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An extension of the compound covariate prediction under the Cox proportional hazard models

Emura , Chen & Chen [2012, PLoS ONE 7(10)]

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Outline:

- 1) Review: Survival data with high-dimensional covariates
- 2) Review: Ridge regression
- 3) Review: Compound covariate (CC) method
- 4) Some theory on CC method
- 5) Extension of the CC method
 - ➔ Propose a new method
- 6) Data example

• Survival data :

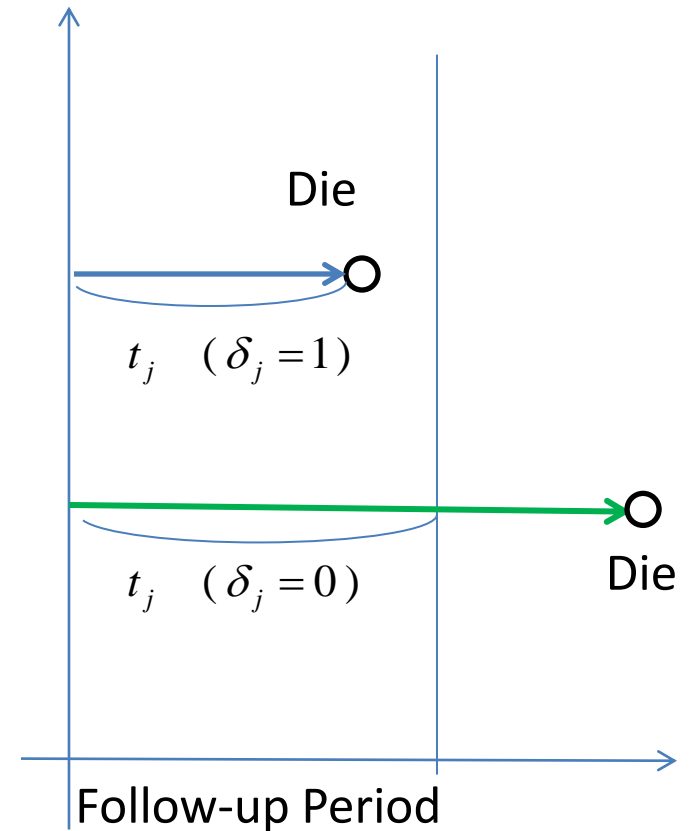
$$\{ (t_i, \delta_i, \mathbf{x}_i); i = 1, \dots, n \}$$

t_i : either time to death or censoring

$$\delta_i = \begin{cases} 1 & \text{if death} \\ 0 & \text{if censoring} \end{cases}$$

$$\mathbf{x}_i = (x_{i1}, \dots, x_{ip})', \text{ possibly } p > n$$

(Gene \Leftrightarrow Covariate)



Lung cancer data from Chen et al. 2007 NEJM

Patient ID	Survival_Status	
100	alive , 47 months (censored)	$t_i = 47, \delta_i = 0$
101	alive, 49 months (censored)	
102	death, 20 months	$t_i = 20, \delta_i = 1$
109	death, 26	
110	alive, 39 (censored)	
113	alive, 35 (censored)	
115	alive, 45 (censored)	
116	death, 9	
128	death, 21	
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.		
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365	alive, 5 months (censored)	

n=125 samples

1st Patient (ID = 100)

- Gene: $\mathbf{x}_i = (x_{i1}, \dots, x_{i672})'$

P=672 covariates >> n = 125

ID_REF	SLOG TRANSFORMED VALUE
1	15.27004532
2	13.17203115
3	14.21802644
4	15.12513123
5	13.20893358
6	14.8388795
7	13.8996511
8	13.93310453
9	14.4358955
10	13.94191912
11	14.80745797
12	13.73624082
13	13.07752608
666	14.63251884
667	14.53994587
668	14.60524106
669	14.48299068
670	11.55074679
671	11.55074679
672	11.55074679

- Genetic information is useful in survival prediction:

Breast cancer:

(Jenssen et al., 2002; van de Vijver et al., 2002;
van't Veer et al., 2002; Zhao et al., 2011)

Lung cancer:

(Beer et al., 2002; Chen et al., 2007; Shedden et al., 2008)

- Demand for statistical prediction methods adapted to high-dimensionality, especially on recent 10 years

