Supervised Learning: Penalized Regression for Other Data Types

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Data of Different Types

- Simple continuous response
- Binary response
- Count data
- Survival outcome

Different Data Need Different Models

- Simple continuous response: squared error
- Binary response: logistic loss (0-1/hinge loss for other methods)
- Count data: Poisson loss
- Survival outcome: Cox loss

Log-Likelihood Loss

Data generating mechanisms $\rightarrow$ (log)likelihood $\rightarrow$ Loss function

Log-Likelihood Loss

Our usual Gaussian model

$$y_i = \beta_0 + x_i^\top \beta + \epsilon_i$$

with ϵ_i iid $N(0, \sigma^2)$

The likelihood:

$$\mathcal{L}(\beta \mid x, y) = (2\pi\sigma^2)^{n/2} \exp - \frac{1}{2\sigma^2} \sum (y_i - x_i^\top \beta)^2$$

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our usual least squares criterion!

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Logistic model

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + x_i^\top \beta$$

with $p_i = P(Y_i = 1 \mid x_i)$

The likelihood:

$$\begin{aligned}
\mathcal{L}(\beta \mid x, y) &= \prod_i p_i^{y_i} (1-p_i)^{(1-y_i)} \\
&= \prod_i \text{expit}(\beta_0 + x_i^\top \beta)^{y_i} \Big(1 - \text{expit}(\beta_0 + x_i^\top \beta)\Big)^{(1-y_i)}
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which is solved in logistic regression.

Log-Likelihood Loss

Other examples:

Log-Likelihood Loss

Other examples:

- Poisson Model:

$$\log\left(E[y_i \mid x_i]\right) = \beta_0 + \beta^\top x_i$$

  is used to model rare events
  - deaths from TB each year in the US
  - counts from sequencing data for gene expression
  - limit of Binomial likelihood for a large number of trials with a really biased coin (e.g. $\pi = 3/1000$)

  give rise to Poisson regression

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- For Poisson regression: `glmnet(x,y,family = "Poisson")`

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Other examples:

- Cox Model (nested multinomials):
  - x_i: features
  - y_i: time on study
  - z_i: indicator of fail/censoring

  Consider likelihood conditional on failure times:

$$P(\text{person } j \text{ fails at time } t \mid \text{a failure at time } t) = \frac{e^{x_j^\top \beta}}{\sum_{k \text{ at risk at } t} e^{x_k^\top \beta}}$$

Survival Outcome

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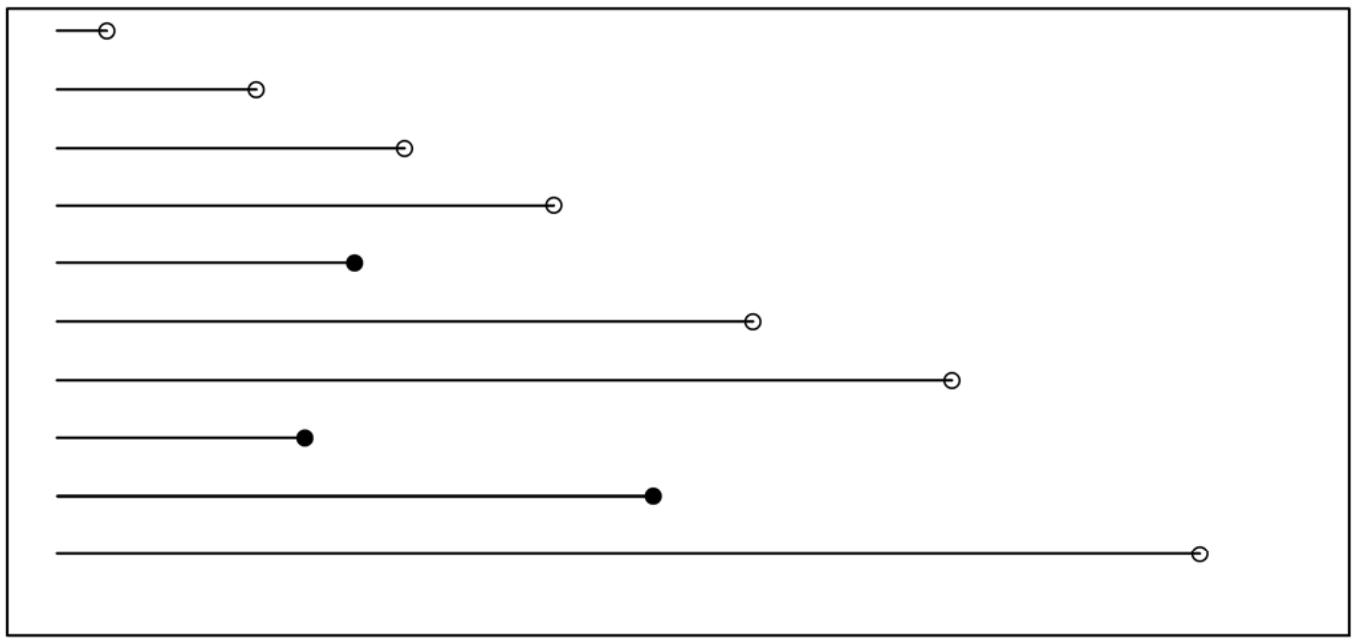
We're interested in **length** of survival time... but not everyone dies;

