Super Learning for Combining Dynamic Predictions for Decision-Making

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1 Background & Motivation

Motivating Study: University of Michigan Prostatectomy Data

- 3634 PCa patients followed-up in 1996–2013
  - aged 40 to 84 years with clinically localized cT1 to cT3 disease
  - received radical prostatectomy

1 Background & Aim (cont'd)

University of Michigan Prostatectomy Data

Patients remain at risk of metastasis

- Follow-up
  - * PSA levels at frequent intervals
  - * when PSA increases, physicians consider Salvage Therapy (ST)
  - * ST androgen deprivation therapy, radiation therapy, chemotherapy, and combinations

1 Background & Motivation (cont'd)

University of Michigan Prostatectomy Data

Use the longitudinal PSA & baseline covariates to predict the risk of metastasis

1 Background & Motivation (cont'd)

- Two main frameworks to obtain such predictions

  ▷ *Landmarking*

    * a series of Cox models at different landmark times
    * biomarker last value as a baseline covariate or a mixed model
    * Breslow estimator of survival probabilities

  ▷ *Joint Models*

    * complete specification of the joint distribution of the outcomes
    * direct derivation of conditional risk probabilities

1 Background & Motivation (cont'd)

Landmarking

- ▷ *Advantages*
  - * easier to use, available in standard software
  - * can generalize to multiple biomarkers without (much) extra computational cost

- ▷ *Disadvantages*
  - * predictions not consistent
  - * not plausible LOCF for biomarkers
  - * does not account for measurement error and endogeneity
  - * not valid causal interpretation

1 Background & Motivation (cont'd)

Joint Models

- ▷ *Advantages*
  - * consistent predictions
  - * accounts for measurement error and endogeneity
  - * biomarkers follow a trajectory
  - * valid causal interpretation

- ▷ *Disadvantages*
  - * computationally intensive
  - * *sensitive to modeling assumptions*

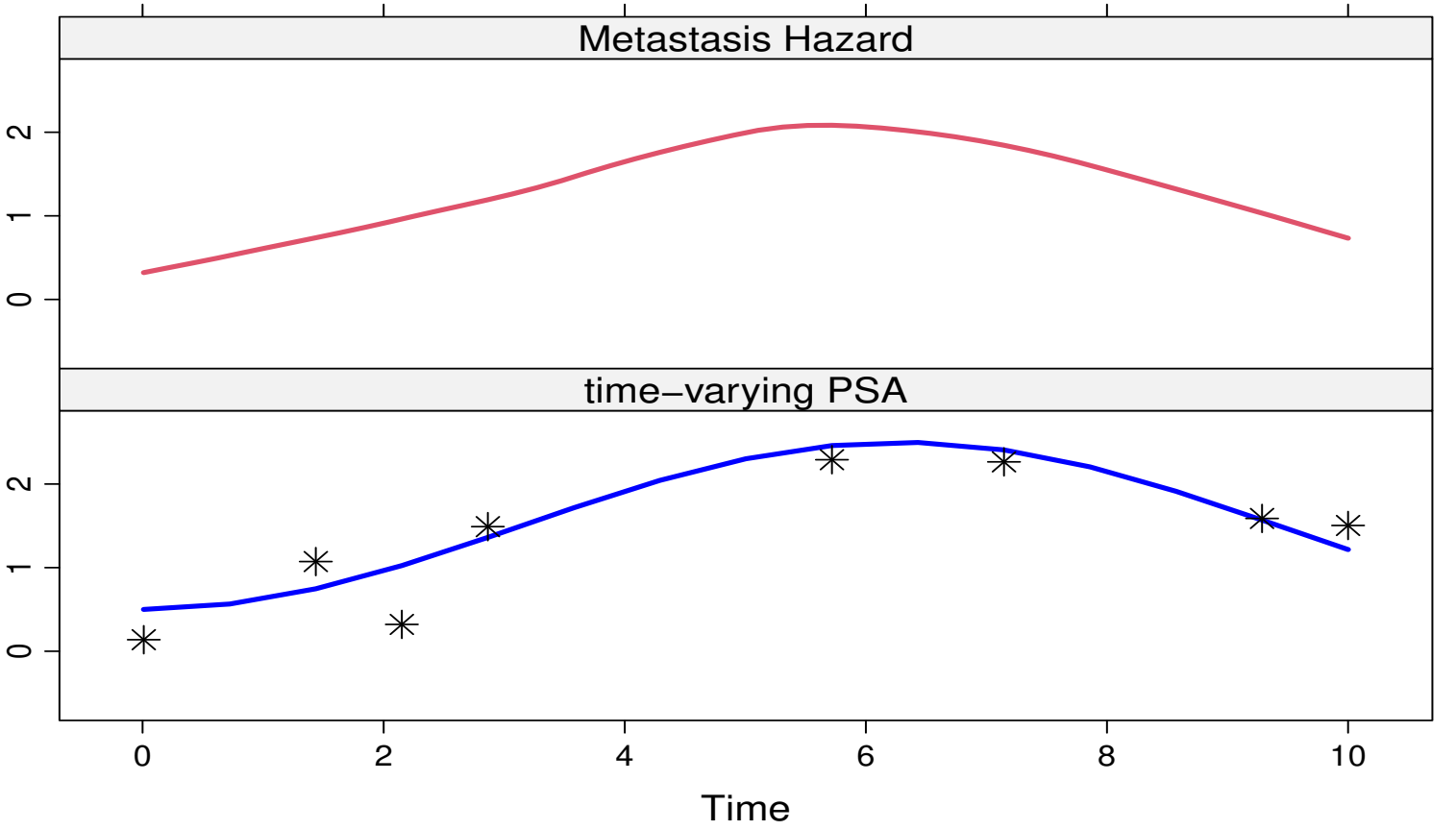
1 Background & Motivation (cont'd)

- *Sensitive to modeling assumptions*
  - ▷ *Longitudinal profiles shape*
    - * non-linear subject-specific trajectories
  - ▷ *Functional form*
    - * how to link the hazard of the event with the longitudinal outcome

Joint Models Framework - Basic Idea

- ▷ Use a model to describe the subject-specific longitudinal trajectories
- ▷ Use these trajectories in a hazard model for the event
- ▷ Random effects explain the association

2 Joint Models (cont'd)



2 Joint Models (cont'd)

More formally

$$
\begin{cases}
h_i(t \mid \mathcal{H}_i(t, \boldsymbol{b}_i)) = h_0(t) \exp\{\boldsymbol{\gamma}^\top \boldsymbol{w}_i + f(\alpha, \mathcal{H}_i(t, \boldsymbol{b}_i))\}, \\
\qquad\qquad\qquad\qquad \mathcal{H}_i(t, \boldsymbol{b}_i) = \{\eta_i(s, \boldsymbol{b}_i); 0 \leq s \leq t\} \\
\\
y_i(t) = \eta_i(t, \boldsymbol{b}_i) + \varepsilon_i(t) \\
\qquad\quad = \boldsymbol{x}_i^\top(t)\boldsymbol{\beta} + \boldsymbol{z}_i^\top(t)\boldsymbol{b}_i + \varepsilon_i(t), \quad \varepsilon_i(t) \sim \mathcal{N}(0, \sigma^2), \\
\\
\boldsymbol{b}_i \sim \mathcal{N}(\boldsymbol{0}, \boldsymbol{D})
\end{cases}
$$

