

# Fitting Joint Models in R using Packages JM and JMbayes

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Joint Statistical Meetings

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# 1.1 Introduction

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- Often in follow-up studies different types of outcomes are collected
- **Explicit** outcomes
  - ▷ multiple longitudinal responses (e.g., markers, blood values)
  - ▷ time-to-event(s) of particular interest (e.g., death, relapse)
- **Implicit** outcomes
  - ▷ missing data (e.g., dropout, intermittent missingness)
  - ▷ random visit times

## 1.2 Illustrative Case Study

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- Aortic Valve study: Patients who received a human tissue valve in the aortic position
  - ▷ data collected by Erasmus MC (from 1987 to 2008);  
77 received sub-coronary implantation; 209 received root replacement
- Outcomes of interest:
  - ▷ death and re-operation → **composite event**
  - ▷ aortic gradient

## 1.3 Research Questions

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- Depending on the questions of interest, different types of statistical analysis are required
- Focus on each outcome separately
  - ▷ does treatment affect survival?
  - ▷ are the average longitudinal evolutions different between males and females?
  - ▷ ...

## 1.3 Research Questions (cont'd)

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- Focus on multiple outcomes
  - ▷ Complex effect estimation: how strong is the association between the longitudinal **outcome** and the hazard rate of death?
  - ▷ Handling implicit outcomes: focus on the longitudinal outcome but with **dropout**

## 1.3 Research Questions (cont'd)

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In the Aortic Valve dataset:

- Research Question:
  - ▷ Can we utilize available aortic gradient measurements to predict survival/re-operation

## 1.4 Goals

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- Methods for the separate analysis of such outcomes are well established in the literature
- Survival data:
  - ▷ Cox model, accelerated failure time models, ...
- Longitudinal data
  - ▷ mixed effects models, GEE, marginal models, ...

## 1.4 Goals (cont'd)

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- **Goals** of this talk:
  - ▷ Introduce joint models
    - \* definition
    - \* association structures
    - \* dynamic predictions
  - ▷ Illustrate software capabilities in R



## 2.1 Joint Modeling Framework

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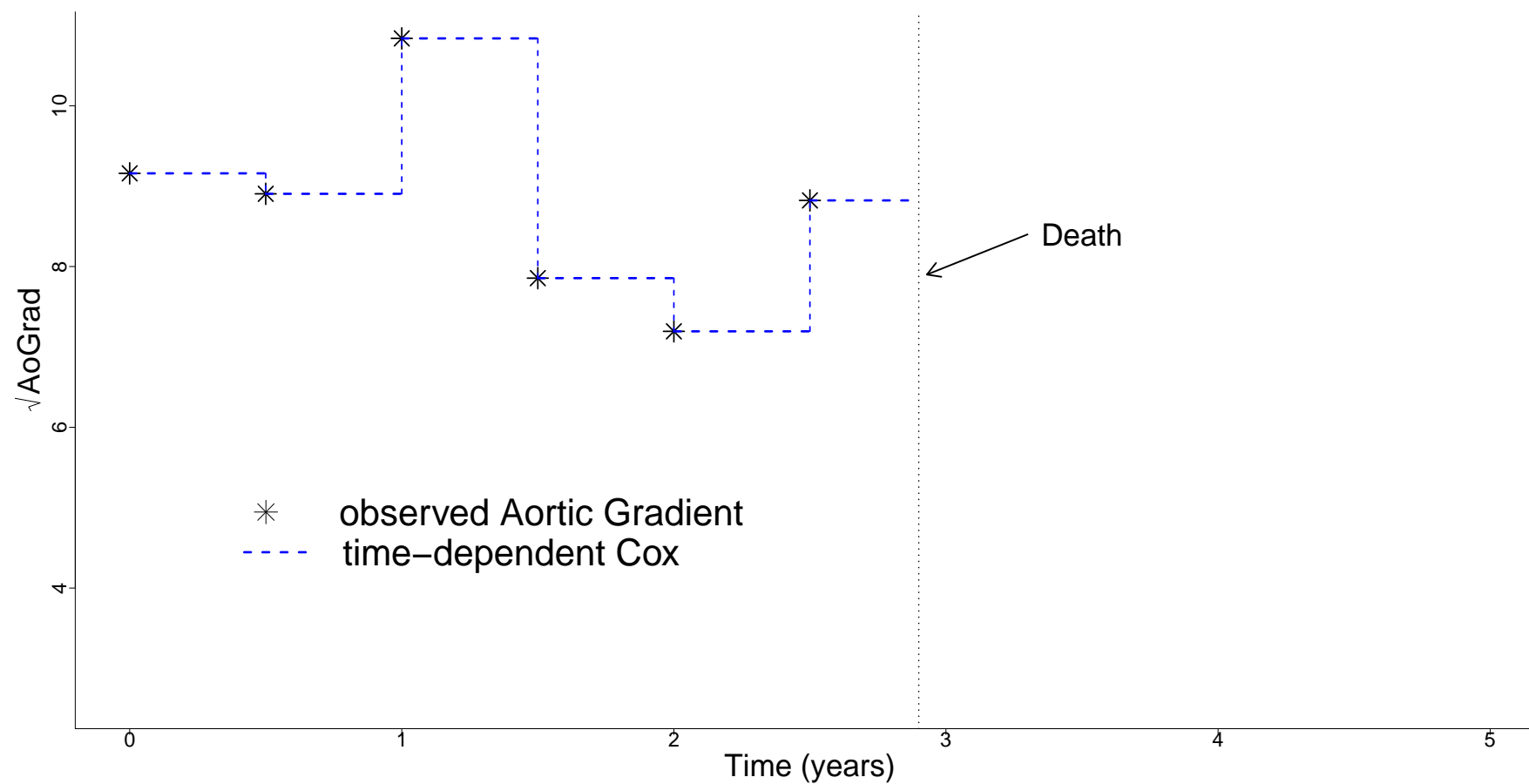
- To answer our questions of interest we need to postulate a model that relates
  - ▷ the aortic gradient with
  - ▷ the time to death or re-operation
- Problem: Aortic gradient is an **endogenous** time-dependent covariate (Kalbfleisch and Prentice, 2002, Section 6.3)
  - ▷ Measurements on the same patient are correlated
  - ▷ Endogenous (aka internal): the future path of the covariate up to any time  $t > s$  IS affected by the occurrence of an event at time point  $s$

## 2.1 Joint Modeling Framework (cont'd)

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- What is special about endogenous time-dependent covariates
  - ▷ measured with error
  - ▷ the complete history is not available
  - ▷ existence directly related to failure status
  
- What if we use the Cox model?
  - ▷ the association size can be severely underestimated
  - ▷ true potential of the marker will be masked

## 2.1 Joint Modeling Framework (cont'd)



## 2.1 Joint Modeling Framework (cont'd)

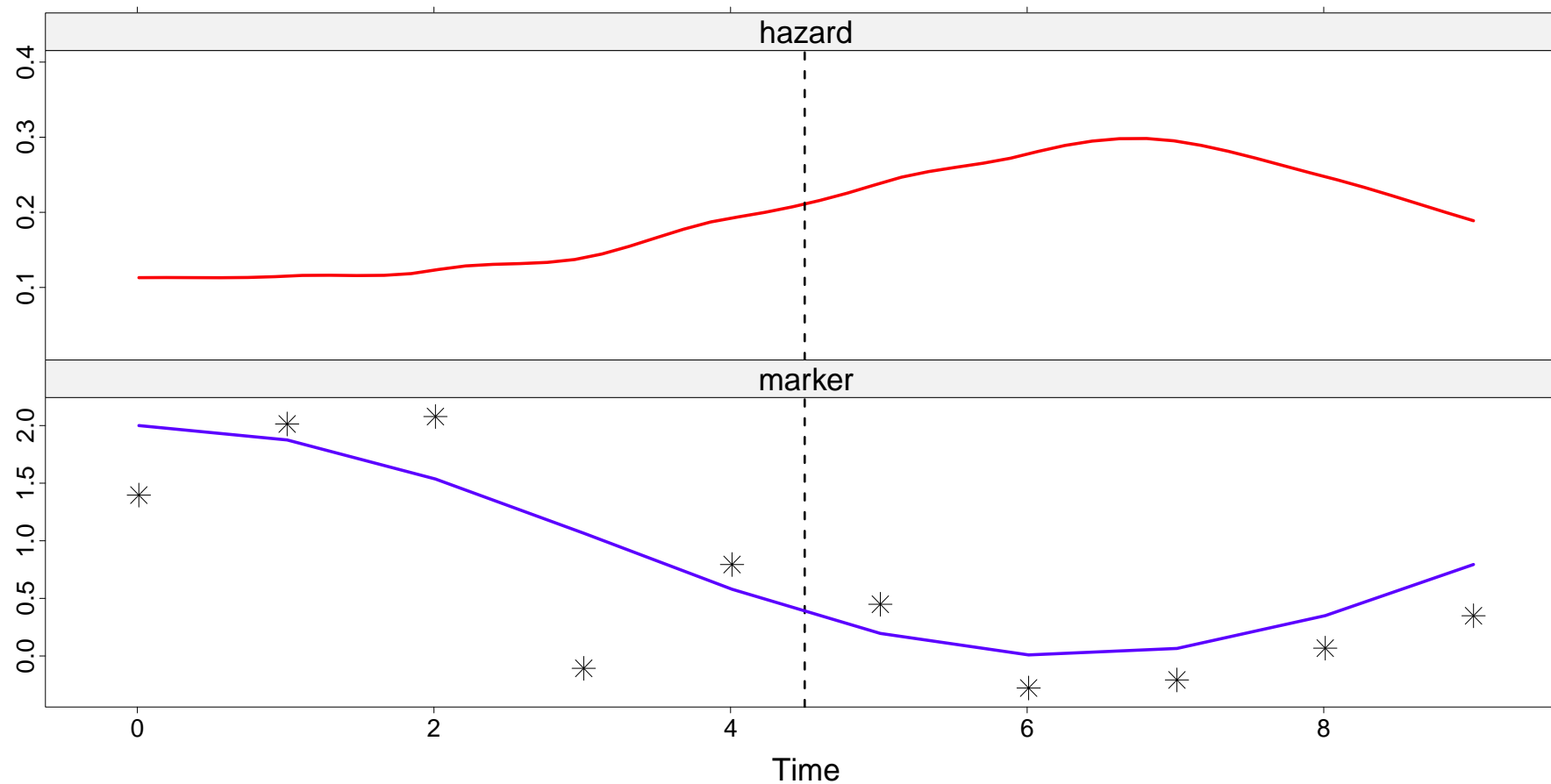
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- To account for the special features of these covariates a new class of models has been developed

