Penalized logistic regression on time-to-event data using casebase sampling

Jesse Islam

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 - Parametric models

Motivations for a new method

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- They believe the stepwise nature is the reason, as it reduces interpretability. [2]
- A streamlined approach for reaching a smooth absolute risk curve. [2]

Dr. Cox's perspective

Reid: How do you feel about the cottage industry that's grown up around it [the Cox model]?

Cox: Don't know, really. In the light of some of the further results one knows since, I think I would normally want to tackle problems parametrically, so I would take the underlying hazard to be a Weibull or something. I'm not keen on nonparametric formulations usually.

Reid: So if you had a set of censored survival data today, you might rather fit a parametric model, even though there was a feeling among the medical statisticians that that wasn't quite right.

Cox: That's right, but since then various people have shown that the answers are very insensitive to the parametric formulation of the underlying distribution [see, e.g., Cox and Oakes, Analysis of Survival Data, Chapter 8.5]. And if you want to do things like predict the outcome for a particular patient, it's much more convenient to do that parametrically.

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- Study to Understand Prognoses and Preferences for Outcomes and Risks Treatments
- Design: Prospective cohort study.
- Setting: 5 academic care centers in the United States.
- Participants: 9105 hospitalized.
- Follow-up-time: 5.56 years.
- 68% incidence rate.

SUPPORT manual imputation [4]

Notorious for missing data

Baseline Variable	Normal Fill-in Value
Bilirubin	1.01
BUN	6.51
Creatinine	1.01
PaO2/FiO2 ratio (pafi)	333.3
Serum albumin	3.5
Urine output	2502
White blood count	9 (thousands)

Table 1: Suggested imputation values. [3]

Mice imputation package (R)

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- 1. PMM (Predictive Mean Matching) For numeric variables

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- 3. polyreg(Bayesian polytomous regression) Factor Variables

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- Surrogate activities of daily living.
- Previous model results. (6)

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- Activities of daily living. (2)

Determined SUPPORT prognostic model on phase I patients.

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- Tested on Phase II.

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- Tested on Phase II.
- Both on the scale of 180 days.

SUPPORT physiology score (SPS) was developed.

```
SPS = 259.9{ARF/MOSF} + 263.4{COPD/CHF} +
241.4{Cirrhosis/Coma} + 281.5{Lung/Colon Cancer} -
0.06174 min(PaO<sub>2</sub>/FiO<sub>2</sub>, 225) - 0.6316 min(Mean BP, 60)
 + 1.0205 WBC - 0.3676(WBC - 8)<sub>+</sub> - 0.5631(WBC -
11) + 0.2691 min(Alb, 4.6) + 0.2312 Aresp - 2.362
Temp + 1.326(Temp - 36.6)<sub>+</sub> + 2.473(Temp - 38.3)<sub>+</sub>
 -1.579 \times 10^{-1} \text{ HR} + 9.770 \times 10^{-5} (\text{HR-55})^3 - 2.189
 \times 10^{-4} (HR - 80)_{+}^{3} + 1.518 \times 10^{-4} (HR - 110)_{+}^{3} -
3.062 \times 10^{-5} (HR - 149)^3 + 0.9763 Bil - 0.7481 (Bil - 149)^3 + 0.9763 (Bil - 149)^3 + 0.9
7) -6.8761 \text{ Cr} + 11.6058(\text{Cr} - 0.600)^3 - 21.8413(\text{Cr}
 -1.000)_{+}^{3} + 10.3574(Cr - 1.500)<sub>+</sub><sup>3</sup> - 0.1219(Cr -
5.399)_{\perp}^{3} - 0.6167096 \text{ Na} + 0.0021118(\text{Na} - 128)_{\perp}^{3} -
0.0036730(Na - 135)^{3}_{+} + 0.0006126(Na - 139)^{3}_{+} +
0.0009486(Na - 148)<sup>3</sup> - 6.278 {COPD/CHF} × mi-
n(Alb, 4.6) - 11.45 {Lung/Colon Cancer} × min(Alb,
4.6) + {ARF/MOSF}[-2.3549 WBC + 2.7494 (WBC -
8)<sub>+</sub> - 0.4638 (WBC - 11)<sub>+</sub>]
```

SUPPORT: my question

How does their SPS perform over 5.56 years?

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- How does the Apache III physiology score (APS) perform over 5.56 years?