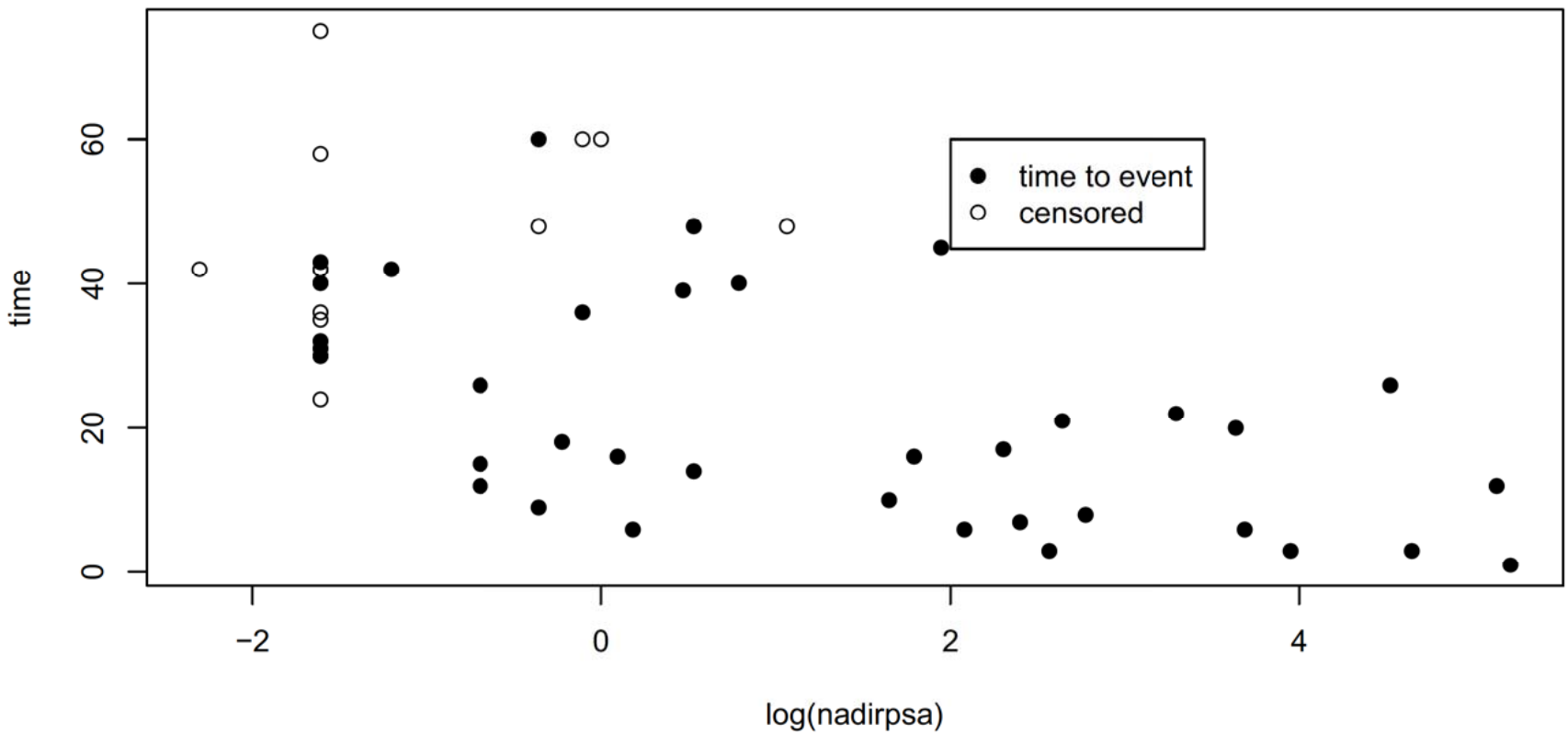


Survival time (all start at zero)

At random, we see survival time T **or** just know that $T > C$

Survival Outcome

Results are *somewhat* intuitive...



