

Supplement 1: Augmented data matrices

Model with smooth baseline coefficients and tree-structured effects of the explanatory variables

Assume a SB model (7) with one split in x_j at split point c_j , where the right node $I(x_j > c_j)$ serves as reference node. For an individual whose event was observed ($\Delta_i = 1$) at time $\tilde{T}_i$ and $x_{ij} \leq c_j$ the augmented data matrix is given by

$$M_i = \begin{matrix} & \mathbf{y_i} & \mathbf{t} & \mathbf{x_j \leq c_j} \\ \begin{matrix} 1 \\ 2 \\ \vdots \\ \tilde{T}_i \end{matrix} & \begin{pmatrix} 0 & 1 & 1 \\ 0 & 2 & 1 \\ \vdots & \vdots & \vdots \\ 1 & \tilde{T}_i & 1 \end{pmatrix} \end{matrix}. \quad (\text{S1})$$

For an individual who was censored ($\Delta_i = 0$) at time $\tilde{T}_i$ and $x_{ij} > c_j$ the augmented data matrix is given by

$$M_i = \begin{matrix} & \mathbf{y_i} & \mathbf{t} & \mathbf{x_j \leq c_j} \\ \begin{matrix} 1 \\ 2 \\ \vdots \\ \tilde{T}_i \end{matrix} & \begin{pmatrix} 0 & 1 & 0 \\ 0 & 2 & 0 \\ \vdots & \vdots & \vdots \\ 0 & \tilde{T}_i & 0 \end{pmatrix} \end{matrix}. \quad (\text{S2})$$

Note that the column $\mathbf{t}$ needs to be coded as a numeric vector, if the baseline hazard is fitted using P-splines.

Model with piecewise constant baseline coefficients and tree-structured effects of the explanatory variables

Assume a PCB model (12) with one split in x_j at split point c_j and one split in t at split point c_t , where the node $I(x_j > c_j)$ serves as the reference node. For an individual whose event was observed ($\Delta_i = 1$) at time $\tilde{T}_i$ and $x_{ij} \leq c_j$ the augmented data matrix is given by

$$M_i = \begin{matrix} & \mathbf{y_i} & \mathbf{t \leq c_t} & \mathbf{t > c_t} & \mathbf{x_j \leq c_j} \\ \begin{matrix} 1 \\ 2 \\ \vdots \\ c_t \\ c_t + 1 \\ c_t + 2 \\ \vdots \\ \tilde{T}_i \end{matrix} & \begin{pmatrix} 0 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 \\ \vdots & \vdots & \vdots & \vdots \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 1 & 1 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & 0 & 1 & 1 \end{pmatrix} \end{matrix}. \quad (\text{S3})$$

For an individual who was censored ($\Delta_i = 0$) at time $\tilde{T}_i$ and $x_{ij} > c_j$ the augmented data matrix is given by

$$M_i = \begin{matrix} & \mathbf{y}_i & \mathbf{t} \leq \mathbf{c}_t & \mathbf{t} > \mathbf{c}_t & \mathbf{x}_j \leq \mathbf{c}_j \\ \begin{matrix} 1 \\ 2 \\ \vdots \\ c_t \\ c_t + 1 \\ c_t + 2 \\ \vdots \\ \tilde{T}_i \end{matrix} & \begin{pmatrix} 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 \\ \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 1 & 0 \end{pmatrix} \end{matrix}. \quad (\text{S4})$$

Tree-structured model including the effects of t and x in a single tree

Assume a ST model (16) with a predictor of the form

$$\eta(t, x_i) = \gamma_0 + [\underbrace{\gamma_1 I(x_{ij} \leq c_j \wedge t \leq c_t)}_{:=I_1} + \underbrace{\gamma_2 I(x_{ij} \leq c_j \wedge t > c_t)}_{:=I_2}],$$

where the node $I(x_j > c_j)$ serves as the reference node. For an individual whose event was observed ($\Delta_i = 1$) at time $\tilde{T}_i$ and $x_{ij} \leq c_j$ the augmented data matrix is given by

$$M_i = \begin{matrix} & \mathbf{y}_i & \mathbf{1} & \mathbf{I}_1 & \mathbf{I}_2 \\ \begin{matrix} 1 \\ 2 \\ \vdots \\ c_t \\ c_t + 1 \\ c_t + 2 \\ \vdots \\ \tilde{T}_i \end{matrix} & \begin{pmatrix} 0 & 1 & 1 & 0 \\ 0 & 1 & 1 & 0 \\ \vdots & \vdots & \vdots & \vdots \\ 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 \\ \vdots & \vdots & \vdots & \vdots \\ 1 & 1 & 0 & 1 \end{pmatrix} \end{matrix}. \quad (\text{S5})$$

For an individual who was censored ($\Delta_i = 0$) at time $\tilde{T}_i$ and $x_{ij} > c_j$ the augmented data matrix is given by

$$M_i = \begin{matrix} & \mathbf{y}_i & \mathbf{1} & \mathbf{I}_1 & \mathbf{I}_2 \\ \begin{matrix} 1 \\ 2 \\ \vdots \\ c_t \\ c_t + 1 \\ c_t + 2 \\ \vdots \\ \tilde{T}_i \end{matrix} & \begin{pmatrix} 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots \\ 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots \\ 0 & 1 & 0 & 0 \end{pmatrix} \end{matrix}. \quad (\text{S6})$$

