Topics in Machine Learning
Machine Learning for Healthcare

Rahul G. Krishnan
Assistant Professor
Computer science & Laboratory Medicine and Pathobiology

Last week

- Supervised machine learning
- Risk stratification
  - Stratification as a prediction problem
  - **Case study:** Predicting the onset of diabetes

Outline

- Clarification to questions
- Risk stratification
  - Deriving labels
  - Evaluating models
- Survival analysis:
  - From binary to continuous valued outcomes
  - Parametric
  - Non-parametric
  - Semi-parametric

Questions from last week

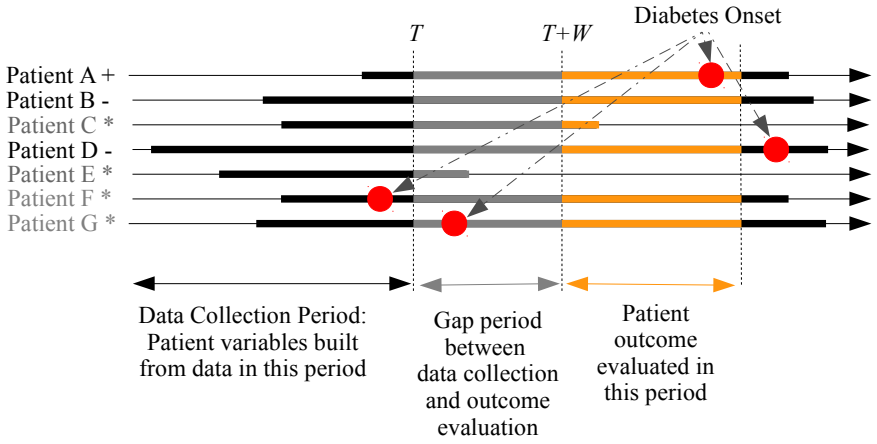
- Is there structure among diagnosis codes:
  - Yes! They are organized in a hierarchy. View ICD10 codes here

    ICD-10-CM Codes › E00-E89 Endocrine, nutritional and metabolic diseases › E08-E13 Diabetes mellitus › Type 2 diabetes mellitus E11

    Type 2 diabetes mellitus E11-

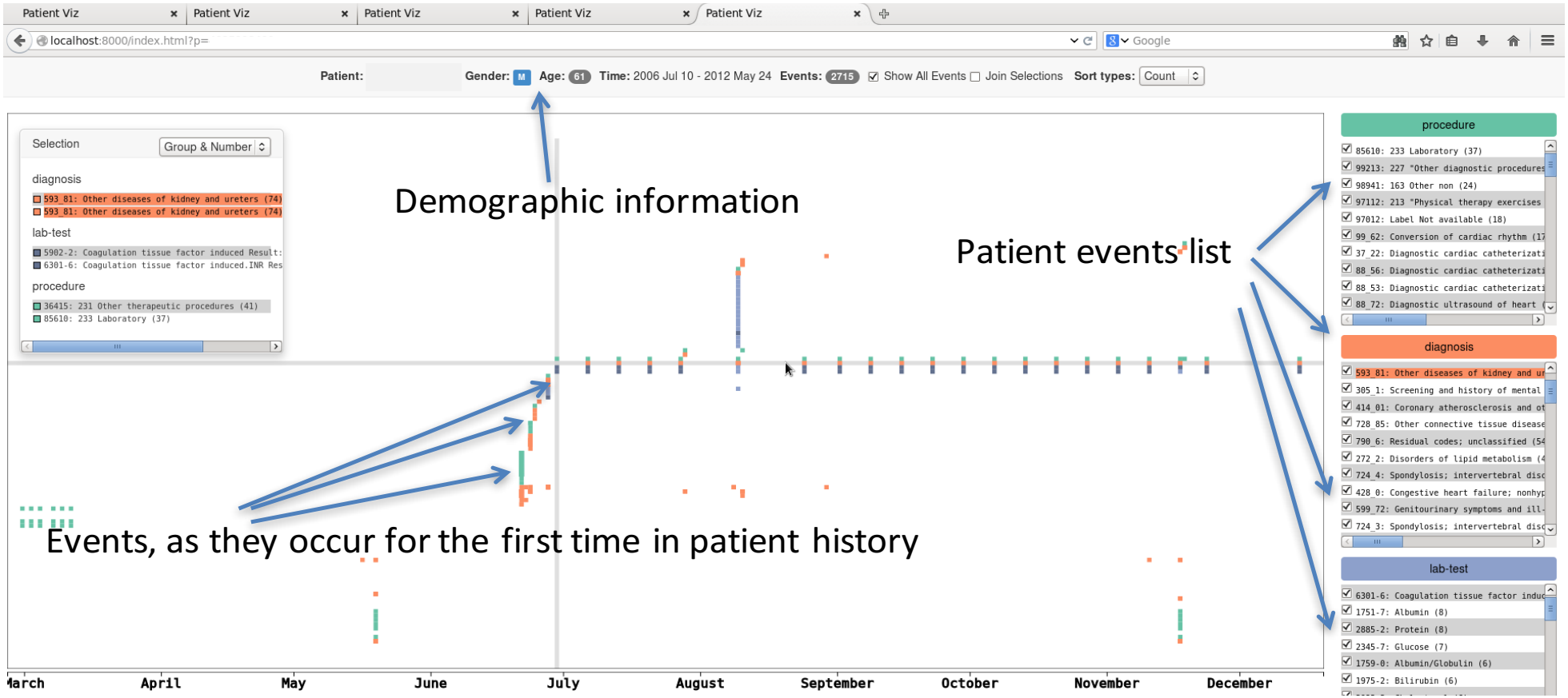
- Using predictive models in the future (on different data):
  - Non-stationarity of data is a challenging problem
    - Means that data distribution changes in unpredictable ways over time
  - Covariate shift can tank good machine learning models deployed in clinics
  - Still a lot of research on good techniques for detection of covariate shift