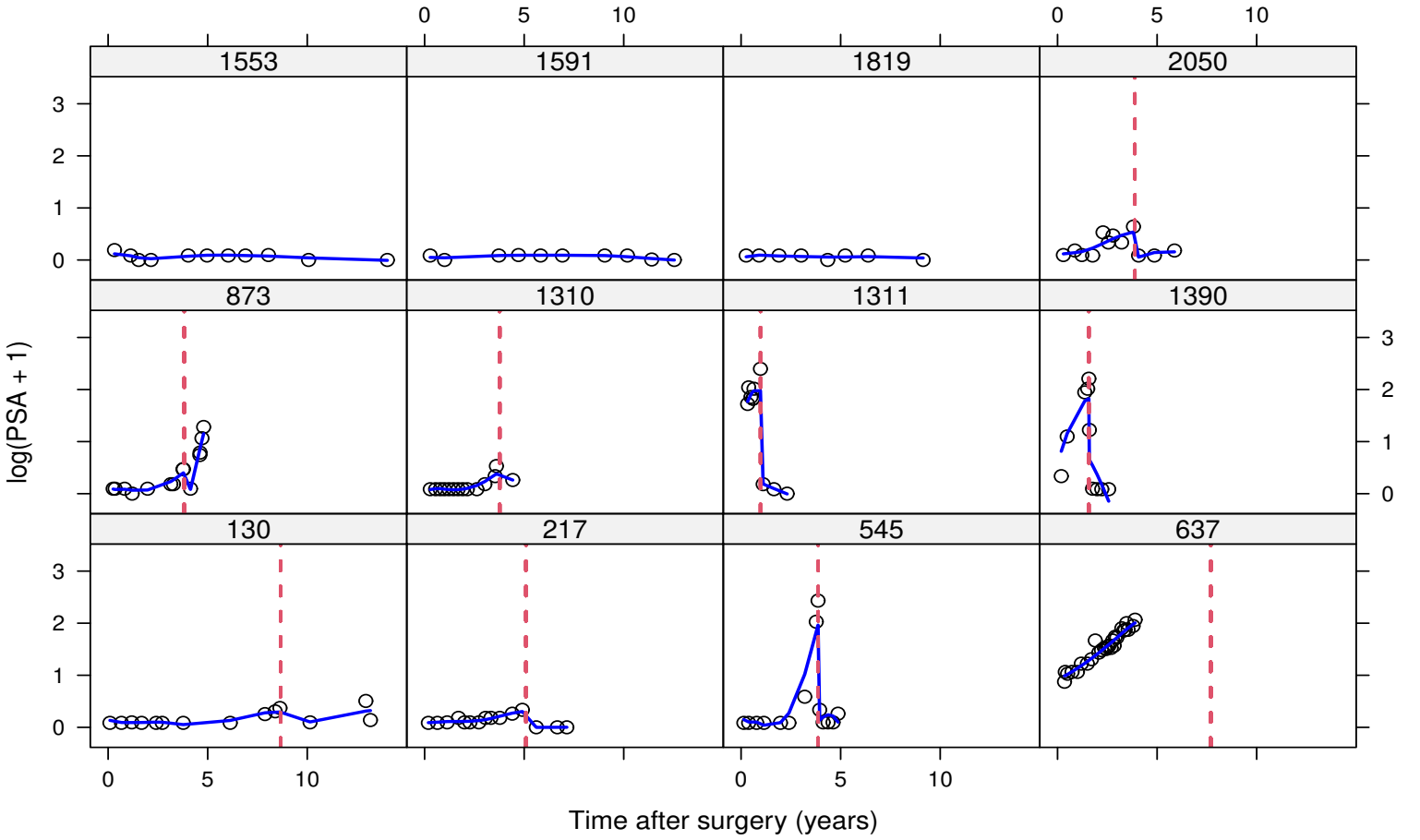
2 Joint Models (cont'd)

- In the context of dynamic predictions,
  - ▷ previous research has shown that predictive accuracy is compromised
  - ▷ when the model does not *adequately* capture the subject-specific trajectories shape

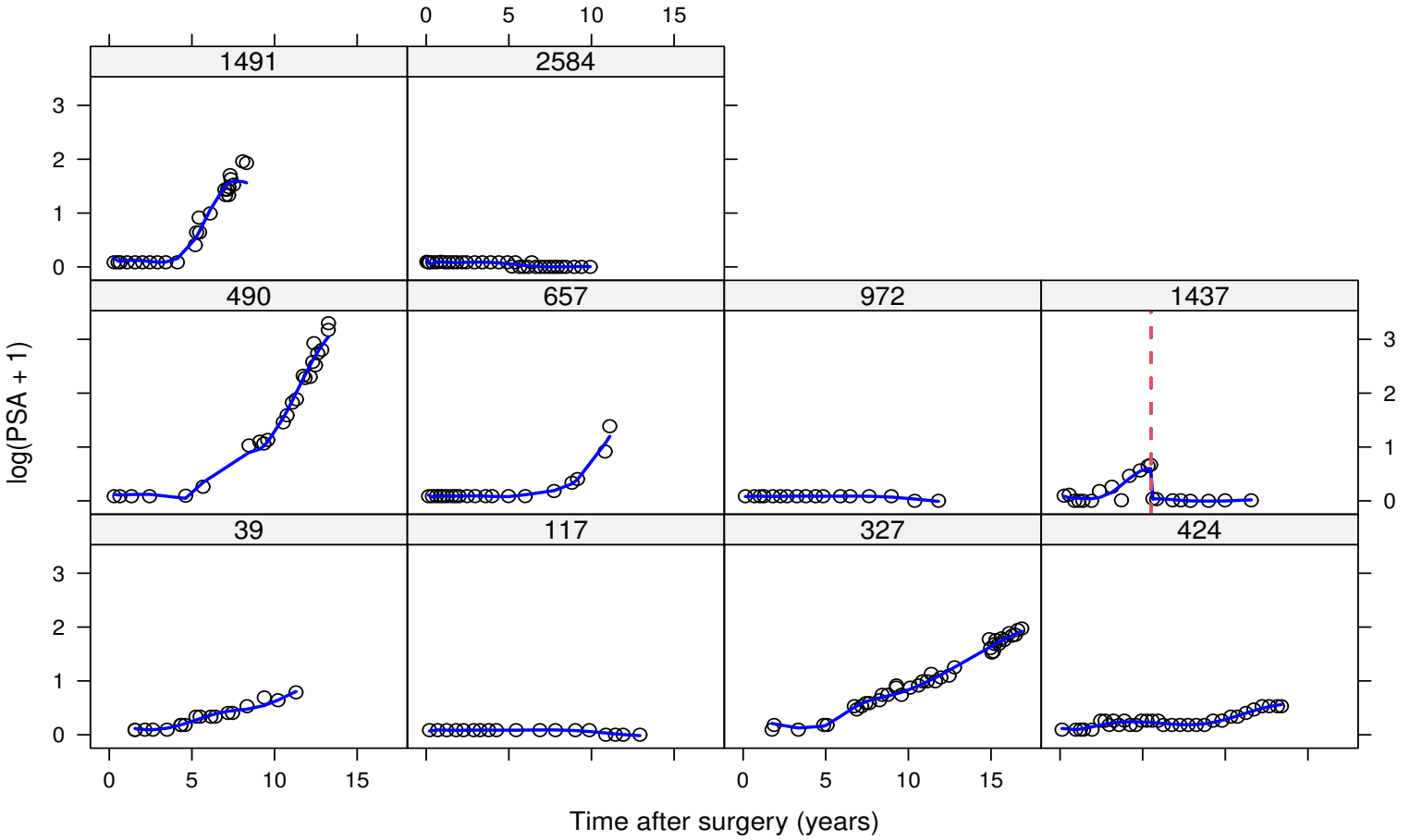
Advice

- ▷ use flexible models, e.g., splines in both fixed- and random-effects parts
- ▷ *increased computational burden*

2 Joint Models (cont'd)



2 Joint Models (cont'd)



3 Functional Forms

There are different ways to link the longitudinal trajectories to the risk of an event

▷ Some standard options are . . .

