Case-Base Neural Networks: survival analysis with time-varying, higher-order interactions

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What is survival analysis?

- Any dataset concerning time to an event.
 - Time to death.
 - Time to graduation.
 - Time to getting a disease.
- Dataset consists of individuals who were followed over time.
 - Study may have a fixed duration or be open ended.
 - The event is not necessarily experienced until the study is over ("Censored").
 - Participants may drop out early for any unrelated reason ("Censored").

Survival time till assignment completion

Time (weeks)



Censored: Individual may experience the event of interest after follow-up has ended.

Hazard function:

Instantaneous potential of experiencing an event at time t, given you survived up to time t.

Hazard ratio:

Cox regression: Assumes proportional hazards... Effect of covariates do not vary with time.

 $h(X,t) = h_0(t)e^{\beta X}$

 $\frac{h(X,t)}{h(0,t)} = \frac{h_0(t)e^{\beta X}}{h_0(t)e^0} = e^{\beta X}$

- *h*(*X*,*t*) : hazard function.
- $h_0(t)$: baseline hazard.
- β*X* : linear predictor

3-week risk?

Time (weeks)



Follow-up time

Case-base sampling with logistic regression

Case-base sampling

Time (weeks)



Time (weeks)



Base: All the person-moments experienced in the study.

Case-base sampling

Time (weeks)



Time (weeks)



- Base: All the person-moments experienced in the study.
- Case series: all the personmoments where an event occurred.

Case-base sampling

Time (weeks)



Time (weeks)



- Base: All the person-moments experienced in the study.
 - Case series: all the personmoments where an event occurred.
- Base series: sample of the base

Case-base sampling and logistic regression



$$e^{\beta(x,t)} = \frac{Pr(Y = 1|x,t)}{Pr(Y = 0|x,t)}$$

$$\frac{Pr(Y = 1|x,t)}{Pr(Y = 0|x,t)} = \frac{h(x,t) * B(x,t)}{b[B(x,t)/B]}$$

$$\frac{h(x,t) * B(x,t)}{b[B(x,t)/B]} = \frac{h(x,t) * B}{b}$$

$$h(x,t) = e^{\beta(x,t)} \frac{b}{B}$$

$$h(x,t) = \beta(x,t) + ln\left(\frac{b}{B}\right) = \# \text{Blue}$$

$$B = \# \text{Moments}$$

Case-base sampling and logistic regression



$$e^{\beta(x,t)} = \frac{Pr(Y=1|x,t)}{Pr(Y=0|x,t)}$$

...

 $ln(\hat{h(x,t)}) = \hat{\beta}(x,t) + ln\left(\frac{b}{B}\right)$ b = # (sample of moments) B = # All moments

To have a flexible baseline hazard:

$$n(\hat{h}(x,t)) = \hat{\beta}_{t_1}t + \hat{\beta}_{t_2}t^2 + \hat{\beta}_{t_3}t^3 + \hat{\beta}x + \ln\left(\frac{b}{B}\right)$$

Case-base sampling and logistic regression



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Case-base sampling permits flexible baseline hazard.

 $h(X,t) = h_0(t) e^{\beta X}$

- h(X,t) : hazard function.
- $h_0(t)$: baseline hazard.
- β*X* : linear predictor

What about flexibility in **Case-base sampling** covariates? permits flexible baseline hazard. $h(X,t) = h_0(t)e^{\beta X}$

- h(X,t) : hazard function.
- $h_0(t)$: baseline hazard.
- β*X* : linear predictor

Exhaustive search with regression is hard

Many covariates.

- How many contribute?
- Interactions?
- Non-linearity?
- Genotypes, CT scans, etc.

Ideally, the model learns from the data.

- Neural networks can be used.
- Case-base + NN = CBNN



State of neural network survival analysis

DeepSurv – Cox neural networks.

- Cox regression extended using neural networks.
- Only uses proportional hazards (PH).

DeepHit – First Hitting Time neural networks.

- Inverse Gaussian distribution used as baseline hazard.
- Does not let model determine baseline hazard.

DeepSurvivalMachines (DSM) – Mixture model used for baseline hazard.

- User specifies a set of distributions to be used as the baseline hazard.
- Does not permit time-varying interactions.

Need a parametric method that permits non-PH and flexible baseline hazard.



Case-Base Neural Networks (CBNN)

- Provides a flexible baseline hazard.
- Permits time-varying interactions among covariates.

CBNN steps



- 1. Case-base sampling.
- 2. Neural network model.
- 3. Set offset to 0 when predicting on new data.