### Joint Models for Longitudinal and Time-to-Event Data

- Intuitive idea behind these models
  1. use an appropriate model to describe the evolution of the marker in time for each patient
  2. the estimated evolutions are then used in a Cox model
- Feature: Marker level is **not** assumed constant between visits

## 2.1 Joint Modeling Framework (cont'd)



## 2.1 Joint Modeling Framework (cont'd)

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- We define a standard joint model

▷ Survival Part: Relative risk model

$$h_i(t) = h_0(t) \exp\{\gamma^\top w_i + \alpha m_i(t)\},$$

where

- \*  $m_i(t)$  = the *true & unobserved* value of aortic gradient at time  $t$
- \*  $\alpha$  quantifies the effect of aortic gradient on the risk for death/re-operation
- \*  $w_i$  baseline covariates

## 2.1 Joint Modeling Framework (cont'd)

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- ▷ **Longitudinal Part:** Reconstruct  $\mathcal{M}_i(t) = \{m_i(s), 0 \leq s < t\}$  using  $y_i(t)$  and a mixed effects model (we focus on continuous markers)

$$\begin{aligned}
 y_i(t) &= m_i(t) + \varepsilon_i(t) \\
 &= x_i^\top(t)\beta + z_i^\top(t)b_i + \varepsilon_i(t), \quad \varepsilon_i(t) \sim \mathcal{N}(0, \sigma^2),
 \end{aligned}$$

where

- \*  $x_i(t)$  and  $\beta$ : Fixed-effects part
- \*  $z_i(t)$  and  $b_i$ : Random-effects part,  $b_i \sim \mathcal{N}(0, D)$

## 3.1 Joint Models in R

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- Joint models are fitted using function `jointModel()` from package **JM**. This function accepts as main arguments a linear mixed model and a Cox PH model based on which it fits the corresponding joint model

```
lmeFit <- lme(CD4 ~ obstime + obstime:drug,
  random = ~ obstime | patient, data = aids)
```

```
coxFit <- coxph(Surv(Time, death) ~ drug, data = aids.id, x = TRUE)
```

```
jointFit <- jointModel(lmeFit, coxFit, timeVar = "obstime",
  method = "piecewise-PH-aGH")
```

```
summary(jointFit)
```



## 3.1 Joint Models in R

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- Argument `method` specifies the type of relative risk model and the type of numerical integration algorithm – the syntax is as follows:

`<baseline hazard>-<parameterization>-<numerical integration>`

Available options are:

- ▷ `"piecewise-PH-GH"`: PH model with piecewise-constant baseline hazard
- ▷ `"spline-PH-GH"`: PH model with B-spline-approximated log baseline hazard
- ▷ `"weibull-PH-GH"`: PH model with Weibull baseline hazard
- ▷ `"weibull-AFT-GH"`: AFT model with Weibull baseline hazard
- ▷ `"Cox-PH-GH"`: PH model with unspecified baseline hazard

`GH` stands for standard Gauss-Hermite; using `aGH` invokes the pseudo-adaptive Gauss-Hermite rule

## 3.1 Joint Models in R

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- Joint models under the Bayesian approach are fitted using function `jointModelBayes()` from package **JMbayes**. This function works in a very similar manner as function `jointModel()`, e.g.,

```
lmeFit <- lme(CD4 ~ obstime + obstime:drug,
  random = ~ obstime | patient, data = aids)
```

```
coxFit <- coxph(Surv(Time, death) ~ drug, data = aids.id, x = TRUE)
```

```
jointFitBayes <- jointModelBayes(lmeFit, coxFit, timeVar = "obstime")
```

```
summary(jointFitBayes)
```

## 3.1 Joint Models in R

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- **JMbayes** is more flexible (in some respects):
  - ▷ directly implements the MCMC
  - ▷ allows for categorical longitudinal data as well
  - ▷ allows for general transformation functions
  - ▷ penalized B-splines for the baseline hazard function
  - ▷ ...

## 3.1 Joint Models in R

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- In both packages methods are available for the majority of the standard generic functions + extras
  - ▷ `summary()`, `anova()`, `vcov()`, `logLik()`
  - ▷ `coef()`, `fixef()`, `ranef()`
  - ▷ `fitted()`, `residuals()`
  - ▷ `plot()`
  - ▷ `xtable()` (you need to load package **xtable** first)

## 4.1 Association Structures

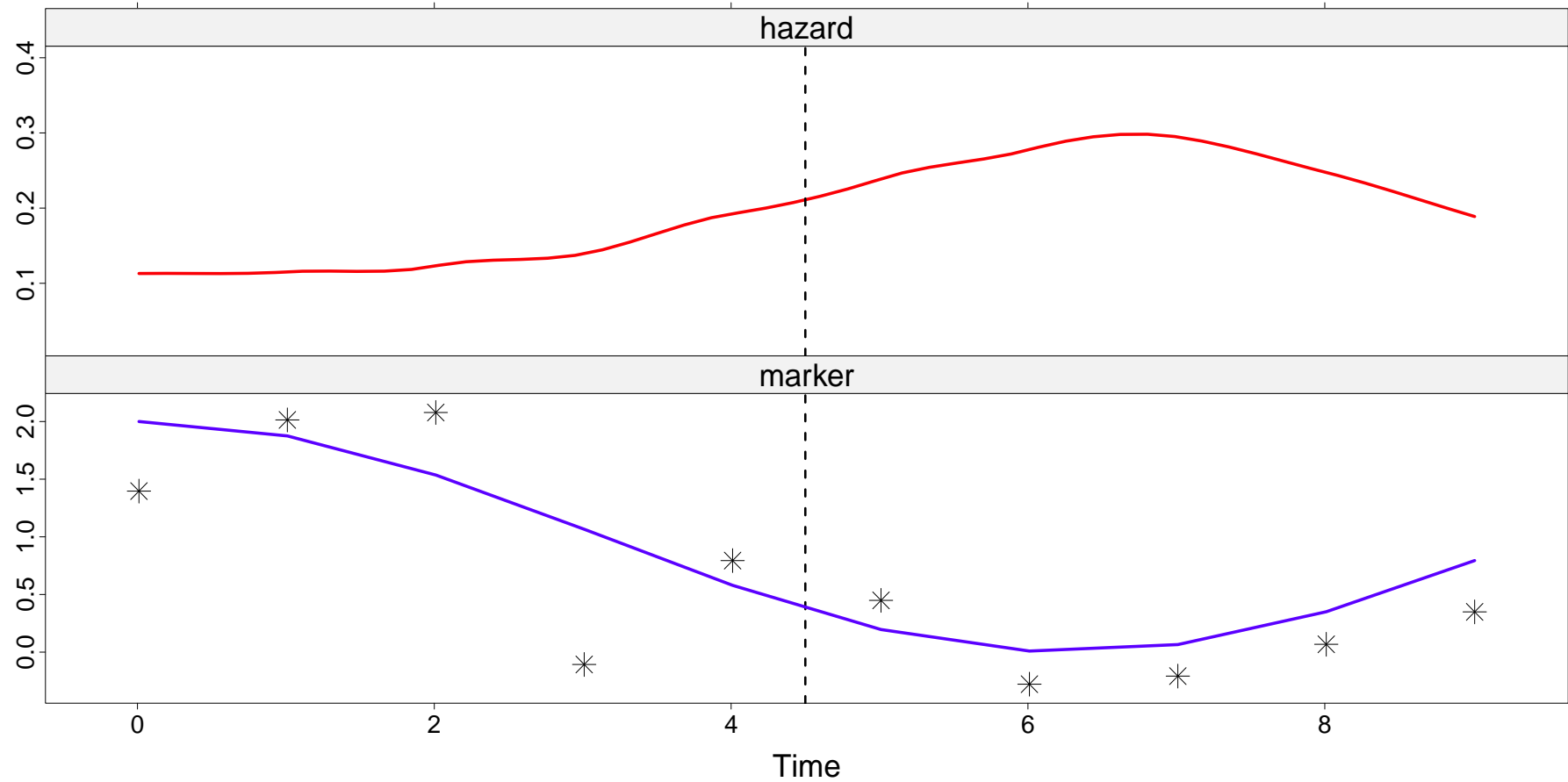
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- The standard assumption is

