Machine Learning for Healthcare HST.956, 6.S897

Lecture 5: Risk stratification (continued)

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Course announcements

- Recitation Friday at 2pm (4-153) optional
- PS1 due tonight; PS2 out Tuesday

Outline for today's class

- 1. Risk stratification (continued)
 - Deriving labels
 - Evaluation
 - Subtleties with ML-based risk stratification
- 2. Survival modeling

Where do the labels come from?



Typical pipeline:

- 1. Manually label several patients' data by "chart review"
- 2. A) Come up with a simple rule to automatically derive label for all patients, **or**

B) Use machine learning to get the labels themselves

Step 1:

Visualization of individual patient data is an important part of chart review



https://github.com/nyuvis/patient-viz

Figure 1: Algorithm for identifying T2DM cases in the EMR.



Source: https://phekb.org/sites/phenotype/files/T2DM-algorithm.pdf

Step 2: Example of a rule-based phenotype

https://www.phekb.org/phenotypes?field_pgx_type_tid_1=398&field_data_model_value=All Login | Request Account PheK a knowledgebase for discovering phenotypes from electronic medical records Search Home Phenotypes Resources Contact Us ᢙ Public Phenotypes Public Collaboration Public phenotypes are believed to be complete and final by their authors. When you are logged in you can view and edit phenotypes in your groups that are non public and in various stages of development. Login To View Private Group Phenotypes Institution Type of Phenotype Owner Phenotyping Groups View Phenotyping Groups Disease or Syndrome -- Þ Data Model Apply - Any --Data Modalities Hae Owner Title Institution and Methods View Groups Phenotyping new Status Type Used Groups content eMERGE Geisinger eMERGE Disease Abdominal Aortic Group, CPT Codes, ICD 9 20 Geisinger Geisinger Final or Aneurysm (AAA) Codes, Vital Signs eMERGE Group Syndrome Phenotype WG ICD 9 Codes, eMERGE Disease ADHD phenotype Medications, eMERGE CHOP Phenotype Final or algorithm Natural Language CHOP Group WG Syndrome Processing CPT Codes, ICD 9 eMERGE eMERGE Disease Codes, Cincinnati Children's Hospital Appendicitis Medications, CCHMC/BCH Phenotype Final or Medical Center Natural Language Group WG Syndrome Processing CPT Codes, ICD 9 Vanderbilt -Disease Vanderbilt -Atrial Fibrillation -Codes, Natural Vanderbilt University SD/RD Final or Demonstration Project Language SD/RD Group Group Syndrome Processing ICD 9 Codes. eMERGE eMERGE Disease Cincinnati Children's Hospital Medications, 3 Autism CCHMC/BCH Phenotype Final or Medical Center Natural Language Group WG Syndrome Processing CPT Codes, ICD 9 eMERGE eMERGE Disease Codes, Marshfield Clinic Research Cataracts Medications, Marshfield Phenotype Final or Foundation Natural Language Group Syndrome WG Processing ICD 9 Codes, Vanderbilt -Disease Medications, Vanderbilt -Crohn's Disease -00/00

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Receiver-operator characteristic curve



Receiver-operator characteristic curve



Receiver-operator characteristic curve

Calibration (note: different dataset)

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Non-stationarity: Diabetes Onset After 2009

→ Automatically derived labels may change meaning

[Geiss LS, Wang J, Cheng YJ, et al. Prevalence and Incidence Trends for Diagnosed Diabetes Among Adults Aged 20 to 79 Years, United States, 1980-2012. JAMA, 2014.]

Non-stationarity: Top 100 lab measurements over time

Time (in months, from 1/2005 up to 1/2014)

→ Significance of features may change over time

[Figure credit: Narges Razavian]

Non-stationarity: ICD-9 to ICD-10 shift

→ Significance of features may change over time

[Figure credit: Mike Oberst]

Re-thinking evaluation in the face of non-stationarity

- How was our diabetes model evaluation flawed?
- Good practice: use test data from a future year:

- Example from today's readings:
 - Patients with pneumonia who have a history of asthma have lower risk of dying from pneumonia
 - Thus, we learn: HasAsthma(x) => LowerRisk(x)
- What's wrong with the learned model?
 - Risk stratification drives interventions
 - If low risk, might not admit to ICU. But this was precisely what prevented patients from dying!

[Caruana et al., Intelligible Models for Healthcare: Predicting Pneumonia Risk and Hospital 30day Readmission. KDD 2015.]

