Models for time-to-event data

From Cox's proportional hazards model to deep learning



Sebastian Pölsterl

Artificial Intelligence in Medical Imaging | Ludwig Maximilian Universität Munich

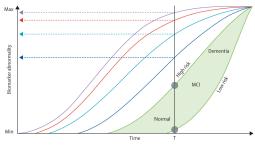
October 2nd 2018

École Centrale de Nantes



- 1 What is Survival Analysis?
- 2 Parametric Survival Models
- **3** Semiparametric Survival Models
- **4** Non-Linear Survival Models
- 5 Survival Analysis with Deep Learning
- 6 Conclusion



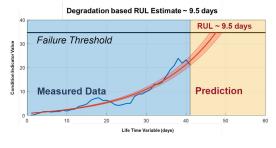


Source: Jack et al. (2013)

- Mild cognitive impairment (MCI) is a common precursor to dementia in Alzheimer's disease and is associated with isolated memory loss.
- Some patients with MCI remain stable, whereas others progress to Alzheimer's disease.
- For an effective therapy, we want to know the probability of conversion at any time point.

Sebastian Pölsterl (Al-Med)

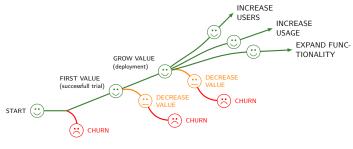






- Most equipment, such as a pump, will experience failure eventually.
- Failure is usually determined by threshold values on various censors: temperature cannot exceed 74°C and pressure must be under 10 bar.
- We want to know the probability of failure at any time point such that replacing the equipment can be scheduled in advance to minimize downtime.

LMU INVIGENTATION Customer relationship management



Source: For Entrepreneurs

- All businesses will lose some of its customers (customer churn).
- For each customer, we have a record of purchases and previous interactions with the company.
- We want to know how likely it is for a customer to turn away (churn) at any given time point so we can provide targeted incentives to induce customers to stay.

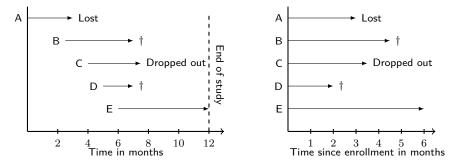
Sebastian Pölsterl (Al-Med)



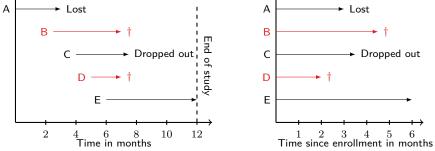
1 What is Survival Analysis?

- 2 Parametric Survival Models
- Semiparametric Survival Models
- 4 Non-Linear Survival Models
- 5 Survival Analysis with Deep Learning
- 6 Conclusion



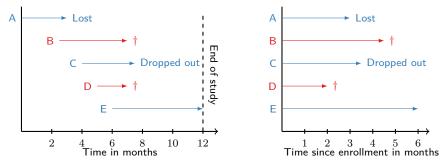






• A record is **uncensored** if an event was observed during the study period: the exact time of the event is known.





- A record is **uncensored** if an event was observed during the study period: the exact time of the event is known.
- A record is **right censored** if a patient remained event-free: it is unknown whether an event occurred after the study ended.



• Right censoring

$$y_i = \min(c_i^{\mathsf{right}}, t_i)$$



• Right censoring

$$y_i = \min(c_i^{\mathsf{right}}, t_i)$$

• Left censoring

$$y_i = \max(c_i^{\mathsf{left}}, t_i)$$



• Right censoring

$$y_i = \min(c_i^{\mathsf{right}}, t_i)$$

• Left censoring

$$y_i = \max(c_i^{\mathsf{left}}, t_i)$$

Interval censoring

 $t_i \in (\tau_i^l; \tau_i^r]$



Right censoring

$$y_i = \min(c_i^{\mathsf{right}}, t_i)$$

• Left censoring

$$y_i = \max(c_i^{\mathsf{left}}, t_i)$$

Interval censoring

$$t_i \in (\tau_i^l; \tau_i^r]$$

• Any combination of left, right, or interval censoring may occur in a study.



Let T denote a **continuous** non-negative random variable corresponding to a patient's survival time with probability density function f(t).

Survival function

$$S(t) = P(T > t) = 1 - P(T \le t) = 1 - F(t) = \int_{t}^{\infty} f(u) du$$



Let T denote a **continuous** non-negative random variable corresponding to a patient's survival time with probability density function f(t).

Survival function

$$S(t) = P(T > t) = 1 - P(T \le t) = 1 - F(t) = \int_{t}^{\infty} f(u) du$$

Hazard function

$$h(t) = \lim_{\Delta t \to 0} \frac{P(t \le T < t + \Delta t \mid T \ge t)}{\Delta t} \ge 0$$



Let T denote a **continuous** non-negative random variable corresponding to a patient's survival time with probability density function f(t).

