Big Data BUS 41201

Week 3: Model Selection

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Model Decisions and Model Building

- ✓Out-of-Sample vs In-Sample performance
- ✓Stepwise strategies
- ✓Regularization and the LASSO
- ✓OOS experiments and Cross Validation
- ✓Information Criteria
  - AIC
  - AICc

Variable Selection as Model Selection

Suppose we observe an outcome y and $\boldsymbol{x} = (x_1, \ldots, x_p)'$ a set of potential inputs.

For *each subset* of the x's, one might consider a *model* for the relating y and that subset.

The variable selection problem:

To find the "best" subset for predicting y.

Particularly of interest when p is large and $x_1, \ldots, x_p$ is thought to contain many redundant inputs.

Variable selection is a special case of model selection, where we focus on a *single model class* $\rightsquigarrow$ **linear models**.

Some basic facts about linear models...

Given a set of covariates $\boldsymbol{x}$, the model is always $\mathbb{E}[y|\mathbf{x}] = f(\mathbf{x}'\boldsymbol{\beta})$.

- Gaussian (linear): $y|\boldsymbol{x} \sim \mathrm{N}(\mathbf{x}'\boldsymbol{\beta}, \sigma^2)$.
- Binomial (logistic): $\mathbb{P}(y = 1|\boldsymbol{x}) = e^{\mathbf{x}'\boldsymbol{\beta}}/(1 + e^{\mathbf{x}'\boldsymbol{\beta}})$.

Estimation of $\boldsymbol{\beta}$: Maximize Likelihood $\Longleftrightarrow$ Minimize Deviance

Likelihood $LHD(\boldsymbol{\beta})$ is

$$\mathbb{P}(data\,|\,\boldsymbol{\beta}) = \mathbb{P}(y_1|\boldsymbol{x}_1, \boldsymbol{\beta}) \times \mathbb{P}(y_2|\boldsymbol{x}_2, \boldsymbol{\beta}) \cdots \times \mathbb{P}(y_n|\boldsymbol{x}_n, \boldsymbol{\beta}).$$

Deviance $dev(\boldsymbol{\beta})$ is defined as $-2 \log LHD(\boldsymbol{\beta})$.

$\widehat{\boldsymbol{\beta}}$ denotes the maximum likelihood estimator of $\boldsymbol{\beta}$ (the most likely value of $\boldsymbol{\beta}$ to have generated the data)

Goodness-of-fit (GOF) is summarized by

$$R^2 = 1 - \frac{dev(\widehat{\boldsymbol{\beta}})}{dev(\boldsymbol{\beta} = \mathbf{0})}.$$

The R^2 we really care about is Out-Of-Sample (OOS) R^2.

The difference between *in* and *out* of sample R^2 is what data are used to fit $\hat{\boldsymbol{\beta}}$ and what the deviances are calculated on.

Example: Linear Regression

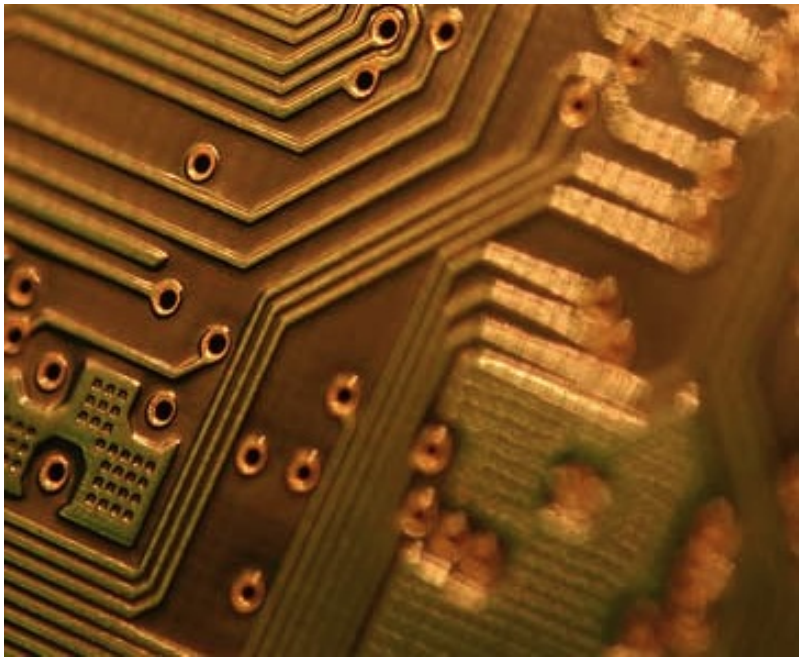
For **In-Sample** (IS) R^2, we have data $[\mathbf{x}_1, y_1] \ldots [\mathbf{x}_n, y_n]$ and you use this data to fit $\hat{\boldsymbol{\beta}}$. The deviance is then

$$dev_{is}(\hat{\boldsymbol{\beta}}) = \sum_{i=1}^{n} (y_i - \mathbf{x}_i' \hat{\boldsymbol{\beta}})^2.$$

For **Out-Of-Sample** (OOS) R^2, observations $1 \ldots n$ are still used to fit $\hat{\boldsymbol{\beta}}$ but the deviance is now calculated over *new* observations, say

$$dev_{oos}(\hat{\boldsymbol{\beta}}) = \sum_{i=n+1}^{n+m} (y_i - \mathbf{x}_i' \hat{\boldsymbol{\beta}})^2.$$

Example: Semiconductor Manufacturing Processes



Very complicated operation
Little margin for error.

Hundreds of diagnostics
Useful or debilitating?

We want to focus reporting and better predict failures.

$\mathbf{x}_i$ is a vector of 200 input signals, y_i is binary PASS/FAIL
There are 100/1477 failures in the dataset.