What do you think the effect of `nadirpsa` is?

Surv objects

The 'outcome' in survival analysis involves both an observed time and a censoring status. These are packaged in a `Surv` object.

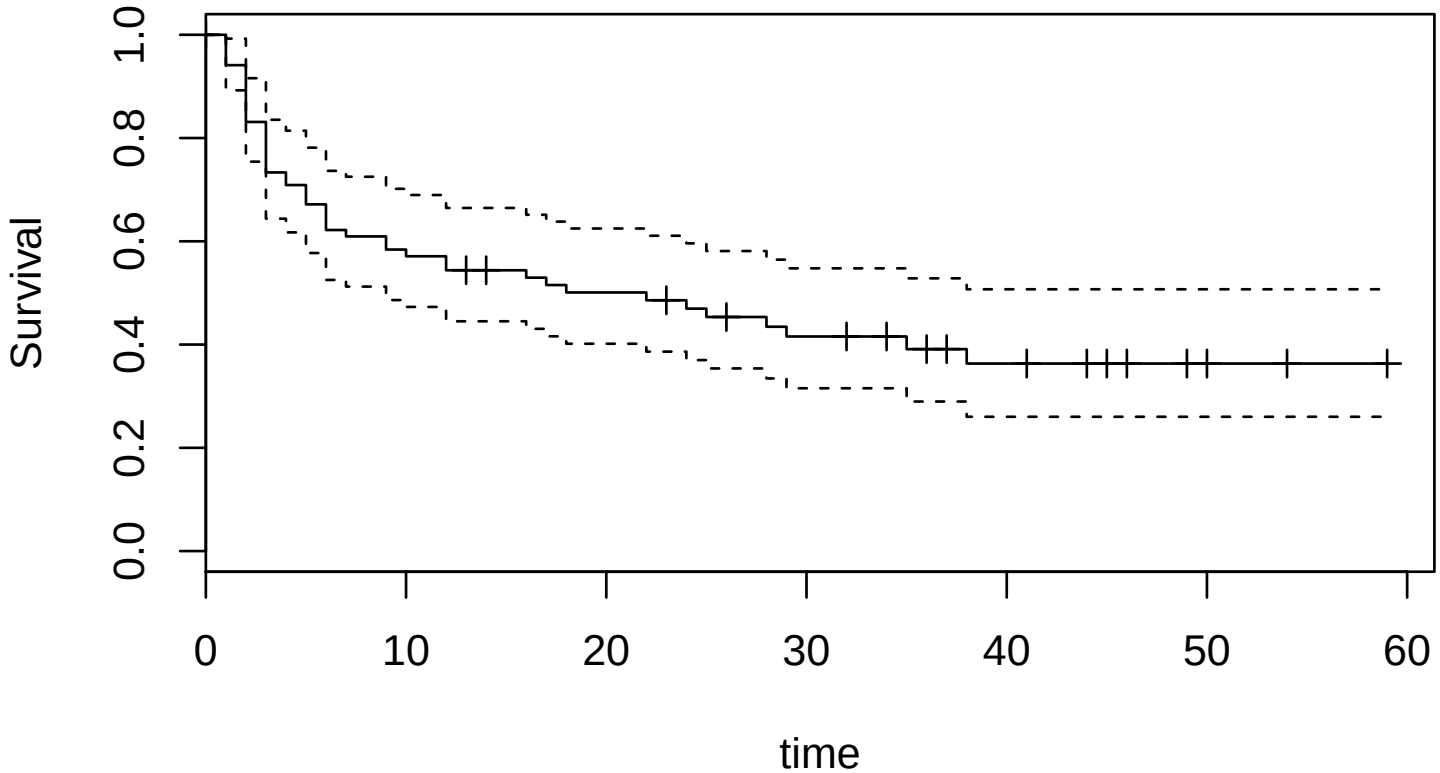
- `library(survival)` has many features for low-dim. data
- `Surv(time,event)` is the simplest form (for simple right-censoring data)
- `event` tells `R` whether we saw T or just $T > C$
- Full T, C terminology a bit cumbersome, censoring is instead shown with a $+$

```
> library(survival)
Loading required package: splines
> tumor.surv <- with(tumor, Surv(time, event) )
> tumor.surv[1:10]
 [1]  0+  1+  4+  7+ 10+  6  14+ 18+  5  12
```

Always check this! Is your censoring setup correctly?