3 Functional Forms (cont'd)

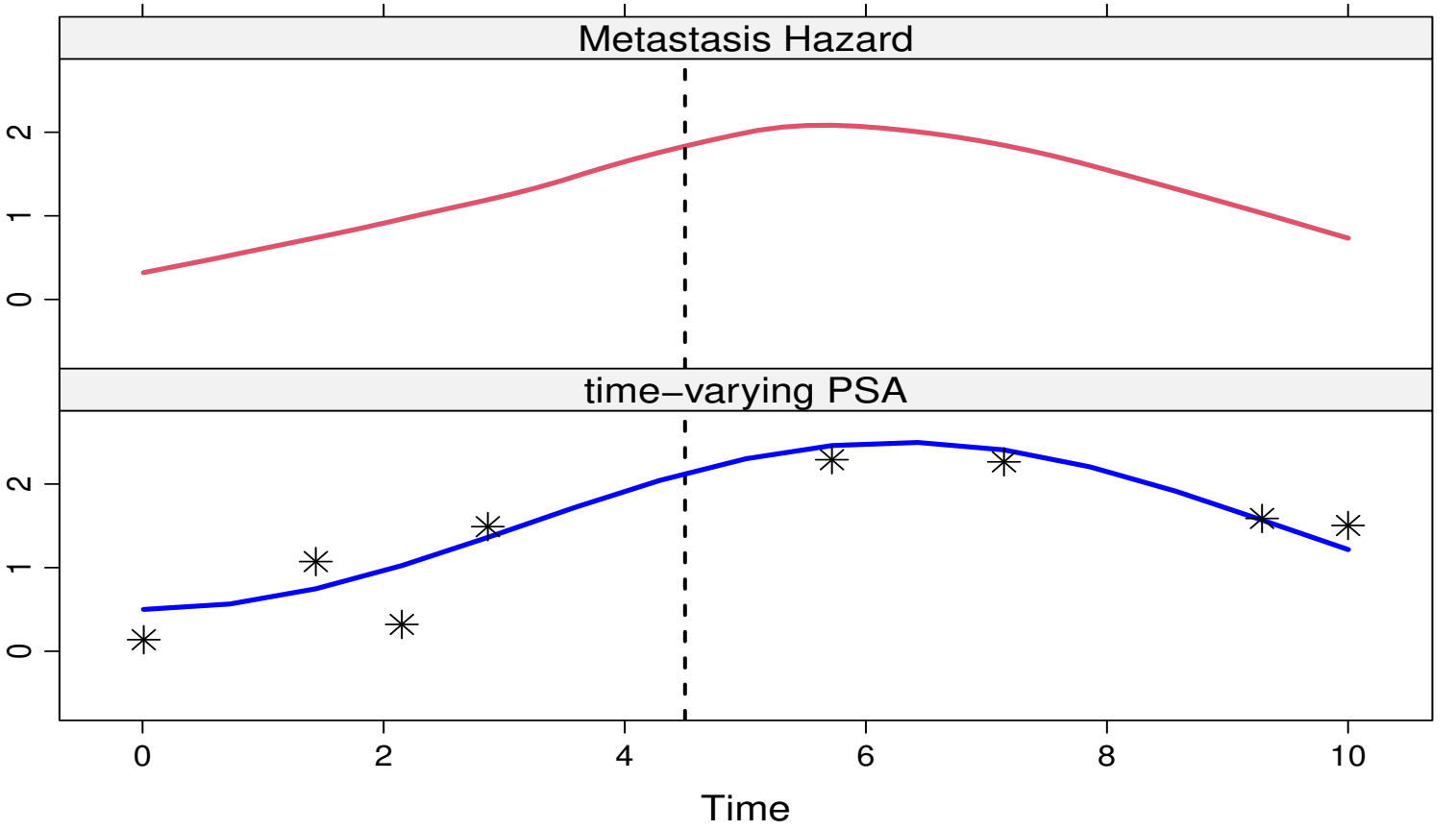
Value: The hazard of metastasis at t is associated with the level of PSA at t:

$$h_i(t \mid \mathcal{H}_i(t, \boldsymbol{b}_i)) \;=\; h_0(t) \exp\{\boldsymbol{\gamma}^\top \boldsymbol{w}_i + \alpha \eta_i(t, \boldsymbol{b}_i)\}$$

where

$$\eta_i(t, \boldsymbol{b}_i) = \boldsymbol{x}_i^\top(t)\boldsymbol{\beta} + \boldsymbol{z}_i^\top(t)\boldsymbol{b}_i$$