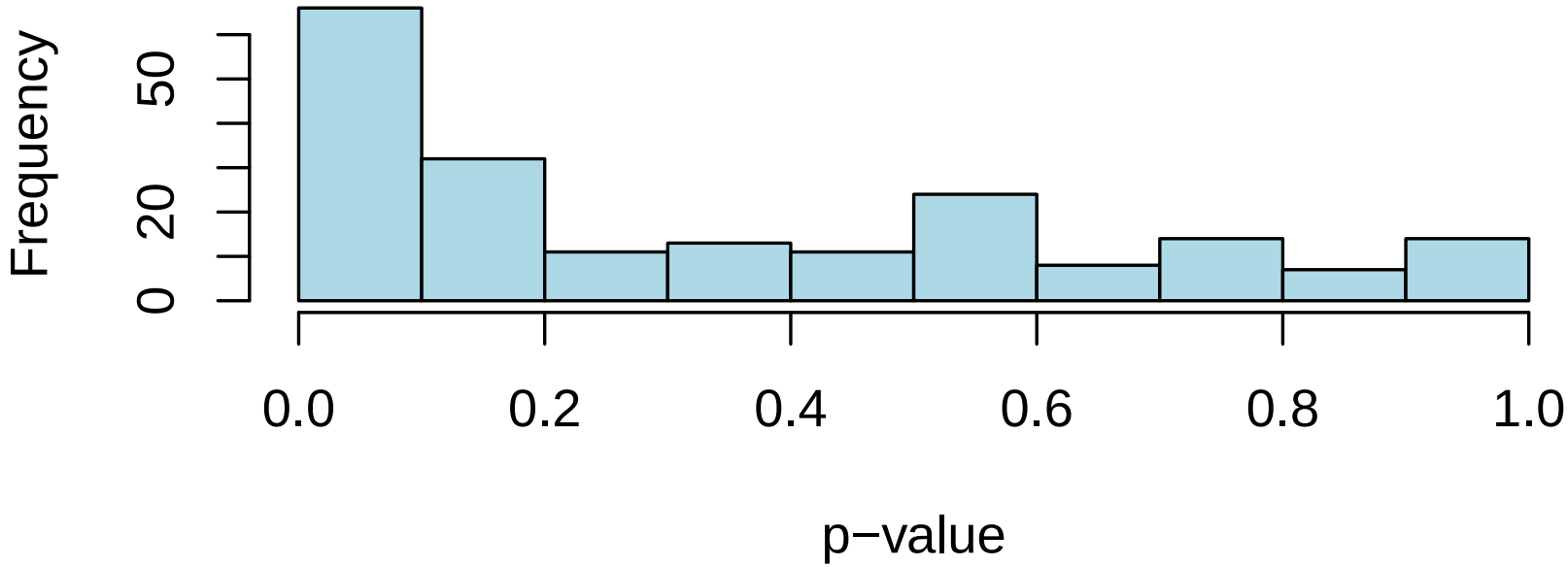
Logistic regression for failure of chip i is

$$p_i = \mathbb{P}(\texttt{fail}_i|\mathbf{x}_i) = e^{\alpha+\mathbf{x}_i'\boldsymbol{\beta}}/(1+e^{\alpha+\mathbf{x}_i'\boldsymbol{\beta}})$$

Semiconductor FDR Control

The full model has $R^2 = 0.56$ (based on *binomial* deviance).

The p-values for these 200 coefficients:



Some are clustered at zero, the rest sprawl out to one.

FDR of $q = 0.1$ yields $\alpha = 0.0122$ p-value rejection cut-off.

Implies 25 'significant', of which approx 22-23 are true signals.

Semiconductors Continued

A *cut* model, using only these 25 signals, has $R^2_{cut} = 0.18$.
This is much smaller than the full model's $R^2_{full} = 0.56$.

In-Sample (IS) R^2

☹ R^2 *always* increases with more covariates.

The larger the model, the more flexibility.

But how well does each model predict *new (unseen)* data?

☹ We can't use In-Sample R^2 for model comparisons.

An Out-Of-Sample (OOS) R^2

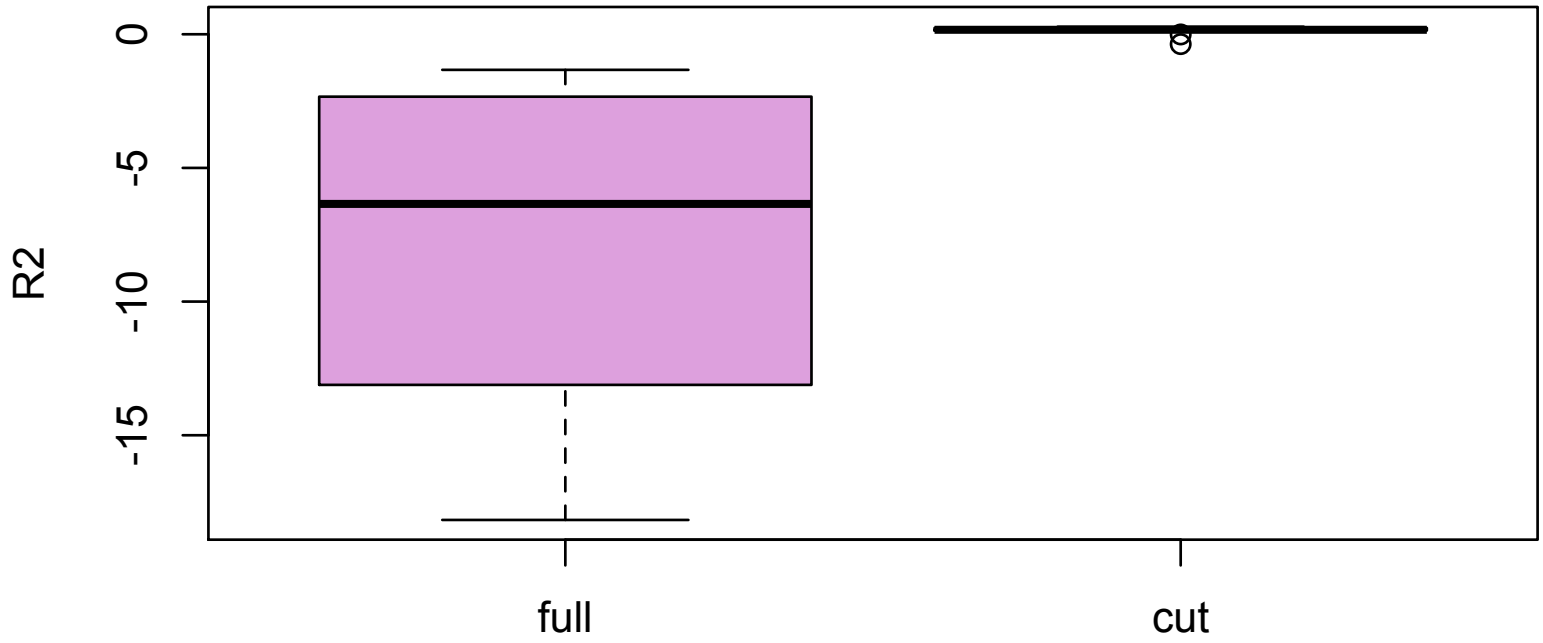
(1) split the data into 10 random subsets ('folds').