Survival function

$$S(t) = P(T > t) = 1 - P(T \le t) = 1 - F(t) = \int_t^\infty f(u) du$$

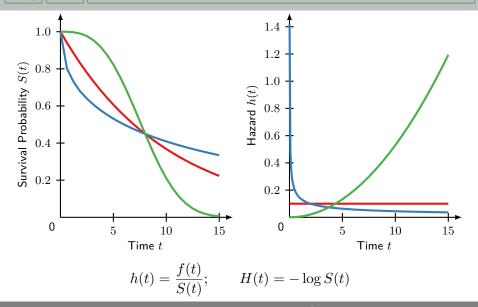
Hazard function

$$h(t) = \lim_{\Delta t \to 0} \frac{P(t \le T < t + \Delta t \mid T \ge t)}{\Delta t} \ge 0$$

Cumulative hazard function

$$H(t) = \int_0^t h(u) du$$

Survival and Hazard Function



Sebastian Pölsterl (AI-Med)



Let T be a **discrete** random variable, which can take on values t_i $(i \in \mathbb{N})$ with probability mass function $P(T = t_i)$ and $t_i < t_j$ if and only if i < j.

Survival function

$$S(t) = \sum_{\{i|t_i>t\}} P(T=t_i) \Leftrightarrow P(T=t_i) = S(t_{i-1}) - S(t_i)$$



Let T be a **discrete** random variable, which can take on values t_i $(i \in \mathbb{N})$ with probability mass function $P(T = t_i)$ and $t_i < t_j$ if and only if i < j.

Survival function

$$S(t) = \sum_{\{i|t_i>t\}} P(T=t_i) \Leftrightarrow P(T=t_i) = S(t_{i-1}) - S(t_i)$$

Hazard function

$$h(t) = P(T = t_i \mid T \ge t_i)$$



Let T be a **discrete** random variable, which can take on values t_i $(i \in \mathbb{N})$ with probability mass function $P(T = t_i)$ and $t_i < t_j$ if and only if i < j.

Survival function

$$S(t) = \sum_{\{i|t_i>t\}} P(T=t_i) \Leftrightarrow P(T=t_i) = S(t_{i-1}) - S(t_i)$$

Hazard function

$$h(t) = P(T = t_i \mid T \ge t_i)$$

Cumulative hazard function

$$H(t) = \sum_{\{i|t_i \le t\}} h(t_i)$$



What is Survival Analysis?

- **2** Parametric Survival Models
- Semiparametric Survival Models
- 4 Non-Linear Survival Models
- 5 Survival Analysis with Deep Learning
- 6 Conclusion

LMU LUDVIG-MAXIMULANG-UNAVIENTAT NORVERIN

• Assume we have a dataset of d covariates for each of n observations:

 $\mathcal{D} = \{(y_i, \boldsymbol{x}_i)\}_{i=1}^n$

- We want to fit a model with parameters Θ to estimate S(t) the probability of survival beyond time t via maximum likelihood optimization.
- Observed times y_i can be
 - 1. uncensored
 - 2. right-censored
 - 3. left-censored
 - 4. interval-censored
- We need to consider carefully what information each observation gives us.



Definition (Noninformative Censoring)

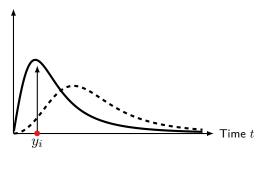
Usually, we assume that the distribution of survival times T is independent of the distribution of censoring times C:

$T\perp C\,|\,\boldsymbol{x}$

This assumption would be violated if the prognosis of individuals who get censored is worse compared to those who are not censored.



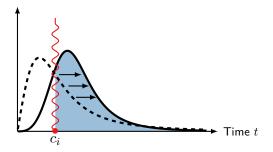
Exact time of event is known



$$\operatorname{argmax}_{\boldsymbol{\Theta}} P(T = y_i; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i) = f(y_i; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i)$$



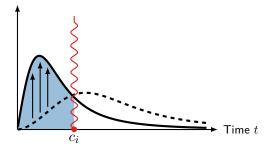
Time of event is right-censored



 $\operatorname*{argmax}_{\boldsymbol{\Theta}} P(T > c_i; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i) = S(c_i; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i)$



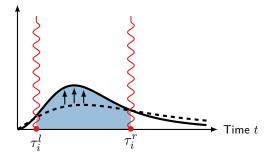
Time of event is left-censored



$$\operatorname{argmax}_{\boldsymbol{\Theta}} P(T \leq c_i; \boldsymbol{\Theta} \mid \boldsymbol{x}_i) = 1 - S(c_i; \boldsymbol{\Theta} \mid \boldsymbol{x}_i)$$



Time of event is interval-censored



$$\underset{\boldsymbol{\Theta}}{\operatorname{argmax}} P(\tau_i^l < T \le \tau_i^r; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i) = \int_{\tau_i^l}^{\tau_i^r} f(u; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i) \, du$$
$$= S(\tau_i^l; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i) - S(\tau_i^r; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i)$$