$$\left\{ \begin{array}{l} h_i(t | \mathcal{M}_i(t)) = h_0(t) \exp\{\gamma^\top w_i + \alpha m_i(t)\}, \\ \\ y_i(t) = m_i(t) + \varepsilon_i(t) \\ \\ = x_i^\top(t)\beta + z_i^\top(t)b_i + \varepsilon_i(t), \end{array} \right.$$

where  $\mathcal{M}_i(t) = \{m_i(s), 0 \leq s < t\}$

# 4.1 Association structures (cont'd)



## 4.1 Association Structures (cont'd)

---

- The standard assumption is

$$\left\{ \begin{array}{l} h_i(t | \mathcal{M}_i(t)) = h_0(t) \exp\{\gamma^\top w_i + \alpha m_i(t)\}, \\ y_i(t) = m_i(t) + \varepsilon_i(t) \\ y_i(t) = x_i^\top(t)\beta + z_i^\top(t)b_i + \varepsilon_i(t), \end{array} \right.$$

where  $\mathcal{M}_i(t) = \{m_i(s), 0 \leq s < t\}$

**Is this the only option? Is this the most optimal for prediction?**

## 4.2 Time-dependent Slopes

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- The hazard for an event at  $t$  is associated with both the current value and the slope of the trajectory at  $t$  (Ye et al., 2008, Biometrics):

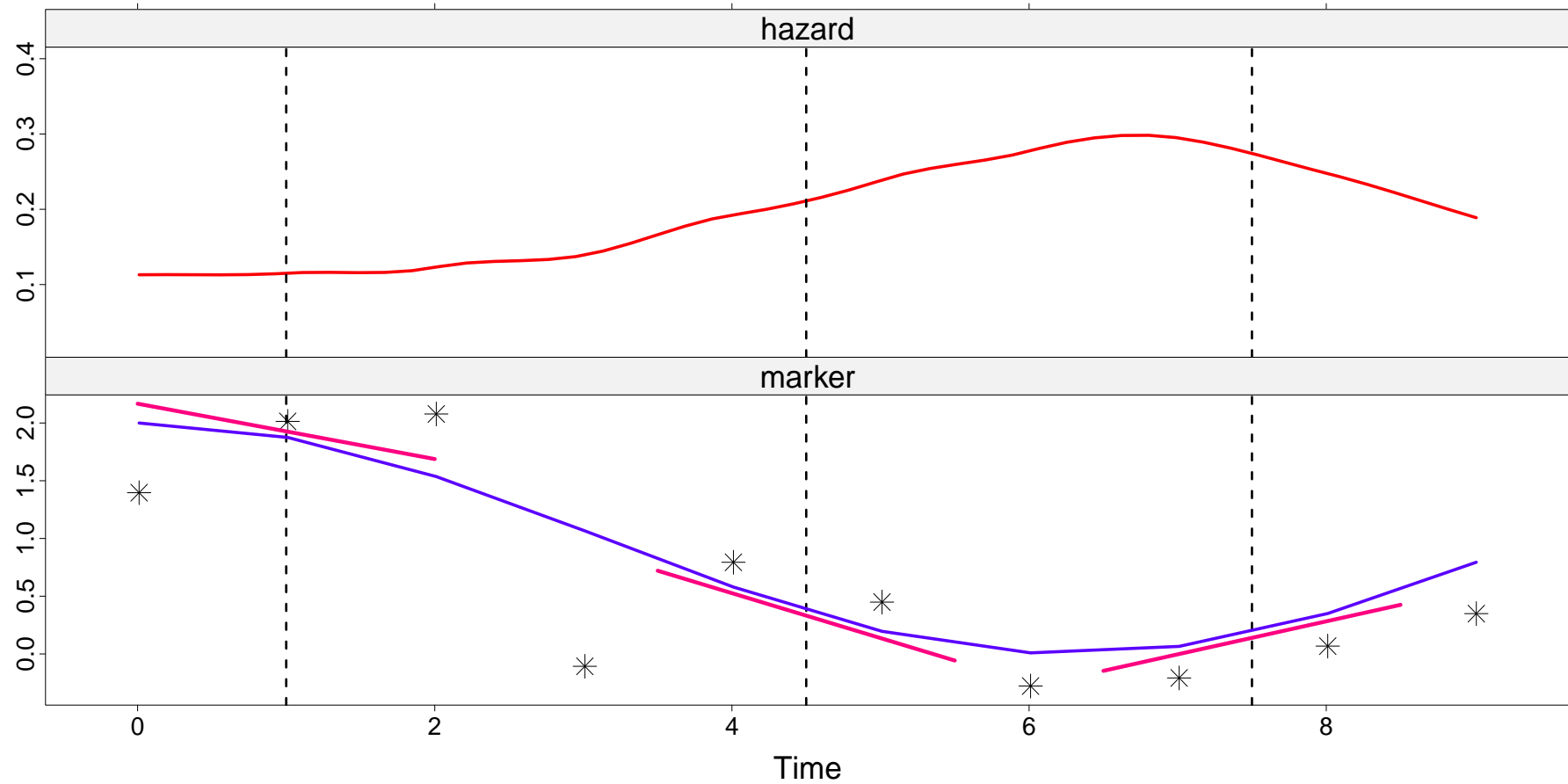
$$h_i(t \mid \mathcal{M}_i(t)) = h_0(t) \exp\{\gamma^\top w_i + \alpha_1 m_i(t) + \alpha_2 m'_i(t)\},$$