(2) repeat 10 times: fit model $\hat{\beta}$ using only 9/10 of data,
and record R^2 on the left-out subset.

☺ *These OOS R^2 give us a sense of how well each model can predict data it has not yet seen.*

OOS experiment for semiconductor failure

We gain predictive accuracy by *dropping* variables.



Cut model has mean OOS R^2 of 0.09, about 1/2 in-sample R2.

The full model is much worse and, more importantly, more variable!

Attention: Why negative R^2?

OOS experimentation

☹ In-Sample R^2 can be misleadingly optimistic.

Using OOS experiments to choose the best model is called *cross validation*. It will be a big part of our big data lives.

Selection of 'the best' model is at the core of all big data.

But before getting to selection, we first need strategies to

come up with a good set of candidate models to choose from.

HOW?

FDR as a selection tool?

A heretical way to think about 'q': a tuning parameter?

Maybe we grab models for $q = 0.1, 0.2, \ldots$ and compare?

Problems with testing/FDR:

☹ FDR theory requires *independence between tests*.

☹ In multiple regression, *multicollinearity* causes problems.

Given two highly correlated x's, you can get big p-values where neither variable is significant. In addition, p-values based on the full model can only be obtained when $p < n$.

☹ In one-at-a-time regression (p models with only one x variable), bringing together variables that are useful *individually* does not mean that they will be useful *collectively*.

Forward stepwise regression

With p predictors, there are 2^p models to choose from.
(Semiconductor example: $2^{200} \approx 1.6 \times 10^{60}$)
☹ We cannot enumerate them all.

Forward stepwise: a heuristic model search procedure starts with a simple 'null' model ($\beta = \mathbf{0}$), and incrementally updates fit (one-variable at a time) to allow for slightly more complexity.

Better than **backwards methods**

- The 'full' model can be expensive or tough to fit, while the null model is usually available in closed form.
- Jitter the data and the full model can change dramatically (because it is overfit). The null model is always the same.

Stepwise approaches are myopic: they find the best solution locally at each step, without much thought about global solution.

Naive forward stepwise regression

The `step()` function in R executes a common stepwise routine:

(1) Fit all *univariate models*. Choose that with highest (IS) R^2 and put that variable – say $x_{(1)}$ – in your model.

(2) Fit all *bivariate models* including $x_{(1)}$ ($y \sim \beta_{(1)}x_{(1)} + \beta_j x_j$), and add x_j from one with highest IS R^2 to your model.

⋮

? When to stop?
When adding a variable does not improve the model much.

You stop when *some model selection rule* (e.g. AIC) is lower for the current model than for any of the models that add one variable. We will talk about model selection rules later.

Forward stepwise regression in R

Easiest way to `step()`: run null and full regressions.

```
null = glm(y ~ 1, data=D)
full = glm(y ~ ., data=D)
fwd = step(null, scope=formula(full), dir="forward")
```

`scope` is the biggest possible model.

Iterate for interactions: `fwd2 = step(fwd, scope=.^2, ...`

Example: semiconductors...

Variable selection options so far...

Subset Selection (SS): Enumerate *all* candidate models and get $\widehat{\beta}$ for each subset of coefficients, with the rest set to zero.

☹ SS is impossible for p as small as 50!

Forward Stepwise is a faster heuristic.

☹ `step()` is still very slow (e.g., 1.5 min for tiny semiconductors)

A related subtle (but massively important) issue is stability.

With small n (relative to p), $\widehat{\beta}$'s have high *sampling variability*: they change a lot from one dataset to another. So which model is 'best' changes a lot.

☹ Predictions based upon the 'best' model will have high variance

$\rightsquigarrow$ big expected errors.

Regularization

The general idea behind regularization:

impose suitable restrictions on $\widehat{\beta}$'s to make them stable and purposeful.

Variable selection achieved with *estimation* rather than p-values.

What do we mean by 'suitable restrictions'?

- *We would like $\widehat{\beta}$ to be less variable,*
- *We would like $\widehat{\beta}$ to yield better prediction,*
- *We would like $\widehat{\beta}$ to have exact zeros.*

We will *penalize* solutions $\widehat{\beta}$ that are not desirable.

Ultimately, we are departing from optimality to stabilize the system.

Regularization continued

Using all predictors $x_1, \ldots, x_p$, the most likely (MLE) values $\widehat{\beta}_{MLE}$ minimize deviance:

$$\widehat{\beta}_{MLE} = \arg\min_{\beta} \left\{ -\frac{2}{n} \log LHD(\beta) \right\}.$$

$\widehat{\beta}_{MLE}$ can only be obtained when $p < n$, can be unstable and cannot have exact zeros. ☹

The *penalized MLE* minimize deviance **plus a penalty**:

$$\widehat{\beta}_{PMLE} = \arg\min_{\beta} \left\{ -\frac{2}{n} \log LHD(\beta) + \lambda \sum_{j=1}^{p} pen(\beta_j) \right\}.$$

Penalty incurs **cost** when choosing solutions that are far from our preferences $\rightsquigarrow \widehat{\beta}_{PMLE}$ is ultimately **biased**.