SUPPORT: my question

- How does their SPS perform over 5.56 years?
- How does the Apache III physiology score (APS) perform over 5.56 years?
- How does a model with all the covariates, excluding SPS and APS, perform?

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- 4. Compare to full model (excluding SPS and APS).

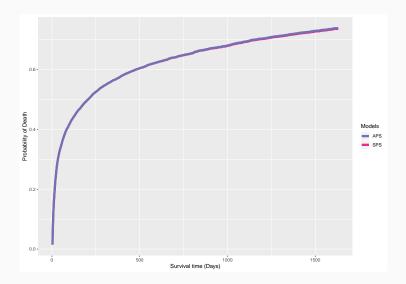
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- All models is trained on 80% of the observations.

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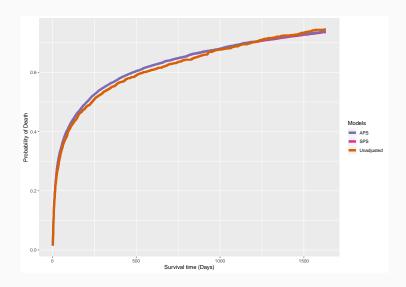
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 - Averaged curve is expected to approach Kaplan-meier curve.

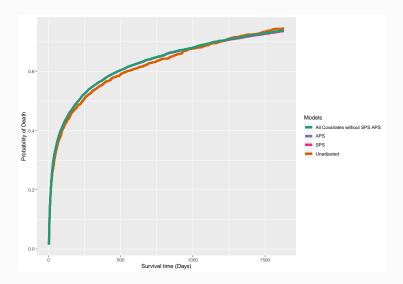
SPS vs APS



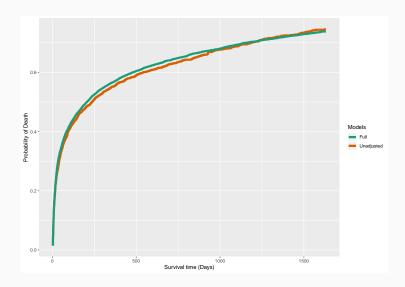
SPS vs. Kaplan-Meier



All covariates vs. physiology scores vs unadjusted



Chosen absolute risk comparisons



Chosen absolute risk comparisons: conclusion

 Linear associations without physiology scores perform similarly to SPS and APS alone.

Chosen absolute risk comparisons: conclusion

- Linear associations without physiology scores perform similarly to SPS and APS alone.
- We choose the linear associations without physiology scores as the model of choice (Full model).

1. Clever sampling.

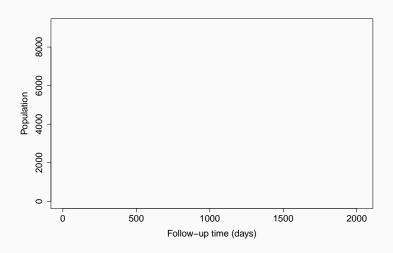
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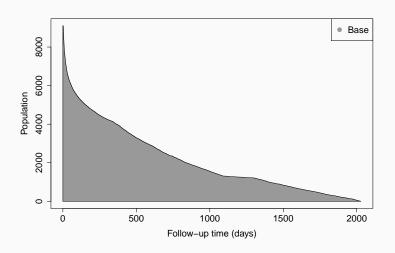
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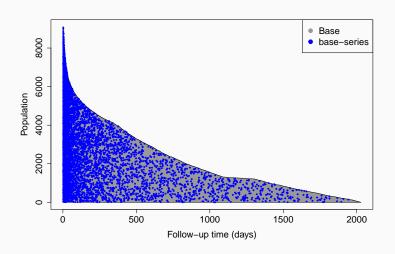
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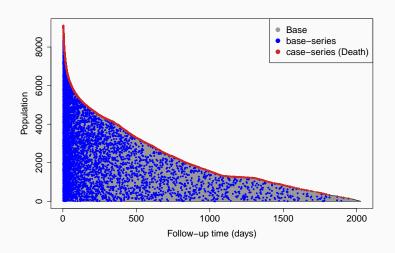
Casebase sampling overview

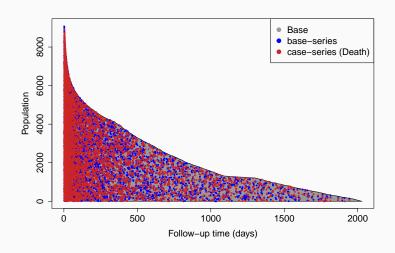
- 1. Clever sampling.
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- 3. Allows a parametric fit using *logistic regression*.
 - Casebase is parametric, and allows different parametric fits by incorporation of the time component.
- Package contains an implementation for generating population-time plots.











