

1. **Glioma Imaging Analysis pipeline based on Histological objects generation, resulting to histogram of Glioma images classification**
2. **A Genomic linkage of DSA-UI may validate this classification of gbm/lgg imaging use case, using mRNA gene expression.**

Pythonic Neuro Image Analysis pipeline to generate object detection

1. Generate random Tiles from selected GBM-SVS slide (grabTiles_forTraining_gbm.py), by doing
 - a). Simple Masking on lowResPILImage
 - b). Getting intended tiles using Girder calls on candygram server
2. Standard Colour deconvolution using HistomicsTK to generate Hematoxylin-stain, Eosin-stain images from the given tile
3. Generate histologic components or histologic objects by quantizing pixels in the above H-Stain and E-Stain channel into following groups (approximation)
 - hp - pixel value in h-channel
 - ep - pixel value in e-channel
 - havg - Average pixel values in h-channel
 - eavg - Average pixel values in e-channel
 - Label pixel p as purple if $hp \leq havg$
 - pink (if $hp > havg$ and $ep \leq eavg$)
 - white if $hp > havg$ and $ep > eavg$

Feature Extraction from the images

In hospitals, biopsies are routinely stained with the hematoxylin-and-eosin technique, which mainly leads to white-like, pink-like, and purple-like pixels. So it is proposed to approximately represent tissue components with circular primitives as the intended objects rather than pixel-domain in this segmentation algorithm.

- a. Purple circular primitive - Cell Nuclei material
 - b. Pink circular primitive - Stroma, Stomal cells' cytoplasms, mucin-poor epithelial cells's cytoplasms
 - c. White circular primitive - Lumina, mucin-rich epithelial cells's cytoplasms
4. Using circle fitting algorithm generate all the possible local histological objects.

https://scipy-cookbook.readthedocs.io/items/Least_Squares_Circle.html

- a. Initially linear algebraic method will be used in implementing circle fitting algorithm

https://dtcenter.org/met/users/docs/write_ups/circle_fit.pdf

Based on algorithm complexity analysis, Graphing methodology will be tried.

5. Using Bag of Words, get the frequency of these objects with the help of k-means and classify tissue images (cancerous vs non-cancerous, gbm vs lgg) using SVM

Referenced publication (Local Object Patterns) has an accuracy 93.03% of representation and classification of pathology images of Colon tissue stained with H&E.

Reference

Image Analysis Pipeline :

1. Local Object Patterns for the Representation and Classification of Colon Tissue Images, Gulden Olgun, Cenk Sokmensuer, and Cigdem Gunduz-Demir, IEEE JOURNAL OF BIOMEDICAL AND HEALTH INFORMATICS, VOL. 18, NO. 4, JULY 2014
2. C.T. Sari and C. Gunduz-Demir, "Unsupervised feature extraction via deep learning for histopathological classification of colon tissue images, IEEE Transactions on Medical Imaging,, May 2019

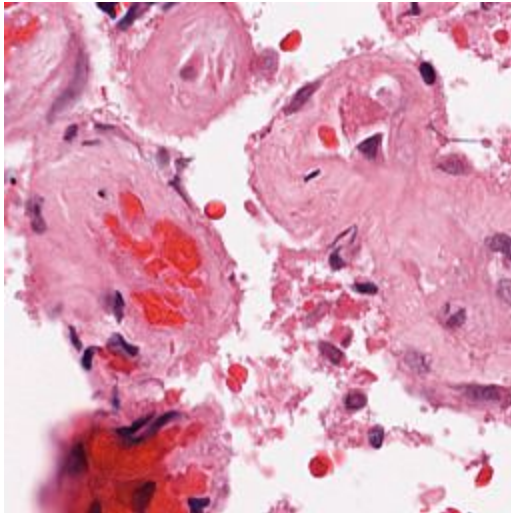
This publication is referenced for Deep Learning

Glioblastoma pathogenesis:

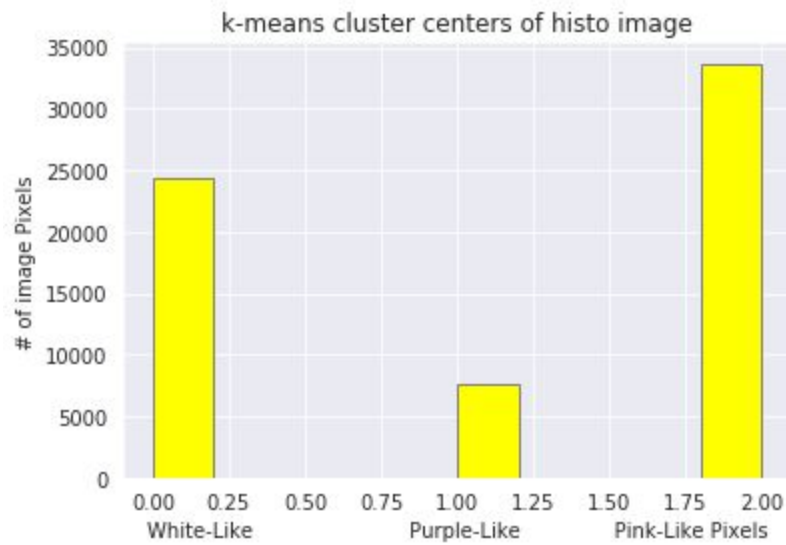
1. Discovery and validation of a glioblastoma co-expressed gene module, Leland J. Dunwoodie¹, William L. Poehlman¹, Stephen P. Ficklin² and Frank Alexander Feltus¹

Sample Tile:

/media/raj/Raj1_5/10ktils/train/gbm/TCGA-02-0001-01Z-00-DX2_20x_7744_32416_256x256.png



After k-means clustering



Largest Object concentration, by applying k-means clustering and circle-fit algorithm

Todo Next: Need to finetune the threshold values and iteratively apply circle-fit , Graph algorithms on all the identified clusters....