Decision theory: Cost in Estimation

Decision theory is about how to behave optimally under uncertainty. It is based on the idea that choices have costs. Estimation and hypothesis testing: what are the costs?

Estimation:

Deviance is the cost of distance between data and the model.
Recall: $\sum_i (y_i - \hat{y}_i)^2$ or $-\sum_i y_i \log(\hat{p}_i) - (1 - y_i) \log(1 - \hat{p}_i)$.

Testing:

Since $\hat{\beta}_j = 0$ is *safe*, it should cost us to decide otherwise.

$\Rightarrow$ The cost of $\hat{\beta}$ is deviance plus a penalty away from zero.

Cost: adding too many parameters in the model

LASSO Regularization

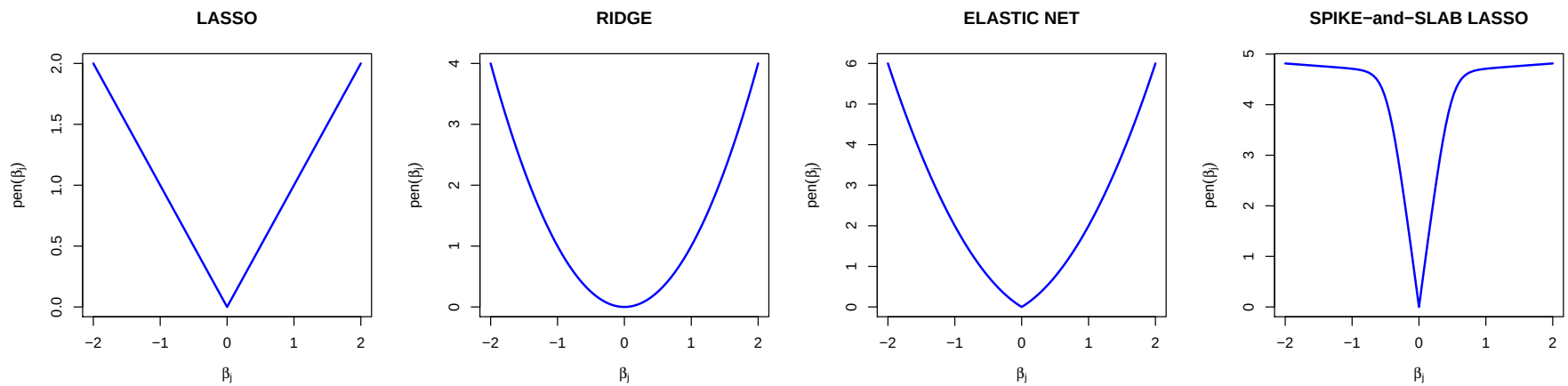
LASSO gives **sparse** solutions:

$$\widehat{\boldsymbol{\beta}}_\lambda = \arg\min_{\boldsymbol{\beta}} \left\{ -\frac{2}{n} \log LHD(\boldsymbol{\beta}) + \lambda \sum_{j=1}^{p} |\beta_j| \right\},$$

where $\lambda > 0$ is the **penalty weight** and $|\beta_j|$ is a cost (penalty) for coefficient β_j.

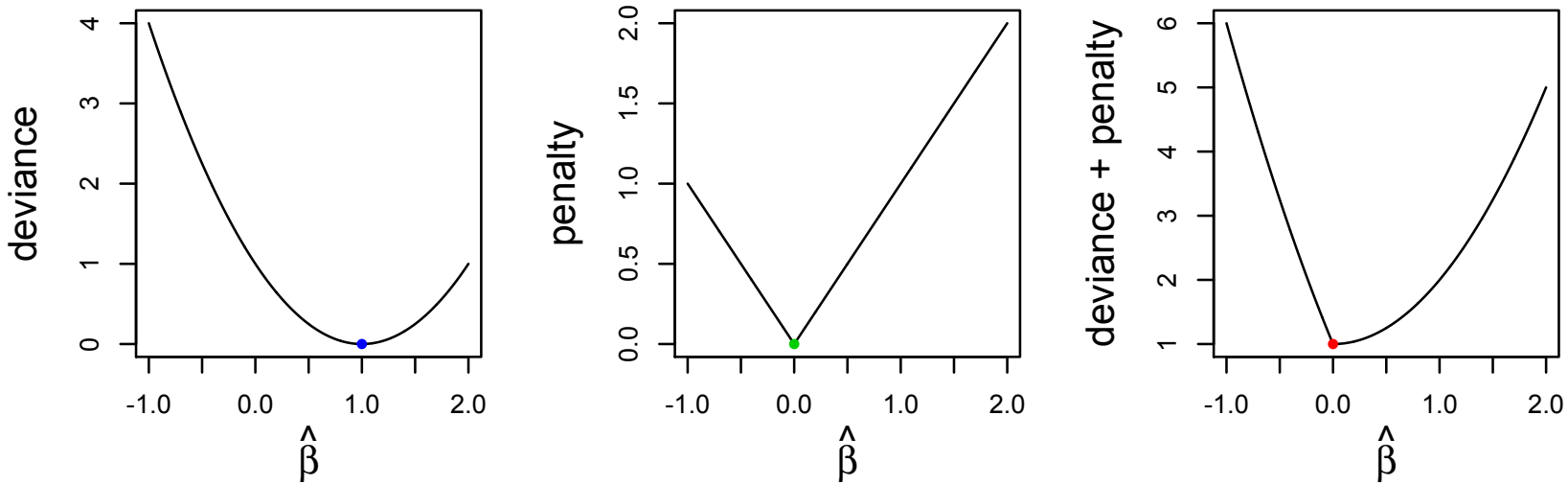
$|\beta_j|$ will be lowest at $\beta_j = 0$ and we pay more for $|\beta_j| > 0$.

Some other penalty options:



Penalization can yield automatic variable selection

The minimum of a smooth + spiky function can be at the spike.



The PMLE estimator is **shrunk to zero** $\rightsquigarrow$ *automatic variable selection* ☺.