Hazard function:

$$h(t | \mathbf{x}_i) = \Pr(t \leq t_i \leq t + dt | t_i \geq t, \mathbf{x}_i) / dt$$

- Cox proportional hazard model (Cox 1972)

$$h(t | \mathbf{x}_i) = h_0(t) \exp(\boldsymbol{\beta}' \mathbf{x}_i), \quad \boldsymbol{\beta} \in \mathbf{R}^p$$

- Partial likelihood estimator:

$$\hat{\boldsymbol{\beta}} \in \mathbf{R}^p : \text{maximize } L_n^1(\boldsymbol{\beta}) = \prod_{i=1}^n \left(\frac{\exp(\boldsymbol{\beta}' \mathbf{x}_i)}{\sum_{t_l \leq t_i} \exp(\boldsymbol{\beta}' \mathbf{x}_l)} \right)^{\delta_i}$$

If $n \rightarrow \infty$, then $\hat{\boldsymbol{\beta}} \rightarrow_p \boldsymbol{\beta}_0$

If $p > n$, $\hat{\boldsymbol{\beta}} \in \mathbf{R}^p$ is **not unique (infinitely many maxima)**

Idea of *Ridge* estimator (Hoerl & Kennard 1970)

Infinitely many
solution in OLS

$$\hat{\beta} = \operatorname{argmin} \|y - X\beta\|^2$$

Unique nearest
point to 0

0

Bayesian Interpretation :
Hastie, Tibshirani, Friedman (2009)
The Element of Statistical Learning

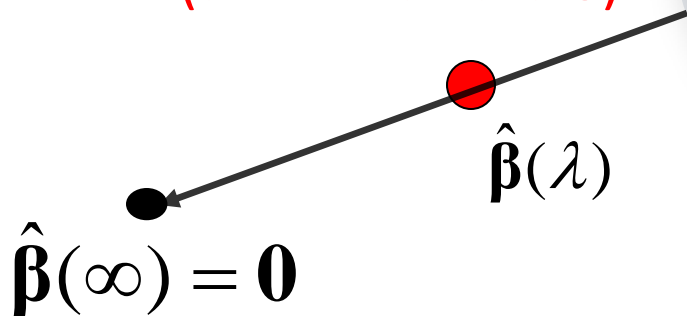
- Penalized partial likelihood
(Verweij & Houwelingen 1994)

$$\hat{\boldsymbol{\beta}}(\lambda) : L_{\lambda}^{Ridge}(\boldsymbol{\beta}) = \prod_{i=1}^n \left(\frac{\exp(\boldsymbol{\beta}' \mathbf{x}_i)}{\sum_{l \in R_i} \exp(\boldsymbol{\beta}' \mathbf{x}_l)} \right)^{\delta_i} - \lambda \|\boldsymbol{\beta}\|^2$$

(Ridge estimator)

Ridge estimator
(shrink toward $\mathbf{0}$)

$$\hat{\boldsymbol{\beta}}(0) : \mathbf{U}(\boldsymbol{\beta}) = \frac{\partial}{\partial \boldsymbol{\beta}} \log L_n^1(\boldsymbol{\beta}) = \mathbf{0}$$



- Prediction by the Ridge estimator

\mathbf{x} : Covariates for a future patient

$\hat{\boldsymbol{\beta}}'(\lambda)\mathbf{x} < c$ (Low hazard --> Good prognosis)

$\hat{\boldsymbol{\beta}}'(\lambda)\mathbf{x} > c$ (High hazard --> Poor prognosis)

where c is the cut-off value

Existing methods for high-dimensional survival data

- Ridge regression (Cox-regression with L_2 penalty)

Verve & van Howelingen(1994 Stat. Med.), Zhao et al. (2011 PLoS ONE)

- Lasso (Cox-regression with L_1 penalty)

Gui & Li (2005 Bioinformatics), Segal (2006 Biostatistics)

- Gene selection via univariate Cox-regression

Jenssen et al. (2002 Nature Med.), Chen et al. (2007 NEJM), name but a few

- Others (Principal component, partial least square, etc.)

