

# Case-base sampling for fitting and validating prognostic models

Workshop on Statistical Issues in Biomarker and Drug Co-development Fields Institute, Toronto

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[Outline](#page-1-0)

#### **Outline**





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- Alternative approaches for fitting flexible hazard models for estimating absolute risks, not requiring this two-step approach?

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- Time matching/risk set sampling (including Cox partial likelihood) eliminates the baseline hazard from the likelihood expression for the hazard ratios.
- If, however, the absolute risks are of interest, they have to be recovered using the semi-parametric Breslow estimator.
- Alternative approaches for fitting flexible hazard models for estimating absolute risks, not requiring this two-step approach?
- There is; it originates from Mantel (1973) and Hanley & Miettinen (2009).

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• Case-base sampling combined with logistic/multinomial regression provides an alternative to risk set sampling-based semi-parametric survival analysis methods.

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- Case-base sampling combined with logistic/multinomial regression provides an alternative to risk set sampling-based semi-parametric survival analysis methods.
- This enables easy fitting of smooth-in-time and non-proportional hazard models with *multiple time scales*.

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- Case-base sampling combined with logistic/multinomial regression provides an alternative to risk set sampling-based semi-parametric survival analysis methods.
- This enables easy fitting of smooth-in-time and non-proportional hazard models with *multiple time scales*.
- Provides an alternative to Kaplan-Meier-based methods for estimating discrimination statistics (e.g. ROC, AUC, risk reclassification probabilities) from censored survival data.

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## Study base

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#### Case series



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## Time matching



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#### **Base series**



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#### Age as the time scale





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#### **Base series**



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#### Base series matched by the Framingham score



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The hazard regression can now be fitted using the conditional likelihood expression

$$
L(\theta) \equiv \prod_{i=1}^n \prod_{t \in (0,\tau]} \left( \frac{\lambda_i(t;\theta)^{\mathrm{d}N_i(t)}}{\rho_i(t) + \lambda_i(t;\theta)} \right)^{\mathrm{d}M_i(t)},
$$

where  $N_i(t)$  counts the cases, and  $M_i(t)$  counts both the case and base series person-moments contributed by individual *i*.

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This is of logistic regression form with the offset term *ρ*i(t) accounting for the base series sampling mechanism.

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where  $N_i(t)$  counts the cases, and  $M_i(t)$  counts both the case and base series person-moments contributed by individual *i*.

- This is of logistic regression form with the offset term *ρ*i(t) accounting for the base series sampling mechanism.
- Generalizes to multinomial regression when competing causes are present.

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### Model specification

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#### Model specification

Consider the following specification of the hazard function:

 $\lambda_i(t;\theta) = \exp\{\theta_0 + f_1(t,\theta_1) + f_2(\text{age at baseline}_i + t, \theta_2)\}$  $+ f_3$ (troponin I<sub>i</sub>,  $\theta_3$ )  $+ \theta_4 \times \text{HDL}$  cholesterol<sub>i</sub>  $+ \theta_5 \times \text{non-HDL}$  cholesterol<sub>i</sub>  $+ \theta_6 \times$  treated systolic blood pressure.  $+ \theta_7 \times$  untreated systolic blood pressure.  $+\theta_8 \times$  smoker<sub>i</sub>  $+ \theta_9 \times$  prevalent diabetes<sub>i</sub>.

• Here  $f_1$ ,  $f_2$  and  $f_3$  are appropriate spline basis functions.

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- Easy to incorporate multiple time scales and interactions between time and other covariates.

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- The likelihood expression does not feature the cumulative hazard, only the hazard function itself evaluated at a discrete number of points.
- The hazard model can be fitted using standard logistic regression procedures.
- The baseline hazard, and consequently, the absolute risk, is obtained as part of the model fit.
- Easy to incorporate multiple time scales and interactions between time and other covariates.
- The time effects themselves can be fitted using flexible specifications, such as regression splines (Hanley & Miettinen, 2009; Saarela & Hanley, 2014).