For instance, LASSO or Spike-and-Slab LASSO have this property.

You can think of the LASSO as the **modern least squares**.

More about the LASSO

LASSO finds $\widehat{\boldsymbol{\beta}}_\lambda$ that minimize $-\frac{2}{n}\log LHD(\boldsymbol{\beta}) + \lambda \sum_j |\beta_j|$.

How to pick λ?

We'll do this for a *sequence* $\lambda_1 < \lambda_2 < ... < \lambda_T$.

Then we can apply model selection tools to choose best $\widehat{\lambda}$.

LASSO path estimation:

(1) *Start with a small* $\lambda_1 \sim 0$ *such that that* $\widehat{\boldsymbol{\beta}}_{\lambda_1} \sim \widehat{\boldsymbol{\beta}}_{MLE}$.

(2) *Choose* $\lambda_2 > \lambda_1$ *and compute* $\widehat{\boldsymbol{\beta}}_{\lambda_2}$

(3) *Keep increasing* λ *until you obtain the null model at* λ_T.

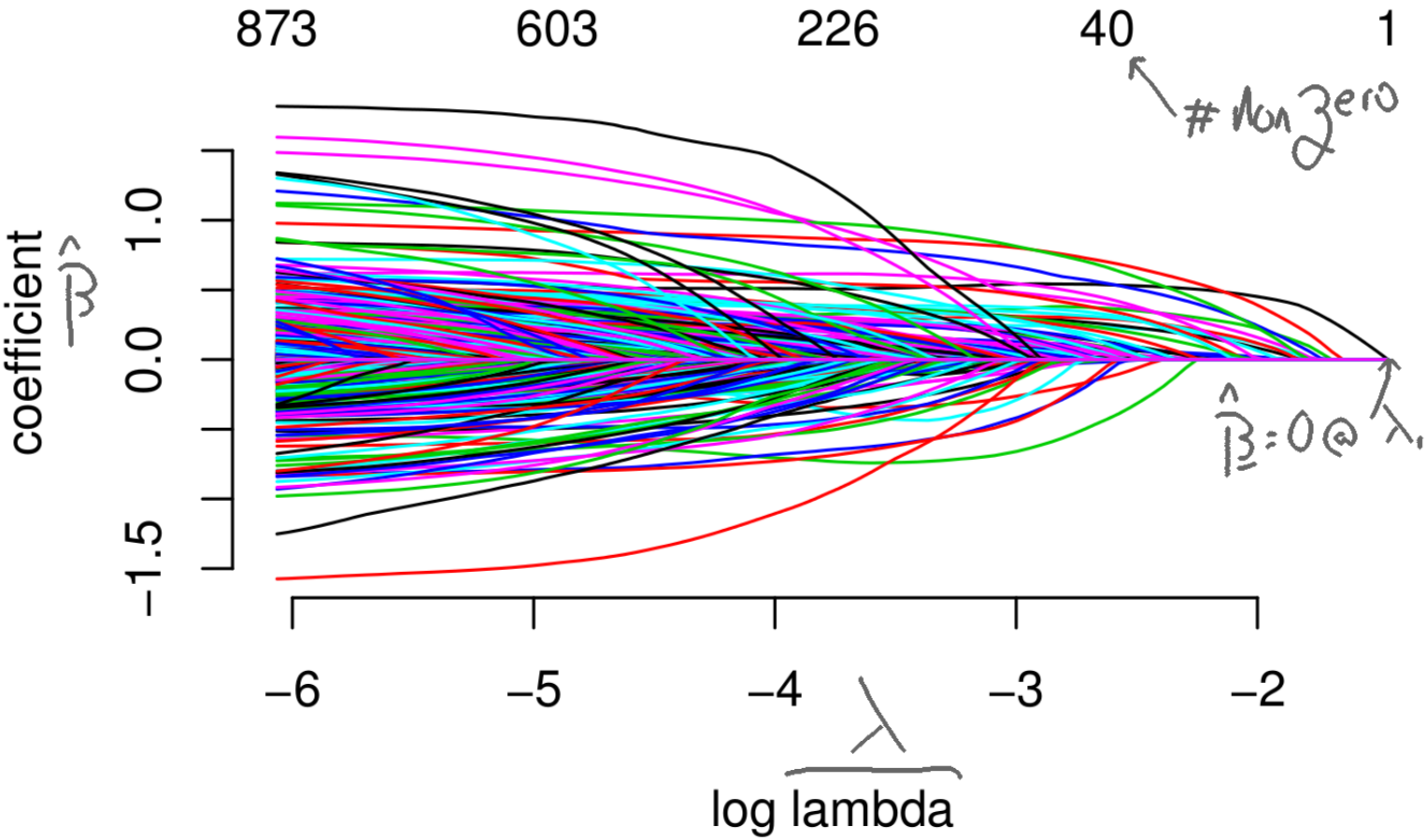
☺ It's fast! Each update is easy.

☺ It's stable: optimal λ_t may change a bit from sample to sample, but that won't affect the model much.

It's a better version of forward stepwise selection.

Path plots

The whole enterprise is easiest to understand visually.



The algorithm moves *right to left*.

The y-axis is $\hat{\boldsymbol{\beta}}$ (each line a different $\hat{\beta}_j$) as a function of λ_t.

Example: Comscore web browser data

The previous plot is household log-online-spend regressed onto % of time spent on various websites (each β_j a different site).

Comscore (available via WRDS) records info on browsing and purchasing behavior for annual panels of households.

Data extracted for the 1000 most heavily trafficked websites and for 10,000 households that spent at least 1$ in 2006.

Why do we care? Predict consumption from browser history.

e.g., to control for base-level spending, say, in estimating advertising effectiveness.

Add-on Packages for R

Much of R's capability comes from its packages,
little pieces of purpose-specific statistical software.

You can add-on with the `install.packages` menu or cmd.

- A good mirror is `http://cran.rstudio.com`.
- You should 'install dependencies' when adding packages.
- Every package has a website on `cran.r-project.org`.