Among above methods, ridge regression has the best performance in terms of survival prediction

(Bovelstad et al., 2007; van Weieringen et al., 2009; Bovelstad and Borgan, 2011)

Objectives of our study:

Propose a new prediction method that generalizes the so-called *compound covariate prediction*

Compound covariate prediction method

*Previously used in medical context

Tukey (1993 Controlled Clinical Trial), Beer et al. (2002 Nature Med.)
Chen et al. (2007 NEJM), Radamacher et al (2002 J. of Theoretical Bio.)
Matsui (2006 BMC Bioinformatics)

* Less known in statistical literature

Compound covariate prediction

Step1: For each gene $j(=1,\dots,p)$, fit a univariate Cox model

$$\Pr(t \leq t_i \leq t + dt | t_i \geq t, x_{ij}) / dt = h_{0j}(t) \exp(\beta_j x_{ij})$$

Step2: A set of p regression coefficients

$$\hat{\boldsymbol{\beta}}(0) = (\hat{\beta}_1, \dots, \hat{\beta}_p)', \quad \text{where } \hat{\beta}_j = \arg \max \prod_{i=1}^n \left(\frac{\exp(\beta_j x_{ij})}{\sum_{t_l \geq t_i} \exp(\beta_j x_{lj})} \right)^{\delta_i}$$

Remark: This is possible even when $p > n$

Step 3: *Compound covariate prediction*

For a future patient with genes $\mathbf{x} = (x_1, \dots, x_p)'$,

$$\hat{\boldsymbol{\beta}}'(0)\mathbf{x} < c \text{ (Good prognosis) ; } \hat{\boldsymbol{\beta}}'(0)\mathbf{x} > c \text{ (Poor prognosis)}$$

Compound covariate method

- is a univariate method to resolve the high dimensionality
- empirically perform well in microarray studies

To motivate our proposal, we first give some theoretical results on the compound covariate method

- **Assumption:** The Cox model holds with

$$h(t | \mathbf{x}_i) = h_0(t) \exp(\boldsymbol{\beta}' \mathbf{x}_i) = h_0(t) \exp(\beta_1 x_{i1} + \dots + \beta_p x_{ip})$$

at the true parameter $\boldsymbol{\beta}' = \boldsymbol{\beta}'_0 = (\beta_{0,1}, \dots, \beta_{0,p}) \neq \mathbf{0}$

- **Remark:** Under the multivariate Cox model assumption, the *univariate Cox model does not hold*, i.e.,

$$h(t | x_{ij}) = -\frac{\partial}{\partial t} \log E[\exp\{-H_0(t) \exp(\boldsymbol{\beta}' \mathbf{x}_i)\} | x_{i1}]$$

~~$\neq h_{0,j}(t) \exp(\beta_j x_{ij})$.~~

- Univariate Cox model for each gene $j (= 1, \dots, p)$

$$\Pr(t \leq t_i \leq t + dt \mid t_i \geq t, x_{ij}) / dt = h_{0j}(t) \exp(\beta_j x_{ij})$$

is a misspecified model (a working model)

Ref:

Struthers & Kalbfleisch (1986) Misspecified proportional hazard models, *Biometrika* 73 pp.363-9.

- Univariate partial likelihood equation

$$\hat{\beta}_j : \text{Solution to } 0 = U_j(\beta_j) = \frac{1}{n} \sum_{i=1}^n \delta_i \left\{ x_{ij} - \frac{\sum_{\ell=1}^n I(t_\ell \geq t_i) x_{\ell j} \exp(\beta_j x_{\ell j})}{\sum_{\ell=1}^n I(t_\ell \geq t_i) \exp(\beta_j x_{\ell j})} \right\}$$

$$\beta_j^* \text{ Solution to } 0 = u_j(\beta_j) \xleftarrow{P} U_j(\beta_j)$$

$$\hat{\beta}_j \xrightarrow{P} \beta_j^* \neq \beta_{0j} \quad (\text{true value in the Assumption})$$

Remark I: If all genes $\mathbf{x} = (x_1, \dots, x_p)'$ are independent

$$\text{sign}(\beta_j^*) = \text{sign}(\beta_{0j}), \quad |\beta_j^*| \leq |\beta_{0j}|$$

Remark II:

Let $\boldsymbol{\beta}^*(0) = (\beta_1^*, \dots, \beta_p^*)'$ and $\mathbf{0} = (0, \dots, 0)'$.

Then, $\boldsymbol{\beta}^*(0)$ is between $\boldsymbol{\beta}_0$ and $\mathbf{0}$.