3 Functional Forms (cont'd)



3 Functional Forms (cont'd)

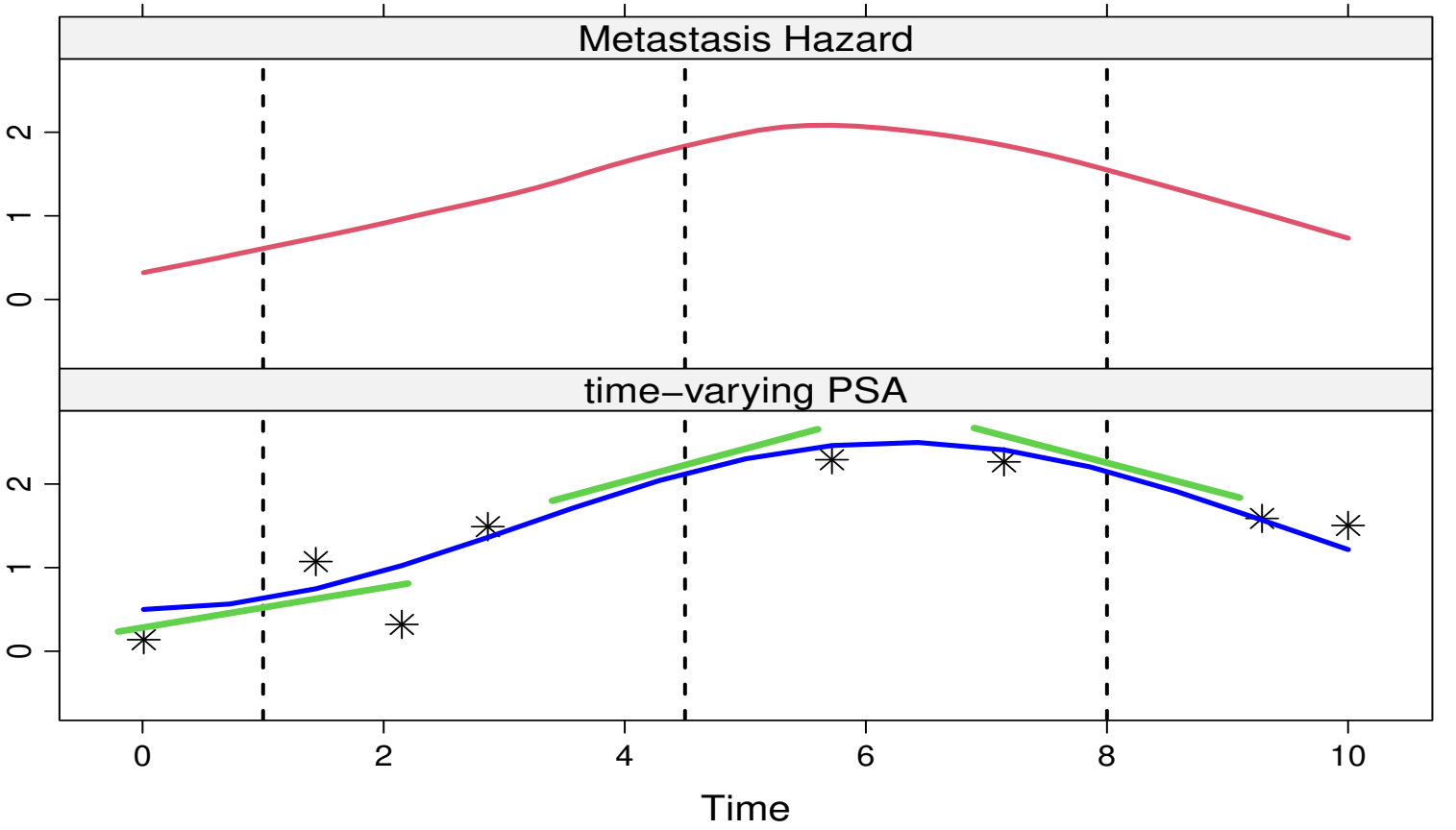
Velocity: The hazard of metastasis at t is associated with the slope of the PSA trajectory at t:

$$h_i(t \mid \mathcal{H}_i(t, \boldsymbol{b}_i)) = h_0(t) \exp\{\boldsymbol{\gamma}^\top \boldsymbol{w}_i + \alpha \eta_i'(t, \boldsymbol{b}_i)\},$$

where

$$\eta_i'(t, \boldsymbol{b}_i) = \frac{\mathsf{d}}{\mathsf{d}t}\{\boldsymbol{x}_i^\top(t)\boldsymbol{\beta} + \boldsymbol{z}_i^\top(t)\boldsymbol{b}_i\}$$

3 Functional Forms (cont'd)



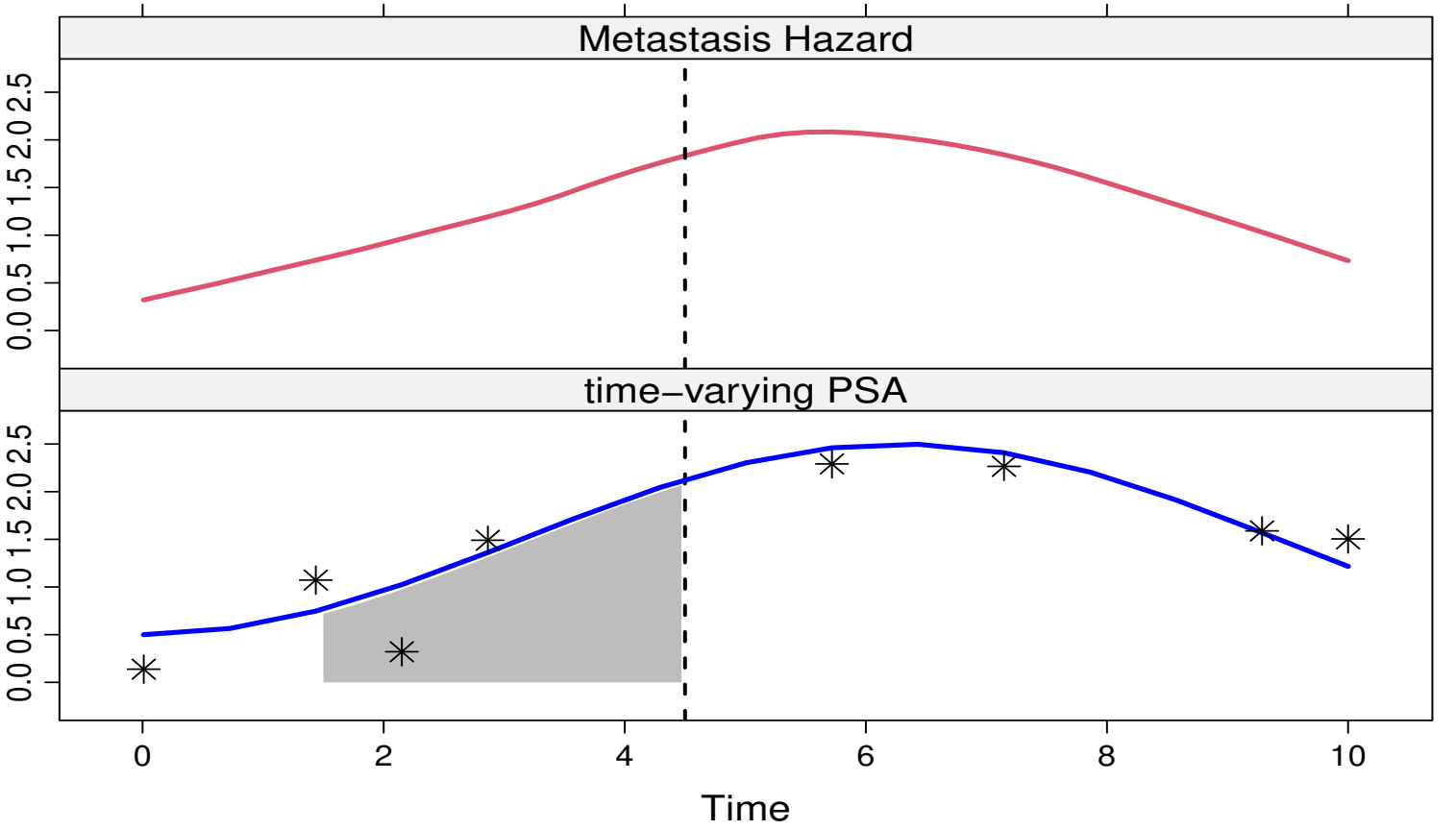
3 Functional Forms (cont'd)

Average Effects: The hazard of metastasis at t is associated with the average PSA in the interval $(t - v, t)$:

$$h_i(t \mid \mathcal{H}_i(t, \boldsymbol{b}_i)) = h_0(t) \exp\left\{ \boldsymbol{\gamma}^\top \boldsymbol{w}_i + \alpha \frac{1}{v} \int_{t-v}^{t} \eta_i(s, \boldsymbol{b}_i) \, \mathrm{d}s \right\}$$