Deriving labels for risk stratification



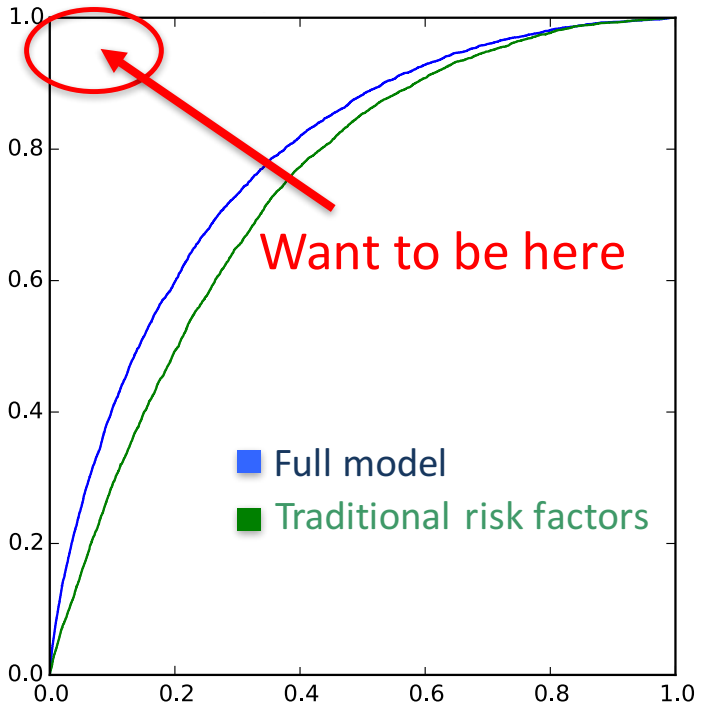
- Typically done via chart review
- Work with doctor to assess criteria that constitute **Diabetic Onset**
  - e.g. does the patient have ICD10 code for diabetes

Evaluation of risk stratification models



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

Evaluation of risk stratification models



Diabetes
1-year gap

AUC = Area under the ROC curve

- Invariant to class imbalance
- Interpretable as the probability that an algorithm ranks a positive patient over a negative patient