Today we'll be using

- `gamlr`: L0 to L1 penalized regression.
- `Matrix`: fancy sparse matrices.

Once installed, do (e.g.) `library(gamlr)` to use a package.

LASSO Software

There are many packages for fitting lasso regressions in R.

`glmnet` is most common. `gamlr` is a useful alternative.
These two are very similar, and they share syntax.

Big difference is what they do beyond a simple lasso:.

- `glmnet` does an 'elastic net': $pen(\beta) = |\beta| + \nu\beta^2$.
- `gamlr` does a 'gamma lasso': $pen(\beta) \approx \log(\nu + |\beta|)$.

Since we stick mostly to lasso, they're nearly equivalent for us.
`gamlr` just makes it easier to apply some model selection rules.

Both use the `Matrix` library representation for sparse matrices.

Diversion: **Simple Triplet Matrices**

Often, your data will be very sparse (i.e, mostly zeros).
It is then efficient to ignore zero elements in storage.

A simple triplet matrix (STM) has three key elements:

The row '`i`', column '`j`', and entry value '`x`'.

Everything else in the matrix is assumed zero.

For example:

$$\begin{bmatrix} -4 & 0 \\ 0 & 10 \\ 5 & 0 \end{bmatrix} \quad \text{is stored as} \quad \left\{ \begin{array}{c} \texttt{i} = 1, 2, 3 \\ \texttt{j} = 1, 2, 1 \\ \texttt{x} = -4, 10, 5 \end{array} \right\}$$

The `Matrix` library provides STM storage and tools.
See `comscore.R` for how to get data into this format.

Running a LASSO

Once you have your `x` and `y`, running a lasso is easy.

```
spender <- gamlr(xweb, log(yspend))
plot(spender)  # nice path plot
spender$beta[c("mtv.com","zappos.com"),]
```

And you can do logistic lasso regression too

```
gamlr(x=SC[,-1], y=SC$FAIL,  family="binomial")
```

You should make sure that `y` is numeric 0/1 here, not a factor.

Some common arguments

- `verb=TRUE` to get progress printout.
- `nlambda`: T, the length of your λ grid.
- `lambda.min.ratio`: λ_1/λ_T.

See `?gamlr` for details and help.

Scale Matters

Penalization is sensitive to the scale of $x_1, \ldots, x_p$.
e.g., $x\beta$ has the same effect as $(2x)\beta/2$, but $|\beta|$ is twice as much penalty as $|\beta/2|$.

It would not be 'fair' to penalize $\beta's$ equally if $x's$ were not on the same scale.

You can multiply β_j by $\text{sd}(x_j)$ in the cost function to standardize.

That is, minimize $-\frac{2}{n}\log LHD(\boldsymbol{\beta}) + \lambda \sum_j \text{sd}(x_j)|\beta_j|$.

$\Rightarrow$ *β_j's penalty is calculated per effect of 1SD change in x_j.*

`gamlr` and `glmnet` both have `standardize=TRUE` by default.
You *only* use `standardize=FALSE` if you have good reason.

How much regularization?

The LASSO minimizes

$$-\frac{2}{n}\log LHD(\boldsymbol{\beta}) + \lambda \sum_{j=1}^{p} |\beta_j|.$$

☺ This *'sparse regularization'* auto-selects the variables.

Sound too good to be true?

☹ You need to choose λ.

Think of $\lambda > 0$ as a signal-to-noise filter: *like squelch on a radio.*

We'll use **cross validation** or **information criteria** to choose.

Path algorithms are key to the whole framework:

⋆ They let us quickly enumerate a set of candidate models.

⋆ This set is stable, so selected 'best' is probably pretty good.

Prediction vs Interpretability

Testing is all about *is this model true*?
We want to know: *what is my best guess*?

None of your models will be 'true' for complicated HD systems.
Instead, just try to get as close to the truth as possible.

Parsimony principle: If two models do similarly well in predicting the unseen data, choose the simpler one.

- Overly simple models will 'underfit' available patterns (λ too large).
- Complicated models 'overfit', and make noisy predictions (λ too small).

The goal is to find the sweet spot in the middle.

Prediction-driven Model Selection

A recipe for model selection.

(1) Find a manageable set of candidate models (i.e., such that fitting all models is fast).

(2) Choose amongst these candidates the one with best predictive performance *on unseen data*.

✓(1) is what the LASSO paths $\widehat{\boldsymbol{\beta}}_{\lambda_1}, \ldots, \widehat{\boldsymbol{\beta}}_{\lambda_T}$ provide.

✓(2) can be achieved with out-of-sample experimentation.

We need to *estimate* the prediction accuracy associated with each model when applied on future unseen data.

Recall that predictive performance can be measured with 'deviance'.

Out-of-sample prediction experiments

We already saw an OOS experiment with the semiconductors. Implicitly, we were estimating predictive deviance (via R^2).

The procedure of using such experiments to do model assessments is called **Cross Validation** (CV). It follows a basic algorithm:

For $k = 1 \dots K$,

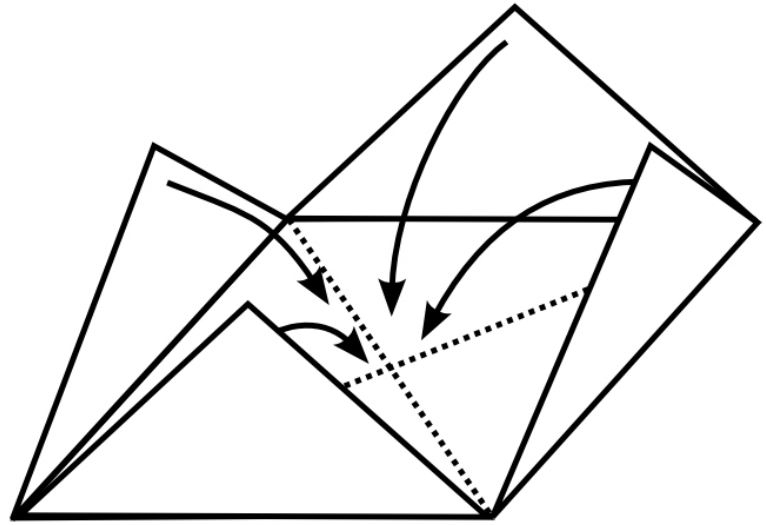
- Use a random subset of $n_k < n$ observations to 'train' the model.
- Record the error rate for predictions from this fitted model on the left-out observations.