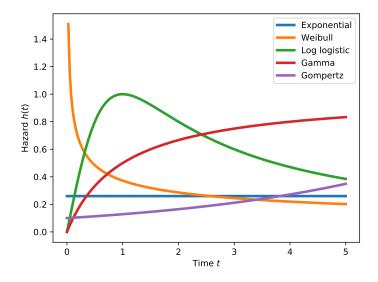
For training, we need to solve the optimization problem

```
\mathop{\mathrm{argmax}}_{\boldsymbol{\Theta}} \quad LL(\boldsymbol{\Theta})
```

where the likelihood function comprises all of the components

$$\begin{split} LL(\boldsymbol{\Theta}) &= \prod_{i \in \text{uncensored}} f(y_i; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i) \\ &\prod_{i \in \text{right-censored}} S(y_i; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i) \\ &\prod_{i \in \text{left-censored}} (1 - S(y_i; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i)) \\ &\prod_{i \in \text{interval-censored}} \left(S(\tau_i^l; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i) - S(\tau_i^r; \boldsymbol{\Theta} \,|\, \boldsymbol{x}_i) \right) \end{split}$$







- What is Survival Analysis?
- 2 Parametric Survival Models
- **3** Semiparametric Survival Models
- 4 Non-Linear Survival Models
- 5 Survival Analysis with Deep Learning
- 6 Conclusion



Parametric Models

- Distribution's parameters are data-dependent based on covariates.
- Work extremely well when survival times follow the chosen distribution.
- Can easily account for various censoring schemes.
- Inference is easy.

Semiparametric Survival Models

Parametric Models

LUDWIG-

- Distribution's parameters are data-dependent based on covariates.
- Work extremely well when survival times follow the chosen distribution.
- Can easily account for various censoring schemes.
- Inference is easy.

Semiparametric Models

- Often, we do not know what distribution we should choose.
- Split the model into 2 parts:
 - 1. part that models influence of covariates.
 - 2. part that models time.
- Usually only account for right-censoring.



• Cox's Proportional Hazards model (Cox PH)

$$h(t \mid \boldsymbol{x}) = h_0(t) \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right) \Leftrightarrow \frac{h(t \mid \boldsymbol{x})}{h_0(t)} = \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right)$$



• Cox's Proportional Hazards model (Cox PH)

$$h(t \,|\, \boldsymbol{x}) = h_0(t) \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right) \Leftrightarrow \frac{h(t \,|\, \boldsymbol{x})}{h_0(t)} = \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right)$$

• Accelerated Failure Time model (AFT)

$$h(t \mid \boldsymbol{x}) = h_0(t \exp(-\boldsymbol{x}^\top \boldsymbol{\beta})) \exp(-\boldsymbol{x}^\top \boldsymbol{\beta})$$

LMU Common Semiparametric Linear Models

• Cox's Proportional Hazards model (Cox PH)

$$h(t \,|\, \boldsymbol{x}) = h_0(t) \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right) \Leftrightarrow \frac{h(t \,|\, \boldsymbol{x})}{h_0(t)} = \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right)$$

• Accelerated Failure Time model (AFT)

$$h(t \mid \boldsymbol{x}) = h_0(t \exp(-\boldsymbol{x}^\top \boldsymbol{\beta})) \exp(-\boldsymbol{x}^\top \boldsymbol{\beta})$$

• Proportional Odds model

$$\frac{P(T > t \mid \boldsymbol{x})}{P(T \le t \mid \boldsymbol{x})} = \frac{1 - S(t \mid \boldsymbol{x})}{S(t \mid \boldsymbol{x})} = \frac{1 - S_0(t)}{S_0(t)} \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right)$$



• Cox's Proportional Hazards model (Cox PH)

$$h(t \mid \boldsymbol{x}) = h_0(t) \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right) \Leftrightarrow \frac{h(t \mid \boldsymbol{x})}{h_0(t)} = \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right)$$

• Accelerated Failure Time model (AFT)

$$h(t \mid \boldsymbol{x}) = h_0(t \exp(-\boldsymbol{x}^\top \boldsymbol{\beta})) \exp(-\boldsymbol{x}^\top \boldsymbol{\beta})$$

• Proportional Odds model

$$\frac{P(T > t \mid \boldsymbol{x})}{P(T \le t \mid \boldsymbol{x})} = \frac{1 - S(t \mid \boldsymbol{x})}{S(t \mid \boldsymbol{x})} = \frac{1 - S_0(t)}{S_0(t)} \exp\left(\boldsymbol{x}^\top \boldsymbol{\beta}\right)$$

• All models are multiplicative.



Definition (Survival data)

Right-censored survival data consists of n triplets:

- $oldsymbol{x}_i \in \mathbb{R}^d$ a d-dimensional feature vector.
 - $y_i > 0$ observed time (time of event *or* time of censoring).
- $\delta_i \in \{0, 1\}$ a boolean event indicator (right censoring).