Survival Curves

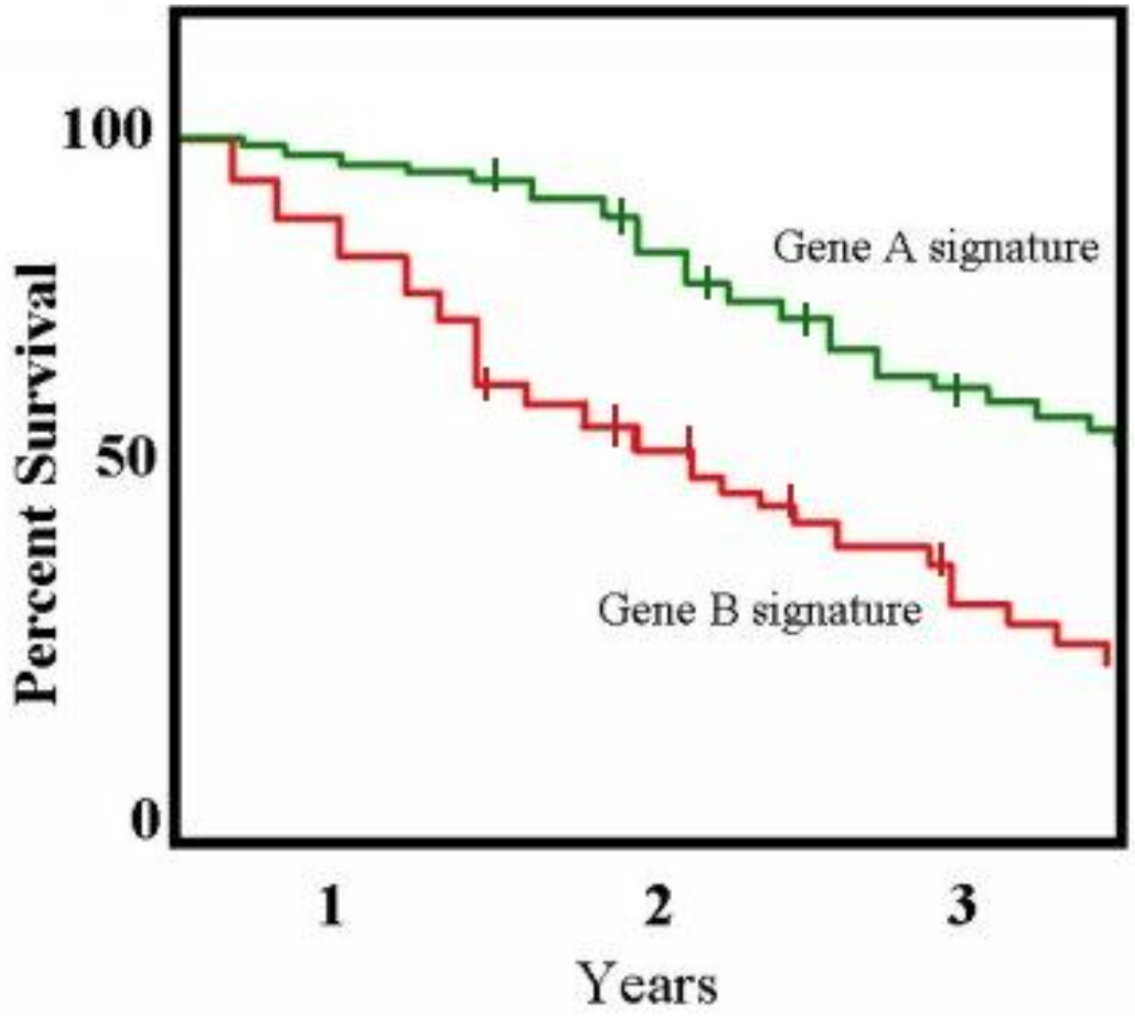
The most common, 'intuitive' summary, also known as Kaplan-Meier curves




```
plot(survfit(tumor.surv ~ 1))
```

Survival Curves

Can e.g. compare different groups



Gene B signature $<$ Gene A signature

Building prognostic survival classifiers

- Generally want a classification of high vs low risk:
- Given a Cox-model
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How do we choose c?

