Testing Statistical Models to Improve Screening of Lung Cancer

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Background

- Over 1 in 4 cancer deaths in the US
- Early-stage detection improves prognosis
- **CT** Scans
- National Lung Screening Trial (NLST)



CT screening detects more early-stage cancers



- CT Scans have a False Positive Rate of 96.4%
- False positives may require invasive procedures to resolve the diagnosis



Overview – Data Collection

- Radiomic features quantified characteristics of tumor/nodule
- Process
 - Image segmentation nodule and parenchyma
 - Feature extraction summary statistics of the following:
 - Intensity
 - Shape
 - Border
 - Texture



Overview – Data Analysis

- Goal: Use radiomic features to improve classification of nodule
- Supervised machine learning
 - Variables

- Input:144 radiomic variables and 2 clinical variables
- Output: Cancer status Malignant or Benign
- 4 models
- Use Cross Validation to estimate predictive performance
- Compare the area under the ROC curve for each combination of tuning parameter(s)

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Data Summary

Variable		Value
Number of Subjects		198 (100%)
	Benign	89 (44.9%)
	Malignant	109 (55.1%)
Clinical Variables		8
	Age (years)	Mean = 59.93 sd = 13.77
	Pack Years	Mean = 26.39 sd = 29.11
Radiomic Variables		144

Cross Validation (CV)

Used to estimate predictive performance

Process (3-Fold CV):

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Protects against "over-fitting" a model

 To improve estimation, we chose to use 10-Fold CV repeated 10 times

Model 4 - Artificial Neural Network

- Thought of as a "black box" inspired by the brain
- Tuning Parameter: number of hidden units
- Hard to interpret
- ROC = 0.79



Model 3– Partial Least Squares

- Linear regression model with fewer variables
 - Orthogonal linear combinations of predictor variables
 - Dimensions are reduced
- Tuning Parameter: number of components
- Hard to interpret
- Continuous outcomes...
- ROC = 0.80

Model 2 – Stochastic Gradient Boosting

- Uses many binary trees
- Final decision based on majority rule
 - (Ties broken at random)
- Variable selection at each node
- Tuning parameters: number of trees, height of tree
- ROC = 0.83



Model 1 – Elastic Net Penalized Logistic Regression

Binomial model is represented by

- $= \log \frac{\Pr(Diagnosis=1 | X=x)}{\Pr(Diagnosis=0 | X=x)} = \beta_0 + \beta^T x$
 - G = {0, 1} where 0 is Benign and 1 is Malignant
 - X is vector of input variables
 - β is vector of coefficients
- Objective function

$$\min_{(\beta_0,\beta)\in\mathbb{R}^{p+1}} \left\{ -\left[\frac{1}{N} \sum_{i=1}^N y_i \cdot \left(\beta_0 + x_i^T \beta\right) - \log(1 + e^{(\beta_0 + x_i^T \beta)}) \right] + \lambda \left[(1-\alpha) \frac{1}{2} \sum_{j=1}^p \beta_j^2 + \alpha \frac{1}{2} \sum_{j=1}^p |\beta_j| \right] \right\}$$

Ridge vs Lasso

Variability vs Bias

11 Elastic Net Penalized Logistic Regression – Optimization



Tuning parameters

- Mixing percentage(α)
- Regularization parameter(λ)

Optimal Performance

 $- \alpha = 0.94$

$$\lambda = 0.03$$

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Tuning parameters

- Mixing percentage(α)
- Regularization parameter(λ)

Optimal Performance

- $\alpha = 0.94$
- $\lambda = 0.03$
- ROC = 0.84

Elastic Net Penalized Logistic Regression – Equation

 $\log \frac{\Pr(Diagnosis = 1 | X = x)}{\Pr(Diagnosis = 0 | X = x)}$

= 0.299

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+ 0.993PackYears

+0.764*Age*

- 0.217PhysSphComp5
- + 0.213NodeFeat6
- + 0.191PhysSphComp6
- 0.189PhysSphComp3
- + 0.157X2DKurtNod3
- + 0.085NodeFeat7
- + 0.048X2DVarSurrTiss5
- + 0.002NodeFeat3



Importance

Elastic Net Penalized Logistic Regression – Variables



Summary

- Models were based on 146 measurements from 198 subjects at the University of Iowa Hospital
 - Clinical variables had a large impact
 - Both nodule and parenchyma features had an impact
- All of our models had similar performance despite design differences
 - ROC between 0.79 and 0.84
 - Approach from uninterpretable black box to a collection of binary trees to logistic regression
- Elastic net model performance
 - Reduced false positive rate (23.6%)
 - At the expense of sensitivity (70.6%)

Future Work

- Set a threshold for false negative then minimize the false positive
- Study the impact of changing the population on the performance of this model
 - Adults aged 55-80 with a history of smoking
 - Multicenter
 - Across US vs. global
 - Beyond academic medical institutions
- Use model to differentiate between types of lung cancer
 - Histology-based
 - Molecular subsets



References

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