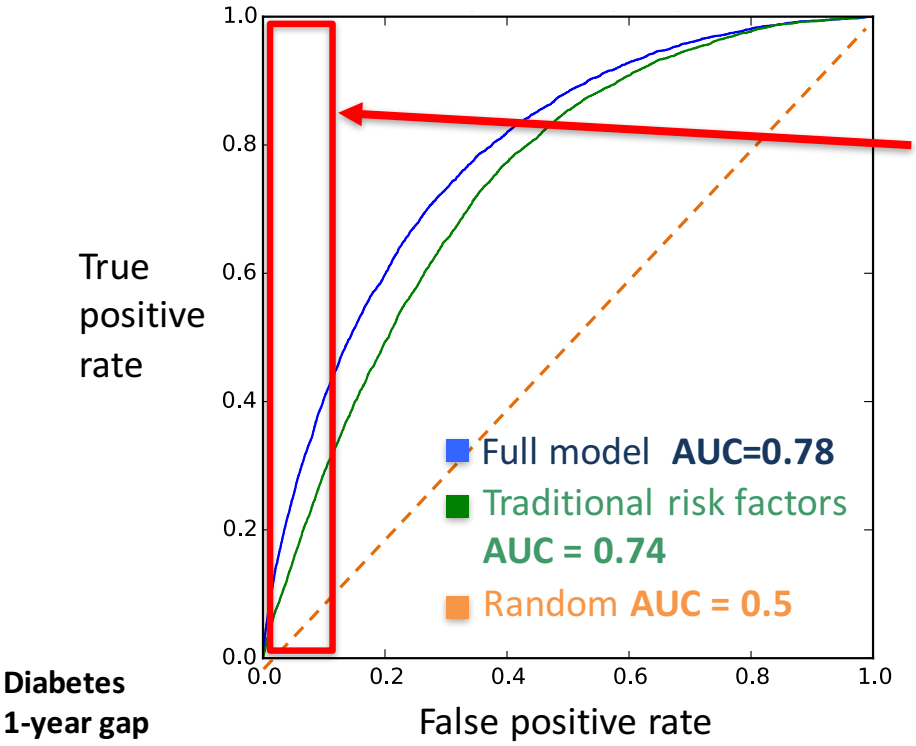
$$TPR = \frac{TP}{Actual\ Positive} = \frac{TP}{TP + FN}$$

$$FNR = \frac{FN}{Actual\ Positive} = \frac{FN}{TP + FN}$$

$$TNR = \frac{TN}{Actual\ Negative} = \frac{TN}{TN + FP}$$

$$FPR = \frac{FP}{Actual\ Negative} = \frac{FP}{TN + FP}$$

Where you want to be on ROC curve



Risk stratification usually focuses on just this region

(because of the cost of interventions)

Diabetes
1-year gap

Many other important statistical considerations when building models

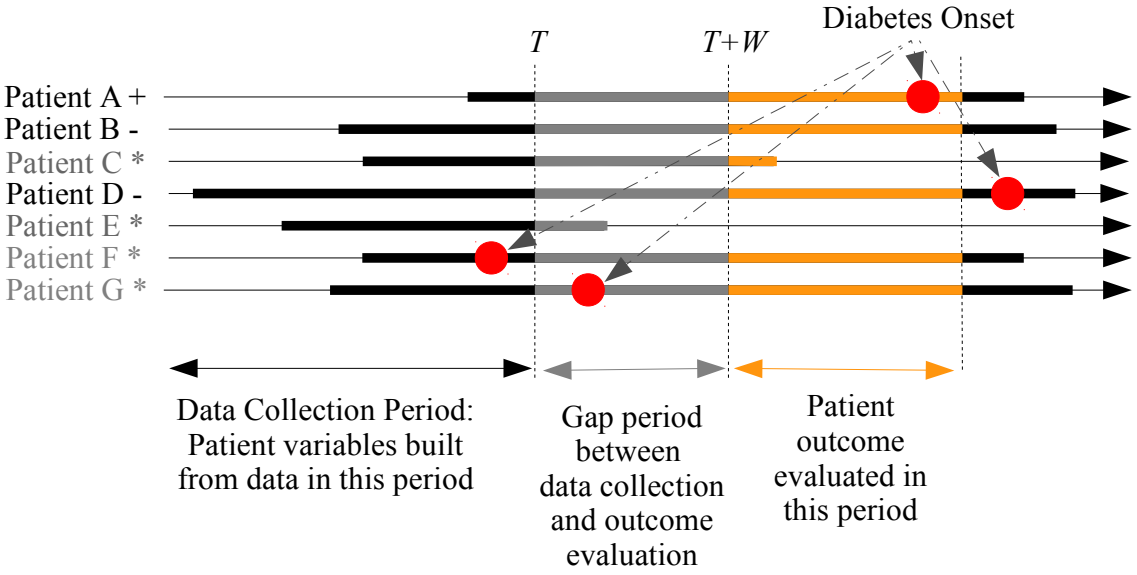
- Calibration
- Sensitivity analysis
- Error bars and confidence intervals on prediction estimates
- Heterogeneity of results:
  - Does the model only work well for a subpopulation?
- Model introspection:
  - For a linear model, are the features used by the models the ones you might expect?
  - Do root nodes in a decision tree make sense?
  - More challenging to do for deep neural networks