• Formally, this is what's happening:

- How do we address this problem?
- First and foremost, must recognize it is happening

 interpretable models help with this

- Hacks:
 - Modify model, e.g. by removing the HasAsthma(x) => LowerRisk(x) rule I do not expect this to work with highdimensional data
 - 2. Re-define outcome by finding a pre-treatment surrogate (e.g., lactate levels)
 - 3. Consider treated patients as **right-censored** by treatment

Example:

Henry, Hager, Pronovost, Saria. A targeted real-time early warning score (TREWScore) for septic shock. *Science Translation Medicine*, 2015

• The rigorous way to address this problem is through the language of **causality**:

Will admission to ICU lower likelihood of death for patient?

• We return to this in Lecture 14

No big wins from deep models on structured data/text

1

2

Health systems collect and store electronic health records in various formats in databases.

All available data for each patient is converted to events recorded in containers based on the Fast Healthcare Interoperability Resource (FHIR) specification. Rajkomar et al., Scalable and accurate deep learning with electronic health records. *Nature Digital Medicine*, 2018

Recurrent neural network & attentionbased models trained on 200K hospitalized patients

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The FHIR resources are placed in temporal order, depicting all events recorded in the EHR (i.e. timeline). The deep learning model uses this full history to make each prediction.

No big wins from deep models on structured data/text

Supplemental Table 1: Prediction accuracy of each task of deep learning model compared to baselines

	Hospital A	Hospital B	
Inpatient Mortality, AUROC ¹ (95% CI)			
Deep learning 24 hours after admission	0.95 (0.94-0.96)	0.93 (0.92-0.94)	Comparison
Full feature enhanced baseline at 24 hours after admission	$0.93(0.92 ext{-}0.95)$	0.91(0.89-0.92)	to Razavian
Full feature simple baseline at 24 hours after admission	$0.93(0.91 ext{-}0.94)$	0.90(0.88-0.92)	et al. '15
Baseline ($aEWS^2$) at 24 hours after admission	$0.85(0.81 ext{-} 0.89)$	$0.86(0.83 ext{-}0.88)$	
30-day Readmission, AUROC (95% CI)			
Deep learning at discharge	0.77 (0.75-0.78)	0.76 (0.75-0.77)	
Full feature enhanced baseline at discharge	$0.75(0.73 extrm{-}0.76)$	$0.75(0.74 ext{-} 0.76)$	
Full feature simple baseline at discharge	0.74(0.73- $0.76)$	$0.73(0.72 ext{-} 0.74)$	
Baseline $(mHOSPITAL^3)$ at discharge	0.70(0.68-0.72)	$0.68(0.67 ext{-}0.69)$	
Length of Stay at least 7 days AUROC (95% CI)			_
Deep learning 24 hours after admission	0.86 (0.86-0.87)	0.85 (0.85-0.86)	
Full feature enhanced baseline at 24 hours after admission	0.85(0.84 - 0.85)	$0.83(0.83 ext{-} 0.84)$	
Full feature simple baseline at 24 hours after admission	$0.83(0.82 ext{-} 0.84)$	0.81(0.80-0.82)	-
Baseline (mLiu ⁴) at 24 hours after admission	0.76(0.75-0.77)	0.74(0.73-0.75)	

[Rajkomar et al. '18 electronic supplementary material: https://static-content.springer.com/esm/art%3A10.1038%2Fs41746-018-0029-1/MediaObjects/41746_2018_29_MOESM1_ESM.pdf]

No big wins from deep models on structured data/text

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Full feBaselinKeep in mind:30-daSmall wins with deep models may disappearDeep 1Small wins with deep models may disappearPull fealtogether with dataset shift or non-stationarityBaselin(Jung & Shab, JBI (15))						
Lengt Deep learning 24 hours after admission Full feature enhanced baseline at 24 hours after admission Full feature simple baseline at 24 hours after admission Baseline (mLiu ⁴) at 24 hours after admission	0.86 (0.86-0.87) 0.85 (0.84-0.85) 0.83 (0.82-0.84) 0.76 (0.75-0.77)	0.85 (0.85-0.86) 0.83 (0.83-0.84) 0.81 (0.80-0.82) 0.74 (0.73-0.75)				

[Rajkomar et al. '18 **electronic supplementary material**: https://static-content.springer.com/esm/art%3A10.1038%2Fs41746-018-0029-1/MediaObjects/41746_2018_29_MOESM1_ESM.pdf] No big wins from deep models on structured data/text – why?