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How do we choose c? cross-validation! (CV survival curves)

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Can use regularization:

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Example: Gene Expression Example

Building a prognostic classifier for patients with advanced bladder cancer receiving chemotherapy:

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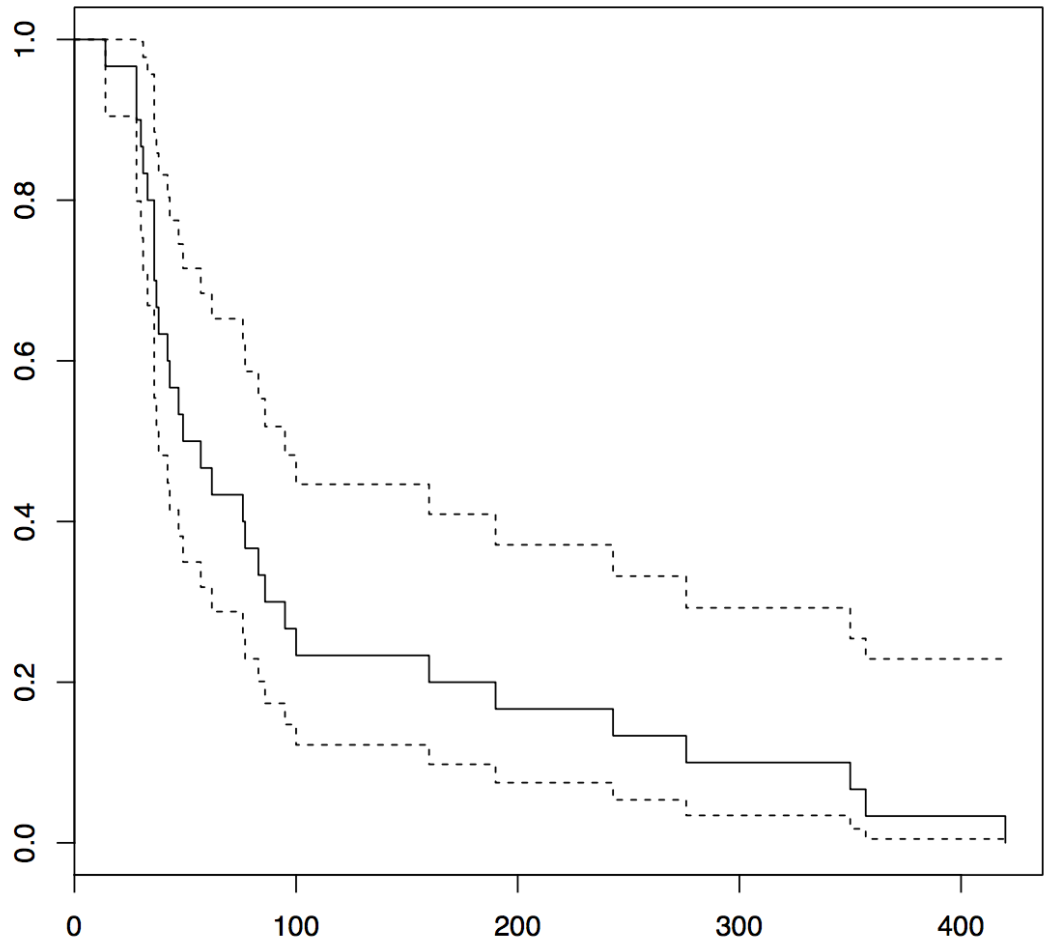
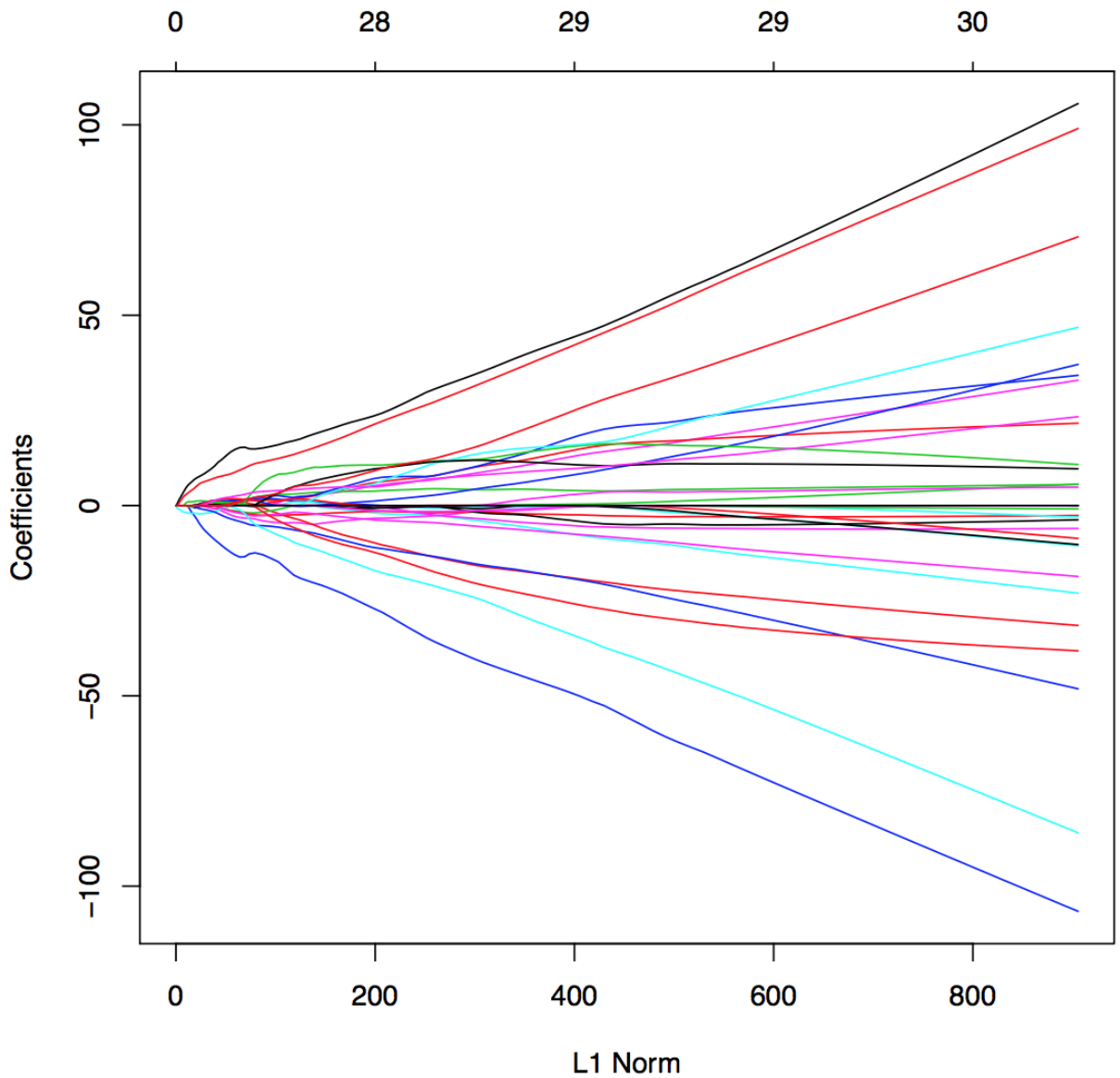