Supplement 2: Fitting the tree-structured models by the R add-on package TSVC

To illustrate the way the proposed models can be fitted in R, consider the data set `data` comprising 10 explanatory variables, which might be generated by the process described in Section 4. In the following example R code, the augmented data matrix is generated and the three proposed models are fitted.

```
library(discSurv)
library(tibble)
library(TSVC)
load("data.rds")

# Data augmentation

data_long <- dataLong(data, timeColumn = "time", censColumn = "status",
                      timeAsFactor = FALSE)
formula <- as.formula("y ~ intC + timeInt + x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8
                      + x9 + x10")
varNames <- c("x1", "x2", "x3", "x4", "x5", "x6", "x7", "x8", "x9", "x10")
dataLong <- add_column(dataLong, intC = 1, .before = 1)
dataLong <- add_column(dataLong, intT = 1, .before = 1)

# Model with smooth baseline coefficients and tree-structured effects
# of the explanatory variables

SB_PT <- TSVC(formula, data = data_long, family = binomial(link = "logit"),
              effmod = varNames, only_effmod = varNames,
              smooth = "timeInt", k = 5, m = 2,
              perm_test = TRUE, nperm = 1000,
              bucket_min = floor(0.1*dim(dataLong)[1]))

SB_MNS <- TSVC(formula, data = data_long, family = binomial(link = "logit"),
              effmod = varNames, only_effmod = varNames,
              smooth = "timeInt", k = 5, m = 2,
              perm_test = FALSE, nodesize_min = 500,
              bucket_min = floor(0.1*dim(dataLong)[1]))

SB_PR <- TSVC(formula, data = data_long, family = binomial(link = "logit"),
              effmod = varNames, only_effmod = varNames,
              smooth = "timeInt", k = 5, m = 2,
              perm_test = FALSE, splits_max = 10,
              bucket_min = floor(0.1*dim(dataLong)[1]))

# Tree-structured model including the effects of t and x in a single tree

ST_PT <- TSVC(formula, data = data_long, family = binomial(link = "logit"),
              effmod = c(varNames, "timeInt"), only_effmod = c(varNames, "timeInt"),
              perm_test = TRUE, nperm = 1000,
              bucket_min = floor(0.1*dim(dataLong)[1]))

ST_MNS <- TSVC(formula, data = data_long, family = binomial(link = "logit"),
              effmod = c(varNames, "timeInt"), only_effmod = c(varNames, "timeInt"),
              perm_test = FALSE, nodesize_min = 500,
              bucket_min = floor(0.1*dim(dataLong)[1]))

ST_PR <- TSVC(formula, data = data_long, family = binomial(link = "logit"),
              effmod = c(varNames, "timeInt"), only_effmod = c(varNames, "timeInt"),
              perm_test = FALSE, splits_max = 10,
              bucket_min = floor(0.1*dim(dataLong)[1]))
```

```

# Model with piecewise constant baseline coefficients and tree-structured effects
# of the explanatory variables

formula_PCB <- as.formula("y ~ intT + intC + timeInt + x1 + x2 + x3 + x4 + x5 + x6
+ x7 + x8 + x9 + x10")

PCB_PT <- TSVC(formula_PCB, data = data_long, family = binomial(link = "logit"),
  effmod = c(varNames, "timeInt"), only_effmod = c(varNames, "timeInt"),
  notmod = list(c("intC", "timeInt"), c("intT", "x1"), c("intT", "x2"),
    c("intT", "x3"), c("intT", "x4"), c("intT", "x5"),
    c("intT", "x6"), c("intT", "x7"), c("intT", "x8"),
    c("intT", "x9"), c("intT", "x10")),
  perm_test = TRUE, nperm = 1000,
  bucket_min = floor(0.1*dim(dataLong)[1]))

PCB_MNS <- TSVC(formula_PCB, data = data_long, family = binomial(link = "logit"),
  effmod = c(varNames, "timeInt"), only_effmod = c(varNames, "timeInt"),
  notmod = list(c("intC", "timeInt"), c("intT", "x1"), c("intT", "x2"),
    c("intT", "x3"), c("intT", "x4"), c("intT", "x5"),
    c("intT", "x6"), c("intT", "x7"), c("intT", "x8"),
    c("intT", "x9"), c("intT", "x10")),
  perm_test = FALSE, nodesize_min = 500,
  bucket_min = floor(0.1*dim(dataLong)[1]))

PCB_PR <- TSVC(formula_PCB, data = data_long, family = binomial(link = "logit"),
  effmod = c(varNames, "timeInt"), only_effmod = c(varNames, "timeInt"),
  notmod = list(c("intC", "timeInt"), c("intT", "x1"), c("intT", "x2"),
    c("intT", "x3"), c("intT", "x4"), c("intT", "x5"),
    c("intT", "x6"), c("intT", "x7"), c("intT", "x8"),
    c("intT", "x9"), c("intT", "x10")),
  perm_test = FALSE, splits_max = 10,
  bucket_min = floor(0.1*dim(dataLong)[1]))

```

The following R code shows how an additional explanatory variable z with linear effect on the outcome can be included in the model. As an example, the SB PT model is considered. For the other proposed models, the inclusion of a variable with linear effect can be done analogously.

```

notmod <- vector(mode = "list", length = 20)
for(i in 1:10){
  notmod[[i]] <- c("z", varNames[i])
}
for(i in 11:20){
  notmod[[i]] <- c(varNames[i], "z")
}
formula <- as.formula("y ~ intC + timeInt + x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8
+ x9 + x10 + z")
SB_PT_L <- TSVC(formula, data = data_long, family = binomial(link = "logit"),
  effmod = varNames, only_effmod = varNames, notmod = notmod,
  smooth = "timeInt", k = 5, m = 2,
  perm_test = TRUE, nperm = 1000,
  bucket_min = floor(0.1*dim(dataLong)[1]))

```

Supplement 3: Additional results of the simulation study

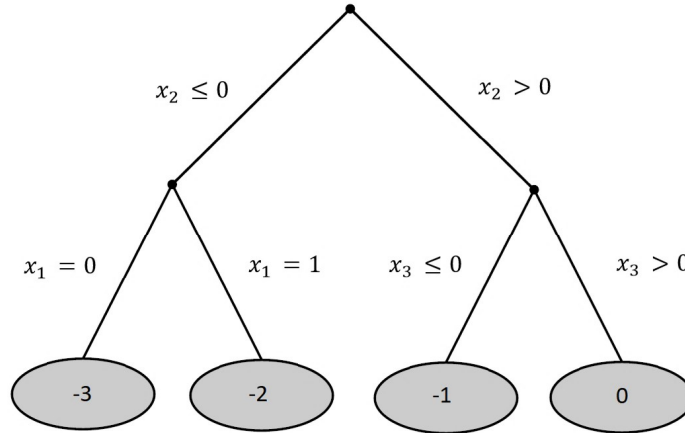


Fig. S1 Effects of the explanatory variables (scenario 1). Tree structure determining the effects of the explanatory variables in simulation scenario 1. The rightmost node on the second level serves as reference node

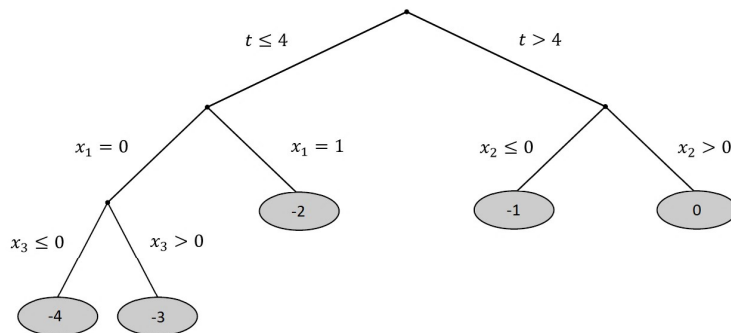


Fig. S2 Effects of the explanatory variables and time (scenario 3). Tree structure determining the effects of the explanatory variables and time in simulation scenario 3. The rightmost node on the second level serves as reference node