where

$$m'_i(t) = \frac{d}{dt} \{x_i^\top(t)\beta + z_i^\top(t)b_i\}$$



## 4.2 Time-dependent Slopes (cont'd)



## 4.3 Cumulative Effects

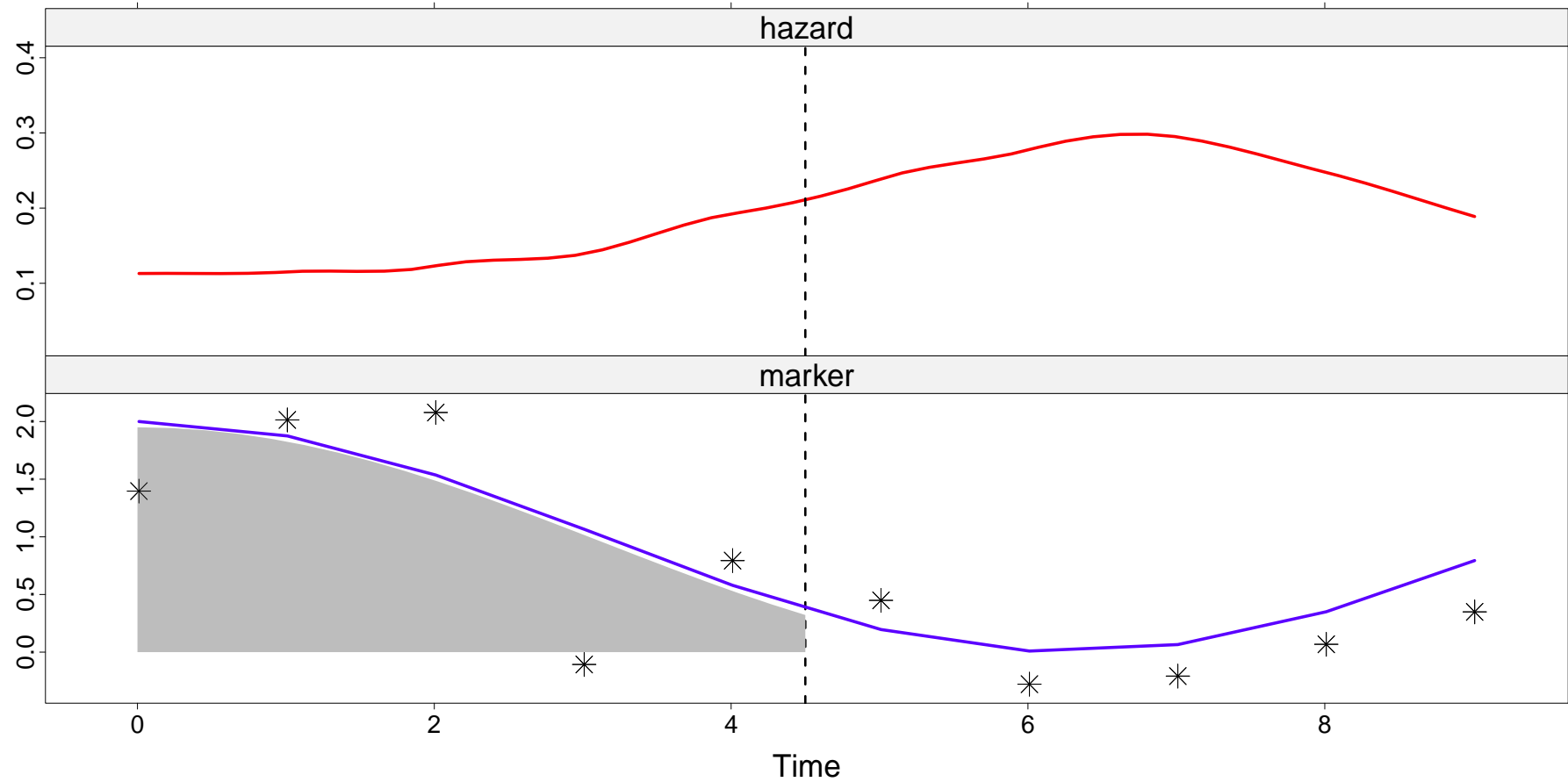
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- The hazard for an event at  $t$  is associated with area under the trajectory up to  $t$ :

$$h_i(t | \mathcal{M}_i(t)) = h_0(t) \exp \left\{ \gamma^\top w_i + \alpha \int_0^t m_i(s) ds \right\}$$

- Area under the longitudinal trajectory taken as a summary of  $\mathcal{M}_i(t)$

# 4.3 Cumulative Effects (cont'd)



## 4.5 Association Structures in JM & JMbayes

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- Both package give options to define the aforementioned association structures
  - ▷ in **JM** via arguments `parameterization` & `derivForm`
  - ▷ in **JMbayes** via arguments `param` & `extraForm`
  
- **JMbayes** also gives the option for general transformation functions, e.g.,

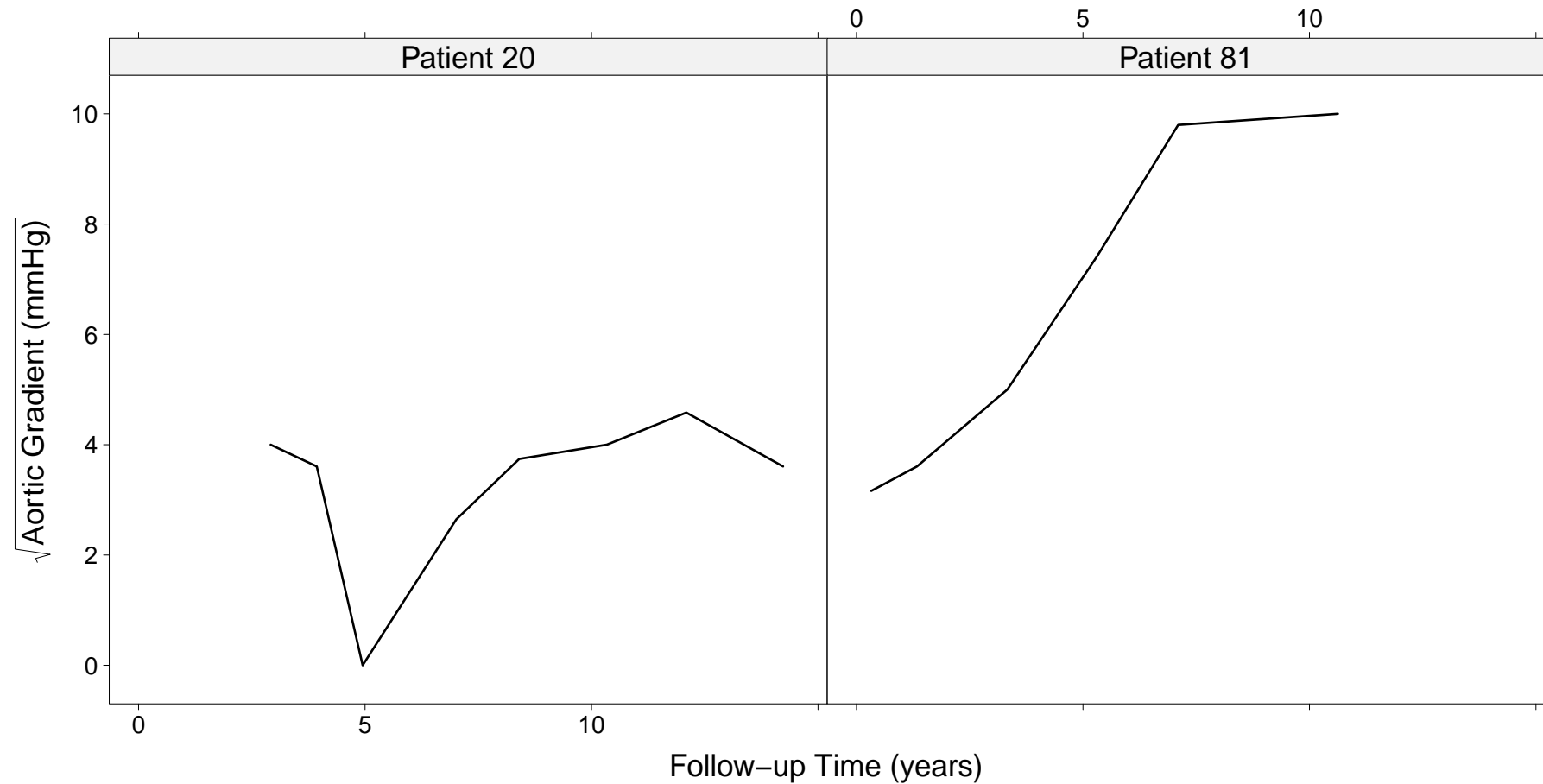
$$h_i(t | \mathcal{M}_i(t)) = h_0(t) \exp\{\gamma^\top w_i + \alpha_1 m_i(t) + \alpha_2 m_i(t) \times \text{Treat}_i + \alpha_3 m'_i(t) + \alpha_3 (m'_i(t))^2\},$$