The importance of interpretability

- Intelligible Models for HealthCare: Predicting Pneumonia Risk and Hospital 30-day Readmission, Caruana et. Al, KDD 2015
- Used generalized additive models to make predictions of pneumonia and readmission
- Learn HasAsthma(x) = LowerRiskOfDying(x)
- Why?
  - Asthmatics w/ pneumonia are prioritized
  - Get aggressive treatment, faster, in ICU
  - Treatment lowers risk of death compared to general population
- Scenario where the prescription of an intervention taints the outcomes
- The consequence:
  - Automated methods might flag asthmatics as not being problematic!

Questions?

Continuous valued outcomes for risk stratification

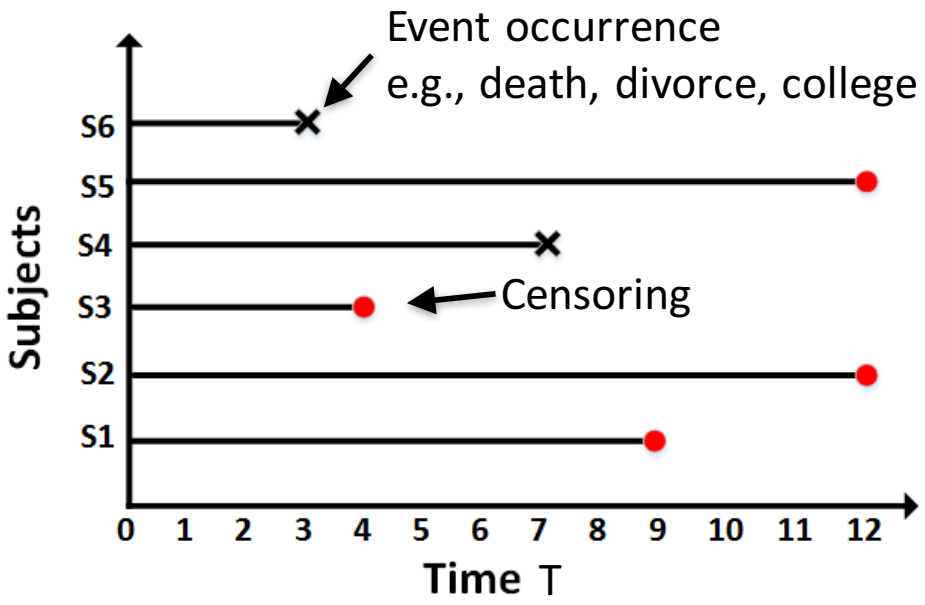


More natural to define patient outcomes as the time taken to reach a clinical endpoint

- Time to re-admission
- Time to death
- Time to progression of disease

Labels are partially missing!

- We may not observe the outcome in the dataset – life, administrative challenges etc.



Event observed

Event not observed

This kind of missingness is known as right censorship!

Censorship

- Censorship is an important to know about when handling longitudinal data
- Three types of censorship:
  - Left censored data:
    - We don't observe the *start* of an event but we do observe longitudinal data after it
    - Example: ICU patient's vitals are continuously recorded from when the enter. If one of the sensor fails and is later fixed, their data is left censored
  - Right censored data [focus for today]
    - We don't observe the *incidence* of an event but we know it occurs after the last observed time
    - We'll see examples soon!
  - Interval censored data:
    - Both left and right censorship
    - Neonatal unit is tracking data on children, observe data sometime after they are born and until they leave the unit (for those who survive)

What can we do when we do not observe when the event occurs?