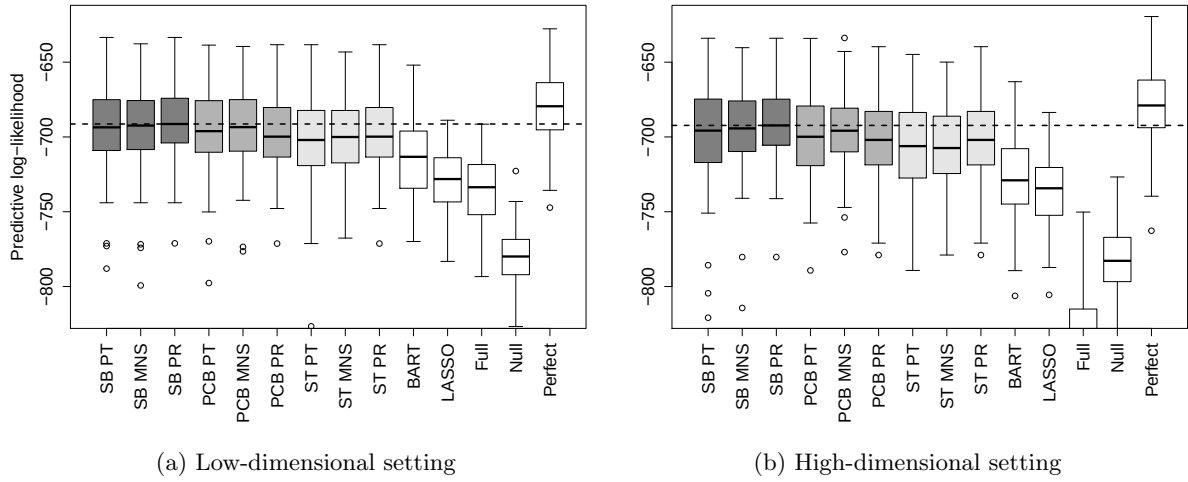


Fig. S3 Results of the simulation study: Predictive performance (scenario 1). The figure shows the predicted log-likelihood obtained from fitting the different models for the low-dimensional setting (left panel) and the high-dimensional setting (right panel) with medium censoring (50%)

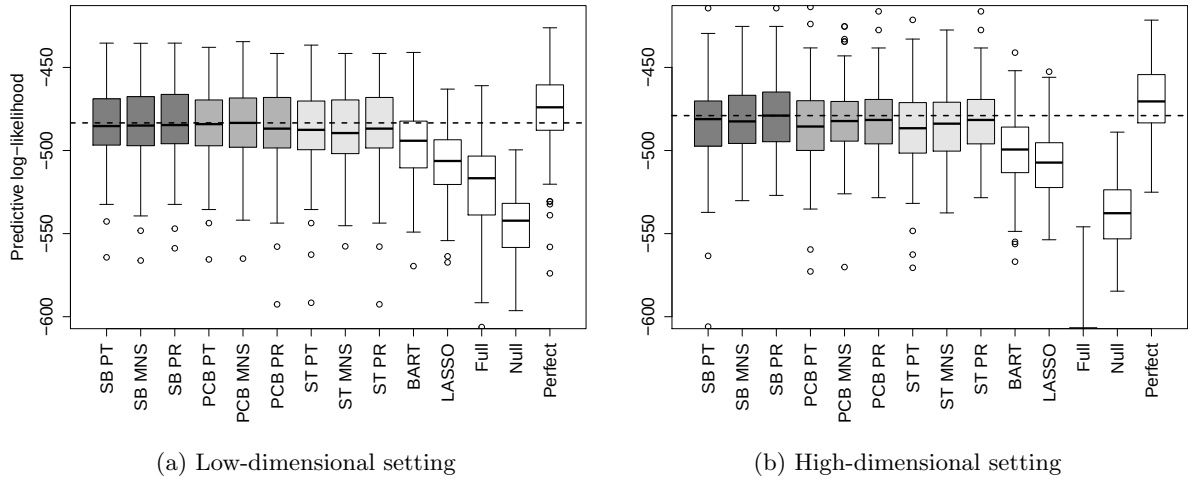
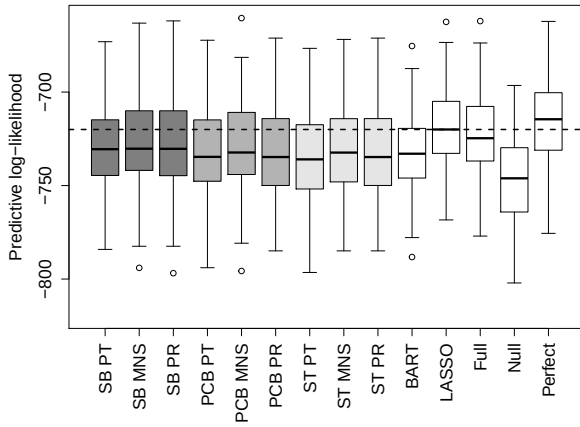
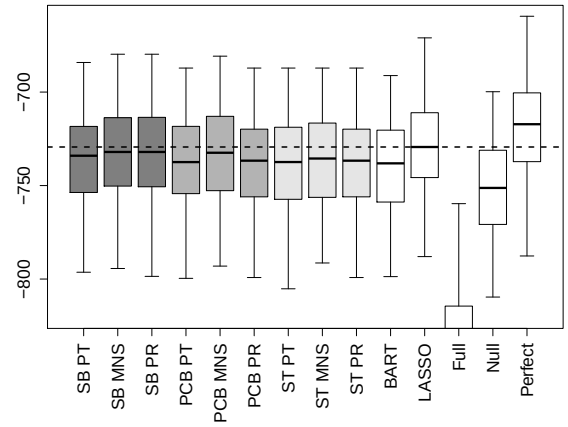


Fig. S4 Results of the simulation study: Predictive performance (scenario 1). The figure shows the predicted log-likelihood obtained from fitting the different models for the low-dimensional setting (left panel) and the high-dimensional setting (right panel) with high censoring (70%)

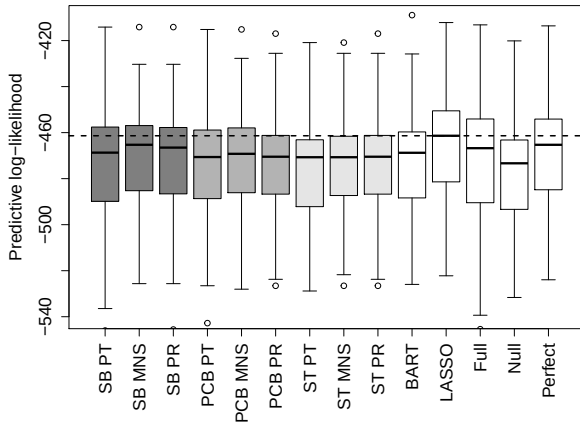


(a) Low-dimensional setting

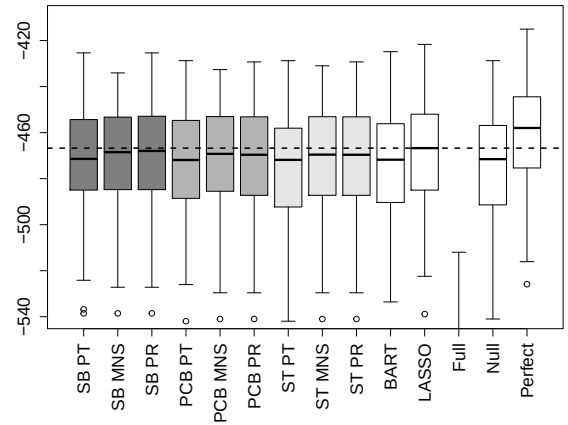


(b) High-dimensional setting

Fig. S5 Results of the simulation study: Predictive performance (scenario 2). The figure shows the predicted log-likelihood obtained from fitting the different models for the low-dimensional setting (left panel) and the high-dimensional setting (right panel) with medium censoring (50%)

