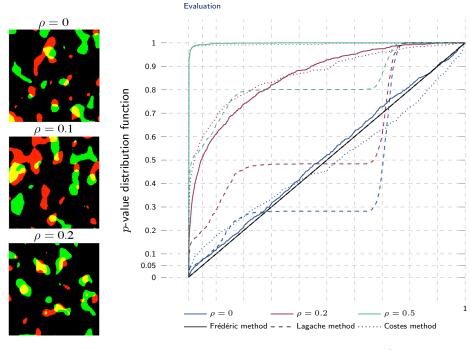
Conclusion

Computation time

	2D image 256x256	2D image 256×256	2D image 256x256	2D+t image 256x256x1000	3D image 256x256x60
	50 objects	200 objects	3500 objects	100 objects	100 objects
Costes method	6.1 s	6.2 s	6.1 s	38 min 20 s	3 min 3 s
with 1000 permutations					
ImageJ plugin					
Lagache method	1 s	1.96 s	12.38 s	12 min 39 s	4.37 s
Icy plugin					
Our method	0.18 s	0.2 s	0.19 s	29.5 s	10 s
C++ implementation					

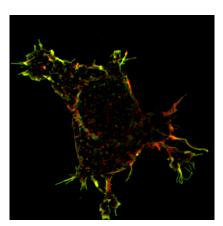




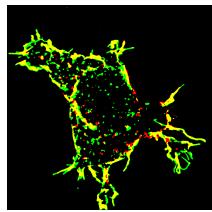


Other evaluations on synthetic images

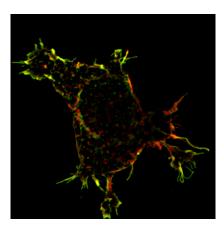
- 3D images
- Different number of objects in each channel
- Different size for objects in channel 1 and objects in channel 2



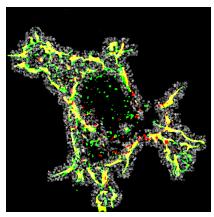
c-Src tyrosine kinase serotonin receptor



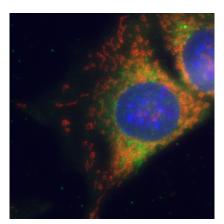
p-value = 0



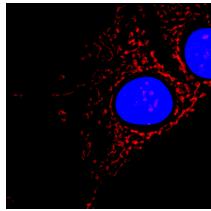
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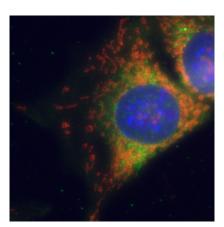
White circles: co-localization hits



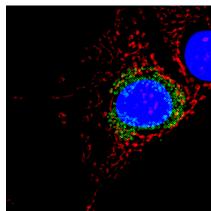
H1B mitochondria EB1 (microtubules plus ends) DNA



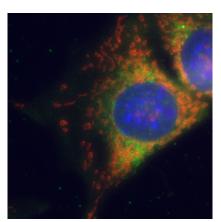
p-value = 0



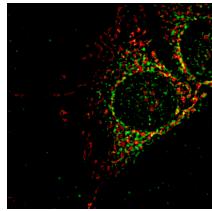
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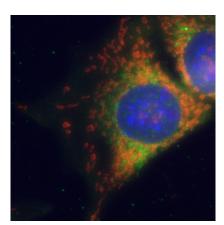
Green circles: anti co-localization hits



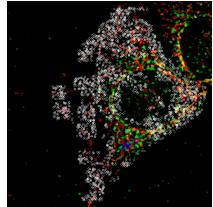
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White circles: co-localization hits Blue circles: anti co-localization hits

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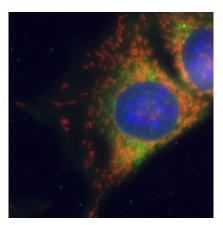
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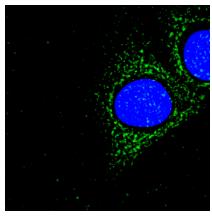
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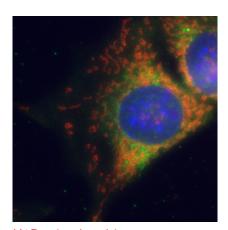
- Non-parametric procedure to test co-localization and anti-colocalization
- Fast and reliable approach
- Method adapted to any size of 2D and 3D objects, enabling localized co-localization



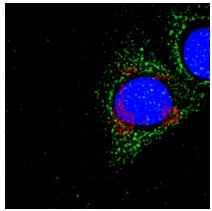
H1B mitochondria EB1 (microtubules plus ends) DNA



p-value = 0.0799



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EB1 (microtubules plus ends)
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White circles: co-localization hits Red circles: anti co-localization hits