- What do we know:
  - x: features
  - y: last observed time
  - b: whether or not the event occurs
- Option: why not throw away all datapoints for which we don't know when the event occurs:
  - Wasteful, might end up with very little data
- Key idea behind survival analysis:
  - Learn to predict time-to-event with all the available data that we have

Preliminaries

- (x, T, b) = (features, time, censoring)
  - b = 0 if censored and b = 1 if event is observed
- f(t) = p(t) = probability of death at time t
- Survival function: $S(t) = P(T > t) = \int_t^\infty f(x)dx$
- Hazard function: $h(t) = \lim_{\epsilon \to 0} p(T \in (t, t+\epsilon] | T \geq t)$
- Cumulative hazard function: $H(t) = \int_0^t h(u)du = \int_0^t \frac{f(u)}{S(u)}du = \int_0^t \frac{-dS(u)}{S(u)}du = -\log\{S(t)\}$
- Hazard function & survival function: $h(t) = \frac{f(t)}{S(t)}$

$$f(t) = h(t)S(t) = h(t)\exp\{-H(t)\}$$

$$S(t) = \exp\{-H(t)\}.$$

Slide credit: Lu Tian and Richard Olshen's course on survival analysis

Preliminaries – (2)

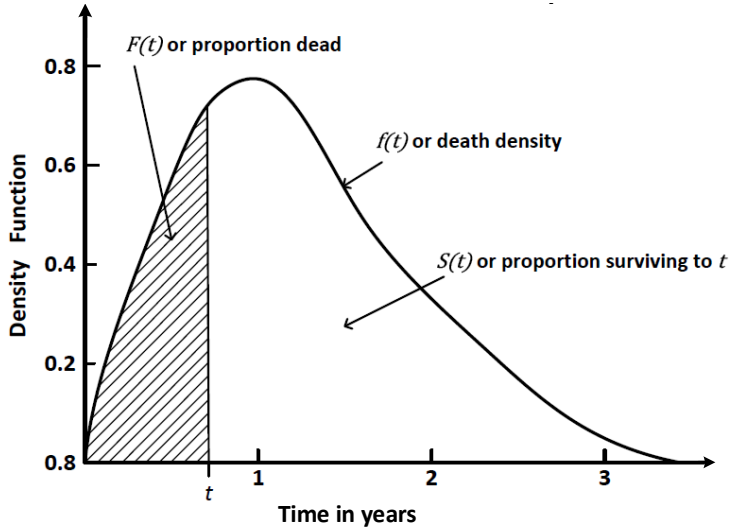


Fig. 2: Relationship among different entities $f(t)$, $F(t)$ and $S(t)$.

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

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

Preliminaries

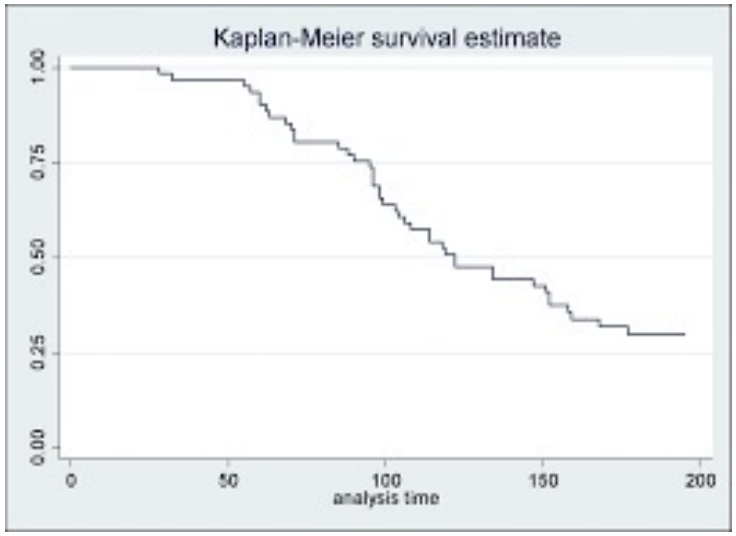
- h(t) dt is approximately the conditional probability of the event occurring in an infinitesimal interval around t conditional on it not having occurred before t

Non-parametric survival analysis

- Let start by ignoring our features and asking about S(t)
  - S(t) is an integral $S(t) = P(T > t) = \int_t^\infty f(x)dx$
  - **Idea:** If we had access to f(x) we could discretize time and evaluate f(x) in each bin and sum them up.
  - **Issue:** We don't have access to f(x) but we **do** have samples!
- **Kaplan Meier curves:**
  - **Non-parametric** estimator of the survival function S(t)
    - We do not assume anything about the underlying distribution of S(t)
  - We'll use our entire dataset to approximate the shape of S(t)

Kaplan Meier estimator

- Derivation out of scope for this class
  - Survival analysis is a rich area of research and is often a course in and of itself
  - E.g. [Lu Tian and Richard Olshen at Stanford]