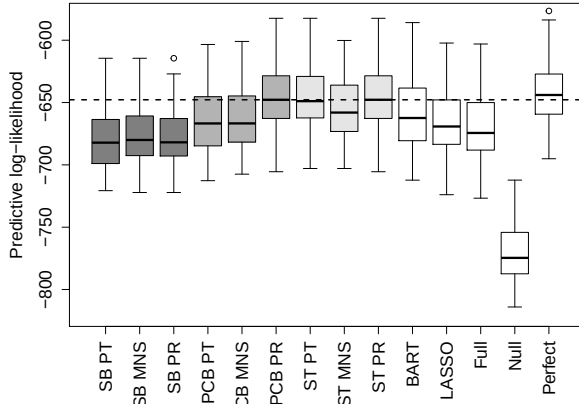


(a) Low-dimensional setting

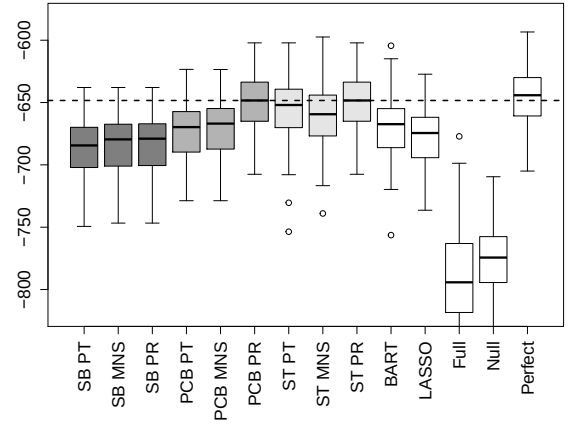


(b) High-dimensional setting

Fig. S6 Results of the simulation study: Predictive performance (scenario 2). The figure shows the predicted log-likelihood obtained from fitting the different models for the low-dimensional setting (left panel) and the high-dimensional setting (right panel) with high censoring (70%)

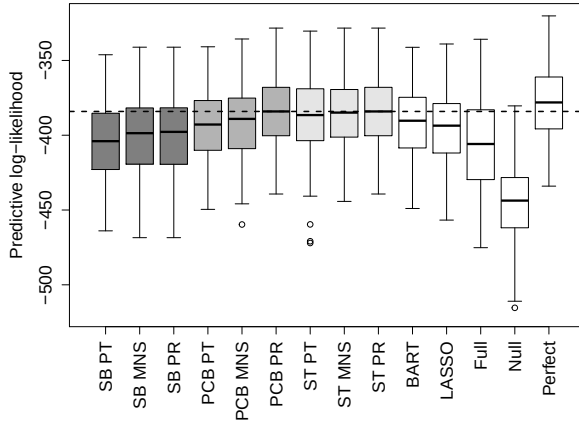


(a) Low-dimensional setting

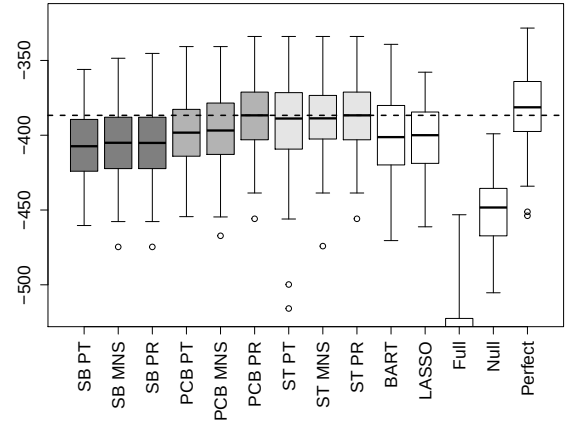


(b) High-dimensional setting

Fig. S7 Results of the simulation study: Predictive performance (scenario 3). The figure shows the predicted log-likelihood obtained from fitting the different models for the low-dimensional setting (left panel) and the high-dimensional setting (right panel) with medium censoring (50%)



(a) Low-dimensional setting



(b) High-dimensional setting

Fig. S8 Results of the simulation study: Predictive performance (scenario 3). The figure shows the predicted log-likelihood obtained from fitting the different models for the low-dimensional setting (left panel) and the high-dimensional setting (right panel) with high censoring (70%)

Table S1 Results of the simulation study: Time (scenario 1). Average true positive rates (TPR.T) and false positive rates (FPR.T) of the thresholds in t for the low-dimensional settings (left) and high-dimensional settings (right) and different degrees of censoring

	Model	Stopping criterion	Low-dimensional			High-dimensional		
Censoring rate			0.3	0.5	0.7	0.3	0.5	0.7
TPR.T	PCB	PT	0.453	0.327	0.210	0.367	0.277	0.193
		MNS	0.740	0.607	0.333	0.690	0.547	0.370
		PR	0.450	0.340	0.223	0.363	0.297	0.197
	ST	PT	0.380	0.270	0.113	0.203	0.203	0.047
		MNS	0.357	0.237	0.083	0.217	0.177	0.067
		PR	0.557	0.417	0.137	0.443	0.297	0.127
FPR.T	PCB	PT	0.030	0.027	0.032	0.033	0.024	0.016
		MNS	0.297	0.273	0.167	0.290	0.243	0.157
		PR	0.035	0.028	0.025	0.032	0.032	0.018
	ST	PT	0.064	0.050	0.024	0.060	0.034	0.007
		MNS	0.071	0.047	0.031	0.067	0.037	0.020
		PR	0.115	0.078	0.047	0.088	0.063	0.018

Table S2 Results of the simulation study: Time (scenario 3). Average true positive rates (TPR.T) and false positive rates (FPR.T) of the thresholds in t for the low-dimensional settings (left) and high-dimensional settings (right) and different degrees of censoring

	Model	Stopping criterion	Low-dimensional setting			High-dimensional setting		
Censoring rate			0.3	0.5	0.7	0.3	0.5	0.7
TPR.T	PCB	PT	1.000	1.000	1.000	1.000	1.000	1.000
		MNS	1.000	1.000	1.000	1.000	1.000	1.000
		PR	1.000	1.000	1.000	1.000	1.000	1.000
	ST	PT	1.000	1.000	1.000	1.000	1.000	1.000
		MNS	1.000	1.000	1.000	1.000	1.000	1.000
		PR	1.000	1.000	1.000	1.000	1.000	1.000
FPR.T	PCB	PT	0.007	0.007	0.004	0.003	0.001	0.002
		MNS	0.116	0.126	0.084	0.133	0.113	0.071
		PR	0.005	0.001	0.000	0.001	0.000	0.000
	ST	PT	0.002	0.002	0.002	0.001	0.000	0.000
		MNS	0.002	0.006	0.000	0.000	0.001	0.000
		PR	0.001	0.000	0.001	0.000	0.000	0.000