## 5.1 Predictions – Definitions

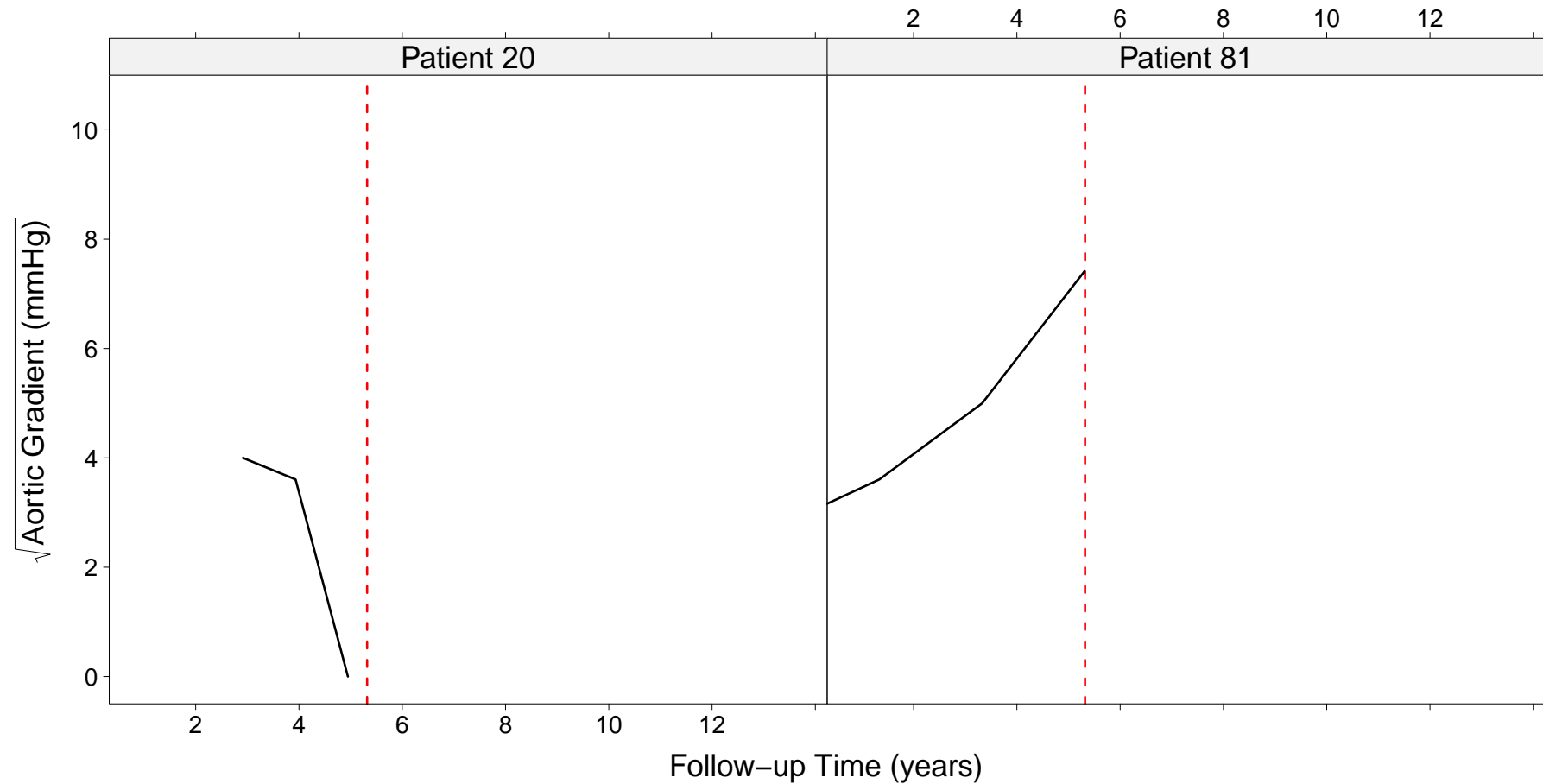
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- We are interested in predicting survival probabilities for a new patient  $j$  that has provided a set of aortic gradient measurements up to a specific time point  $t$
- Example: We consider Patients 20 and 81 from the Aortic Valve dataset

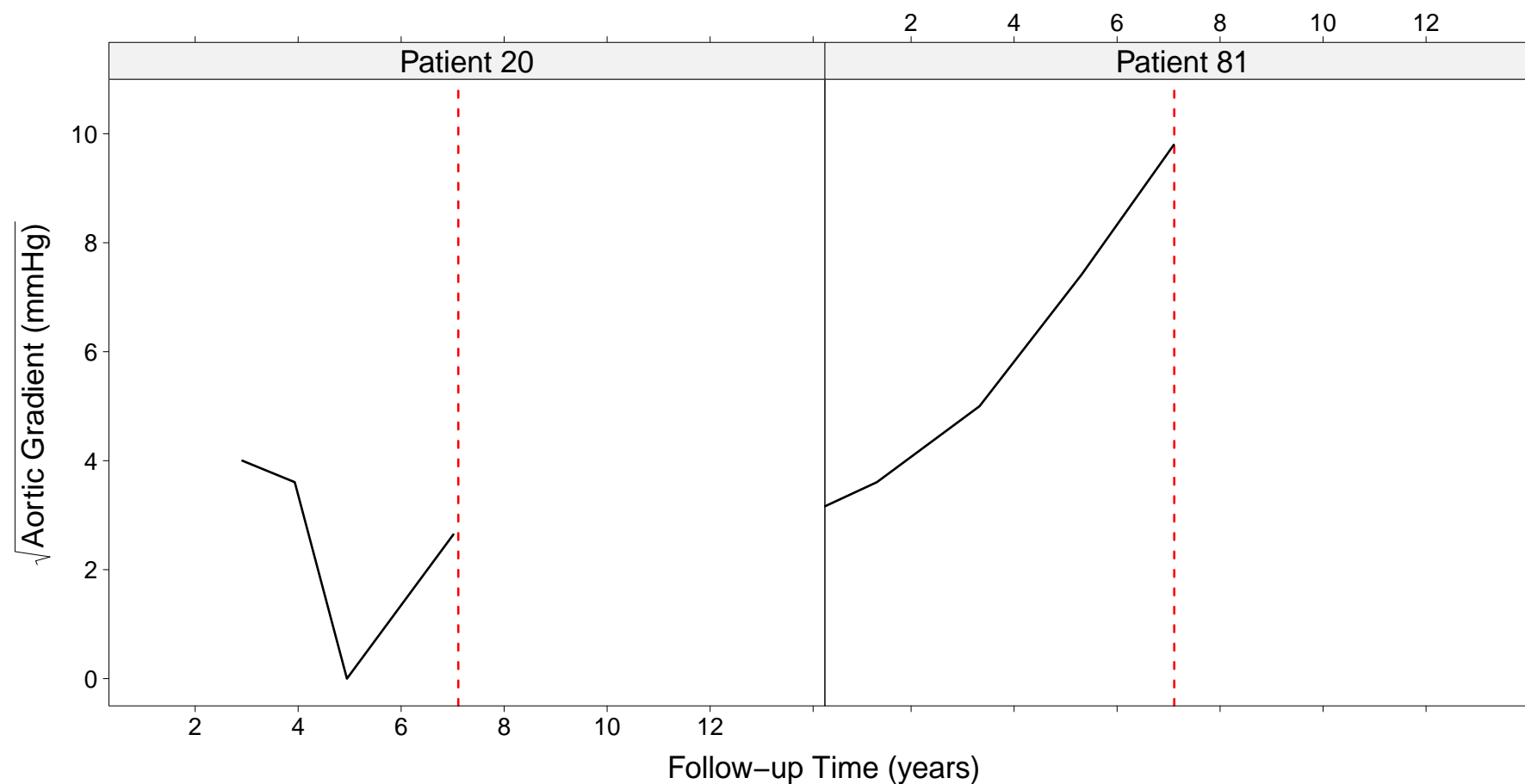
## 5.1 Predictions – Definitions (cont'd)