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Since the hazard model specification was fully parametric, Bayesian measures of uncertainty may be calculated for any function of these parameters.

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- Consequently, we can obtain posterior predictive distributions for discrimination measures such as ROC curves, areas under the curve (AUC), or risk reclassification probabilities.

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- Overfitting?

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- Since the hazard model specification was fully parametric, Bayesian measures of uncertainty may be calculated for any function of these parameters.
- Consequently, we can obtain posterior predictive distributions for discrimination measures such as ROC curves, areas under the curve (AUC), or risk reclassification probabilities.
- Overfitting?
- The procedure works similarly if the risk score has been derived in another sample.

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Consider for example sensitivity, that is, the probability of the estimated  $10$ -year risk  $\pi(X; \theta)$  being at least some threshold risk  $\pi^*,$ given the occurrence of the event during the 10 years, and data  $D$ :

$$
P(\pi(X; \theta) \geq \pi^* \mid N(10) = 1, \theta, D) = \frac{\int_X \mathbf{1}_{\{\pi(x; \theta) \geq \pi^*\}} \pi(x; \theta) P(\mathrm{d}x \mid D)}{\int_X \pi(x; \theta) P(\mathrm{d}x \mid D)}.
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The sources of uncertainty here are the unknown parameters *θ* of the hazard regression model, and the unknown predictive distribution  $P(X | D)$  of the prognostic factors.

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- The sources of uncertainty here are the unknown parameters *θ* of the hazard regression model, and the unknown predictive distribution  $P(X | D)$  of the prognostic factors.
- If we take  $P(\mathrm{d} x\mid D)=\sum_{i=1}^n\frac{1}{n}$  $\frac{1}{n}\delta_{x_i}(\mathrm{d} x)$ , a point estimate is given by

$$
\frac{\sum_{i=1}^n \mathbf{1}_{\{\pi(x_i;\hat{\theta})\geq \pi^*\}} \pi(x_i;\hat{\theta})}{\sum_{i=1}^n \pi(x_i;\hat{\theta})}.
$$

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## Parametric ROC curves



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## Kaplan-Meier ROC curves (Heagerty et al. 2000)

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The hazard model parameters *θ* are drawn from the posterior distribution  $P(d\theta | D) \propto L(\theta)P(d\theta)$ .

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- The posterior predictive distribution of the prognostic factors may be approximated by the Bayesian bootstrap (Rubin, 1981).

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- The posterior predictive distribution of the prognostic factors may be approximated by the Bayesian bootstrap (Rubin, 1981).
- This corresponds to  $P(\text{d}x \mid D) = \sum_{i=1}^{n} w_i \delta_{x_i}(\text{d}x)$ , where (w1*, . . . ,*wn) ∼ Dirichlet(1*, . . . ,* 1).

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- The posterior predictive distribution of the prognostic factors may be approximated by the Bayesian bootstrap (Rubin, 1981).
- This corresponds to  $P(\text{d}x \mid D) = \sum_{i=1}^{n} w_i \delta_{x_i}(\text{d}x)$ , where (w1*, . . . ,*wn) ∼ Dirichlet(1*, . . . ,* 1).
- The ROC curve and corresponding AUC are calculated at each realization of  $\theta$  and  $(w_1, \ldots, w_n)$ .

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#### Posterior AUCs for the five models



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- This enables easy fitting of smooth-in-time and non-proportional hazard models with multiple time scales.
- Similarly, this provides an alternative to Kaplan-Meier-based methods for estimating discrimination statistics (e.g. ROC, AUC, risk reclassification probabilities) from censored survival data.

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- Bayesian measures of uncertainty can be obtained for these.

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- Similarly, this provides an alternative to Kaplan-Meier-based methods for estimating discrimination statistics (e.g. ROC, AUC, risk reclassification probabilities) from censored survival data.
- Bayesian measures of uncertainty can be obtained for these.
- Improving the prediction of CVD in healthy populations, beyond the classic risk factors of CVD, has been challenging.

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