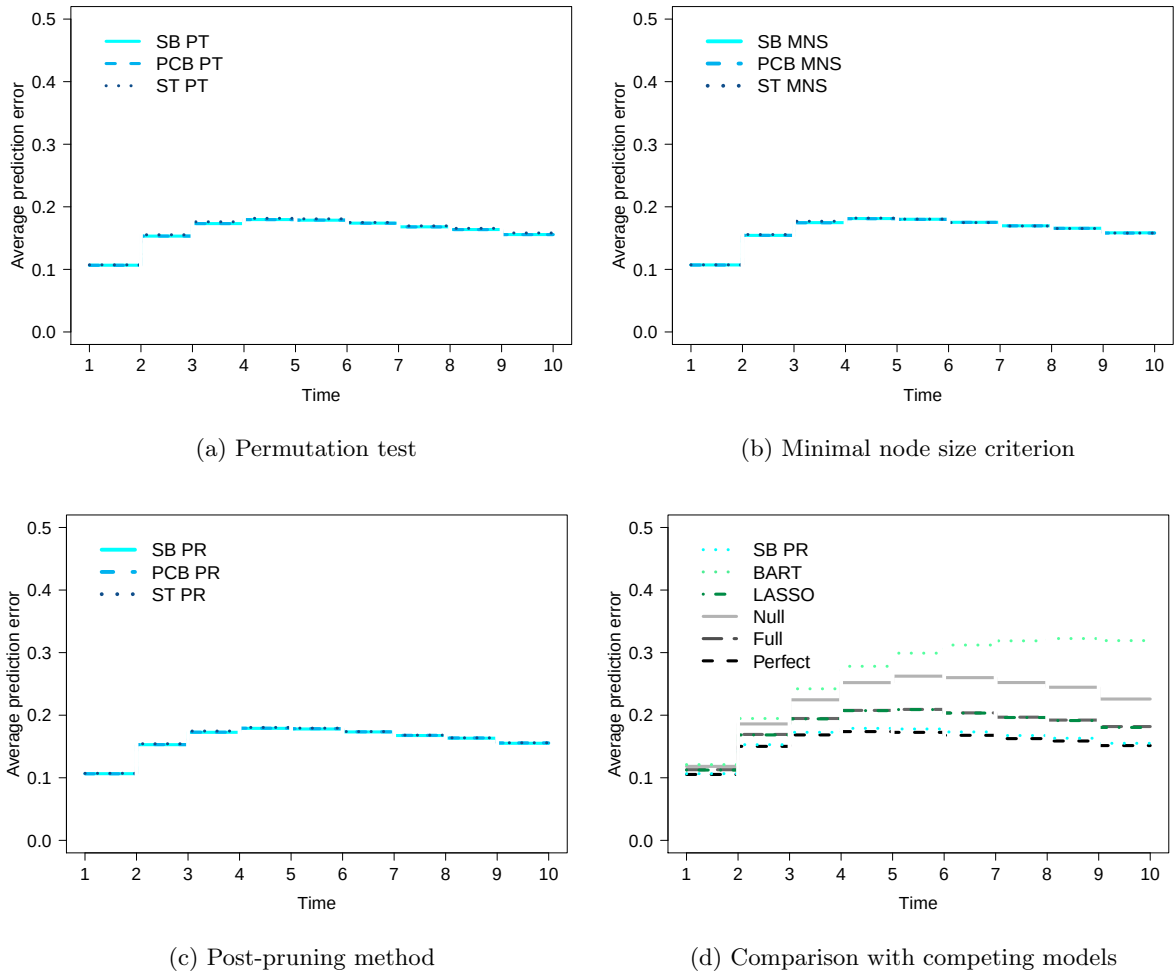
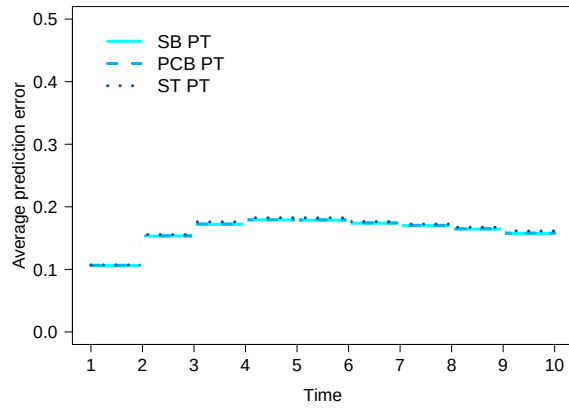
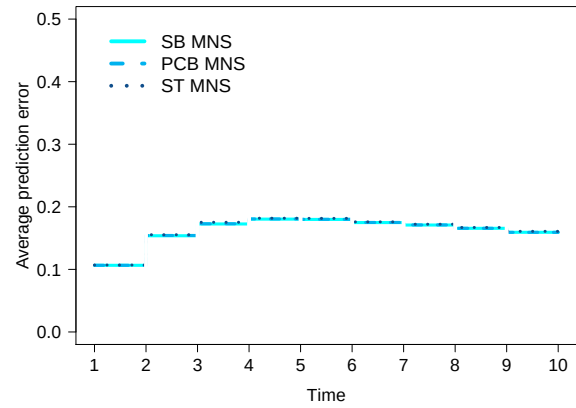


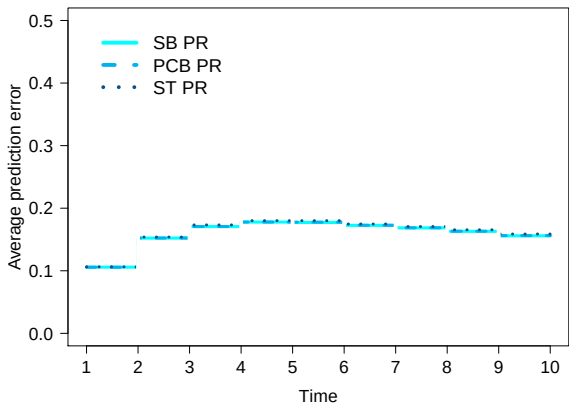
Fig. S9 Results of the simulation study: Prediction error curves (scenario 1). The figures show the prediction error curves of the different models for a low-dimensional setting with low censoring (30%). The four panels show the following: top left panel: proposed models with permutation test as stopping criterion; top right panel: proposed models with minimal node size as stopping criterion; bottom left panel: proposed models applying the post-pruning method; bottom right panel: proposed model with lowest integrated prediction error and the competing models