LMU Cox's Proportional Hazards model

- Cox PH is by far the most popular survival model.
- Coefficients can be interpreted in terms of hazard ratio:

$$\frac{h(t \mid x_1, \dots, x_j, \dots, x_p)}{h(t \mid x_1, \dots, x_j + 1, \dots, x_p)} = \exp\left(\frac{\beta_j}{\beta_j}\right).$$

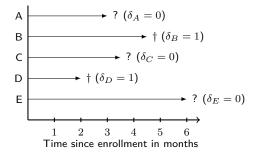
- The hazard ratio is a constant *independent of time* (proportional hazards assumption).
- Optimization is easy: baseline hazard function $h_0(t)$ can be ignored until β has been estimated (*partial likelihood optimization*):

$$\underset{\boldsymbol{\beta}}{\operatorname{argmax}} \quad \sum_{i=1}^{n} \delta_{i} \left[\boldsymbol{x}_{i}^{\top} \boldsymbol{\beta} - \log \left(\sum_{j \in \mathcal{R}_{i}} \exp(\boldsymbol{x}_{j}^{\top} \boldsymbol{\beta}) \right) \right],$$

where $\mathcal{R}_i = \{j \mid y_j \ge t_i\}$ denotes the risk set.



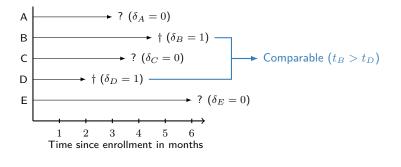
$$\mathcal{P} = \{(i,j) \mid y_i > y_j \land \delta_j = 1\}_{i,j=1,\dots,n}$$



$$\mathcal{P} = \{\}$$



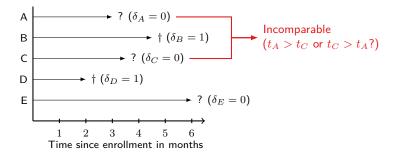
$$\mathcal{P} = \{(i,j) \mid y_i > y_j \land \delta_j = 1\}_{i,j=1,\dots,n}$$



 $\mathcal{P} = \{(\mathbf{B}, \mathbf{D})\}$



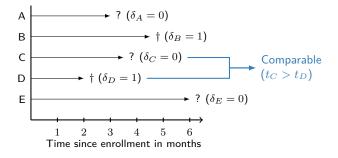
$$\mathcal{P} = \{(i,j) \mid y_i > y_j \land \delta_j = 1\}_{i,j=1,\dots,n}$$



$$\mathcal{P} = \{(B,D)\}$$



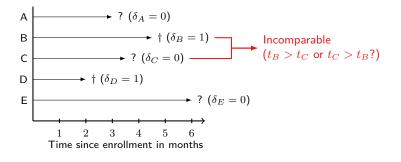
$$\mathcal{P} = \{(i,j) \mid y_i > y_j \land \delta_j = 1\}_{i,j=1,\dots,n}$$



$$\mathcal{P} = \{(B, D), (\mathbf{C}, \mathbf{D})\}\$$



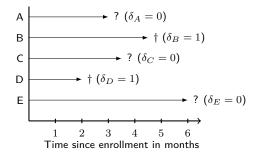
$$\mathcal{P} = \{(i,j) \mid y_i > y_j \land \delta_j = 1\}_{i,j=1,\dots,n}$$



 $\mathcal{P} = \{(B, D), (C, D)\}$



$$\mathcal{P} = \{(i,j) \mid y_i > y_j \land \delta_j = 1\}_{i,j=1,\dots,n}$$



 $\mathcal{P} = \{(B, D), (C, D), (A, D), (E, D), (E, B)\}$



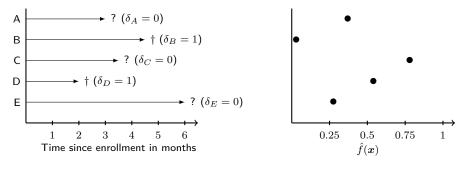
- The concordance index (c index) is a measure of rank correlation between predicted risk scores $\hat{f}(x)$ and observed time points y.
- It is the ratio of correctly ordered (concordant) pairs to comparable pairs:

$$\hat{c}_{\mathsf{Harrell}} = \frac{1}{|\mathcal{P}|} \sum_{(i,j) \in \mathcal{P}} I(\hat{f}(\boldsymbol{x}_i) < \hat{f}(\boldsymbol{x}_j)).$$

- A random model has c index 0.5, a perfect model 1.0
- Risk scores can be on any scale, only their relative ordering matters.
- *c* index is independent of time.