Observed event times

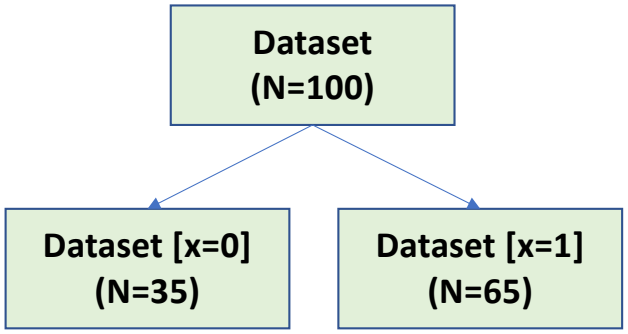
$$y_{(1)} < y_{(2)} < \cdots < y_{(D)}$$

$d_{(k)}$ = # events at this time

$n_{(k)}$ = # of individuals alive and uncensored

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

What do we do if we have features (x)?



Evaluate KM estimator on each strata

Right [survival probability of patients who have multiple myeloma stratified by genetic marker]

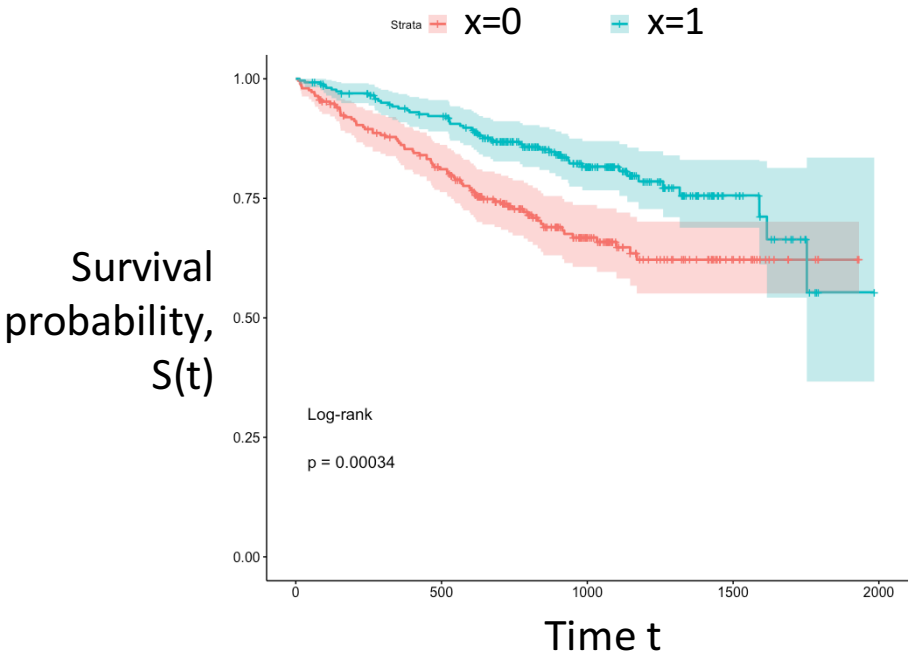
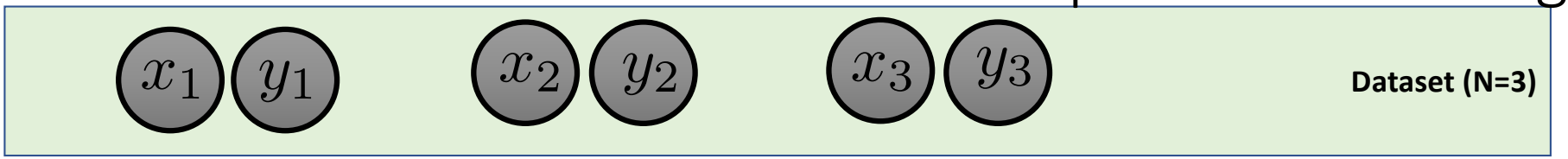


Figure credit: Rebecca Boiarsky

What if x is high-dimensional?