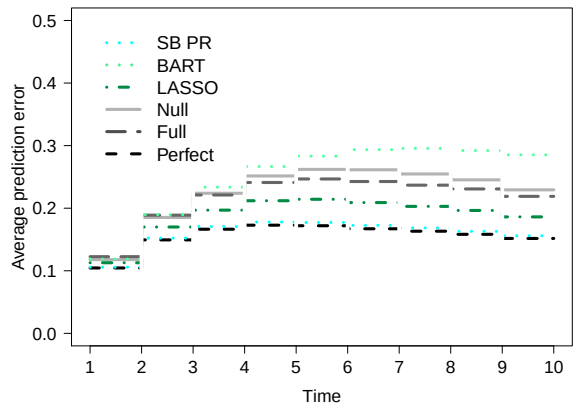
(a) Permutation test



(b) Minimal node size criterion

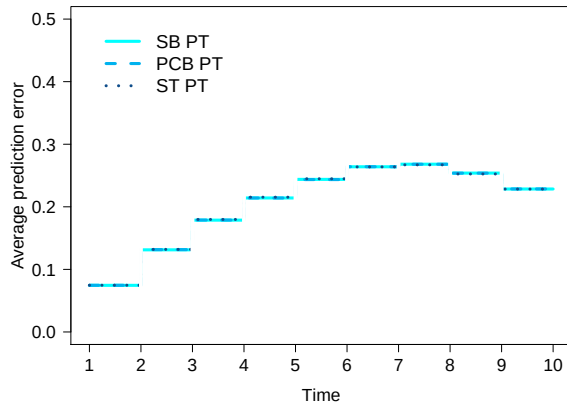


(c) Post-pruning method

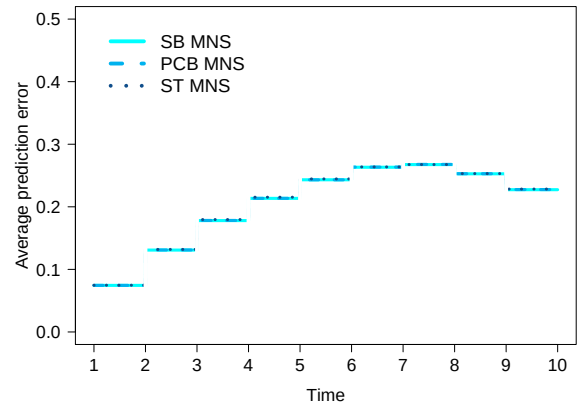


(d) Comparison with competing models

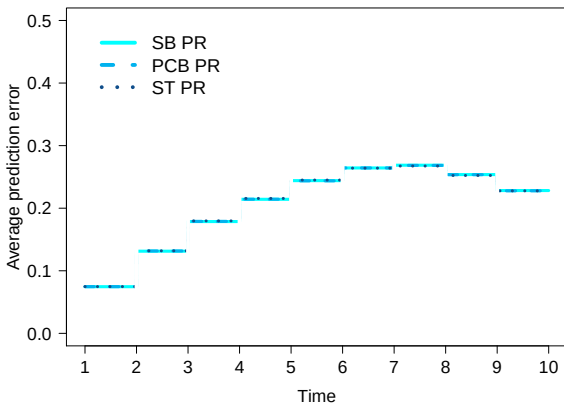
Fig. S10 Results of the simulation study: Prediction error curves (scenario 1). The figures show the prediction error curves of the different models for a high-dimensional setting with low censoring (30%). The four panels show the following: top left panel: proposed models with permutation test as stopping criterion; top right panel: proposed models with minimal node size as stopping criterion; bottom left panel: proposed models applying the post-pruning method; bottom right panel: proposed model with lowest integrated prediction error and the five competing models



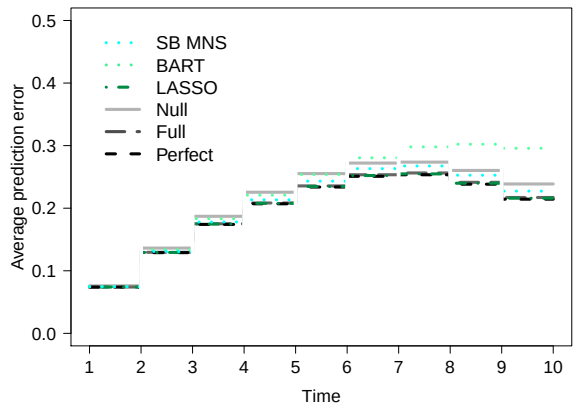
(a) Permutation test



(b) Minimal node size criterion

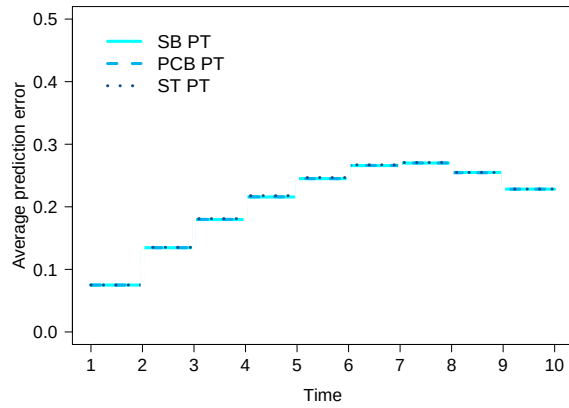


(c) Post-pruning method

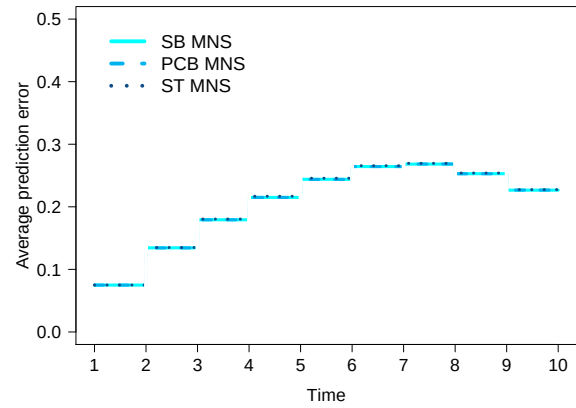


(d) Comparison with competing models

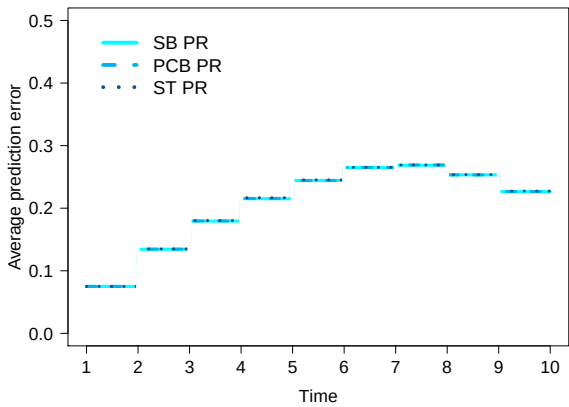
Fig. S11 Results of the simulation study: Prediction error curves (scenario 2). The figures show the prediction error curves of the different models for a low-dimensional setting with low censoring (30%). The four panels show the following: top left panel: proposed models with permutation test as stopping criterion; top right panel: proposed models with minimal node size as stopping criterion; bottom left panel: proposed models applying the post-pruning method; bottom right panel: proposed model with lowest integrated prediction error and the competing models