We account for the observation period

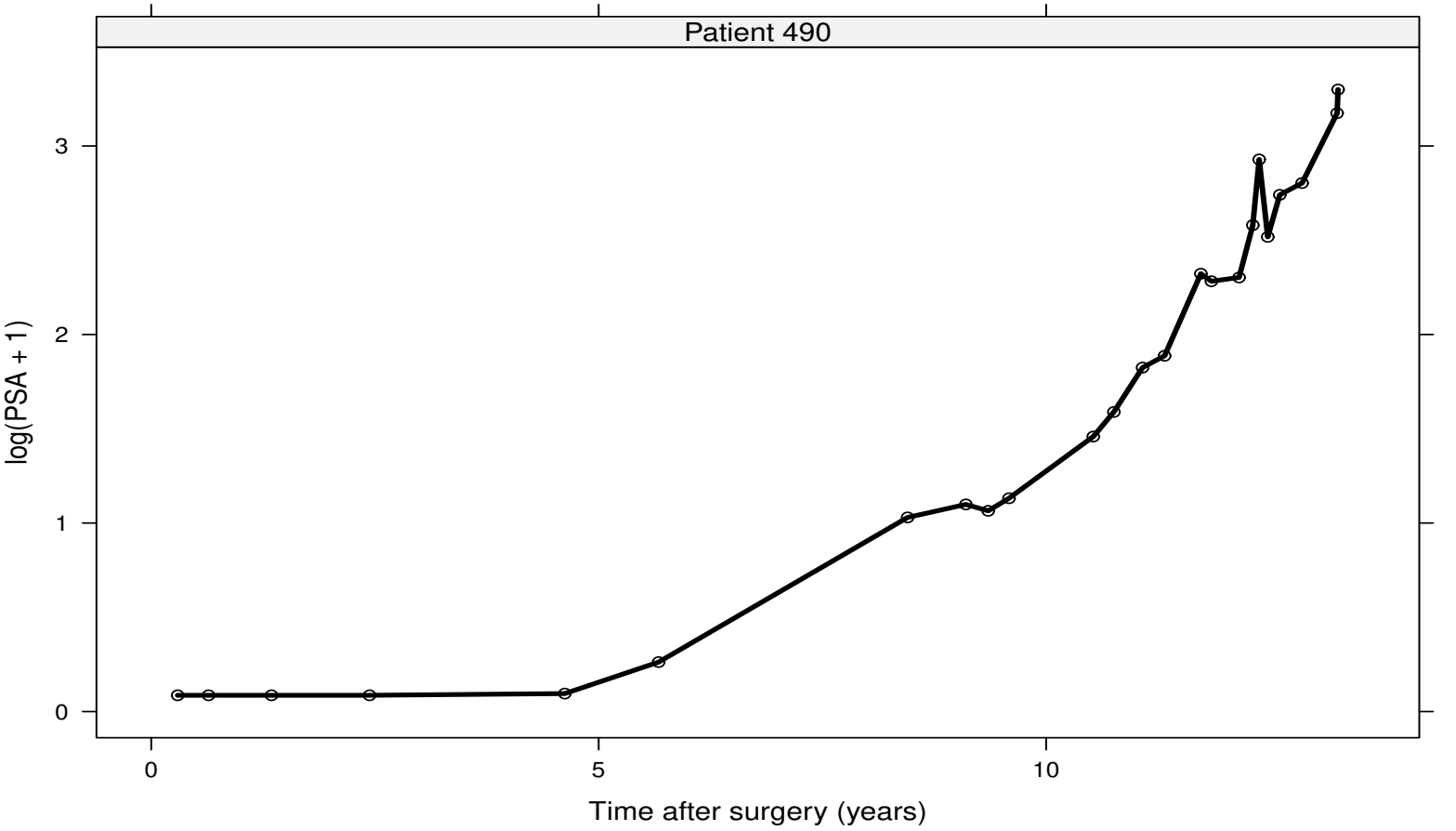
3 Functional Forms (cont'd)



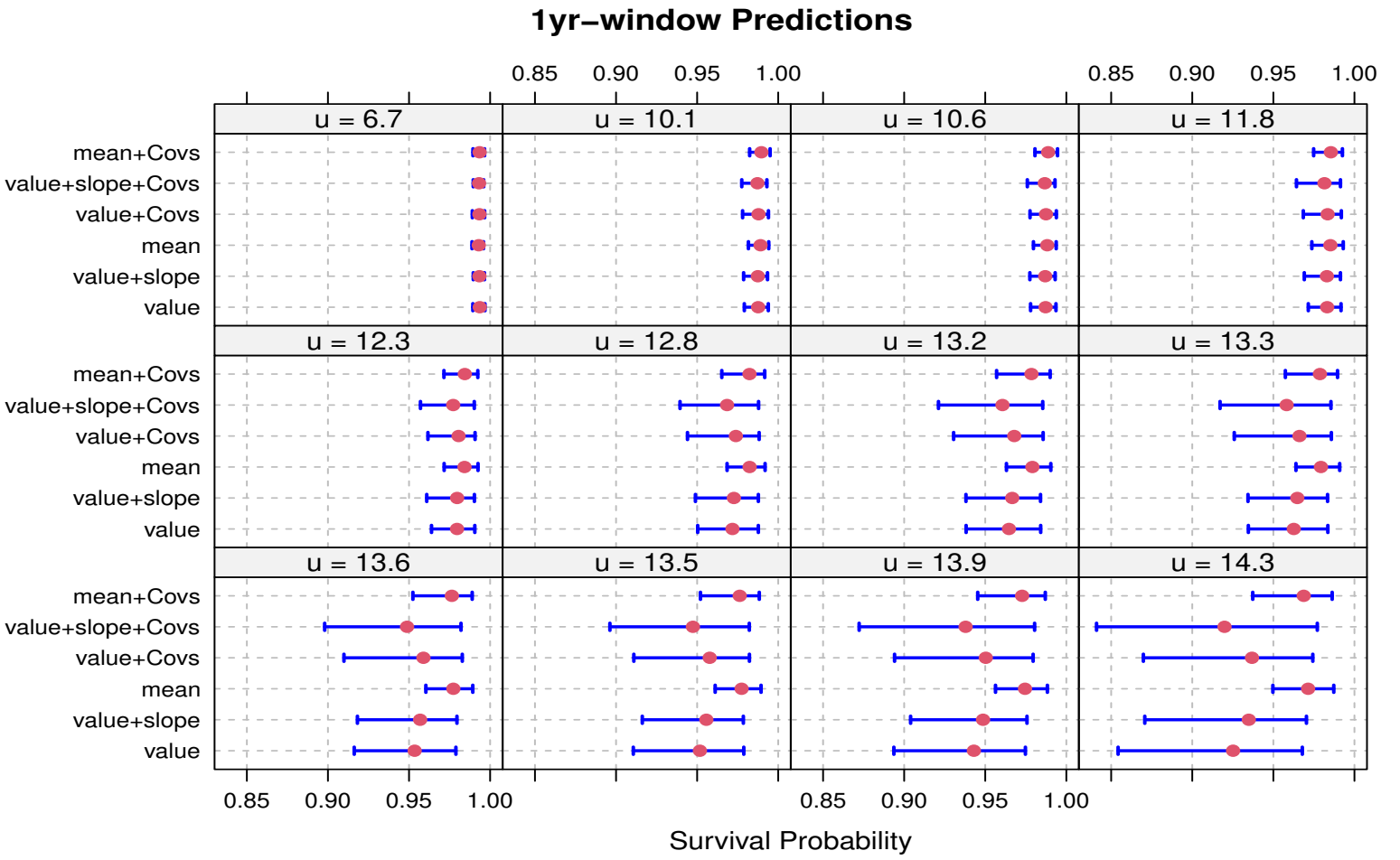
3 Functional Forms (cont'd)

How significant is the choice of the functional form for dynamic predictions?