Cox Regression in HD

Very easy to run lasso:

```
fit <- glmnet(X, Surv(time,status), family = "cox")
plot(fit)
```

Cox Regression in HD



Cross validation for KM in HD

This is a bit more tricky, as we may need to cross validate for each pair of candidate c and λ:

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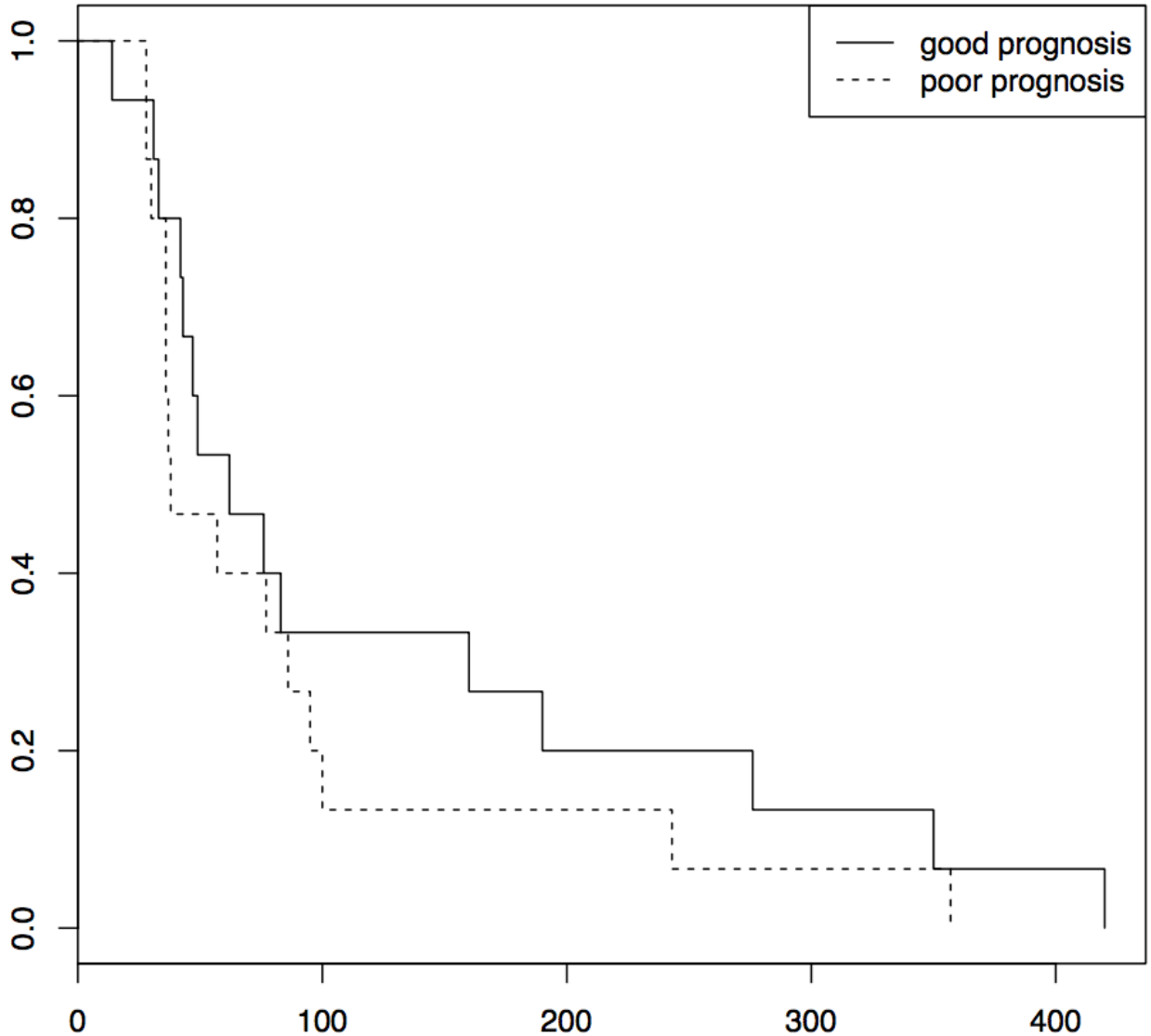
This is a bit more tricky, as we may need to cross validate for each pair of candidate c and λ:

1. Break data into folds
2. For each fold k
   2.1. Train on all data except kth fold to find $\hat{\beta}$
   2.2. Calculate score $\eta_i = x_i^\top \hat{\beta}$ for all i in the left-out fold
3. Split the data into i with $\eta_i \leq c$ and $\eta_i > c$
4. Plot KM curves!

Choose the best KM plot!

```
> unord <- match(1:30,obs.ord)
> test.pred <- matrix(0,ncol = 100, nrow = 30)
> for(fold in 1:3){
+ ind.train <- obs.ord[((fold-1)*10 + 1):(fold*10)]
+ fit.train <- glmnet(X[ind.train,], Surv(time[ind.train],status[ind.train]), family="cox")
+ test.pred[-ind.train,] <- predict(fit.train, X[-ind.train,])
+}
> k <- 80
> plot(survfit(Surv(time,status)~(test.pred[,k] > median(test.pred[,k]))),
+ lty = c(1,2))
> legend("topright", c("good prognosis","poor prognosis"), lty = c(1,2))
```


good prognosis
poor prognosis
1.0
0.8
0.6
0.4
0.2
0.0
0
100
200
300
400

Not so great!