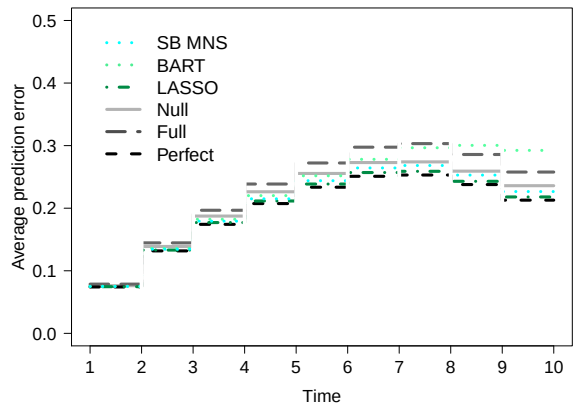
(a) Permutation test



(b) Minimal node size criterion

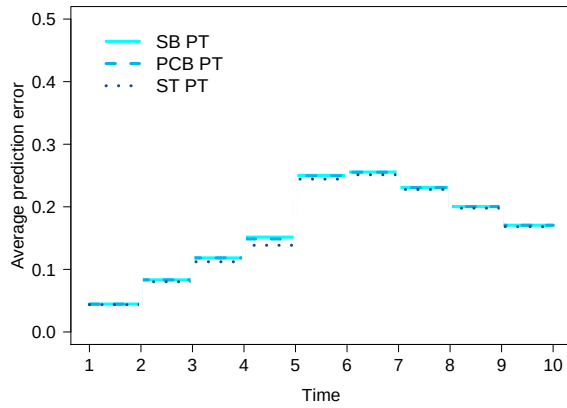


(c) Post-pruning method

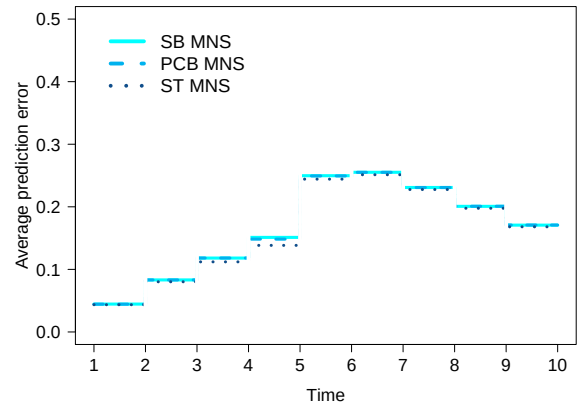


(d) Comparison with competing models

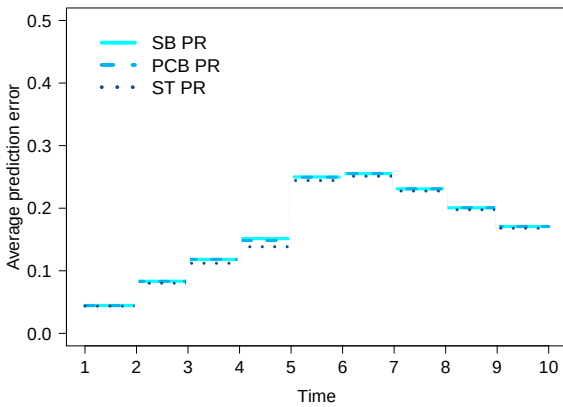
Fig. S12 Results of the simulation study: Prediction error curves (scenario 2). The figures show the prediction error curves of the different models for a high-dimensional setting with low censoring (30%). The four panels show the following: top left panel: proposed models with permutation test as stopping criterion; top right panel: proposed models with minimal node size as stopping criterion; bottom left panel: proposed models applying the post-pruning method; bottom right panel: proposed model with lowest integrated prediction error and the competing models



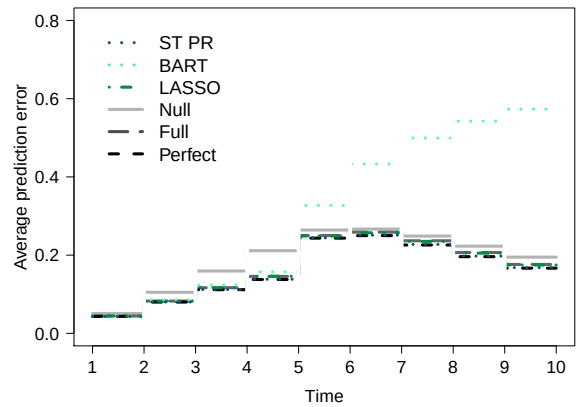
(a) Permutation test



(b) Minimal node size criterion

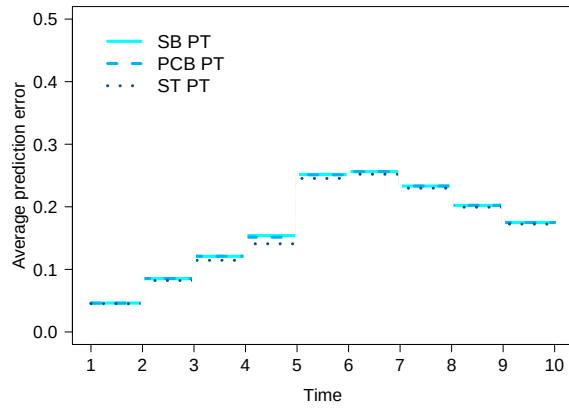


(c) Post-pruning method

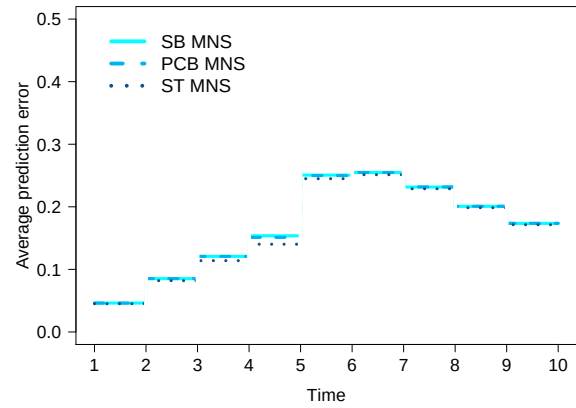


(d) Comparison with competing models

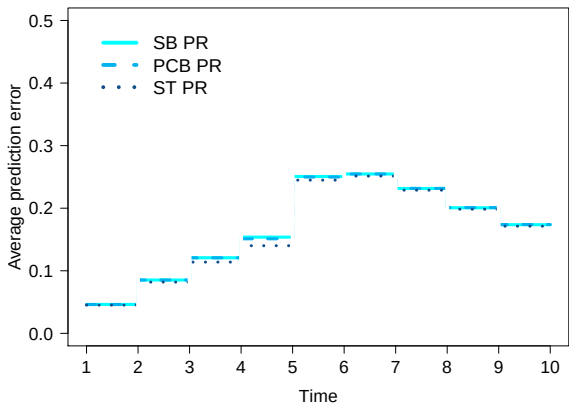
Fig. S13 Results of the simulation study: Prediction error curves (scenario 3). The figures show the prediction error curves of the different models for a low-dimensional setting with low censoring (30%). The four panels show the following: top left panel: proposed models with permutation test as stopping criterion; top right panel: proposed models with minimal node size as stopping criterion; bottom left panel: proposed models applying the post-pruning method; bottom right panel: proposed model with lowest integrated prediction error and the competing models



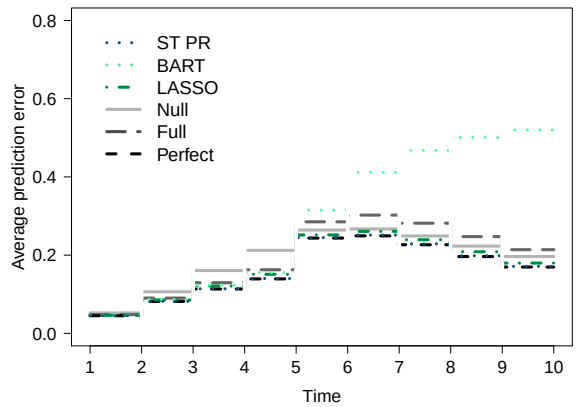
(a) Permutation test



(b) Minimal node size criterion



(c) Post-pruning method



(d) Comparison with competing models

Fig. S14 Results of the simulation study: Prediction error curves (scenario 3). The figures show the prediction error curves of the different models for a high-dimensional setting with low censoring (30%). The four panels show the following: top left panel: proposed models with permutation test as stopping criterion; top right panel: proposed models with minimal node size as stopping criterion; bottom left panel: proposed models applying the post-pruning method; bottom right panel: proposed model with lowest integrated prediction error and the competing models