CBNN to hazard

$$\log\left(h(t \mid X_i)\right) = \log\left(\frac{\operatorname{sigmoid}\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}{1 - \operatorname{sigmoid}\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}\right) + \log\left(\frac{b}{B}\right)$$

$$\begin{split} \log\left(h(t \mid X_i)\right) &= \log\left(\frac{\operatorname{sigmoid}\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}{1 - \operatorname{sigmoid}\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}\right) + \log\left(\frac{b}{B}\right) \\ &= \log\left(\frac{\frac{\exp\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}{\exp\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right) + 1}}{1 - \frac{\exp\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}{\exp\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right) + 1}}\right) + \log\left(\frac{b}{B}\right) \end{split}$$

$$\begin{split} \log\left(h(t \mid X_i)\right) &= \log\left(\frac{\operatorname{sigmoid}\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}{1 - \operatorname{sigmoid}\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}\right) + \log\left(\frac{b}{B}\right) \\ &= \log\left(\frac{\frac{\exp\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}{\exp\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right) + 1}}{1 - \frac{\exp\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)}{\exp\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right) + 1}}\right) + \log\left(\frac{b}{B}\right) \\ &= \log\left(\exp\left(f_{\theta}(X, T) + \log\left(\frac{B}{b}\right)\right)\right) + \log\left(\frac{b}{B}\right) \end{split}$$

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Metrics and hyperparameters

Right-censored Brier score

$$\mathrm{BS}(t) = \frac{1}{N} \sum_{i=1}^{N} \left(\frac{\left(\widehat{CI}(X,t) - 1\right)^2 \cdot \mathbf{1}_{S_i \le t, \delta_i = 1}}{\widehat{G}(S_i)} + \frac{\left(\widehat{CI}(X,t)\right)^2 \cdot \mathbf{1}_{S_i > t}}{\widehat{G}(t)} \right)$$

- S_i <- Survival time of i-th individual.
- *t* <- Survival time of interest.
- $\widehat{CI}(X,t)$ <- Cumulative incidence.
- $\hat{G}(m)$ <- Inverse probability censoring weighting (IPCW) at time m.
- δ_i <- Indicator: 1 = event , 0 = censored.

Index of Prediction Accuracy



- IPA > 0: model performs better than null.
- IPA < 0: model performs worse than null.

Kattan, M. W., & Gerds, T. A. (2018). The index of prediction accuracy: an intuitive measure useful for evaluating risk prediction models. *Diagnostic and prognostic research*, *2*(1), 1-7.

Hyperparameters

- Epochs = 2000
- Batch size = 512
- Learning rate = 10e-3
- Decay = 10e-7
- Hidden layers = {50,50,25,25}
 - 50% dropout after each hidden layer.
- 60/20/20% train/validation/test.
- Stopping condition: minimum change in loss = 10e-7.

Simulation studies

Simulated covariates

 $z_1 \sim \text{Bernoulli}(0.5)$

$$z_2 \sim \begin{cases} N(0, 0.5) & \text{if } z_1 = 0 \\ N(10, 0.5) & \text{if } z_1 = 1 \end{cases}$$

$$z_3 \sim \begin{cases} N(8, 0.5) & \text{if } z_1 = 0\\ N(-3, 0.5) & \text{if } z_1 = 1 \end{cases}$$

Simple simulation

$$h(t \mid X_i) = \lambda \cdot e^{\beta_1 z_1 + \beta_2 z_2 + \beta_3 z_3}$$

•
$$\beta 1 = \beta 2 = \beta 3 = 0.1$$

• $\lambda = 1.0$

Simple simulation result



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Complex simulation

$$h(t \mid X_i) = \sum_{i=1}^{5} (\gamma_i \cdot basis_i) + \beta_1 \cdot z_1 + \beta_2 \cdot z_2 + \beta_3 \cdot z_3 + \boxed{\tau_1 \cdot z_1 \cdot z_2 \cdot time} + \boxed{\tau_2 \cdot z_1 \cdot z_3 + \tau_3 \cdot z_2 \cdot z_3}$$

 $\beta 1 = \beta 2 = \beta 3 = 1$

 $\tau 1 = 10, \, \tau 2 = 2, \, \tau 3 = 2$

 $\gamma 1 = 3.9, \gamma 2 = 3, \gamma 3 = -0.43, \gamma 4 = 1.33, \gamma 5 = -0.86$

- Breast cancer dataset from the *Flexsurv* package.
- 686 patients with primary node positive breast cancer.
 - 43% die over 7.28 years.
 - Breast cancer dataset originally used to demonstrate the benefit of flexible baseline hazards.

Complex simulation result



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Real data studies

SUPPORT study

Study to Understand Prognoses Preferences Outcomes and Risks of Treatment (SUPPORT) Phase I 8873 hospitalized adults.

- Followed up to 5.56 years.
- 68% incidence (death).
- 14 covariates (after imputation).

Requires imputation. For comparison with competitors a preprocessed version from DeepSurv is used.

• Age, sex, race, number of comorbidities, presence of diabetes/dementia/cancer, blood pressure, heart/respiration rate, temperature, white blood cell count, sodium and creatinine.



SUPPORT result



METABRIC study

Molecular Taxonomy of Breast Cancer International Consortium (METABRIC)

1980 individuals:

- 57.72% die due to breast cancer.
- with 30 years of follow-up.

There are 9 covariates in total for this study (from Deepsurv):

- 4 genes (MKI67, EGFR, PGR, and ERBB2).
- 5 clinical features:
 - (hormone treatment/radiotherapy/chemotherapy/ER-positive indicator and age at diagnosis).

Pre-processed version from DeepSurv is used.



Case series

METABRIC result



Conclusion

If time varying interactions and a flexible baseline hazard without user specification are of interest, CBNN Should be strongly considered.

- Provides a parametric, flexible baseline hazard.
- Permits time-varying effects of covariates.
- Applicable to high-dimensional datasets.

https://github.com/Jesse-Islam/cbnn

https://github.com/Jesse-Islam/cbnnManuscript