- Option 1: stratify based on clusters of x
- Option 2: Let the survival function **depend on x**
- Lets study what happens in supervised learning:
- In linear regression: $y \sim \mathcal{N}(w^T x + b; 1)$
  - Outcome is a Gaussian function centered around [w^Tx + b]
  - Known as a parametric model for y:
    - There are some parameters that govern the behavior of y as a function of x

Maximum likelihood estimation for supervised learning



- Given a dataset, the model parameters are learned via **maximum likelihood estimation**

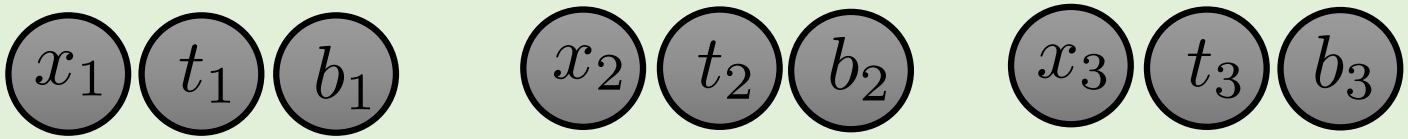
$$\mathcal{L}(y, x) = \log p(y|x; \theta)$$

Score function (high is good, low is bad)

$$\theta = \arg\max_{\theta} \sum_{i=1}^{N} \mathcal{L}(y_i, x_i)$$

Solve this optimization problem to **learn** the model. Often formulated as a minimization of the negative of the log-likelihood function

Maximum likelihood estimation for survival analysis



- Given a dataset, the model parameters are learned via **maximum likelihood estimation**

$$p(T = t|x;\theta) = f(t)$$

Uncensored likelihood

$$p(T > t|x;\theta) = S(t)$$

Censored likelihood

$$\sum_{i=1}^{N} b_i \log p(T = t_i|x_i;\theta) + (1 - b_i) \log p(T > t_i|x_i;\theta)$$

Maximize the following objective function to learn model parameters

What distribution should I use?

Table 2.1 Useful parametric distributions for survival analysis

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 ($\sigma > 0, \mu \in R$)	$1 - \Phi\{(\ln t - \mu)/\sigma\}$	$\varphi\{(\ln t - \mu)/\sigma\}(\sigma t)^{-1}$
Log-logistic ($\lambda > 0, \phi > 0$)	$1/(1 + \lambda t^{\phi})$	$(\lambda \phi t^{\phi-1})/(1 + \lambda t^{\phi})^2$
Gamma ($\lambda, \phi > 0$)	$1 - I(\lambda t, \phi)$	$\{\lambda^{\phi}/\Gamma(\phi)\} t^{\phi-1} \exp(-\lambda t)$
Gompertz ($\lambda, \phi > 0$)	$\exp\{\frac{\lambda}{\phi}(1 - e^{\phi t})\}$	$\lambda e^{\phi t} \exp\{\frac{\lambda}{\phi}(1 - e^{\phi t})\}$

(parameters can be a function of x)

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

CoxPH: Interpretability in survival analysis

- Parameteric models that depend on x change parameters of a distribution in linear/non-linear ways as a function of x
- **Goal:** Link variation to covariates directly to the survival function
- The Cox Proportional Hazard's model is one of the most popular tools in survival analysis

$$h(t|X = x; \theta) = \underbrace{h_0(t)}_{\text{Baseline hazard}} \exp(\beta^T x)$$

Baseline hazard reflects the hazard for subjects with all covariates equal to 0

Interpretation in the univariate case

$$\frac{h(t|X = x_1; \theta)}{h(t|X = x_2; \theta)} = \frac{\exp(\beta^T x_1)}{\exp(\beta^T x_2)} \quad \frac{h(t|X = x + 1)}{h(t|X = x)} = \exp(\beta)$$

Hazard ratio is independent of time

Parameters have an intuitive meaning

CoxPH: Linear model for log of the hazard ratio

CoxPH for binary data

- X = [received drug (0 no, 1 yes) , gender (0 male, 1 female)]

$$h(t|x_1, x_2) = h_0(t)\exp(\beta_1 z_1 + \beta_2 z_2)$$

$$h(t|X) = h_0(t)$$ No treatment, Male

$$h(t|X) = h_0(t)\exp(\beta_1)$$ Yes treatment, Male

$$h(t|X) = h_0(t)\exp(\beta_2)$$ No treatment, Female

$$h(t|X) = h_0(t)\exp(\beta_1 + \beta_2)$$ Yes treatment, Female

Key advantage of the CoxPH model

- We can estimate the model parameters β
- Notably we can do so without estimation the baseline hazard
- This is a **semi-parametric model**
  - We make no assumptions about the baseline hazard rate but we do learn parameters corresponding to how it is modified based on patient covariates
- How do we learn this model?
  - Won't derive from scratch
  - Useful reference: Course notes by Ronghui (Lily) Xu

