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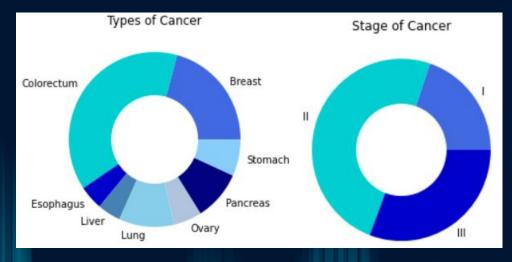
Introduction

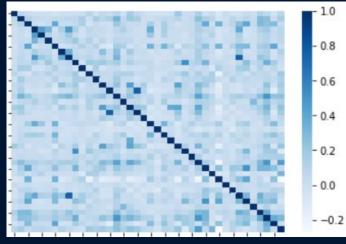
- Early cancer diagnosis and treatment can drastically alter the outcome of the disease
- CancerSeek Algorithm uses DNA and protein analysis on over 1800 blood samples from healthy individuals and cancer patients
 - Created a logistic regression to predict whether a sample was cancerous using a scored number from DNA analysis and 8 protein levels
- Our goal is to improve the prediction algorithms by building our own models
 - We will use an **optimized subset of data** from the dataset (additional protein levels, individual characteristics)
 - We will compare various classification methods (logistic regression, neural networks, random forests)



Data

- 1005 cancer patients, 812 healthy patients
- **Diverse** data (8 types of cancer, 3 stages of cancer, 41 protein biomarkers)





Data + Datasets

Biomarker Data

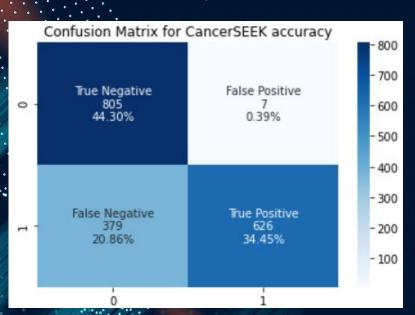
- 41 common protein levels that can be assayed and have known potential link to cancerous phenomena
- Circulating Tumor Mutant DNA
 Score (score of mutant driver genes from tumors found in plasma)

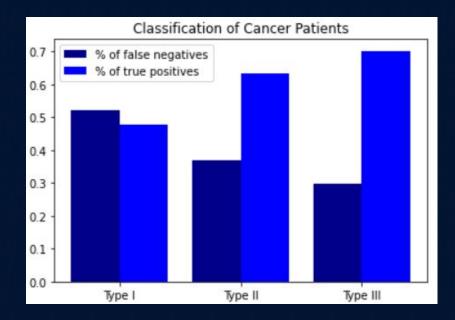
Datasets

- Demographic + Biomarker
 - Age, sex
 - All biomarkers
- Biomarker
 - Just biomarkers
- Replicated Dataset from Paper
 - Subset of 8 proteins and ctDNA score

CancerSEEK Baseline

- CancerSEEK accurately predicts patients **78.8%** of the time
- Specificity of 99.6% and sensitivity of 79.1%
- The accuracy rate for CancerSEEK is proportional to the cancer stage

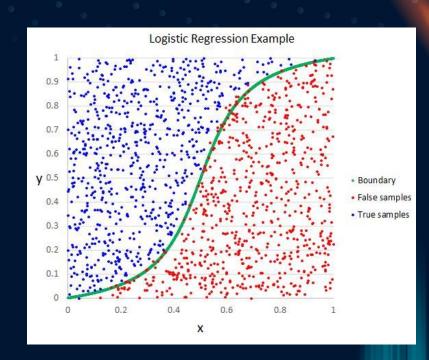




Logistic Regression Model

- Trained with Cross Validation
- Created 3 models:
 - Demographic and Bio Data
 - Bio Data
 - Replicated Data from the original study

- Future Possibilities:
 - Shift the decision boundary
 - Try different kinds of regression (linear)

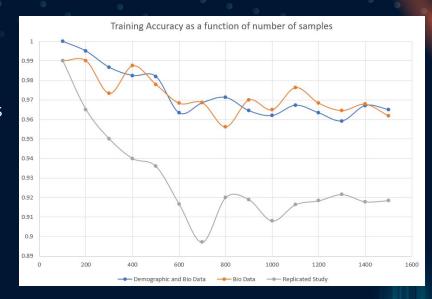


Logistic Regression Results

N = 100 Test Data	Accuracy	Specificity N = 769	Sensitivity N = 948
Demographic and Bio Data	82.9%	84.4%	82.6%
Biological Data	65.1%	31.0%	92.6%
Replicated Study Data	82.9%	84.3%	82.6%

Random Forest Model

- Performed Cross Validation to find the best model
 - Grid Cross Validation to tune the hyper parameters with our Train and Dev sets
- To be further explored:
 - Investigating the decision path for interpretability
 - Analyzing the parameters to see which aspects impact the decisions
 - Improving specificity for RF model



Random Forest Test Accuracy

N = 100 Test Data	Accuracy	Specificity N = 769	Sensitivity N = 948
Demographic and Bio Data	96.4%	94.8%	97.5%
Biological Data	96.3%	95.2%	97.2%
Replicated Study Data	91.5%	92.8%	90.4%

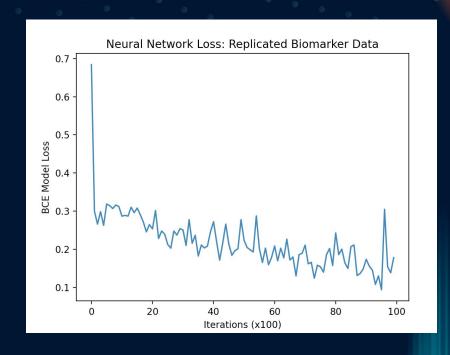
Neural Network Model

Model Structure

- 2-Hidden Layer NN with Dropout
 - ReLu and PReLu Activation
- Hidden Layer Widths = 100
- LR = .005
- Dropout Rate = 0.2
- Epochs = 4000

Next Steps

 Further hyperparameter tuning (structure, rates, etc.)



Neural Network

N = 600 Test Data	Accuracy	Specificity (n = 274)	Sensitivity (n = 326)
Demographic and Bio Data	88.5%	99.3%	79.4%
Bio Data	86.0%	98.2%	75.8&
Replicated Study Data	75.7%	97.8%	57.1%

Model Evaluation

- Logistic Regression
 - Baseline
 - Worst accuracy, worst specificity
- Random Forest
 - Best performing model
 - High accuracy (96%), specificity O.K. (94%) but lower than
 clinical-grade specificity requirements for diagnostics
- Neural Networks
 - Good performance overall
 - Very high specificity, can improve on sensitivity

Next Steps

- Continue tuning models
 - Change size of neural network
 - Tune hyper-parameters (e.g. shift logistic regression)
- Potentially try linear regression
- Interpretability analysis
 - How did our models go wrong?
 - How can they be improved?

Update on Deliverables

- Must accomplish
 - Logistic Regression ✔
 - Neural Network
 - AdaBoost, Random Forests
- Expect to accomplish
 - Advanced Data Pre-Processing
 - Interpretability Analysis
 - Multi-Class Classification of Cancer Type
- Would like to accomplish
 - High Specificity
 - Additional Data
 - Cancer Localization

Feedback?