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

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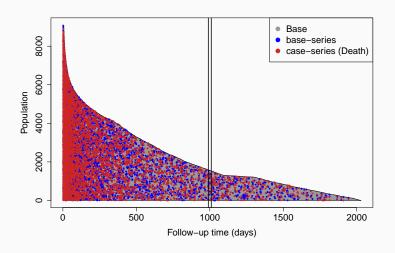
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- B(x,t) = Risk-set for survival time t.

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log-odds = log hazard

$$e^{L} = \frac{\hat{h}(x,t) * B}{b}$$
$$\hat{h}(x,t) = \frac{b * e^{L}}{B}$$
$$log(\hat{h}(x,t)) = L + log(\frac{b}{B})$$

Maximum log-likelihood [1]

$$log(I(\beta_0, \beta)) = \frac{1}{N} \sum_{i=1}^{N} \{ y_i (\beta_0 + x_i^T \beta) - log(1 + e^{\beta_0 + x_i^T \beta}) \}$$

Maximum log-likelihood, with offset

$$log(I(log(\frac{b}{B}),\beta)) = \frac{1}{N} \sum_{i=1}^{N} \{ y_i(log(\frac{b}{B}) + x_i^T \beta) - log(1 + e^{log(\frac{b}{B}) + x_i^T \beta}) \}$$

Maximum log-likelihood, with offset and lasso

$$log(l(log(\frac{b}{B}),\beta)) = \frac{1}{N} \sum_{i=1}^{N} \{ y_i(log(\frac{b}{B}) + x_i^T \beta) - log(1 + e^{log(\frac{b}{B}) + x_i^T \beta}) \} - \lambda ||\beta||$$

Casebase: Parametric families

• We can now fit models of the form:

$$log(h(t;\alpha,\beta)) = g(t;\alpha) + \beta X$$

Casebase: Parametric families

• We can now fit models of the form:

$$log(h(t; \alpha, \beta)) = g(t; \alpha) + \beta X$$

• By changing the function $g(t; \alpha)$, we can model different parametric families easily:

Casebase: Parametric models

Exponential: $g(t; \alpha)$ is equal to a constant

casebase::fitSmoothHazard(status ~ X1 + X2)

Gompertz: $g(t; \alpha) = \alpha t$

casebase::fitSmoothHazard(status ~ time + X1 + X2)

Weibull: $g(t; \alpha) = \alpha log(t)$

casebase::fitSmoothHazard(status ~ log(time) + X1 + X2)

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- CI(x,t)= Cumulative Incidence (Absolute Risk)
- h(x,u)= Hazard function
- Lets use the weibull hazard.

 Recall: Case study to demonstrate regularization using our method.

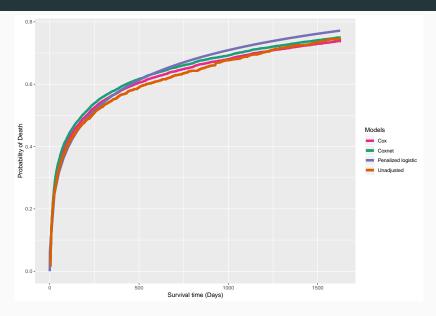
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- **Coxnet**: (death, time) $\sim \beta X <$ Lasso
- **Penalized logistic**: death $\sim \log(\text{time}) + \beta X < -\text{Lasso}$

Survival comparison



Conclusions / take homes

 Classical survival analysis requires methods to encorporate censorship in our data.

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Conclusions / take homes

- Classical survival analysis requires methods to encorporate censorship in our data.
- Case-base sampling is a technique that implicitly encorporates censorship implicitly.
- Logistic regression on SUPPORT dataset had slightly different results near the end of follow-up time.

Future work

• Comparative measure.

Future work

- Comparative measure.
- Survival GWAS.

References 1

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Tutorial and slides

Tutorial:

http://sahirbhatnagar.com/casebase/

Slides:

 $https://github.com/Jesse-Islam/ATGC_survival_presentation_Feb.27.2020$

Questions?