Machine Learning Classifier to Predict Liver and Pancreatic Carcinoma

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Learning Problem and Motivation

- Predict Hepatocellular Carcinoma (HCC) and Pancreatic Adenocarcinoma (PAAD) using DNA methylation and protein expression.

- DNA methylation profile and protein expression are known to be different between cancer and normal cells.

- Potential to be used as effective biomarker indicators for gene targeted treatment.

Existing Research

- Existing work:
  - DNA methylation profile individually
  - Gene expression individually
  - Comparison between DNA methylation and gene expression

- Not much has been done using protein expression in comparison to other biomarkers as an indicator of cancer.

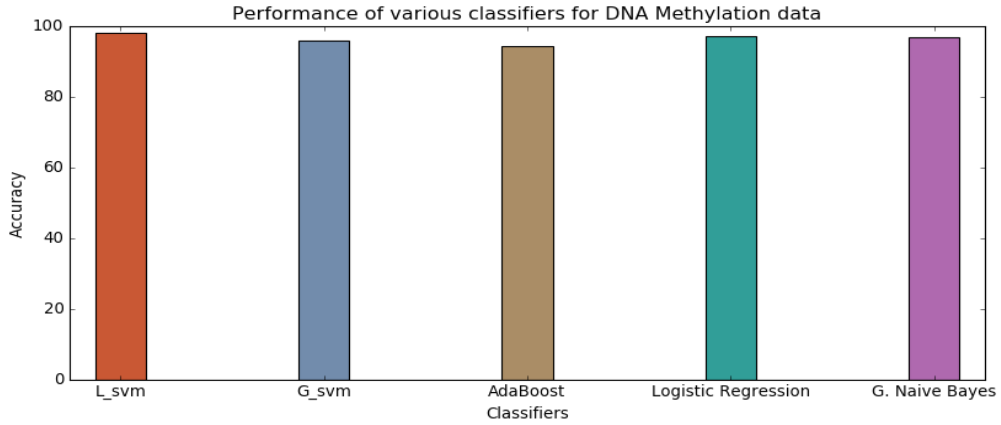
Dataset

- Data from TCGA for HCC and PAAD:
  - DNA methylation (Processed data: ~4GB)
    - 485577 features for both HCC and PAAD
    - 430 samples for HCC
    - 195 samples for PAAD
  - Protein expression (Processed data: ~1MB)
    - 205 overall features for HCC and PAAD
    - 184 samples for HCC
    - 123 samples for PAAD

Pipeline

- Imputation and normalization of data
- K-Means - with 2 and 4 centroid
- Models
  - AdaBoost - on reduced dimension
  - Linear and Gaussian SVM – on reduced dimension
  - Gaussian Naïve Bayes – on full feature set and reduced dimension
  - Logistic Regression – on full feature set and reduced dimension

Comparison of models



Conclusion

- DNA methylation – best model: Linear SVM with 98.09% accuracy
- Protein expression – best model: Gaussian SVM with 93.51% accuracy
- Tradeoff: Accuracy vs Resource Utilization
  - DNA methylation: Higher accuracy – Running Time of ~4 hours – Requires ~4GB data
  - Protein expression: Relatively lower accuracy – Running Time of ~15 minutes – Requires ~1MB data

References

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