



# Brain Mapping Visualization: Computation Contorting and Neuron Selection

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## Abstract

In our current medical technology advances today, our data collection equipments and methods are going far into the microscopic regions to extract necessary information that allow us to have a better understanding of the relationships in the mammalian brain. The dataset of neuroimaging are extracted from the microscope that is mounted to the head of the mouse. The eventual goal of this type of data collection is to gain a deeper understanding of the behaviors in relation to neuron activities. Normally a human task would be to classify images consisting of a single neuron or types of noise or disarray, but with the extraction process of the images, the task can be perplexed because of the imaging optics from the microscope that creates the abnormalities present in the image features. This work describes the automated neuron selection process and extractions of abnormalities from a dataset of over 1000 images that requires processing. The neuron selection process will contain the process that involves matched filtering, image segmentation, and region classification. The abnormalities extraction process will contain an initialization of fitting a 2-D function to the major axis length distribution will result in every pixel in the image to have a value. This function presents us two things: an estimate of the abnormality center and a measure of the expansion caused at each concentric ring around the center. The fitted function will be used to estimate the shape of the imaging surface.

## Neuron Selection Method - Region Classification Method (Part 2)

### Applicable Regions

#### - Template modeling

- Create a window around the brightest pixel
- Determine which of the 25 tiles it will best match
- Normalize each pixel by its time average for the tile
- Filter each tile by corresponding tiles for each image

### Analysis of the Regions (Filter Response)

#### - If Maximum Response is too small

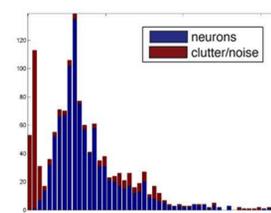


Fig. 2. Distribution of maximum response. Local matched filter: Acceptable images (Blue) Non-neuron images (Red).

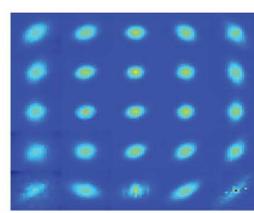


Fig. 3. Local Filters (Neuron Extractions)

### Image Segmentation and Morphological Classification

- Binarize at half maximum brightest pixel
- Checking conditions
  - Area of the foreground
  - Proximity of the brightest image to the edge of the image
- Region classification
- Checking conditions on brightest regions

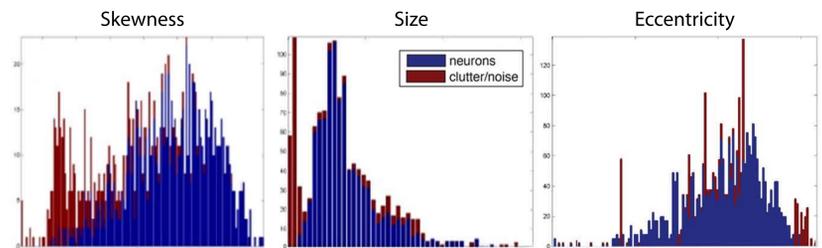
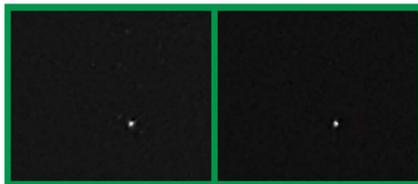


Fig. 4. Distribution of imbalances of region brightness and distribution of the area of the largest region. Local matched filter: Acceptable images (Blue) and non-neuron images (Red).

## Neuron Selection Method (Part 1)

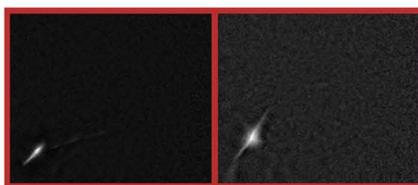
In order to perform the automated process of neuron selections, a creation of a neuron-shaped template to match again each image is the first step. Since abnormalities make neurons look distinct in various parts of the image, the plate will be modified by the location in the image. Matching this criterion will lead to the process of eliminating images that are not neuron-like with the average-neuron filters. A process of binarization and characterization will be implemented on the remaining unfiltered images and regulate images to a series of morphological tests to further eliminate images with other undesirable features.

### Match



### Neurons

### Eliminated



### Blood Vessels

### Eliminated



### Dusts

Fig. 1. Applicable Regions

## Abnormalities Extraction Algorithm

To remove the contorting caused by optical abnormalities, the procedure of characteristics of classified neurons to assess the location of each pixel on the contour imaging surface was determined. In order to start, the first step would be to take the set of all classified neurons and measure the major axis length of each cell. An initialization of fitting a 2-D function to the major axis length distribution will result in every pixel in the image to have a value. This function presents us two things: an estimate of the abnormality center and a measure of the expansion caused at each concentric ring around the center. The fitted function will be used to estimate the shape of the imaging surface. For each concentric ring around the computed center, the estimation of a "expansion factor" by calculating the ratio of the fitted major axis length function along that ring to the fitted major axis length function in the center is to be performed.