Log-Likelihood Recap

- Losses are often based on generative model or error structure
- Minimize Negative Log Likelihood
- Can add sparsity/ridge/other penalties

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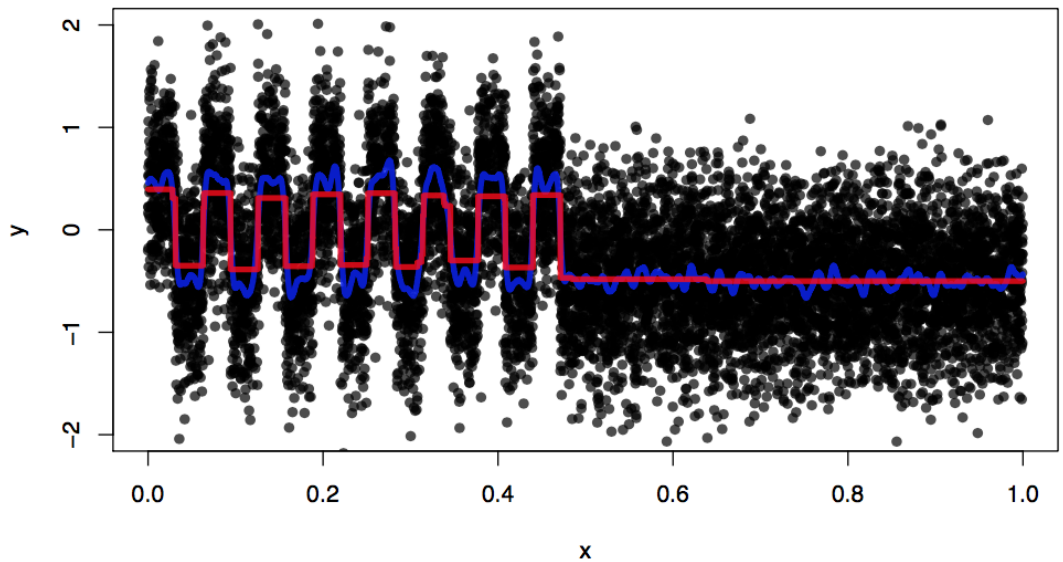

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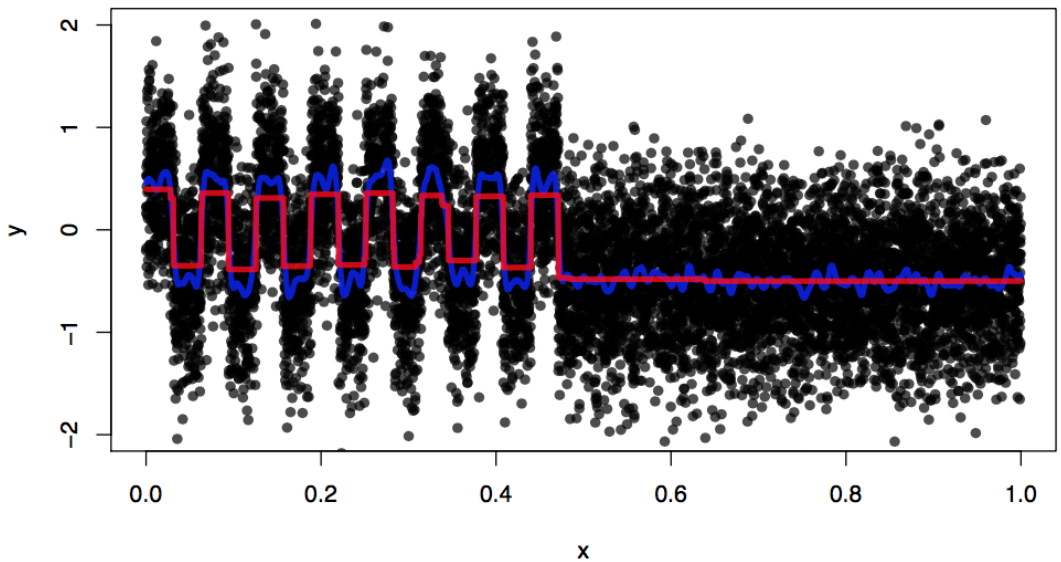

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$$\min \ell(\beta) + \lambda \sum_j |\beta_j - \beta_{j-1}|$$

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- There are various other types of penalties
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  - ...
- This is a very active area of research!!