GeneExpressMap Quickstart Guide

Getting Started
Requirements
GeneExpressMap is a MATLAB GUI application and as such requires a working installation of MATLAB

Installation
Click the "Download Source" button above and extract the archive into a folder of your choosing. Start MATLAB and change its working directory to the folder in which you have extracted the downloaded archive. At the MATLAB prompt, type "GeneExpressMap" to begin!

Example Run
Loading data sets
On opening, GeneExpressMap displays four empty image windows on the right side of the GUI as well a set of processing buttons and settings on the left side. GeneExpressMap is designed to operate on three sets of data per experiment. The first data set is a nuclear stain, the second and third are fluorescent whole mount *in situ* hybridization (F-WMISH) data sets. To populate the GUI with data, select **Start New Analysis** from the **File** menu and load tif stacks of the appropriate data when prompted. If you wish to analyze a single channel F-WMISH data set, simple select the F-WMISH to be analyzed data twice.

Setting Analysis Parameters
Once the nucleus and FISH data sets are loaded into GeneExpressMap, the default settings for all analysis parameters are set for the GUI. The user must set the **X/Y Resolution** and **Z Resolution** for their data set. These values will be unique to each dataset depending on how the data was acquired. For **Threshold Level**, these settings are calculated for each data set. For all other parameters, the defaults are general settings that have yielded satisfactory results on a variety of data sets. The user may start with these settings and refine them later if desired.

Image Processing
A typical run through GeneExpressMap will next proceed with image thresholding, denoising, and dilation of the data sets in order to produce an overlap between the nuclear stain and F-WMISH signals. These steps are carried about by pressing the threshold, denoise, and dilate buttons as they become active on the left hand side of the GUI.

Nucleus identification and F-WMISH Expression assignment
A model of all nuclei in the data set is next constructed by pressing the **Find Nuclei** button. This constructs a three dimensional model of all nuclei from the the two dimensional stack of processed images in the nuclear stain data set.