IMAGING MASS SPECTROMETRY IN DETECTING TUMOR HETEROGENEITY

Project Summary

Intratumor heterogeneity is a key factor in tumor progression, affecting patient outcomes and treatment. Tumor subpopulations can be histologically indistinguishable but still have molecular phenotypes that drive tumor progression and determine disease out-come. The identification of the proteins that cause tumor heterogeneity is of utmost importance for understanding cancer development and the management of cancer patients.

Team Members

Ibrahim ElSayed Mostafa Yehia Donia Abd Elsalam Renad Taher Mariem Ahmed Hemasayed600@gmail.com Mustafayehia4@gmail.com Donia.199887@gmail.com Renad.taher12@gmail.com

Mariem.ahmed.1608@gmail.com

Materials and Methods

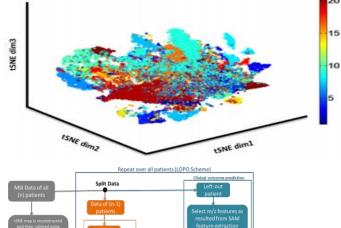
Tumor-specific signatures obtained by protein matrix-assisted laser desorption MSI analysis of primary tumors of gastric cancer (n = 63) and breast cancer (n = 32) were nonlinearly mapped to a 3D space using t-SNE. Using the perceptually linear L*a*b color map to color each pixel according to its position in the t-SNE space. To segment the image into a discrete number of clusters, bisecting k-means and edge-correlation algorithms were applied. The resulting clusters, or tumor subpopulations, were then statistically compared with the patients' clinical data (survival for gastric cancer and lymph node metastasis for breast cancer) to identify the subpopulations statistically associated with patient phenotype. LOPO pixel-based and patient-based classifiers were built to cross-validate the identification of tumor subpopulations and patient outcomes.

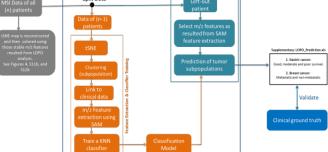
Techniques Used

Mass spectrometry-based proteomics is applied following isolation of the proteins from cell lysates or tissue samples by biochemical fractionation or affinity selection leading to better cancer diagnosis and treatment, we will use one type which is (MALDI).

Machine Learning algorithms to visualize proteins and its peaks in which we will use (t-SNE) technique and then apply component analysis and dimension reduction to better view of data in 2D and in this step we will use (PCA) technique. Analysis of resulted data for each patient and determine which protein causes the two types of cancer which are (Gastric Cancer and Breast Cancer) for better diagnosis and treatment.

Methods Diagram





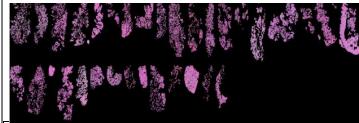


Figure 1: t-SNE Technique

Figure 2: Project Flow using LOPO Cross Validation

Figure 3: Image of All biopsies under microscope

using HE technique

Expertise

- Improving Deep Neural Network (Coursera)
- Neural Network (Coursera)
- Sequence Models (Coursera)
- Introduction to Data Visualization with ggplot2 (Datacamp)
- Machine Learning Foundations: A Case Study Approach (Coursera)
- Front-End Web UI Frameworks and Tools: Bootstrap 4 (Coursera)

- Machine Learning (Andrew Coursera)
- Computer Vision Basics (Coursera)
- Machine Learning with Python (Coursera)
- Embedded Systems
- CNN (Coursera)

Fund Reasons

- 1. Amazon account to access data and deal with it.
- 2. PC with high GPU to apply deep learning and image processing on data or Any laptop with high GPU too.
- 3. Work station (RAM, Hard Disk, Processor ... etc.).