# 5.1 Predictions – Definitions (cont'd)



# 5.1 Predictions – Definitions (cont'd)



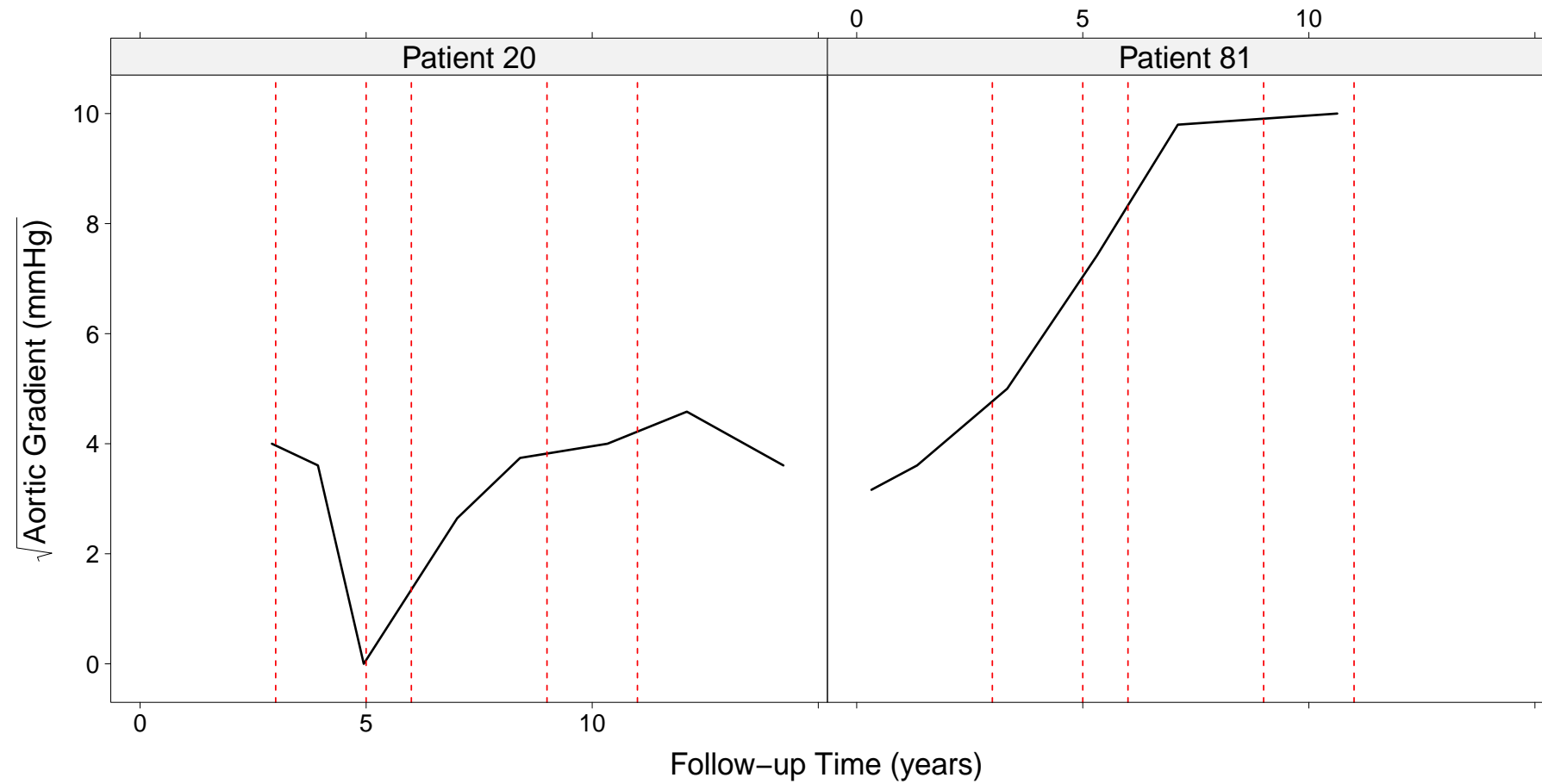


## 5.1 Predictions – Definitions (cont'd)

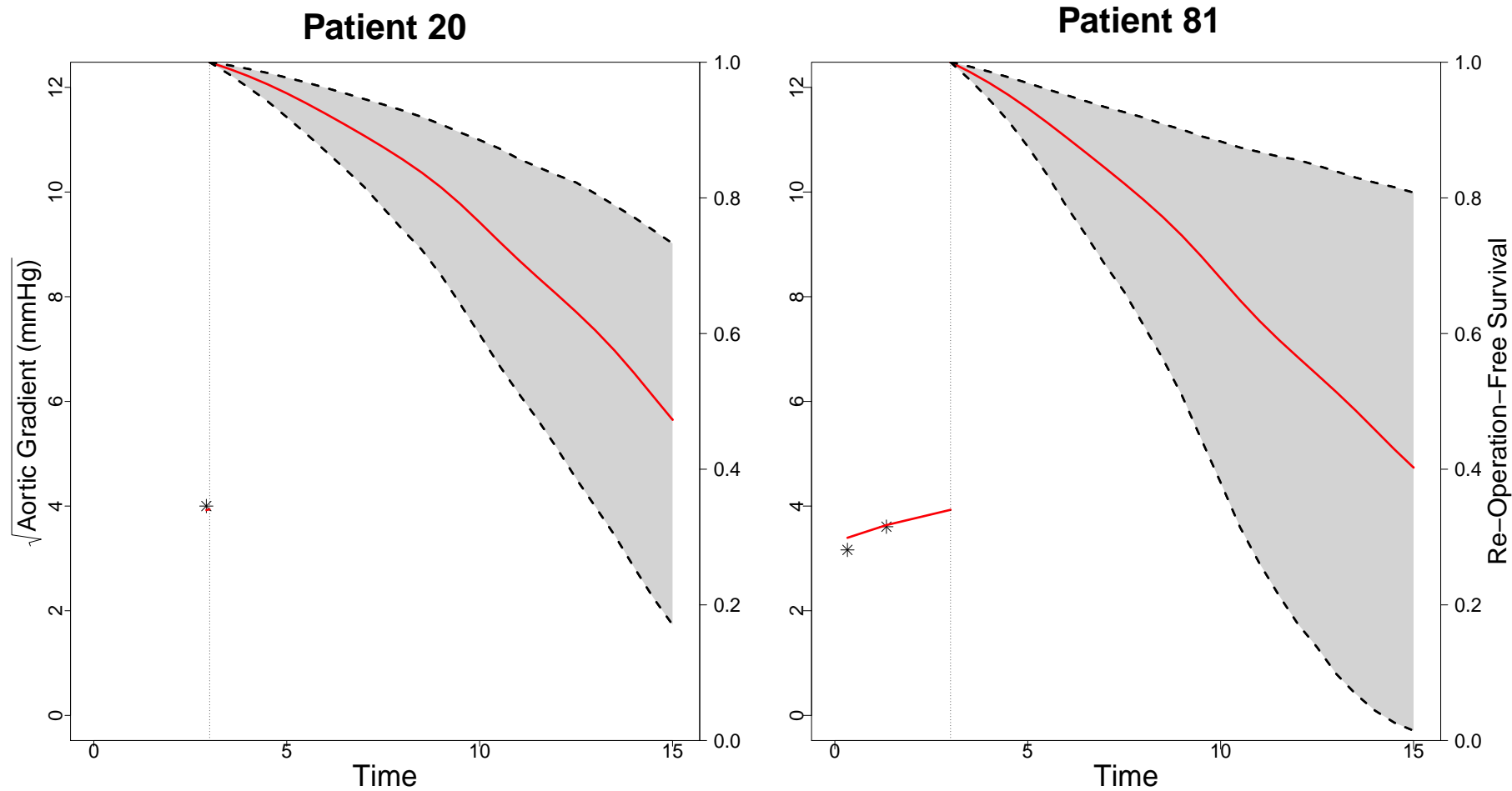
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- What do we know for these patients?
  - ▷ a series of aortic gradient measurements
  - ▷ patient are event-free up to the last measurement
- **Dynamic Prediction** survival probabilities are dynamically updated as additional longitudinal information is recorded