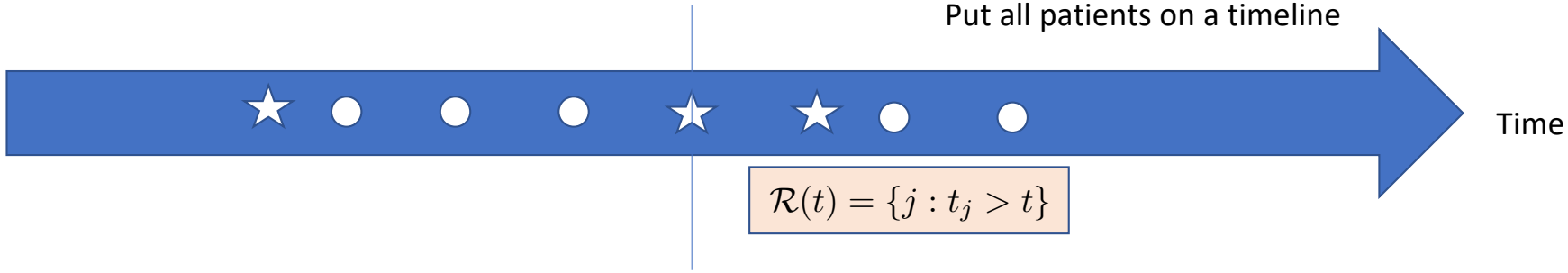
Cox Partial Likelihood

Scan from left to right in time, at each discrete point, calculate the risk set

$$\mathcal{R}(t) = \{j : t_j > t\}$$

$$\mathcal{L}(\beta) = \sum_{i=1}^{K} b_i \log \frac{\exp(\beta^T X_i)}{\sum_{l \in \mathcal{R}(t_i)} \exp(\beta^T X_l)}$$

Visualizing the computation of the partial likelihood



$$\mathcal{L}(\beta) = \sum_{i=1}^{K} b_i \log \frac{\exp(\beta^T X_i)}{\sum_{l \in \mathcal{R}(t_i)} \exp(\beta^T X_l)}$$

Censored event

Event

Intuition: How likely are the features of this patient to explain their elevated risk of having the event occur now compared to all the individuals whose event occurs later!

Advances in machine learning for survival analysis

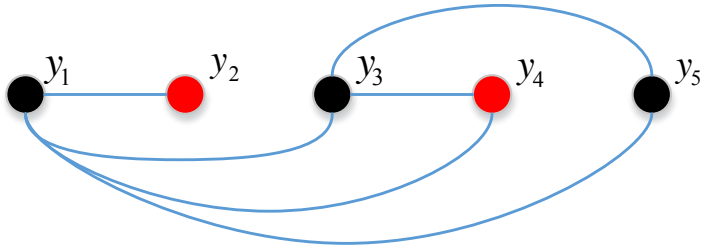
- DeepSurv, Katzman et. al, 2017
  - One of the readings for this week uses a deep neural network to parameterize the modification to the hazard function
  - Parameter estimation by taking derivatives of the
- Advanced reading Deep survival analysis, Ranganath et. al, 2016
  - What if x is very high dimensional?
  - Rather than condition on x directly, learn a latent representation of x while jointly modeling survival time

Evaluation in survival analysis

- Concordance index (aka C-statistic) – predicts how well the model ranks patients based on survival (i.e. predicts relative survival time)
- Equivalent to AUC (when there is no censoring)

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

Black = uncensored
Red = censored



Other ways to evaluate models

- Mean squared error [for just those who are uncensored]
- Held out likelihood (censored + uncensored)

Questions?

Why not use classification?

If T has a non-uniform distribution,

Thresholds for classification may not be known at training time

Why not use regression?

When outcomes are missing [event time not observed] you may have to throw data out

- Leads to limited training data
- Might introduce bias into the dataset

Announcements

- Piazza now has a pinned post to help you start looking for teammates to work on problems
- Watch MIMIC data and analysis tutorials [posted to course website]
- Friday:
  - 30 minutes - Discussion with Alistair Johnson, Scientist, SickKids Hospital
  - 20 minutes - Breakout rooms to brainstorm ideas for group projects