General Information

This README file pertains to code hosted at:

https://github.com/uomsystemsbiology/epidermal_data

It is designed to run for the analysis of data hosted on GigaDB, the GigaScience data repository:

http://www.url.to.be/designated

doi: to-be-assigned

Detailed technical information on these data can be found within a corresponding Data Note:

Cursons *et al.* (2015). Spatially-transformed fluorescence image data for ERK-MAPK and selected proteins within human epidermis. *GigaScience*. Submitted Sep 2015.

doi: to-be-known

These MATLAB scripts have several dependencies upon MATLAB Toolboxes and MATLAB File Exchange functions, as detailed in the Script/Function Overview (p2).

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Script/Function Overview

Within the base code folder, there are a number of scripts:

/code/sample_to_loessDiscCentroids.m

This MATLAB script reads in the sample location data, extracts pixel intensities from the raw image data, maps to the normalised distance co-ordinate, performs loess smoothing, and outputs .csv/.tiff at various stages.

/code/recreate_pMEK_heterogeneity_fig.m

This MATLAB script reproduces Fig. AF4.1 of the GigaScience Data Note described above (NB: this output was tidied in GIMP to produce the final figure).

There are also a number of functions used by the scripts above:

/functions/calculateDistancesToBoundary.m

/functions/calculateLoessCurve.m

/functions/calculateSpatialDivisions.m

/functions/convertSmpAnaToAbundVector.m

/functions/extractSampleInformation.m

/functions/initSamplingKernel.m

/functions/loadImageStack.m

/functions/loadImageStackAsSparse3DCellArrays.m

/functions/produceSmpAna.m

/functions/rescaleNormDist.m

sample_to_loessDiscCentroids.m (will be updated 05/09/15)

This MATLAB script reads in the sample location data, extracts pixel intensities from the raw image data, maps to the normalised distance co-ordinate, performs loess smoothing, and outputs .csv/.tiff at various stages. A graphical overview of this script, the functions used, and the outputs at each stage is given below:

Dependencies:

recreate_pMEK_heterogeneity_fig.m

This MATLAB script reproduces Fig. AF4.1 of the GigaScience Data Note described above. A Graphical overview of this script is given below:
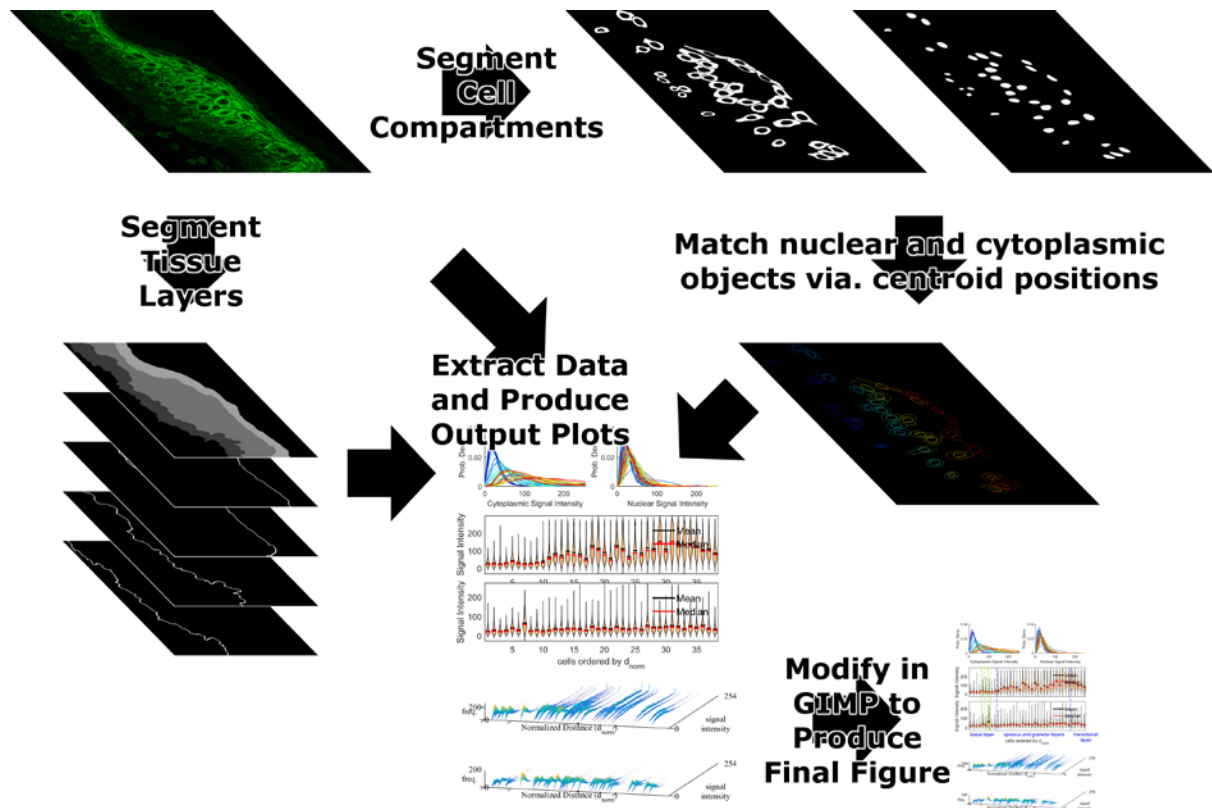
1. The image data were loaded and used for segmentation of tissue layers and sub-cellular compartments (note that these segmented files have already been generated for this figure; however, they can be modified or adapted).
2. The centroids of segmented cytoplasm and nuclei were identified using functions from the image processing toolbox, and the nearest cytoplasm/nuclei were matched using the dist function from the Neural Network Toolbox
      Lines 115 ~ 185
3. Pixel locations of segmented objects were also extracted using the Image Processing Toolbox, and signal intensity data were extracted from these.
      Lines 150 ~ 180
4. The nucleus centroid of each cell was mapped on to the normalised-distance co-ordinate [1], and the distribution of pixel intensities was examined by looking at the probability density functions, violin plots, and mapping the probability density functions on to the normalised distance as surface plots.
      Lines 185 ~ 510
5. The create Fig. 4A of the GigaScience Data Note, the output image underwent minor modifications within GIMP.

Dependencies:

This script executes several functions with MATLAB ToolBox dependencies:

- Image Processing Toolbox
    - `bwlabel`, `regionprops`, `bwmorph`
    - `calculateDistancesToBoundary` → `bwlabel`, `regionprops`
- Neural network Toolbox
    - `dist`
- Statistics and Machine Learning Toolbox
    - `ksdensity`

This script also executes `violin` from the MATLAB File Exchange (File ID: #45134), created by Holger Hoffman: hhoffmann@uni-bonn.de

- http://www.mathworks.com/matlabcentral/fileexchange/45134-violin-plot-based-on-kernel-density-estimation

References

1. Cursons J, Gao J, Hurley DG, Print CG, Dunbar PR, Jacobs MD et al. Regulation of ERK-MAPK signaling in human epidermis. BMC systems biology. 2015;9:41. doi:10.1186/s12918-015-0187-6.