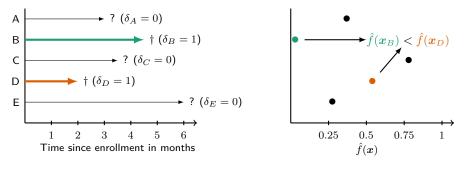
$$\frac{1}{|\mathcal{P}|} \sum_{(i,j)\in\mathcal{P}} I(\hat{f}(\boldsymbol{x}_i) < \hat{f}(\boldsymbol{x}_j))$$



 $\mathcal{P} = \{(B,D), (C,D), (A,D), (E,D), (E,B)\} \Rightarrow \hat{c} = ?$



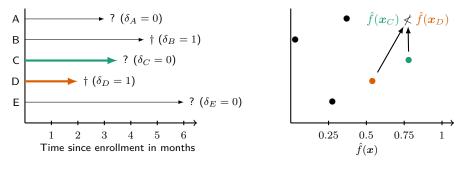
$$\frac{1}{|\mathcal{P}|} \sum_{(i,j)\in\mathcal{P}} I(\hat{f}(\boldsymbol{x}_i) < \hat{f}(\boldsymbol{x}_j))$$



 $\mathcal{P} = \{ (\mathbf{B}, \mathbf{D}), (C, D), (A, D), (E, D), (E, B) \} \Rightarrow \hat{c} = ?$



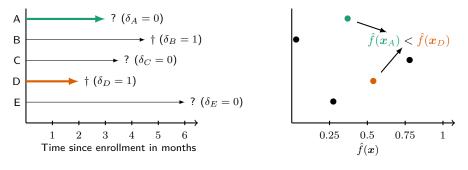
$$\frac{1}{|\mathcal{P}|} \sum_{(i,j)\in\mathcal{P}} I(\hat{f}(\boldsymbol{x}_i) < \hat{f}(\boldsymbol{x}_j))$$



 $\mathcal{P} = \{ (B, D), (\mathbf{C}, \mathbf{D}), (A, D), (E, D), (E, B) \} \Rightarrow \hat{c} = ?$



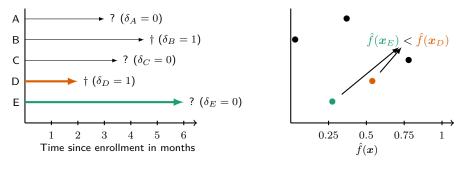
$$\frac{1}{|\mathcal{P}|} \sum_{(i,j)\in\mathcal{P}} I(\hat{f}(\boldsymbol{x}_i) < \hat{f}(\boldsymbol{x}_j))$$



 $\mathcal{P} = \{ (B, D), (C, D), (A, D), (E, D), (E, B) \} \Rightarrow \hat{c} = ?$



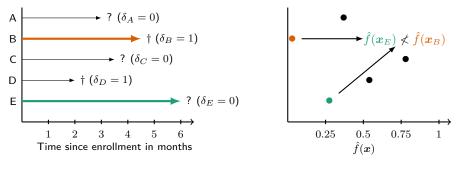
$$\frac{1}{|\mathcal{P}|} \sum_{(i,j)\in\mathcal{P}} I(\hat{f}(\boldsymbol{x}_i) < \hat{f}(\boldsymbol{x}_j))$$



 $\mathcal{P} = \{(B, D), (C, D), (A, D), (\mathbf{E}, \mathbf{D}), (E, B)\} \Rightarrow \hat{c} = ?$



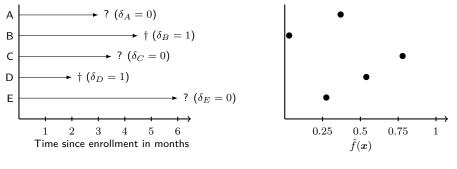
$$\frac{1}{|\mathcal{P}|} \sum_{(i,j)\in\mathcal{P}} I(\hat{f}(\boldsymbol{x}_i) < \hat{f}(\boldsymbol{x}_j))$$



 $\mathcal{P} = \{(B, D), (C, D), (A, D), (E, D), (\mathbf{E}, \mathbf{B})\} \Rightarrow \hat{c} = ?$



$$\frac{1}{|\mathcal{P}|} \sum_{(i,j)\in\mathcal{P}} I(\hat{f}(\boldsymbol{x}_i) < \hat{f}(\boldsymbol{x}_j))$$



 $\mathcal{P} = \{(B,D), (C,D), (A,D), (E,D), (E,B)\} \Rightarrow \hat{c} = 3/5$



- What is Survival Analysis?
- 2 Parametric Survival Models
- Semiparametric Survival Models
- **4** Non-Linear Survival Models
- 5 Survival Analysis with Deep Learning
- 6 Conclusion