Above results deduced from :

Struthers & Kalbfleisch (1986 Biometrika) ; Bretagnolle & Huber-Carol(1988 Scand. JS)

Proposed estimator

- Univariate *compound* likelihood (unique maxima)

$$L_n^0(\boldsymbol{\beta}) = \prod_{j=1}^p \prod_{i=1}^n \left(\frac{\exp(\beta_j x_{ij})}{\sum_{t_l \geq t_i} \exp(\beta_j x_{lj})} \right)^{\delta_i}$$

- Multivariate likelihood (infinitely many maxima when $p > n$)

$$L_n^1(\boldsymbol{\beta}) = \prod_{i=1}^n \left(\frac{\exp(\boldsymbol{\beta}' \mathbf{x}_i)}{\sum_{l \in R_i} \exp(\boldsymbol{\beta}' \mathbf{x}_l)} \right)^{\delta_i}$$

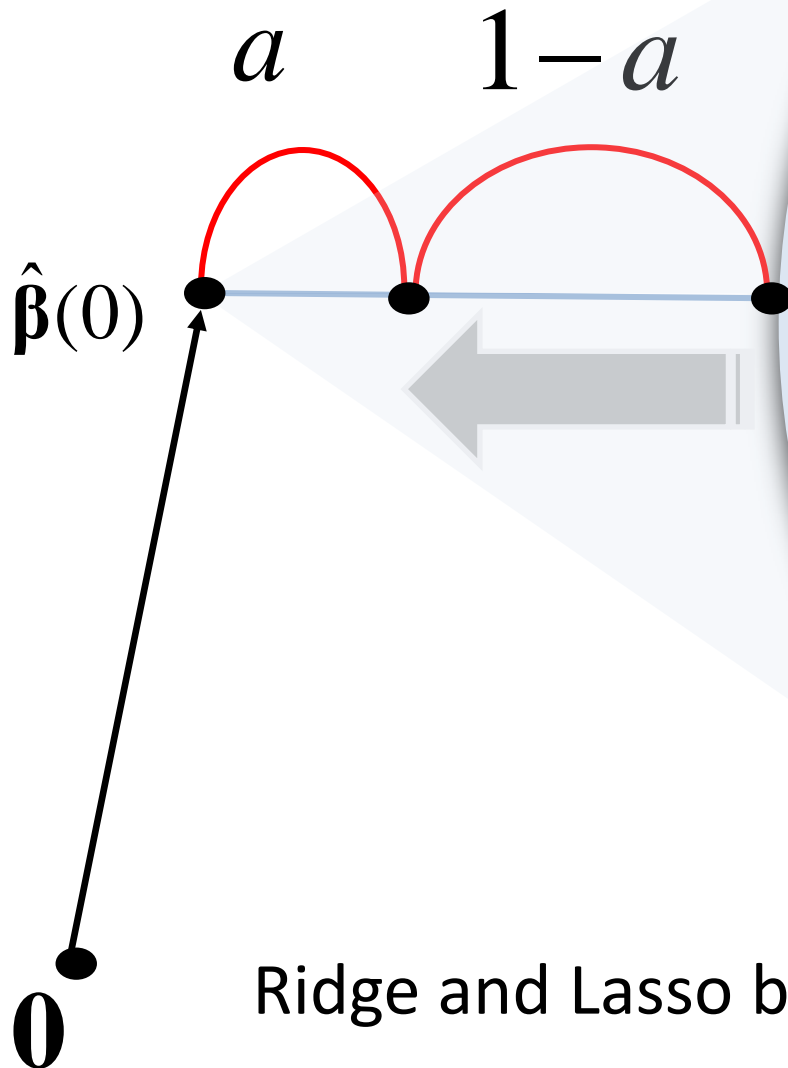
- Idea: Mixture of univariate and multivariate likelihood

$$\hat{\boldsymbol{\beta}}(a) = \operatorname{argmax} \left\{ a \log L_n^1(\boldsymbol{\beta}) + (1-a) \log L_n^0(\boldsymbol{\beta}) \right\}, \quad a \in [0, 1]$$

We call it “compound shrinkage estimator”

Compound shrinkage estimator :

$$\hat{\boldsymbol{\beta}}(a) = \operatorname{argmax} \left\{ a \log L_n^1(\boldsymbol{\beta}) + (1-a) \log L_n^0(\boldsymbol{\beta}) \right\}$$