- Sequential data in medicine is very different from language modeling
 - Many time scales, significant missing data, and multi-variate observations
 - Likely *do exist* predictive nonlinear interactions, but subtle
 - Not enough data to naively deal with the above two
- Medical community has already come up with some very good features

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Survival modeling

• We focus on <u>right-censored</u> data:

[Wang, Li, Reddy. Machine Learning for Survival Analysis: A Survey. 2017]

Survival modeling

- Why not use classification, as before?
 - Less data for training (due to exclusions)
 - Pessimistic estimates due to choice of window
- What about regression, e.g. minimizing meansquared error?
 - T is non-negative, may want long tails
 - If we just naively removed censored events, we would be introducing bias

Notation and formalization

- Data are (x, T, b)=(features, time, censoring), where b=0,1 denotes whether time is of censoring or event occurrence
- Let f(t) = P(t) be the probability of death at time t
- Survival function: the probability of an individual surviving beyond time *t*,

$$S(t) = P(T > t) = \int_{t}^{\infty} f(x)dx$$

[Ha, Jeong, Lee. Statistical Modeling of Survival Data with Random Effects. Springer 2017]

Notation and formalization

Fig. 2: Relationship among different entities f(t), F(t) and S(t). [Wang, Li, Reddy. Machine Learning for Survival Analysis: A Survey. 2017]

Kaplan-Meier estimator

 Example of a non-parametric method; good for unconditional density estimation

Observed event times $y_{(1)} < y_{(2)} < \cdots < y_{(D)}$

- $d_{(k)}$ = # events at this time
- $n_{(k)} = #$ of individuals alive and uncensored

$$\widehat{S}_{K-M}(t) = \prod_{k:y_{(k)} \le t} \left\{ 1 - \frac{d_{(k)}}{n_{(k)}} \right\}$$

[Figure credit: Rebecca Peyser]

Maximum likelihood estimation

• Commonly parametric densities for f(t):

Distribution		Survival function $S(t)$	Density function $f(t)$
Exponential ($\lambda > 0$)		$\exp(-\lambda t)$	$\lambda \exp(-\lambda t)$
Weibull $(\lambda, \phi > 0)$		$\exp(-\lambda t^{\phi})$	$\lambda \phi t^{\phi-1} \exp(-\lambda t^{\phi})$
Log-normal $(\sigma > 0, \mu \in R)$	(parameters can be a	$1 - \Phi\{(\ln t - \mu)/\sigma\}$	$\varphi\{(\ln t - \mu)/\sigma\}(\sigma t)^{-1}$
Log-logistic $(\lambda > 0, \phi > 0)$	function of x)	$1/(1+\lambda t^{\phi})$	$(\lambda\phi t^{\phi-1})/(1+\lambda t^{\phi})^2$
Gamma ($\lambda, \phi > 0$)		$1 - I(\lambda t, \phi)$	$\{\lambda^{\phi}/\Gamma(\phi)\}t^{\phi-1}\exp(-\lambda t)$
$\begin{array}{l} \text{Gompertz} \\ (\lambda, \phi > 0) \end{array}$		$\exp\{\frac{\lambda}{\phi}(1-e^{\phi t})\}$	$\lambda e^{\phi t} \exp\{\frac{\lambda}{\phi}(1-e^{\phi t})\}$

Table 2.1 Useful parametric distributions for survival analysis

[Ha, Jeong, Lee. Statistical Modeling of Survival Data with Random Effects. Springer 2017]

Maximum likelihood estimation

• Two kinds of observations: censored and uncensored

Uncensored likelihood

$$p_{\theta}(T=t \,|\, \mathbf{x}) = f(t)$$

Censored likelihood

$$p_{\theta}^{\text{censored}}(t \mid \mathbf{x}) = p_{\theta}(T > t \mid \mathbf{x}) = S(t)$$

• Putting the two together, we get:

$$\sum_{i=1}^{n} b_i \log p_{\theta}^{\text{censored}}(t | \mathbf{x}) + (1 - b_i) \log p_{\theta}(t | \mathbf{x})$$

Optimize via gradient or stochastic gradient ascent!

Evaluation for survival modeling

 Concordance-index (also called C-statistic): look at model's ability to predict *relative* survival times:

$$\hat{c} = \frac{1}{num} \sum_{i:b_i = 0} \sum_{j:y_i < y_j} I[S(\hat{y}_j | X_j) > S(\hat{y}_i | X_i)]$$

• Illustration – blue lines denote pairwise comparisons:

• Equivalent to AUC for binary variables and no censoring

[Wang, Li, Reddy. Machine Learning for Survival Analysis: A Survey. 2017]

Final thoughts on survival modeling

- Could also evaluate:
 - Mean-squared error for uncensored individuals
 - Held-out (censored) likelihood
 - Derive binary classifier from learned model and check calibration
- Partial likelihood estimators (e.g. for coxproportional hazards models) can be much more data efficient