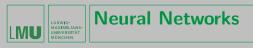
- Take a linear model and replace the linear predictor $x_i^\top \beta$ with an unknown, more complex function f(x).
- We can model f(x) as an additive model by performing gradient descent in function space (gradient boosting).
- Loss function:
 - Cox PH (Binder and Schumacher, 2008; Li and Luan, 2005; Ridgeway, 1999)
 - AFT (Hothorn et al., 2006; Schmid and Hothorn, 2008; Wang and Wang, 2010)
 - c index (Benner, 2002; Mayr and Schmid, 2014)
- Base learner:
 - regression tree (Breiman et al., 1984)
 - componentwise least squares (Bühlmann and Yu, 2003)



- We can treat survival analysis as ranking problem (Van Belle et al., 2008).
- We want to optimize a smooth approximation of the *c* index:

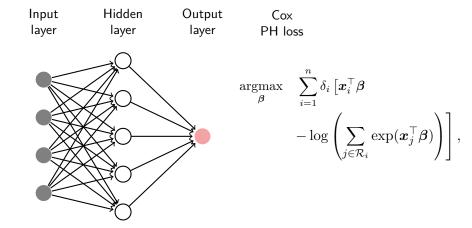
$$\begin{split} \min_{\boldsymbol{w}} \quad & \frac{1}{2} \|\boldsymbol{w}\|_2^2 + \gamma \sum_{(i,j) \in \mathcal{P}} \xi_{ij} \\ \text{subject to} \quad & \boldsymbol{w}^\top \boldsymbol{x}_i - \boldsymbol{w}^\top \boldsymbol{x}_j \geq 1 - \xi_{ij}, \quad \forall (i,j) \in \mathcal{P}, \\ & \xi_{ij} \geq 0, \qquad \qquad \forall (i,j) \in \mathcal{P} \end{split}$$

- Optimization algorithm needs to be clever to avoid dependency on kernel matrix of size $O(|\mathcal{P}|^2) = O(n^4)$ (Pölsterl et al., 2015, 2016).
- Alternative models: regression with non-symmetric loss (Khan and Zubek, 2008; Shivaswamy et al., 2007), quantile regression (Eleuteri, 2008; Eleuteri and Taktak, 2012).

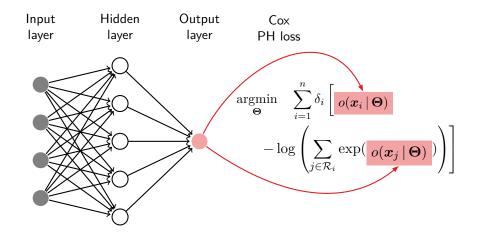


- Faraggi and Simon (1995) proposes a multi-layer perceptron that extends the Cox PH model.
- Biganzoli et al. (1998) and Liestøl et al. (1994) propose the *Partial Logistic Artificial Neural Network* that considers survival times grouped into mutually exclusive intervals and a loss based on a piecewise exponential model.

MU LUNIG-



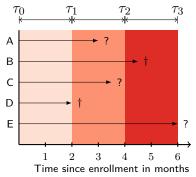
Loss by Faraggi and Simon



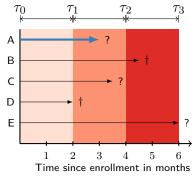


- Samples need to be sorted by observed time y_i due to sum over $\mathcal{R}_i = \{j \mid y_j \ge t_i\}.$
- Batch size needs to be large, otherwise gradient is very noisy.
- Only considers **time-invariant features** (proportional hazards assumption).







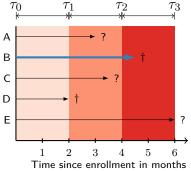


Event in k-th interval?

$$\delta_{A1} = 0, \quad \delta_{A2} = 0, \quad \delta_{A3} = 0$$

Time spent in k-th interval: $\tilde{y}_{A1} = 2$, $\tilde{y}_{A2} = 1$, $\tilde{y}_{A3} = 0$

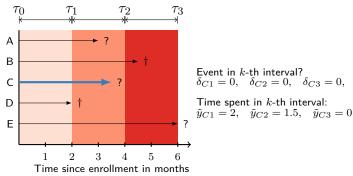




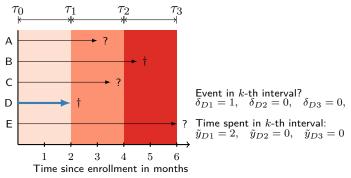
Event in k-th interval? $\delta_{B1} = 0, \quad \delta_{B2} = 0, \quad \delta_{B3} = 1$

Time spent in k-th interval: $\tilde{y}_{B1}=2, \quad \tilde{y}_{B2}=2, \quad \tilde{y}_{B3}=0.5$











• A piecewise exponential model has a constant hazard rate $\lambda_l > 0$ in the l-th interval and has survival function

$$S(t) = \exp(-\lambda_l(t - \tau_{l-1})) \prod_{k=1}^{l-1} \exp(-\lambda_k(\tau_k - \tau_{k-1}))$$



• A piecewise exponential model has a constant hazard rate $\lambda_l > 0$ in the l-th interval and has survival function

$$S(t) = \exp(-\lambda_l(t - \tau_{l-1})) \prod_{k=1}^{l-1} \exp(-\lambda_k(\tau_k - \tau_{k-1}))$$