- Calculate the distance along the ring by dividing the distance around the ring by expansion factor
- Numerically compute the latitude and longitude of each point
- Checking goodness of the fit
- Find the best function to fit to the major axis length
- Estimation of the 3-D position acquired
- Apply map projection to flatten sphere to a plane with less abnormalities

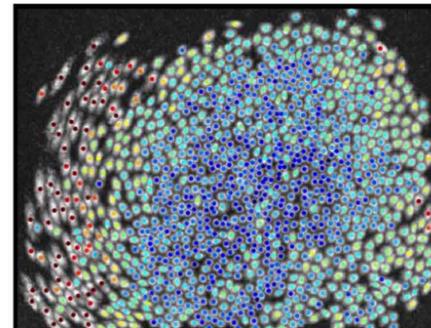


Fig. 5. Abnormality cell map with colored dots correlating to major axis lengths.

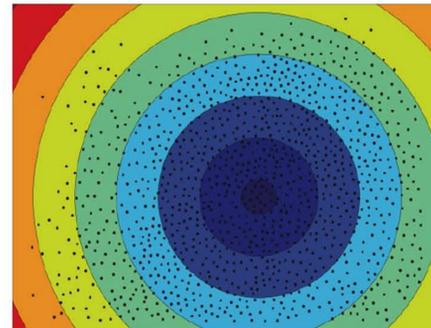


Fig. 6. Conic function fit level sets.

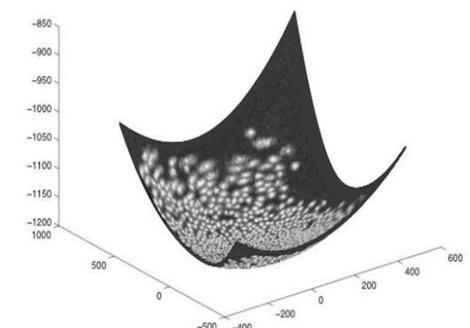


Fig. 7. Cell map projected on the estimated spherical imaging contour.

## Results and Conclusion

In result, the algorithm has an exceptionally low probability of accepting a defective image, while rejecting a tolerable number of effective images. On a dataset of 1300 of applicable images composed by the PCA/ICA, there was a false acceptance rate of 0.3% and false rejection rate of 13%

After the estimation of the 3-D coordinates of all pixels on the imaging surface was acquired existing map projections can be utilized to flatten the spherical surface in a way that improves the shapes of the neurons and does not compile extraneous expansion. Numerous testing of large number of map projections were ran and the most visually appealing results with projections are either azimuthally, projecting from the base to upward, or conic, area of the sphere is projected onto a cone whose vertex is usually above one of the poles, then unrolled onto a flat surface. Several projections were chosen, which were visually pleasing in many ways, and measured their success by calculating the standard deviation of the major axis lengths of the cells in the new projected cell maps. The projection that executed best was the Lambert projection by this measure, a conic projection designed to sustain area. The Lambert projection, however, misconstrue the peripheral view into a different contour. For this logic, a preferable choice to choose an azimuthal projection such as the Wiechel projection, which transform the peripheral view into a more circular contour.

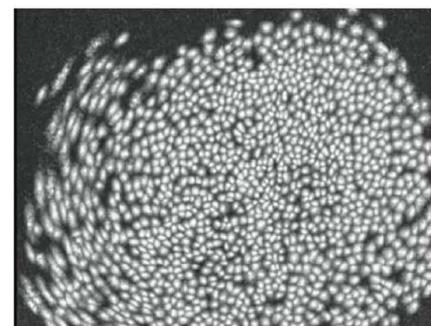


Fig. 8. Original Cell Map

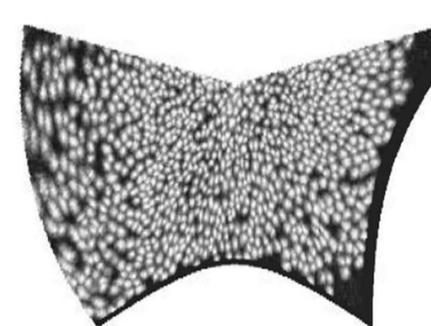


Fig. 9. Lambert Projection

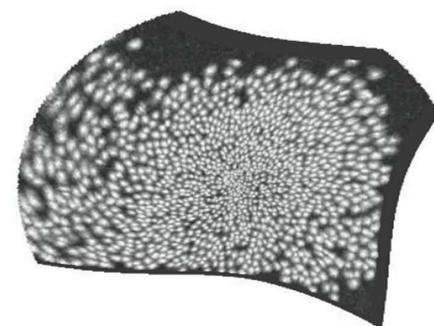


Fig. 10. Wiechel Projection

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