We'll usually measure 'error rate' as deviance. But alternatives include MSE, misclass rate, integrated ROC, or error quantiles.

You care about both average and spread of OOS error.

K-fold Cross Validation

One option is to just take
repeated random samples.
It is better to 'fold' your data.



- Sample a random ordering of the data
  (important to avoid order dependence)
- Split the data into K folds: 1st 100/K%, 2nd 100/K%, etc.
- Cycle through K CV iterations with a single fold left-out.

This guarantees each observation is left-out for validation,
and lowers the sampling variance of CV model selection.

Leave-one-out CV, with $K = n$, is nice but takes a long time.
$K = 5$ to 10 is fine in most applications.

CV LASSO

The LASSO path indexed by $\lambda_1 < \lambda_2 < \cdots < \lambda_T$ gives T fitted coefficient vectors, $\widehat{\boldsymbol{\beta}}_{\lambda_1} \ldots \widehat{\boldsymbol{\beta}}_{\lambda_T}$, each yielding deviance for *new data:*

$$-\log \mathbb{P}(\mathbf{y}^{new} \mid \mathbf{X}^{new}, \widehat{\boldsymbol{\beta}}_{\lambda_T})$$

Cross-validation to select λ:

For a given set of candidate penalties $\lambda_1 \ldots \lambda_T$ and for each of $k = 1 \ldots K$ folds,

(1) Fit the path $\widehat{\boldsymbol{\beta}}^k_{\lambda_1} \ldots \widehat{\boldsymbol{\beta}}^k_{\lambda_T}$ on all data except fold k.

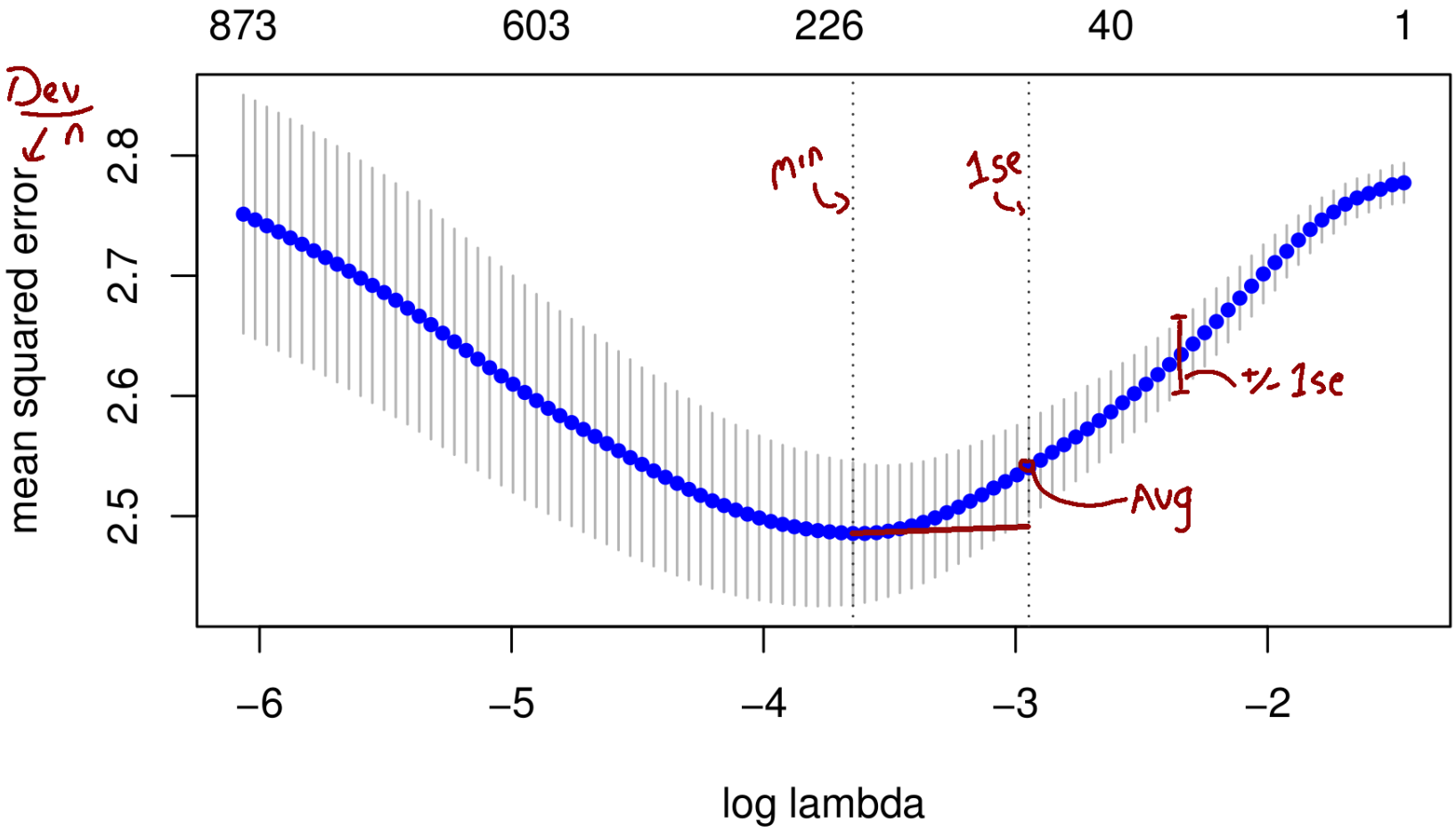
(2) Get fitted deviance on left-out data: $-\log \mathbb{P}(\mathbf{y}^k \mid \mathbf{X}^k, \widehat{\boldsymbol{\beta}}^k_{\lambda_t})$.