3 Functional Forms (cont'd)



3 Functional Forms (cont'd)



4 Super Learning

- The selected functional form and time effect for the longitudinal outcome can influence the derived predictions
  - ▷ especially for the survival outcome

How to select between the different functional forms and trajectory shapes?

4 Super Learning (cont'd)

- The standard answer is to employ information criteria, e.g., DIC, WAIC, ...

- However, the longitudinal information dominates the joint likelihood
  $\Rightarrow$ will not be sensitive enough wrt predicting survival probabilities

- In addition, will *a single model* be the most appropriate
  - ▷ for all future patients?
  - ▷ for all follow-up times?

4 Super Learning (cont'd)

Solution: *Super Learning*

- *Consider multiple plausible models with different*
  - longitudinal outcomes
  - assumptions for the longitudinal profiles
  - functional forms
  - baseline covariates, interaction terms
  - ...

- *Obtain the desired predictions from these models*

- *Combine predictions using weights*
  - *how to select the weights?*

4 Super Learning (cont'd)

Solution: *Super Learning*

- ▷ select weights to optimize prediction metric *of your choice*
- ▷ account for over-fitting using cross-validation

4 Super Learning (cont'd)

How it works:

- Assume we have a library of L *base-learners* (models) $\mathcal{L} = \{M_1, \ldots, M_L\}$
- Specify time t to optimize the dynamic predictions, and a medically-relevant time window Δt
- Split $\mathcal{D}_n$ in V-folds
- For $v \in \{1, \ldots, V\}$, train the learners in library $\mathcal{L}$ in $\mathcal{D}_n^{(-v)}$

4 Super Learning (cont'd)

How it works:

▷ For the subjects in $\mathcal{D}_n^{(v)}$, not used when training the learner, calculate the predictions

$$\hat{\pi}_i^{(v)}(t + \Delta t \mid t, M_l) = \Pr\{T_i^* < t + \Delta t \mid T_i^* > t, \mathcal{H}_i(t), M_l, \mathcal{D}_n^{(-v)}\}$$

do this for all $v = 1, \ldots, V$ to get the *cross-validated predictions*

4 Super Learning (cont'd)

How it works:

▷ We define the ensemble of *cross-validated predictions*

$$\hat{\bar{\pi}}_i^v(t+\Delta t \mid t) = \sum_{l=1}^{L} \varpi_l(t)\hat{\pi}_i^{(v)}(t+\Delta t \mid t, M_l), \quad v = 1, \ldots, V$$

* the weights depend on $t \Rightarrow$ *different weights at different follow-up times*

4 Super Learning (cont'd)

How it works:

- Select $\varpi_l(t)$ to optimize your *meta-learner* (predictive accuracy metric), e.g.,
  - Brier Score (*Proper scoring rule*)
  - Expected Predictive Cross-Entropy (*Proper scoring rule*)
  - AUC (*Not a proper scoring rule*)
  - ...

- Under the constraints
  - $\widehat{\varpi}_l(t) > 0$ for all $l = 1, \ldots, L$
  - $\sum_{l=1}^{L} \widehat{\varpi}_l(t) = 1$

5 UM Data Analysis

A library $\mathcal{L}$ with twelve joint models

- PSA models
  - ▷ M_{l1}: *linear* subject-specific time trends that change after salvage
  - ▷ M_{l2}: the same as M_{l1} + covariates
  - ▷ M_{l3}: *nonlinear* subject-specific time trends that change after salvage
  - ▷ M_{l4}: the same as M_{l3} + covariates
- Baseline covariates: age at surgery, Charlson's index, Gleason score, and baseline PSA

5 UM Data Analysis (cont'd)

A library $\mathcal{L}$ with twelve joint models

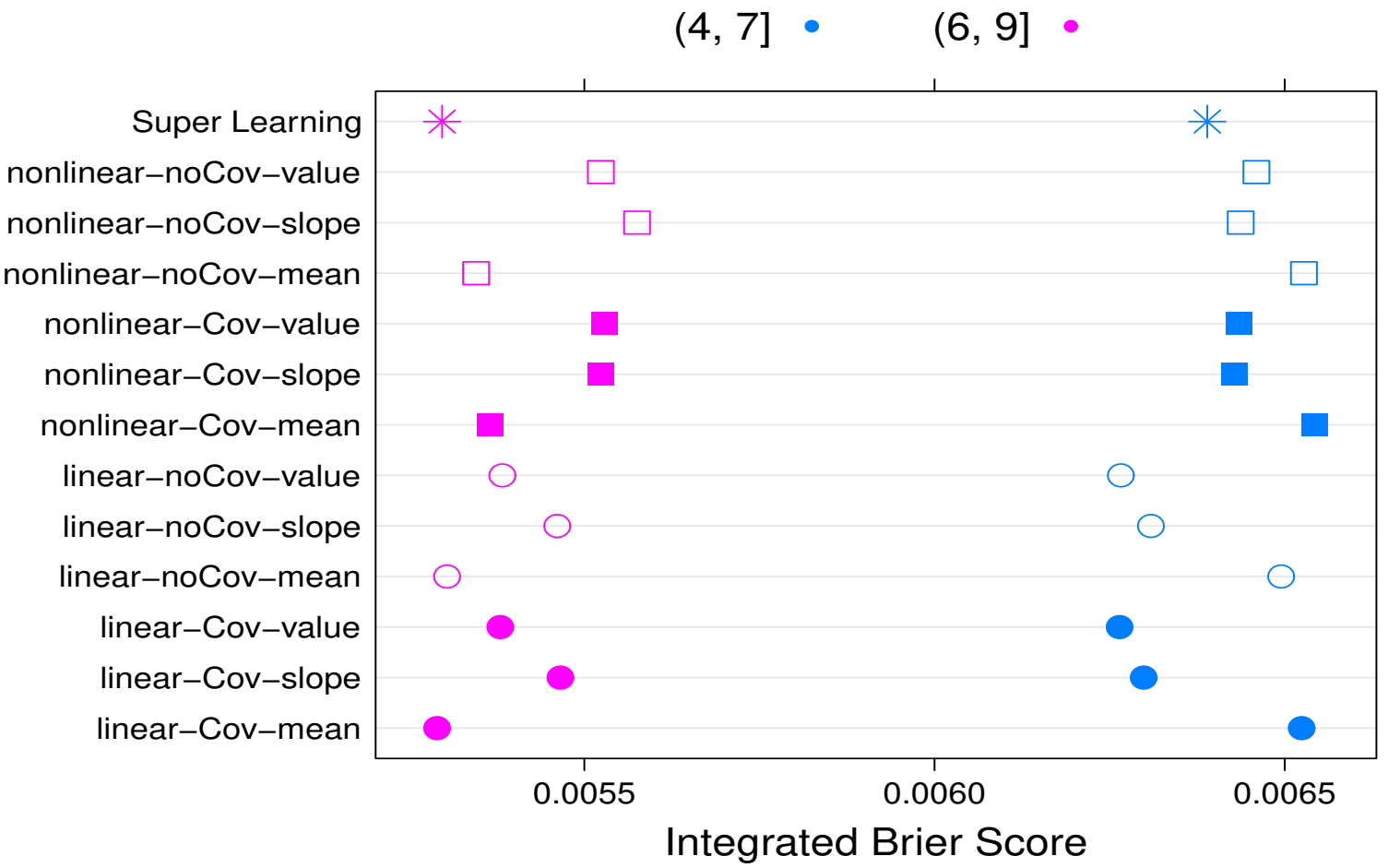
- Metastasis models
  - ▷ M_{s1}: value of $\log(\text{PSA} + 1)$
  - ▷ M_{s2}: velocity of $\log(\text{PSA} + 1)$
  - ▷ M_{s3}: average $\log(\text{PSA} + 1)$
- Time varying salvage therapy
- Baseline covariates: the same as in the PSA models