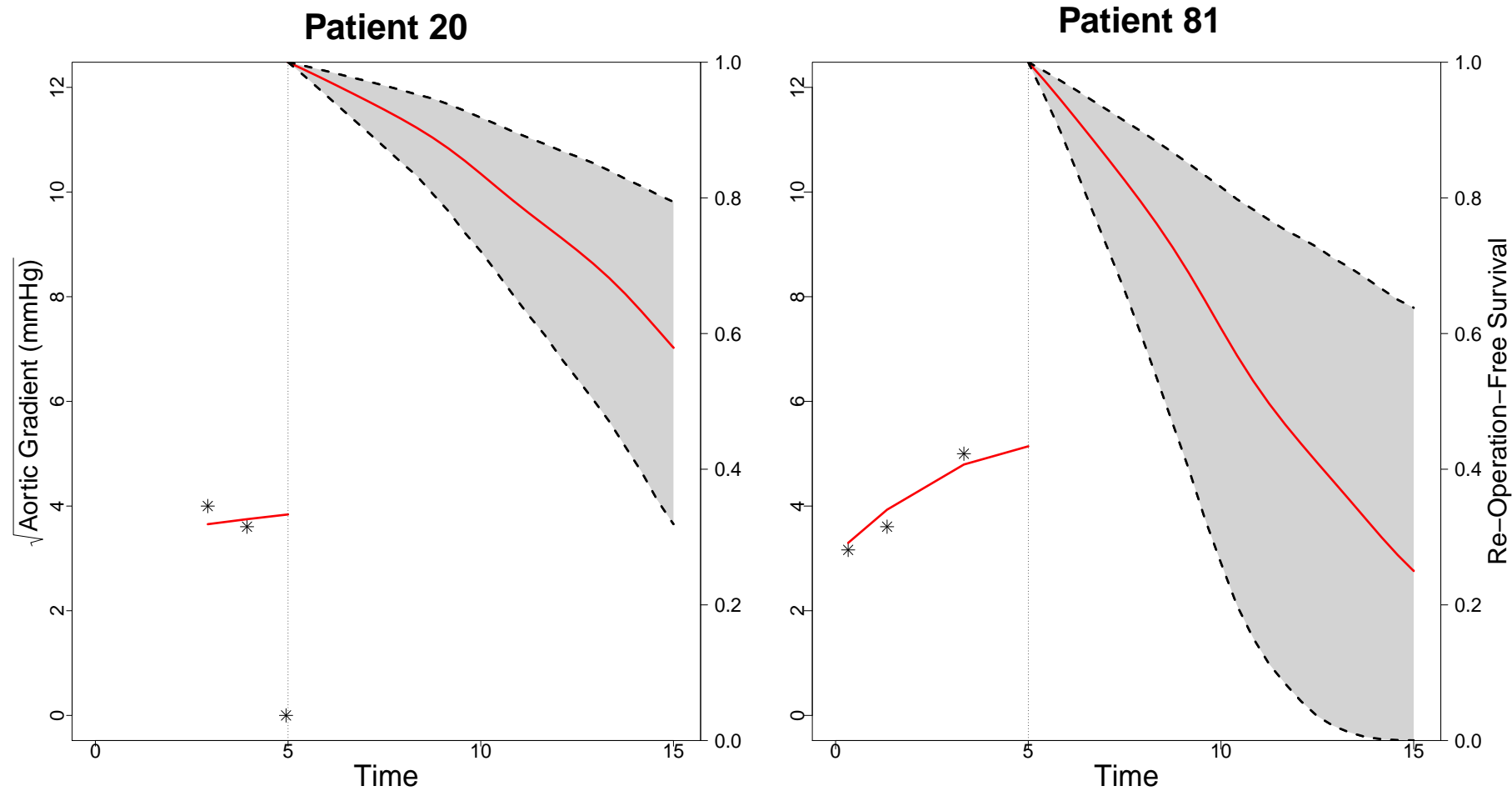
## 5.3 Dyn. Predictions – Illustration



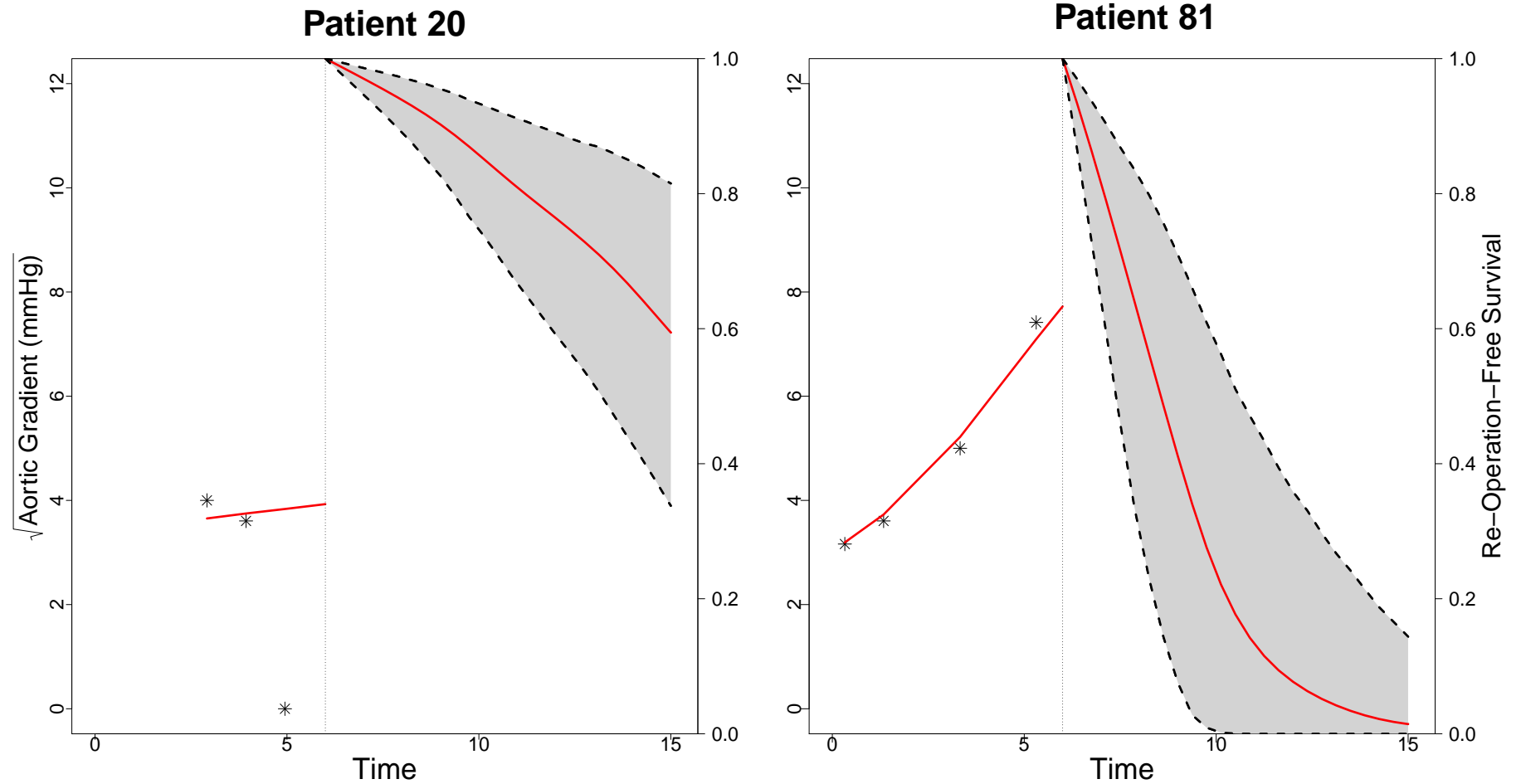
## 5.3 Dyn. Predictions – Illustration (cont'd)



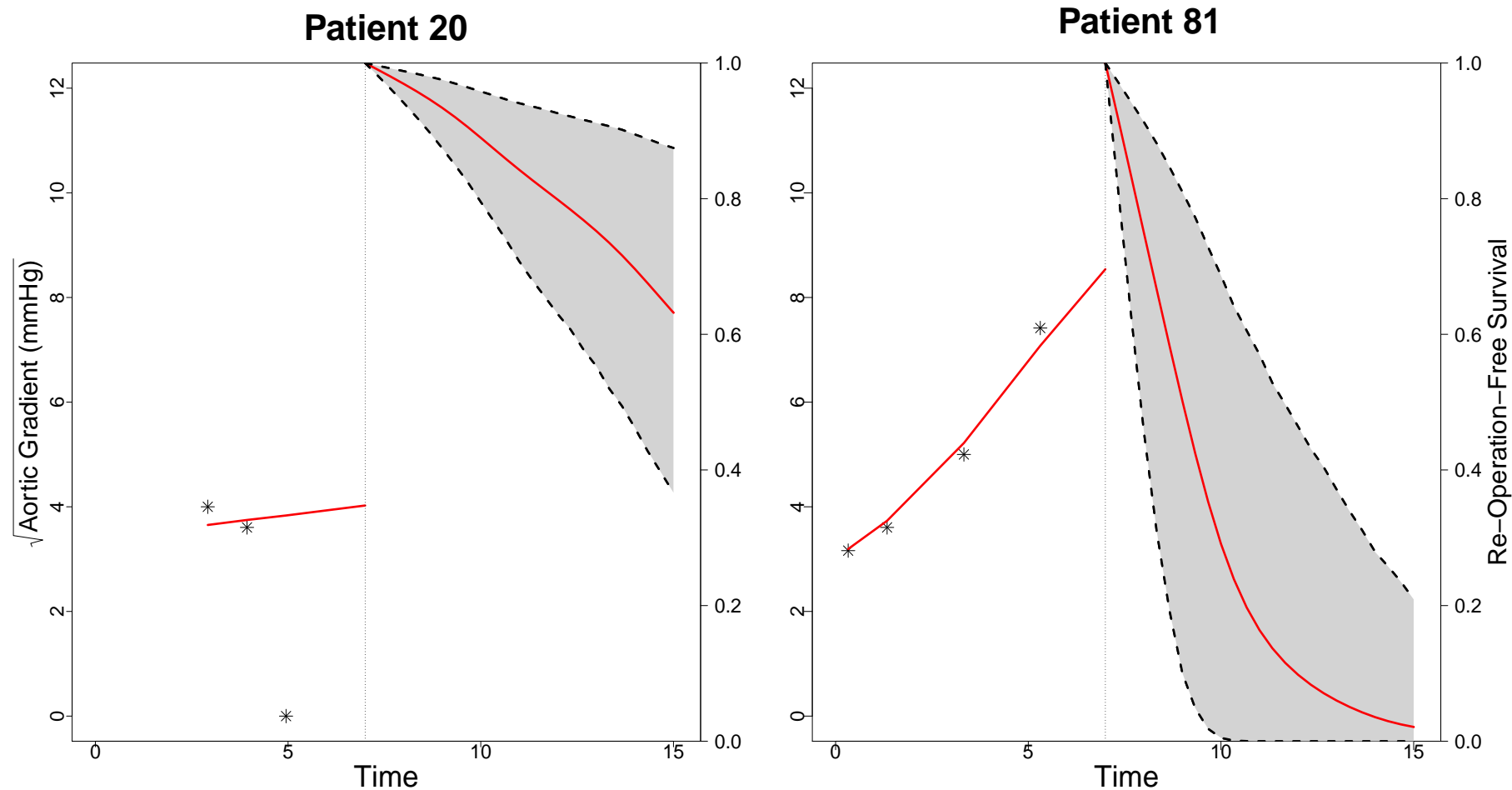
## 5.3 Dyn. Predictions – Illustration (cont'd)



