Call4Help Feedback

Please preface your comment with your [first name] and/or [e-mail@address] so you can be contacted for further discussion

Notes (please preface your comment with your [first name] so you can be contacted for further discussion)

1. Igor Golic

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Website:
Raw data:
I agree to publish this submission on Call4Help webpage: YES

Title

Measuring mitochondria from TEM images of BAT

Keywords

Abstract

Image processing and analysis of TEM images of brown adipose tissue (BAT); how to automate mitochondrial size analyses (area, length, width); problems - high density of mitochondria, separating touching mitochondria, differences in mitochondrial size and shape, TEM contrast.

Link to presentation

https://docs.google.com/presentation/d/1xC_yr9YnQBWc_i-q6gHYyVzJxSY2x37Clt1uiZ0JRIE/edit?usp=sharing

Notes

- (Stefan) try CLAHE filtering for homogenize contrast differences in different areas and in between different sections
- [simon] ilastik, but that is mainly my reaction whenever I see EM images

- [Michael] Could start by looking into a circular hough transform to take advantage of the circular nature of your objects. This might not be optimum, but if it work it will be robust against touching objects.
- Moritz: Skeletonize and calculate average curvature on all segments of a certain length. Then filter based on this to get rid of objects which do not have the typical radius of the Mitos.

2. Elisa Nerli

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Title

High Content Imaging screening in primary neurons

Keywords

Abstract

My project aims at set up an high content phenotypic screening assay using primary neuronal cultures. This requires an automated acquisition of fluorescence images and analysis of neuronal morphology. In order to guarantee a good reproducibility of the assay, manual interaction must be avoided as much as possible and the images acquired across different experiments must be similar in intensity.
I need to normalize the contrast of the images in order to obtain similar histograms, because the yield of fluorescence is different depending on external factors and I might not be able to compare images coming from different experiments.

Link to presentation

https://docs.google.com/presentation/d/1GN8CCKyQOfRgNnOWUuFS4cVmw8Tq_-JWszrpZG4ANiA/edit?usp=sharing

Notes

- [AS] calibration slide, mounting media (RI mismatch), sealing media when you prepare the slides: try valap
- [Sebastian] Have you tried the FIJI-plugins “Skeletonize” and “AnalyzeSkeleton”? Might help with segmentation even if you have different signals.
- [simon] Consider CellProfiler for all the book-keeping of variable names, plate names etc. You can call ImageJ and ilastik from CellProfiler. Beware of including cells that are near the edge: they will bias your results due to incomplete information. To make histograms similar: this is called histogram equalisation
- [Michael] You can try classify your images into categories based on signal to noise and do your statistical tests on images within the same catagory.
- []bleach correction plugin in ImageJ

3. Christina Braunsdorf

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I agree to publish this submission on Call4Help webpage: YES

Title

Automatic quantification of filaments

Keywords

Abstract

In our lab we are working with Candida albicans a fungus that can cause superficial as well as systemic infections. It is dimorphic and can grow as budding yeast but switch to hyphal form under inducing conditions.
Since the hyphal growth of C. albicans is related to virulence and tissue invasion we would like to quantify and compare the total hyphal length of different strains.

Link to presentation

https://docs.google.com/presentation/d/1SMdLKJ5-BAIzZR3RCr3OfBF07J8VRao-cK_8uHMFgLw/edit?usp=sharing

Notes

- []Machine learning - you will first need to find the rules that isolate what you want...
- []image segmentation followed by skeletonization. Use the imagej plugins on these skeletons and pull out the properties you would like, like the length.
- [Michael] To distinguish between elongated cells and hypahae you could combine a skeletonisation with a distance map. Once you have the skeleton for each of those pixels you can compare that to the distance map. if the membranes are parallel the distance map shouldn't change much along the distance map.
- [simon] try out Imaris, it has some toolboxes for filament tracing
- [szymon] try ilastik, with the correct choice of features
- [] before starting image processing, do some preprocessing and correct the images for their background differences.
- []