5 UM Data Analysis (cont'd)

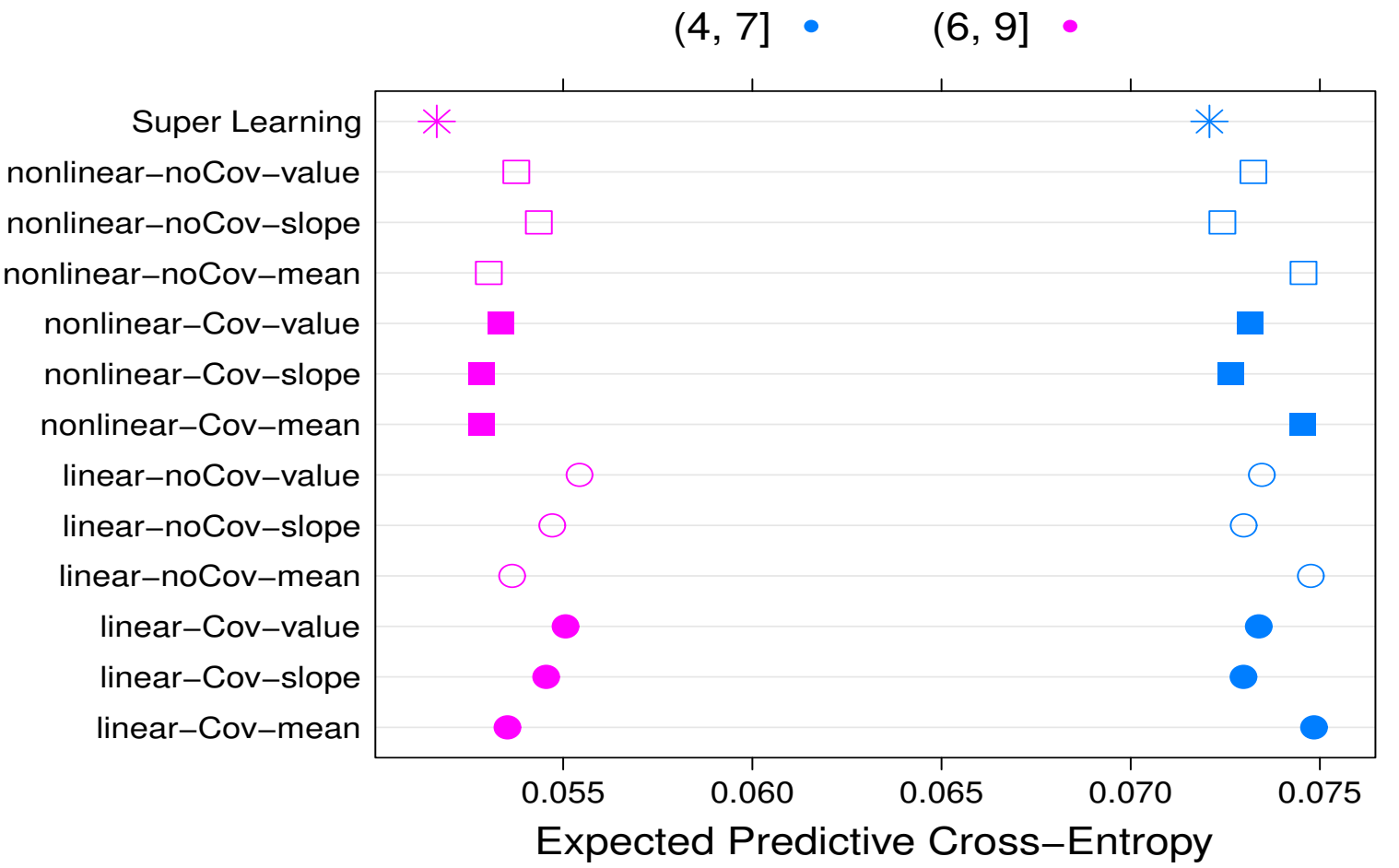
- We evaluated predictive accuracy in two time intervals
  - ▷ $(4, 7]$: 2514 patients at risk; 28 metastasis
  - ▷ $(6, 9]$: 1914 patients at risk; 16 metastasis

- Metrics
  - ▷ Integrated Brier Score
  - ▷ Expected Predictive Cross-Entropy

5 UM Data Analysis (cont'd)



5 UM Data Analysis (cont'd)



6 Software

- Available in **JMbayes2**
  - ▷ cross-validated fitting of models
  - ▷ combination of dynamic predictions
    https://drizopoulos.github.io/JMbayes2/articles/Super_Learning.html

Thank for your attention!

https://www.drizopoulos.com/

7 Choice of the Meta-Learner

We focus on two meta-learners

▷ *Integrated Brier Score*

$$\text{IBS}(t+\Delta t, t) = \frac{1}{\Delta t}\int_t^{t+\Delta t} E\left[\left\{\mathbb{I}(T_i^* \leq s) - \pi_i(s \mid t)\right\}^2 \,\middle|\, T_i^* > t\right] \mathrm{d}s$$

▷ *Expected Predictive Cross-Entropy*

$$\text{EPCE}(t+\Delta t, t) = E\left\{-\log\left[p\left\{T_i^* \mid t < T_i^* \leq t+\Delta t, \mathcal{Y}_i(t)\right\}\right]\right\}$$

7 Choice of the Meta-Learner (cont'd)

- For the estimation of the Brier score, we need to account for censoring in $[t, t + \Delta t)$
  * inverse probability of censoring weighting
  * model-based weights

7 Choice of the Meta-Learner (cont'd)

- Brier Score with IPCW

$$\widehat{\mathsf{BS}}_{IPCW}(t+\Delta t,t)=\frac{1}{n}\sum_{i=1}^{n}\widehat{W}_i(t+\Delta t,t)\Big\{\mathbb{I}(T_i\leq t+\Delta t)-\hat{\hat{\pi}}_i^v(t+\Delta t\mid t)\Big\}^2$$

where

$$\widehat{W}_i(t+\Delta t,t)=\frac{\mathbb{I}(t<T_i\leq t+\Delta t)\delta_i}{\hat{G}(T_i\mid t)}+\frac{\mathbb{I}(T_i>t+\Delta t)}{\hat{G}(t+\Delta t\mid t)},$$

with $\hat{G}(\cdot)$ denoting Kaplan-Meier estimate of the censoring distribution $\Pr(C_i>t)$

