CLINICAL PREDICTION MODELS

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COPRH Con

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OUTLINE

- The Modelling Process
- Building Prediction Models
- Assessment and Validation



"This just isn't doing it for me. Could we go back to using the crystal ball?"



MODELLING PROCESS

• Plan

- o Identify goal
- o Assemble the data
- o Handle data issues

• Build

- o Identify model/technique
- o Identify metrics for assessment
- o Internal validation
- o External validation

Implement

- o Identify outputs
- o Make model available
- \circ $\,$ Continued monitoring $\,$







PLAN: SCOPE

- **Goal:** "Predict Prostate cancer specific mortality (PCSM) in patients with prostate cancer"
 - PCSM or Overall Survival?

• Existing literature:

- AJCC criteria for prediction models
- \circ $\,$ Alternative prediction models and methods $\,$
- \circ What is the gap?





PLAN: PREPARE

• Data: Obtained patient data from 10 centers (n=~20,000)

Data issues:

- Missing data: To impute or not?
- Variable coding
- o Inconsistencies

• Training and Validation:

- Split based on center?
- Random split?
- Percentage split?

Transparency

- Circulate model building plan
- Hold validation data externally



BUILD

- Model/Technique
- Assess
- Validate



"The boss wants me to create a computer algorithm that can convert hindsight into foresight."



BUILD: MODEL/TECHNIQUE

- Regression Methods (stepwise, penalized)
- Tree-based Methods
- Random Forest
- Other methods
 - o Neural nets
 - Deep learning
 - Support Vector Machines
 - \circ Boosting



Regression Methods

Stepwise

• Penalized regression (Lasso, Ridge, Elastic net)

Advantages:

- Good prediction (all penalized regression methods)
- Variable selection and prediction (Lasso and Elastic net)

Disadvantages

- No variable selection (Ridge)
- o Inference is more difficult





Tree-based Methods

Algorithm:

- Start will all patients in top node
- For every variable, evaluate every possible binary split
- Choose the best variable/threshold combination
- Repeat for all terminal nodes until no split is possible
- Stop when terminal node size is too small





Tree-based Methods

• Advantages:

- o Simple, easy to understand and use
- Naturally identify thresholds (when they exist, which is not always)
- Naturally identify interactions

• Disadvantages:

- \circ Poor prediction
- Unstable (small changes to the data can result in large changes to the tree)





- A forest is comprised of many trees
- "Ensemble" method

Advantages:

- Can be used for both regression and classification tasks
- Easy to view relative importance of input variables
- Won't overfit (with enough trees)

• Disadvantages:

- Very slow with large number of trees
- o Ineffective for real-time predictions
- \circ Not a descriptive tool



Variable Importance



- 1. The size, quality, nature of your data
- 2. What you want to do with your data
- 3. The available computation time
- Match the method to your goal
- Goal: Parsimonious model
 - Method: Lasso (NOT Ridge or Random Forest)
- Goal: Interpretable model
 - **Method:** Elastic net, Survival Tree, Regression
- Choice of model can be less important than getting the basics right (confounding, censoring, etc.)



BUILD: ASSESS

- Identify the metrics to assess predictive performance
- Discrimination
 - Area under the ROC curve (AUC), Concordance-index (C-index)
- Calibration
 - o Calibration plots

Overall measures of prediction error

- o Brier Score
- Provide comparison
 - To null model (with no covariates)
 - o To alternate models



BUILD: VALIDATE

- Apparent: Performance of model on data used to develop the model
 - Will get optimistic estimates of performance
- Internal: Performance on population underlying the sample ("reproducibility")
 - Test/training set, cross-validation, bootstrap
- External: Performance on related but slightly different population
 - o Different centers, years, therapies, variable definitions



IMPLEMENT: OUTPUTS

- Nomograms
- Point estimates
- Tree-based methods
- Score charts
- Web-based applications (R Shiny apps)



IMPLEMENT: DEPLOY & MONITOR



R Shiny App (Small Cell Lung Cancer)

Input parameters	Kaplan Meier estimator
Age (0 <= value <= 120)	risk score = 10.85
50	ç –
Gender	ä –
Male	tili 8 .
Race	
White v	
Spanish Origin?	0 - 0 -
FALSE T	° -
Charison/Deyo Score	0 20 40 60 80 100 120
0	Time (Months)
AJCC V8 TNM Stage	Time (Months) Survival Probability
AJCC V8 TNM Stage	Time (Months) Survival Probability 0 1
AJCC V8 TNM Stage IA Surgery?	Time (Months)Survival Probability0160.729
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AJCC V8 TNM Stage IA Surgery? No Surgery Chemotherapy?	Time (Months)Survival Probability0160.729120.486240.234
AJCC V8 TNM Stage IA Surgery? No Surgery Chemotherapy? No Chemo	Time (Months) Survival Probability 0 1 6 0.729 12 0.486 24 0.234 36 0.148
AJCC V8 TNM Stage IA V Surgery? Chemotherapy? No Chemo V	Time (Months) Survival Probability 0 1 6 0.729 12 0.486 24 0.234 36 0.148 48 0.109
AJCC V8 TNM Stage IA ▼ Surgery? ▼ No Surgery ▼ Chemotherapy? ▼ Radiation Therapy? ▼	Time (Months) Survival Probability 0 1 6 0.729 12 0.486 24 0.234 36 0.148 48 0.109 60 0.081
AJCC V8 TNM Stage IA ▼ Surgery? ▼ No Surgery ▼ Chemotherapy? No Chemo ▼ Radiation Therapy? No Radiation	Time (Months) Survival Probability 0 1 6 0.729 12 0.486 24 0.234 36 0.148 48 0.109 60 0.081 72 0.061
AJCC V8 TNM Stage IA V Surgery? No Surgery V Chemotherapy? No Chemo V Radiation Therapy? Laterality	Time (Months) Survival Probability 0 1 6 0.729 12 0.486 24 0.234 36 0.148 48 0.109 60 0.081 72 0.061 84 0.046
AJCC V8 TNM Stage IA ▼ Surgery? ▼ No Surgery ▼ Chemotherapy? ▼ No Chemo ▼ Radiation Therapy? ▼ No Radiation ▼ Laterality ▼ Not a paired site ▼	Time (Months) Survival Probability 0 1 6 0.729 12 0.486 24 0.234 36 0.109 48 0.109 60 0.081 72 0.061 84 0.046 96 0.035

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SUMMARY