- $\boldsymbol{\beta}_0$ (true)

Infinitely many solutions
for a multivariate Cox regression

$$\hat{\boldsymbol{\beta}}: \mathbf{U}(\boldsymbol{\beta}) = \frac{\partial}{\partial \boldsymbol{\beta}} \log L_n^1(\boldsymbol{\beta}) = \mathbf{0}$$

Ridge and Lasso both shrink toward zero

- Proposition 2: (in our paper)

$$\sqrt{n}(\hat{\boldsymbol{\beta}}(\hat{a}) - \boldsymbol{\beta}_0) \rightarrow N(\mathbf{0}, \boldsymbol{\Sigma}(\boldsymbol{\beta}_0)) \text{ with } \hat{a} = \operatorname{argmax} CV(a).$$

(CV = Cross-Validated likelihood of Verveij & Houwelingen 1993)

- Plug-in variance estimator $\boldsymbol{\Sigma}_n^{\hat{a}}(\hat{\boldsymbol{\beta}}(\hat{a}))$

$$\boldsymbol{\Sigma}_n^a(\boldsymbol{\beta}) = \mathbf{A}_n^a(\boldsymbol{\beta}) \{ \mathbf{V}_n^a(\boldsymbol{\beta}) / n \}^{-1} \mathbf{A}_n^a(\boldsymbol{\beta})'$$

$$\mathbf{A}_n^a(\boldsymbol{\beta}) = \mathbf{V}_n^a(\boldsymbol{\beta})^{-1} \dot{\mathbf{h}}_n(\boldsymbol{\beta}) \{ -d^2 CV(a) / da^2 \}^{-1} \dot{\mathbf{h}}_n(\boldsymbol{\beta})' + \mathbf{I}_p$$

$$\dot{\mathbf{h}}_n(\boldsymbol{\beta}) = \partial \mathbf{U}_n^a(\boldsymbol{\beta}) / \partial a, \text{ where } \mathbf{U}_n^a(\boldsymbol{\beta}) = \text{Score function}$$

$$\frac{d}{da} CV(a) = \text{Estimating function of } a,$$

$$\mathbf{V}_n^a(\boldsymbol{\beta}) = \text{observed Fisher information}$$

* Reasonable performance even when $p > n$.

Numerical comparison

Compare 4 methods

1. Compound covariate (CC) estimator

$\hat{\boldsymbol{\beta}} = (\hat{\beta}_1, \dots, \hat{\beta}_p)'$, where $\hat{\beta}_j$ = univariate Cox regression estimators

2. Compound shrinkage (CS) estimator

$\hat{\boldsymbol{\beta}}(\hat{a}) : a \log L_n^1(\boldsymbol{\beta}) + (1-a) \log L_n^0(\boldsymbol{\beta}) \quad \leftarrow$ R compound.Cox package
(Emura and Chen, 2012)

3. Ridge estimator

$\hat{\boldsymbol{\beta}}(\hat{\lambda}) : \log L_n^1(\boldsymbol{\beta}) - (\lambda/2) \sum_{j=1}^p \beta_j^2 \quad \leftarrow$ R penalized package