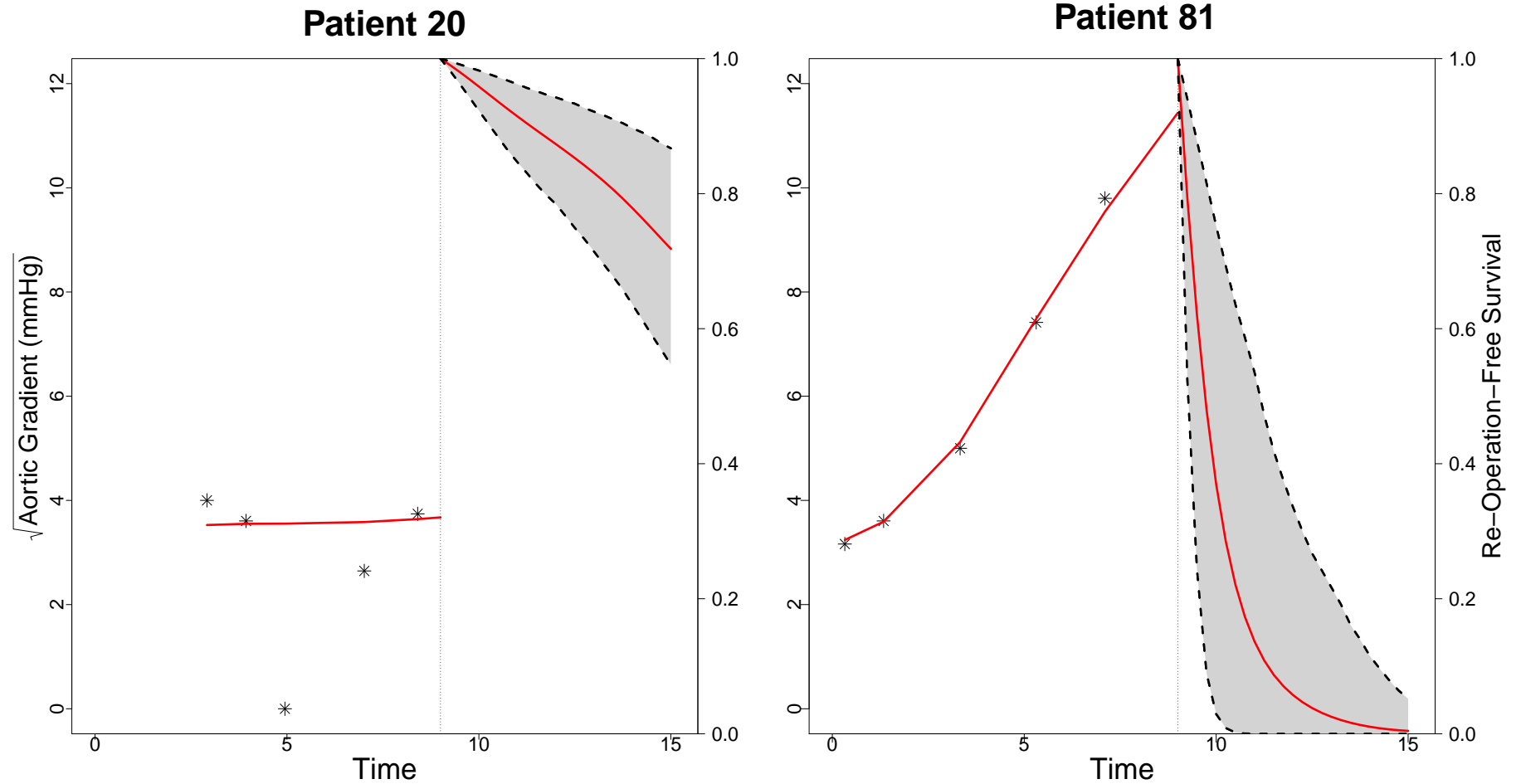
## 5.3 Dyn. Predictions – Illustration (cont'd)



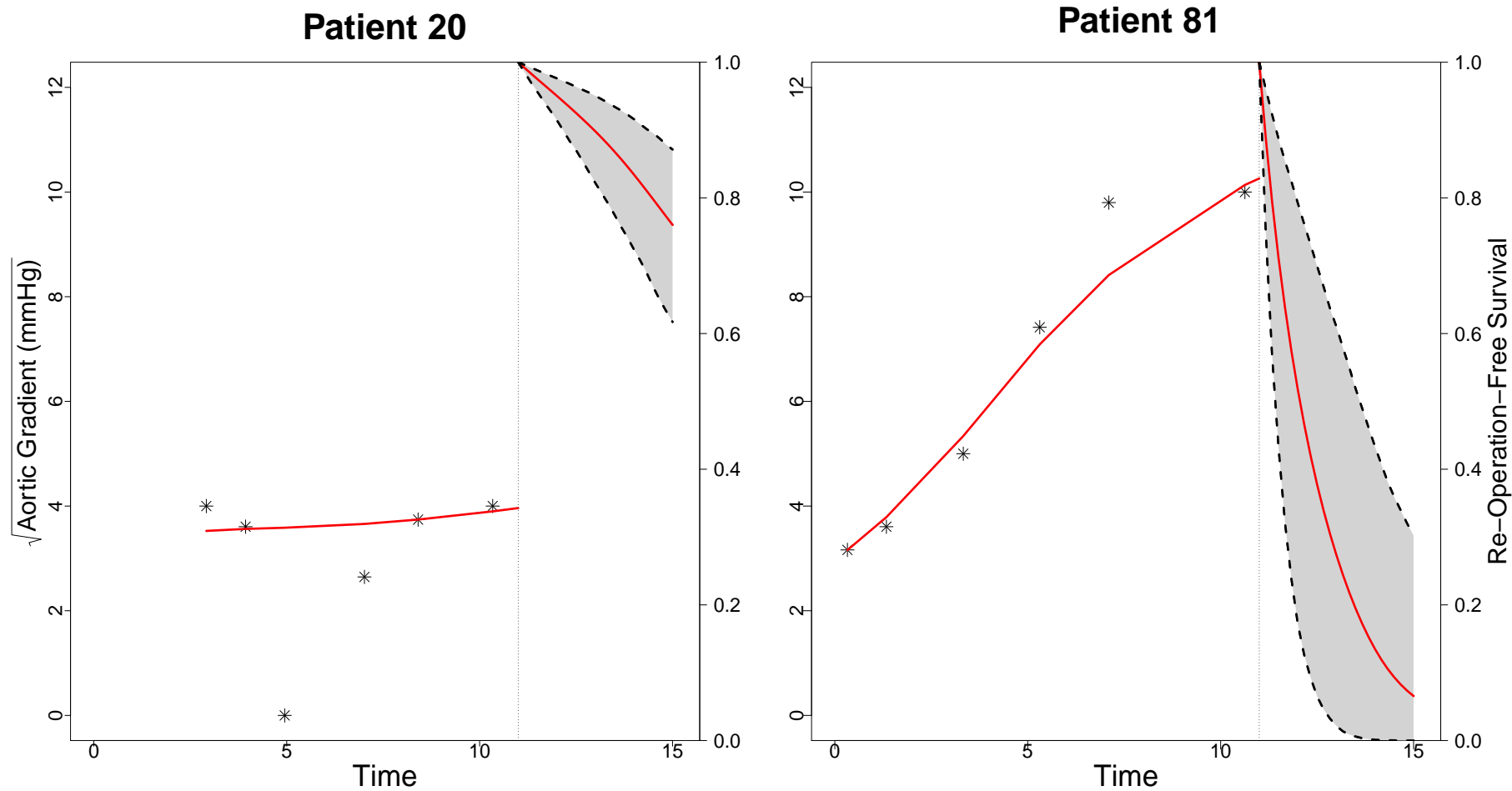
## 5.3 Prediction Survival – Illustration (cont'd)



## 5.3 Dyn. Predictions – Illustration (cont'd)



## 5.3 Dyn. Predictions – Illustration (cont'd)





## 5.2 Predictions – JM & JMbayes

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- Individualized predictions of survival probabilities are computed by function `survfitJM()` – for example, for Patient 2 from the PBC dataset we have

```
sfit <- survfitJM(jointFit, newdata = pbc2[pbc2$id == "2", ])
```

```
sfit
```

```
plot(sfit)
```

```
plot(sfit, include.y = TRUE)
```

```
# shiny app in JMbayes
```

```
JMbayes::runDynPred()
```

## 6. Resources

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- **JM**

- ▷ JSS paper (<http://www.jstatsoft.org/v35/i09/>)
- ▷ book for joint models (<http://jmr.r-forge.r-project.org/>)

- **JMbayes**

- ▷ JSS paper (<http://arxiv.org/abs/1404.7625>; to appear)

**Thank you for your attention!**