• Substituting the definition into the log-likelihood function of a parametric model, we obtain

$$\underset{\{\lambda_1,\dots,\lambda_L\}}{\operatorname{argmax}} \quad \sum_{i=1}^n \sum_{k=1}^L \left[\delta_{ik} \log(\lambda_k) - \lambda_k \tilde{y}_{ik}\right]$$



• A piecewise exponential model has a constant hazard rate $\lambda_l > 0$ in the l-th interval and has survival function

$$S(t) = \exp(-\lambda_l(t - \tau_{l-1})) \prod_{k=1}^{l-1} \exp(-\lambda_k(\tau_k - \tau_{k-1}))$$

• Substituting the definition into the log-likelihood function of a parametric model, we obtain

$$\underset{\{\lambda_1,\dots,\lambda_L\}}{\operatorname{argmax}} \quad \sum_{i=1}^n \sum_{k=1}^L \left[\delta_{ik} \log(\lambda_k) - \lambda_k \tilde{y}_{ik} \right]$$

• Finally, the parameters λ_k are modeled by a neural network $o(x_i | \Theta)$ conditional on feature vectors x_i as

$$\lambda_k(\boldsymbol{x}_i) = \exp(\underbrace{\log \lambda_{0k}}_{\substack{\mathsf{baseline} \\ =\mathsf{bias term}}} + \boldsymbol{w}^\top o(\boldsymbol{x}_i \,|\, \boldsymbol{\Theta}))$$



- What is Survival Analysis?
- 2 Parametric Survival Models
- Semiparametric Survival Models
- 4 Non-Linear Survival Models
- 5 Survival Analysis with Deep Learning

6 Conclusion

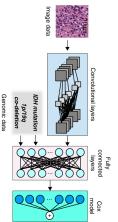


- I could find 24 papers using deep learning¹ techniques with a loss accounting for censored event times.
- 10 use the Cox PH loss of Faraggi and Simon (1995).
- 18 have been applied to medical data.
 - 8 to medical images (6 of which are on histopathology images).
 - 4 to genomic data.
 - The remaining use tabular clinical data or EHR.

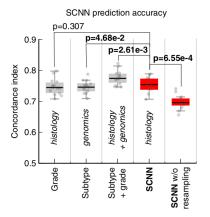
¹excluding work using Deep Gaussian Processes

Mobadersany et al. (2018), "Predicting cancer outcomes from histology and genomics using convolutional networks", PNAS.

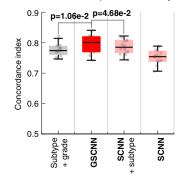
- Objective: Survival prediction of patients with diffuse gliomas.
- Network integrates information from both histology images and genomic biomarkers.
- Uses a modified VGG-19 architecture with loss of Faraggi and Simon.
- Training and testing use random sampling of patches from region of interest.
- Genomic markers (IDH mutation status and 1p/19q co-deletion) are integrated as input to shared FC layer.







GSCNN prediction accuracy



Grob et al. (2018), "A RNN Survival Model: Predicting Web User Return Time", ECML-PKDD.

- Objective: Predict the return times of users to a website.
- Each user has a sequence of previous sessions.
- Each session is has a start time and a set of features.
- Time T is defined as the period between the end of a session and the beginning of the succeeding session.
- The hazard function up to the *j*-th session $h_j(t)$ is modeled as a recurrent marked temporal point process:

$$h_j(t) = \exp\left(\underbrace{\boldsymbol{v}^{(t)}\boldsymbol{h}_j}_{\text{past}} + \underbrace{\boldsymbol{w}(t-t_j)}_{\text{temporal}} + \underbrace{\boldsymbol{b}^{(t)}}_{\text{bias}}\right)$$



	Baseline	Cox PH	RNN-MSE	RNN-SM
RMSE (days)	43.25	49.99	28.69	59.99
Concordance	0.500	0.816	0.706	0.739
Non-returning AUC	0.743	0.793	0.763	0.796
Non-returning recall	0.000	0.246	0.000	0.538



- What is Survival Analysis?
- 2 Parametric Survival Models
- Semiparametric Survival Models
- 4 Non-Linear Survival Models
- 5 Survival Analysis with Deep Learning
- 6 Conclusion



- Time-to-event analysis is applicable across a wide range of domains.
- It is a well studied topic in statistics.
- Most classical machine learning models have been modified for time-to-event data.
- It is slowly being adapted by the deep learning community, although most of the approaches are rather naive.
- Cox PH model is surprisingly hard to beat.