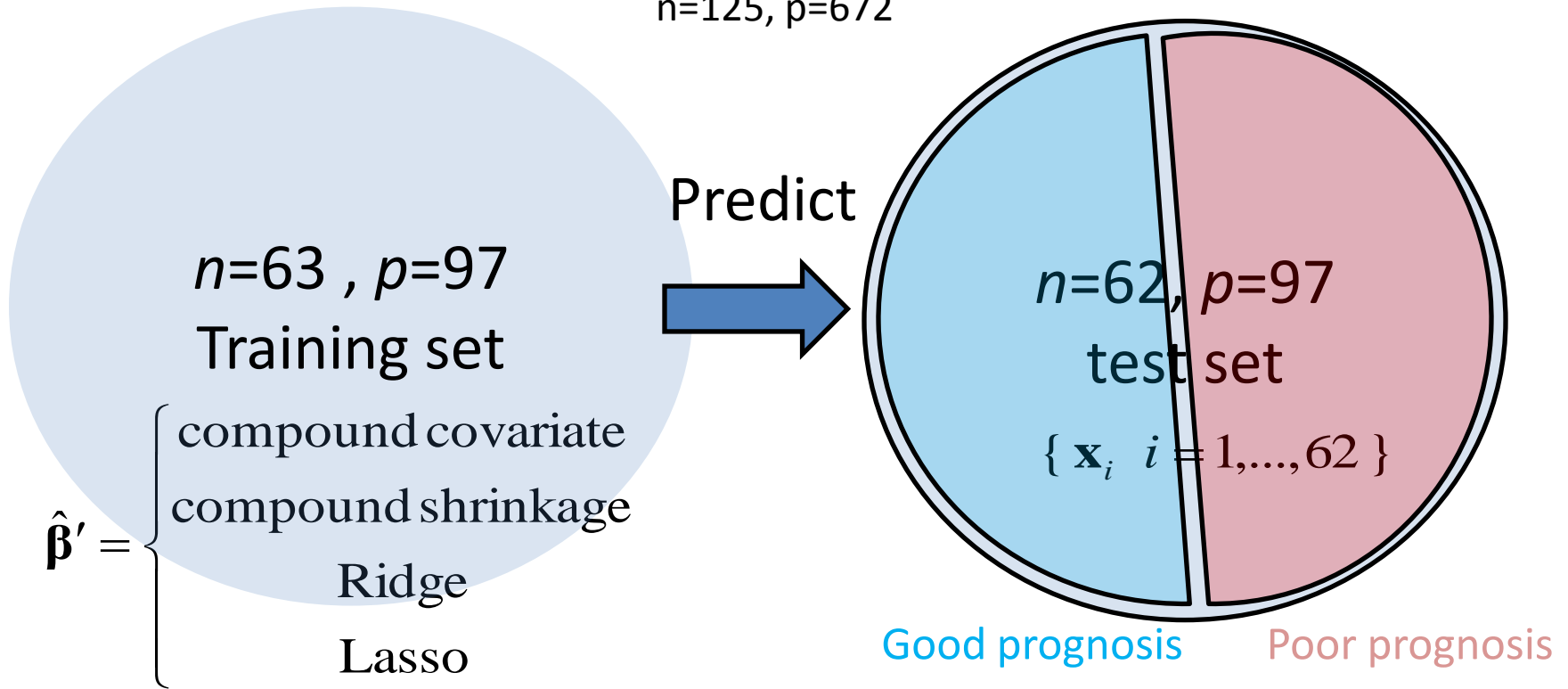
4. Lasso estimator

$\hat{\boldsymbol{\beta}}(\hat{\lambda}) : \log L_n^1(\boldsymbol{\beta}) - \lambda \sum_{j=1}^p |\beta_j| \quad \leftarrow$ R penalized package

* \hat{a} or $\hat{\lambda}$ is obtained by cross-validation (Verveij & Houwelingen 1993 Stat.Med.)

•Data: Lung cancer data (Chen et al., 2007 NEJM)

$n=125, p=672$

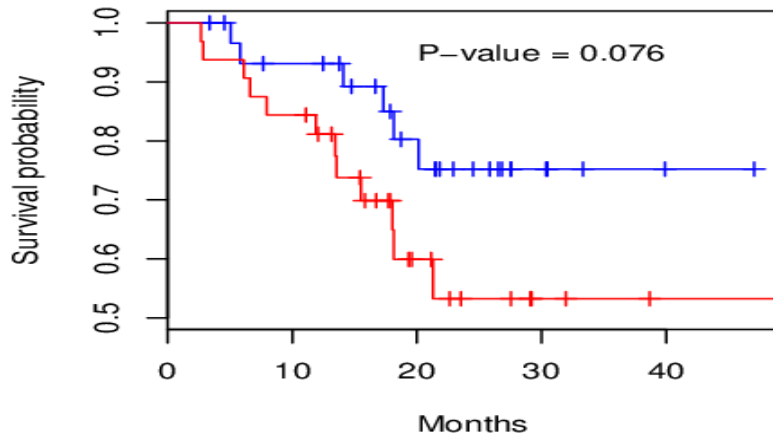


$\hat{\beta}' \mathbf{x}_i < c$ (Good prognosis) ; $\hat{\beta}' \mathbf{x}_i > c$ (Poor prognosis),