Table S3 Results of the simulation study: Prediction errors (scenario 1). Average integrated prediction errors for the low-dimensional settings (left) and high-dimensional settings (right) and different degrees of censoring. To avoid inflated integrated PE values due to unstable inverse-probability-of-censoring weights for the later time intervals, time intervals in which less than 10% of the 500 simulated individuals were still at risk were excluded from the calculation

Censoring rate	Model	Stopping criterion	Low-dimensional			High-dimensional		
			0.3	0.5	0.7	0.3	0.5	0.7
SB	PT	PT	0.152	0.193	0.249	0.152	0.195	0.251
		MNS	0.153	0.194	0.250	0.153	0.194	0.251
		PR	0.151	0.192	0.251	0.151	0.193	0.251
PCB	PT	PT	0.152	0.193	0.249	0.153	0.196	0.251
		MNS	0.153	0.194	0.250	0.153	0.194	0.250
		PR	0.152	0.193	0.251	0.151	0.194	0.251
ST	PT	PT	0.154	0.195	0.250	0.155	0.198	0.252
		MNS	0.154	0.195	0.251	0.155	0.197	0.252
		PR	0.153	0.194	0.252	0.153	0.196	0.251
BART	—	—	0.245	0.306	0.378	0.229	0.288	0.358
LASSO	—	—	0.172	0.219	0.278	0.175	0.224	0.285
Null	—	—	0.206	0.263	0.332	0.206	0.264	0.330
Full	—	—	0.172	0.220	0.281	0.200	0.266	0.361
Perfect	—	—	0.148	0.187	0.238	0.147	0.186	0.237

Table S4 Results of the simulation study: Prediction errors (scenario 2). Average integrated prediction errors for the low-dimensional settings (left) and high-dimensional settings (right) and different degrees of censoring. To avoid inflated integrated PE values due to unstable inverse-probability-of-censoring weights for the later time intervals, time intervals in which less than 10% of the 500 simulated individuals were still at risk were excluded from the calculation

Censoring rate	Model	Stopping criterion	Low-dimensional			High-dimensional		
			0.3	0.5	0.7	0.3	0.5	0.7
	SB	PT	0.198	0.288	0.378	0.200	0.290	0.377
		MNS	0.198	0.286	0.377	0.199	0.289	0.373
		PR	0.198	0.286	0.377	0.199	0.289	0.373
	PCB	PT	0.199	0.287	0.379	0.200	0.291	0.377
		MNS	0.198	0.286	0.377	0.199	0.289	0.374
		PR	0.199	0.287	0.379	0.200	0.289	0.375
	ST	PT	0.198	0.287	0.379	0.201	0.291	0.375
		MNS	0.198	0.286	0.378	0.200	0.289	0.374
		PR	0.199	0.287	0.378	0.200	0.290	0.374
	BART	—	0.230	0.314	0.387	0.229	0.311	0.384
	LASSO	—	0.191	0.275	0.362	0.194	0.282	0.368
	Null	—	0.208	0.293	0.379	0.208	0.295	0.376
	Full	—	0.191	0.277	0.366	0.224	0.344	0.463
	Perfect	—	0.189	0.273	0.360	0.190	0.274	0.359

Table S5 Results of the simulation study: Prediction errors (scenario 3). Average integrated prediction errors for the low-dimensional settings (left) and high-dimensional settings (right) and different degrees of censoring. To avoid inflated integrated PE values due to unstable inverse-probability-of-censoring weights for the later time intervals, time intervals in which less than 10% of the 500 simulated individuals were still at risk were excluded from the calculation

Censoring rate	Model	Stopping criterion	Low-dimensional			High-dimensional		
			0.3	0.5	0.7	0.3	0.5	0.7
SB	PT	PT	0.202	0.301	0.525	0.204	0.304	0.520
		MNS	0.202	0.300	0.521	0.202	0.302	0.514
		PR	0.202	0.301	0.544	0.202	0.313	0.514
PCB	PT	PT	0.201	0.301	0.522	0.203	0.304	0.518
		MNS	0.201	0.300	0.519	0.202	0.302	0.512
		PR	0.202	0.300	0.547	0.200	0.202	0.512
ST	PT	PT	0.197	0.293	0.507	0.199	0.295	0.505
		MNS	0.197	0.301	0.516	0.198	0.301	0.507
		PR	0.197	0.293	0.538	0.198	0.305	0.503
BART	—	—	0.365	0.504	0.688	0.345	0.459	0.658
LASSO	—	—	0.203	0.301	0.516	0.206	0.306	0.516
Null	—	—	0.221	0.324	0.550	0.222	0.324	0.543
Full	—	—	0.204	0.304	0.526	0.237	0.373	0.700
Perfect	—	—	0.196	0.285	0.497	0.197	0.291	0.489

Supplement 4: Additional information on the applications

Table S6 Analysis of the odontogenic infection data. Summary statistics of the LOS and the patients characteristics incorporated in the analysis ($n = 303$)

Variable		Summary statistics				
	x_{min}	$x_{0.25}$	x_{med}	$\bar{x}$	$x_{0.75}$	x_{max}
LOS	1	4	5	5.9	7	18
Age	6	31	48	48.6	64	92
Gender	0: 146 (48.2%)					1: 157 (51.8%)
Spreading	0: 268 (88.4%)					1: 35 (11.6%)
Location	0: 263 (86.8%)					1: 40 (13.2%)
Antibiosis	0: 263 (86.8%)					1: 40 (13.2%)
Diabetes	0: 278 (91.7%)					1: 25 (8.3%)
Remaining focus	0: 118 (38.9%)					1: 185 (61.1%)

Table S7 Analysis of the lymphatic filariasis data. Summary statistics of the patients characteristics incorporated in the analysis ($n = 118$)

Variable	Summary statistics					
	x_{min}	$x_{0.25}$	x_{med}	$\overline{x}$	$x_{0.75}$	x_{max}
Age	18	40.75	50	47.83	57	60
Weight	40	54.75	62.50	65.12	73.50	120
Microfiliariae count	0	0	0	16.87	0	752
Gender	0: 85 (72.0%)				1: 33 (28.0%)	
Infection status	0: 72 (61.0%)				1: 46 (11.6%)	
Drug	Placebo (0)				38 (32.20%)	
	Amoxicillin (1)				35 (29.66%)	
	Doxycycline (2)				45 (38.14%)	
Lymphedema stage before treatment	1	2 (1.69%)				
	2	52 (44.07%)				
	3	57 (48.31%)				
	4	1 (0.85%)				
	5	6 (5.08%)				
Hygiene status before treatment	Poor (0)				21 (0.69%)	
	Moderate (1)				69 (58.47%)	
	Good (2)				28 (23.73%)	