7 Choice of the Meta-Learner (cont'd)

- Brier Score with model-weights

$$\widehat{\mathsf{BS}}_{model}(t+\Delta t,t)=\frac{1}{n_t}\sum_{i:T_i>t}\delta_i\mathbb{I}(T_i\leq t+\Delta t)\Big\{1-\hat{\tilde{\pi}}_i^v(t+\Delta t\mid t)\Big\}^2$$
$$+\,\mathbb{I}(T_i>t+\Delta t)\Big\{\hat{\tilde{\pi}}_i^v(t+\Delta t\mid t)\Big\}^2$$
$$+(1-\delta_i)\mathbb{I}(T_i\leq t+\Delta t)\Bigg[\hat{\tilde{\pi}}_i^v(t+\Delta t\mid T_i)\Big\{1-\hat{\tilde{\pi}}_i^v(t+\Delta t\mid t)\Big\}^2$$
$$+\Big\{1-\hat{\tilde{\pi}}_i^v(t+\Delta t\mid T_i)\Big\}\Big\{\hat{\tilde{\pi}}_i^v(t+\Delta t\mid t)\Big\}^2\Bigg]$$

7 Choice of the Meta-Learner (cont'd)

- IPCW
  - ▷ *Advantage:* it provides unbiased estimates even when the model is misspecified
  - ▷ *Disadvantage:* it requires that the model for the weights is correct
    * challenging because censoring may depend on the longitudinal outcomes in a complex manner
    * sensitive to (unobserved) instrument by confounder interactions

7 Choice of the Meta-Learner (cont'd)

- Model-based Weights
  - ▷ *Advantage:* it allows censoring to depend on the longitudinal history (in any possible manner)
  - ▷ *Disadvantage:* it requires that the model is well-specified

7 Choice of the Meta-Learner (cont'd)

- An estimate of EPCE$(t + \Delta t, t)$ that accounts for censoring

$$\widehat{\text{EPCE}}(t + \Delta t, t) = \frac{1}{n_t} \sum_{i:T_i > t} - \log\Big[p\{\tilde{T}_i, \tilde{\delta}_i \mid T_i > t, \mathcal{Y}_i(t), \mathcal{D}_n\}\Big]$$

  with

  - $\tilde{T}_i = \min(T_i, t + \Delta t)$
  - $\tilde{\delta}_i = \delta_i \mathbb{I}(t < T_i \leq t + \Delta t)$

- Features

  - it allows censoring to depend on the longitudinal history
  - *problem:* it is not written as a function of the predictions

7 Choice of the Meta-Learner (cont'd)

- The conditional predictive log-likelihood

$$\log\Big[p\{\tilde{T}_i, \tilde{\delta}_i \mid T_i > t, \mathcal{Y}_i(t), \mathcal{D}_n\}\Big] =$$
$$\tilde{\delta}_i \log[h_i\{\tilde{T}_i \mid \mathcal{Y}_i(t), \mathcal{D}_n\}] + \log \frac{\Pr\{T_i^* > \tilde{T}_i \mid \mathcal{Y}_i(t), \mathcal{D}_n\}}{\Pr\{T_i^* > t \mid \mathcal{Y}_i(t), \mathcal{D}_n\}}$$

  - ▷ the second term is $\log\{\pi_i(\tilde{T}_i \mid t)\}$
  - ▷ for the first term, we write the hazard function as

$$h_i\{\tilde{T}_i \mid \mathcal{Y}_i(t), \mathcal{D}_n\} = \frac{p(\tilde{T}_i)}{S(\tilde{T}_i)} = -\frac{\frac{\mathrm{d}}{\mathrm{d}t}\Pr\{T_i^* > t \mid \mathcal{Y}_i(t), \mathcal{D}_n\}\Big|_{t=\tilde{T}_i}}{\Pr\{T_i^* > \tilde{T}_i \mid \mathcal{Y}_i(t), \mathcal{D}_n\}}$$

7 Choice of the Meta-Learner (cont'd)

- We approximate the derivative with a forward difference and we get

$$\widehat{\mathsf{EPCE}}(t+\Delta t, t) =$$

$$-\frac{1}{n_t}\sum_{i:T_i>t}\tilde{\delta}_i\left[\log\{1-\hat{\tilde{\pi}}_i^v(\tilde{T}_i+\epsilon \mid \tilde{T}_i)\}-\log(\epsilon)\right]+\log\{\hat{\tilde{\pi}}_i^v(\tilde{T}_i \mid t)\}$$

that can be used to optimize $\varpi_l(t)$

7 UM Data Analysis (cont'd)

	$(t, t+\Delta t] = (4, 7]$		$(t, t+\Delta t] = (6, 9]$	
	IBS	weights	IBS	weights
SL	0.00639		0.00530	
linear-noCov-value	0.00627	0.08334	0.00538	0.00352
linear-noCov-slope	0.00631	0.08342	0.00546	0.00136
linear-noCov-mean	0.00649	0.08329	0.00530	0.31705
linear-Cov-value	0.00626	0.08344	0.00538	0.01732
linear-Cov-slope	0.00630	0.08342	0.00547	0.00124
linear-Cov-mean	0.00652	0.08327	0.00529	0.52883
nonlinear-noCov-value	0.00646	0.08331	0.00552	0.00009
nonlinear-noCov-slope	0.00644	0.08332	0.00558	0.00002
nonlinear-noCov-mean	0.00653	0.08327	0.00535	0.08450
nonlinear-Cov-value	0.00643	0.08332	0.00553	0.00008
nonlinear-Cov-slope	0.00643	0.08333	0.00552	0.00008
nonlinear-Cov-mean	0.00654	0.08326	0.00537	0.04589

7 UM Data Analysis (cont'd)

	$(t, t+\Delta t] = (4, 7]$		$(t, t+\Delta t] = (6, 9]$	
	EPCE	weights	EPCE	weights
SL	0.07208		0.05166	
linear-noCov-value	0.07347	0.00026	0.05543	0.03259
linear-noCov-slope	0.07299	0.00004	0.05471	0.15417
linear-noCov-mean	0.07476	0.00235	0.05365	0.01329
linear-Cov-value	0.07338	0.00000	0.05506	0.02167
linear-Cov-slope	0.07298	0.00006	0.05455	0.09639
linear-Cov-mean	0.07484	0.00274	0.05353	0.02836
nonlinear-noCov-value	0.07324	0.00000	0.05376	0.01562
nonlinear-noCov-slope	0.07242	0.79539	0.05436	0.00317
nonlinear-noCov-mean	0.07457	0.18346	0.05303	0.02524
nonlinear-Cov-value	0.07316	0.00000	0.05337	0.10840
nonlinear-Cov-slope	0.07265	0.00121	0.05283	0.08131
nonlinear-Cov-mean	0.07454	0.01448	0.05284	0.41979