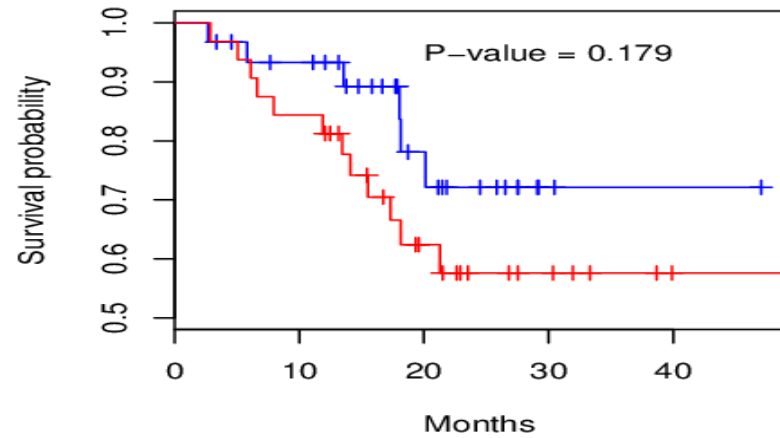
where c is the median of $\{ \hat{\beta}' \mathbf{x}_i, i = 1, \dots, n \}$

Survival curves for **Poor** vs. **Good** prognosis groups in n=62 testing data; p-value for Log-rank test