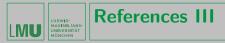


- Benner, A. (2002). "Application of "Aggregated Classifiers" in Survival Time Studies". In: *Proc. in Computational Statistics: COMPSTAT*. Ed. by W. Härdle and B. Rönz, pp. 171–176.
- Biganzoli, E., P. Boracchi, L. Mariani, and E. Marubini (May 1998). "Feed forward neural networks for the analysis of censored survival data: a partial logistic regression approach". In: *Stat. Med.* 17.10, pp. 1169–1186. ISSN: 0277-6715.
- Binder, H. and M. Schumacher (2008). "Allowing for mandatory covariates in boosting estimation of sparse high-dimensional survival models". In: *BMC Bioinformatics* 9, p. 14.
- Breiman, L., J. H. Friedman, C. J. Stone, and R. A. Ohlsen (1984). *Classification and Regression Trees.* Wadsworth International Group.
- Bühlmann, P. and B. Yu (2003). "Boosting With the L_2 Loss". In: J Am Stat Assoc 98.462, pp. 324–339.
- Eleuteri, A. (2008). "Support vector survival regression". In: 4th IET International Conference on Advances in Medical, Signal and Information Processing, pp. 1–4.



Eleuteri, A. and A. F. Taktak (2012). "Support Vector Machines for Survival Regression". In: Computational Intelligence Methods for Bioinformatics and Biostatistics. Ed. by E. Biganzoli, A. Vellido, F. Ambrogi, and R. Tagliaferri. Vol. 7548. LNCS. Springer, pp. 176–189.

- Faraggi, D. and R. Simon (Jan. 1995). "A neural network model for survival data". In: *Stat. Med.* 14.1, pp. 73–82. ISSN: 02776715.
- Grob, G. L., A. Cardoso, C. H. B. Liu, D. A. Little, and B. P. Chamberlain (2018). "A Recurrent Neural Network Survival Model: Predicting Web User Return Time". In: Eur. Conf. Mach. Learn. Princ. Pract. Knowl. Discov. Databases.
- Hothorn, T., P. Bühlmann, S. Dudoit, A. Molinaro, and M. J. van der Laan (2006). "Survival ensembles". In: *Biostatistics* 7.3, pp. 355–373.
- Jack, C. R., D. S. Knopman, W. J. Jagust, R. C. Petersen, M. W. Weiner, et al. (Feb. 2013). "Tracking pathophysiological processes in Alzheimer's disease: an updated hypothetical model of dynamic biomarkers". In: *The Lancet Neurology* 12.2, pp. 207–216.



- Khan, F. M. and V. B. Zubek (2008). "Support Vector Regression for Censored Data (SVRc): A Novel Tool for Survival Analysis". In: 8th IEEE International Conference on Data Mining, pp. 863–868.
- Li, H. and Y. Luan (2005). "Boosting proportional hazards models using smoothing splines, with applications to high-dimensional microarray data". In: *Bioinformatics* 21.10, pp. 2403–2409.
- Liestøl, K., P. K. Andersen, and U. Andersen (June 1994). "Survival analysis and neural nets". In: *Stat. Med.* 13.12, pp. 1189–1200. ISSN: 02776715.
- Mayr, A. and M. Schmid (2014). "Boosting the concordance index for survival data a unified framework to derive and evaluate biomarker combinations". In: *PLoS One* 9.1, e84483.
- Mobadersany, P., S. Yousefi, M. Amgad, D. A. Gutman, J. S. Barnholtz-Sloan, J. E. Velázquez Vega, D. J. Brat, and L. A. D. Cooper (Mar. 2018). "Predicting cancer outcomes from histology and genomics using convolutional networks". In: *Proc. Natl. Acad. Sci.* 115.13, E2970–E2979. ISSN: 0027-8424.



- Pölsterl, S., N. Navab, and A. Katouzian (2015). "Fast Training of Support Vector Machines for Survival Analysis". In: *Machine Learning and Knowledge Discovery in Databases*. Ed. by A. Appice, P. P. Rodrigues, V. Santos Costa, J. Gama, A. Jorge, and C. Soares. Lecture Notes in Computer Science, pp. 243–259.
- (Sept. 2016). "An Efficient Training Algorithm for Kernel Survival Support Vector Machines". In: 3rd Workshop on Machine Learning in Life Sciences.
- Ridgeway, G. (1999). "The state of boosting". In: *Computing Science and Statistics*, pp. 172–181.
- Schmid, M. and T. Hothorn (2008). "Flexible boosting of accelerated failure time models". In: *BMC Bioinformatics* 9, p. 269.
- Shivaswamy, P. K., W. Chu, and M. Jansche (2007). "A Support Vector Approach to Censored Targets". In: 7th IEEE International Conference on Data Mining, pp. 655–660.
- Van Belle, V., K. Pelckmans, J. A. K. Suykens, and S. Van Huffel (2008). "Survival SVM: a practical scalable algorithm". In: *ESANN*, pp. 89–94.



Wang, Z. and C. Wang (2010). "Buckley-James Boosting for Survival Analysis with High-Dimensional Biomarker Data". In: Statistical Applications in Genetics and Molecular Biology 9.1.