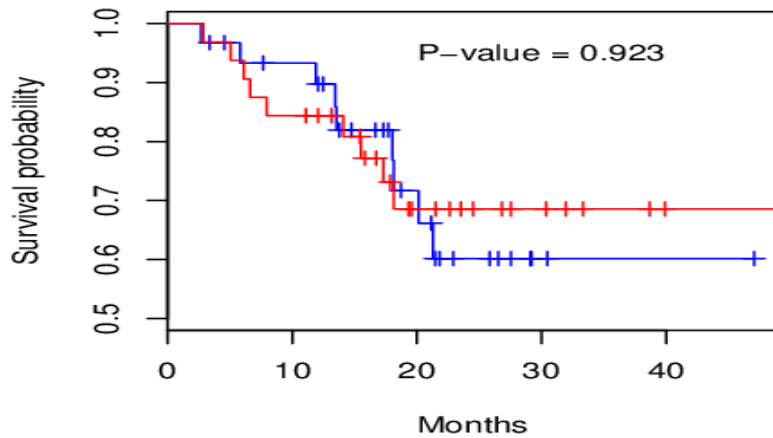
Compound covariate



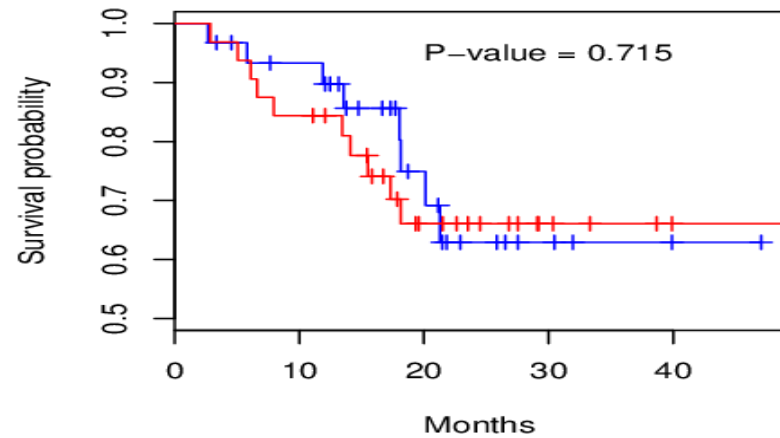
Compound shrinkage



Ridge regression

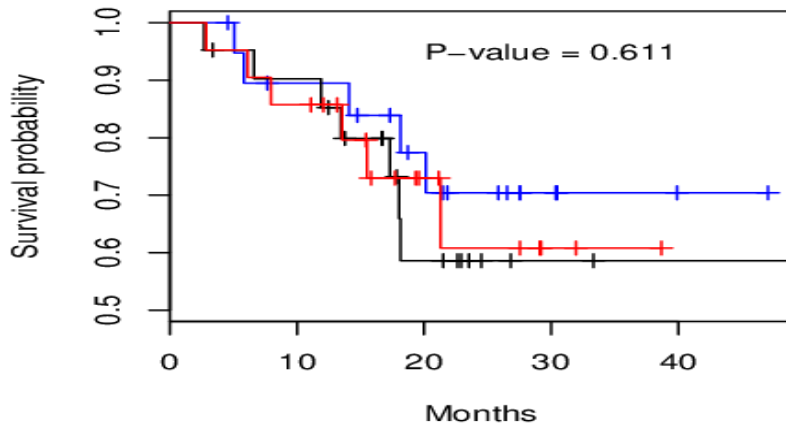


Lasso

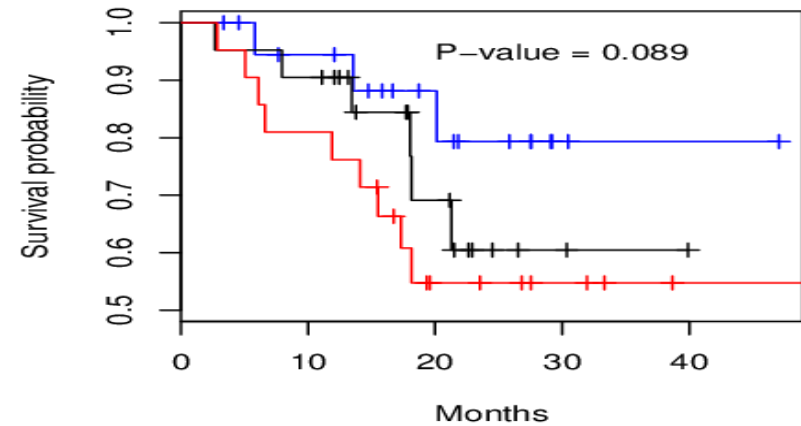


Survival curves for **Poor**, Medium, **Good** prognosis groups for n=62 testing data; p-value for Log-rank trend test

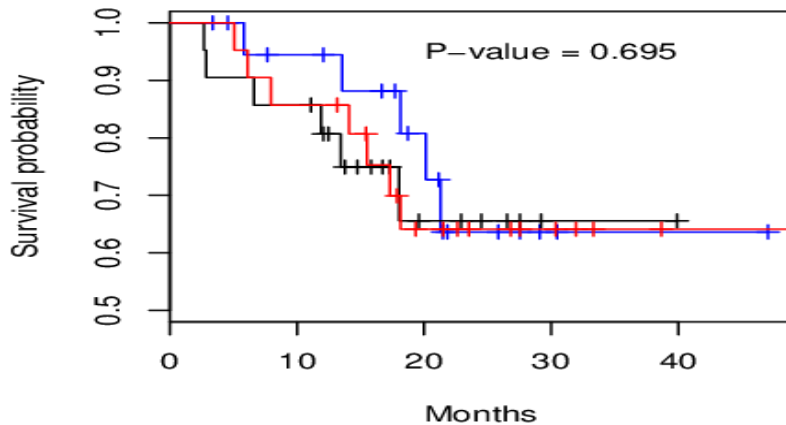
Compound covariate



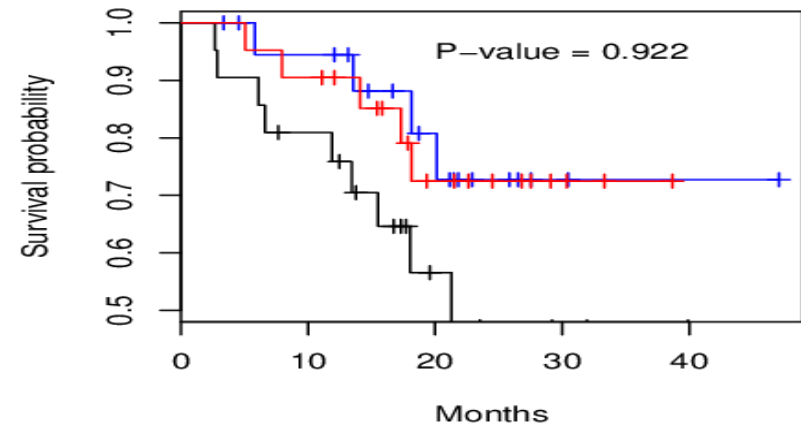
Compound shrinkage



Ridge regression



Lasso



Thank you for your attention