This gives us K draws of OOS deviance for each λ_t.

Finally, use these to choose the 'best' $\widehat{\lambda}$, then re-fit the model to *all of the data* by minimizing $-\frac{2}{n} \log \text{LHD}(\boldsymbol{\beta}) + \widehat{\lambda} \sum_j |\beta_j|$.

How do we choose the best $\widehat{\lambda}$?

Again, the routine is most easily understood visually.



Both selection rules are good; `1se` has extra bias for simplicity.

CV Lasso

Both `gamlr` and `glmnet` have functions to wrap this all up.
The syntax is the same; just preface with `cv.`.

```
cv.spender <- cv.gamlr(xweb, log(yspend))
```

Then, `coef(cv.spender)` gives you $\hat{\beta}_t$ at the 'best' λ_t

- `select="min"` gives λ_t with *min average OOS deviance*.
- `select="1se"` defines best as *biggest* λ_t *with average OOS deviance no more than 1SD away from the minimum.*

`1se` is default, and balances prediction against false discovery.
`min` is purely focused on predictive performance.

Problems with Cross Validation

☹ It is time consuming: When estimation is not instant, fitting K times can become infeasible even for K in 5-10.

☹ It can be unstable (especially when n is small): imagine doing CV on many different samples. There can be large variability on the model chosen.

Still, some form of CV is used in most DM applications.

Also, be careful to not cheat: for example, with the FDR cut model we've already used the full n observations to select the 25 strongest variables. It is not surprising they do well 'OOS'.

The rules: *never use the same data twice (for selection and validation).*

Alternatives to CV: Information Criteria

'Information Criteria' (IC): measure how much information is lost when we use our model to represent our data. They approximate distance between a model and 'the ideal'.

IC provide an avenue for **in-sample model comparisons**, by trading off *in-sample* deviance and *model complexity*.

You can apply them by choosing the model with minimum IC.

Most common is Akaike's AIC = Deviance + $2\#parms$.

$\#parms$ = number of parameters used in your model fit.
For lasso and MLE, this is just the # of nonzero $\hat{\beta}_j$.

For example, the `summary.glm` output reports

```
    Null deviance: 731.59 on 1476 degrees of freedom
Residual deviance: 599.04 on 1451 degrees of freedom
AIC: 651.04
```

AIC overfits in high dimensions

The AIC is actually estimating OOS deviance: what your deviance would be on another *independent* sample of size n.

IS deviance is too small, since the model is tuned to this data.
Some deep theory shows that .

$$\text{AIC} \approx \textit{OOS deviance}.$$

Its common to claim this approx (i.e., AIC) is good for 'big n'.
Actually, its only good for big $\frac{n}{\#parms}$.

In Big Data, # parameters can be huge. Often $\#parms \approx n$.
In this case the AIC will be a bad approximation: it overfits!

AIC corrected: AICc

AIC approximates OOS deviance, but does a bad job for big $\#parms$.

In linear regression an improved approx to OOS deviance is

$$\text{AICc} = \text{Deviance} + 2\#parms\frac{n}{n - \#parms - 1}$$

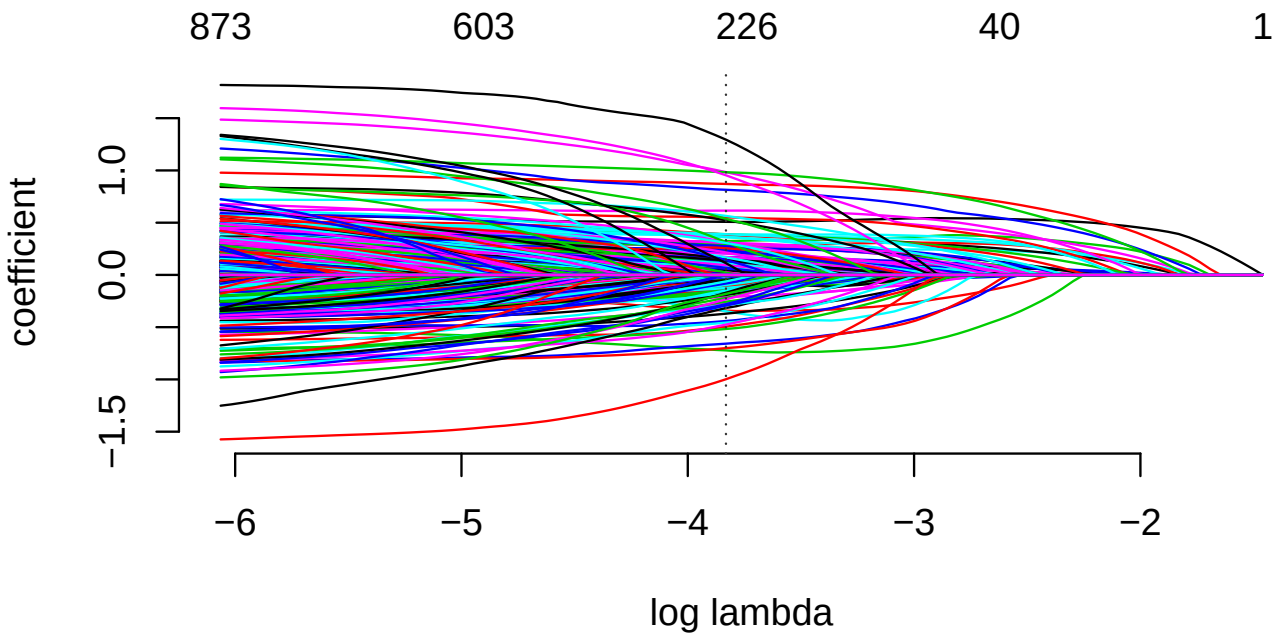
This is the corrected AIC, or AICc.

It also works nicely in logistic regression, or for any `glm`.

Notice that for big $\frac{n}{\#parms}$, AICc $\approx$ AIC. So *always* prefer AICc.

gamlr uses AICc

It's marked on the path plot

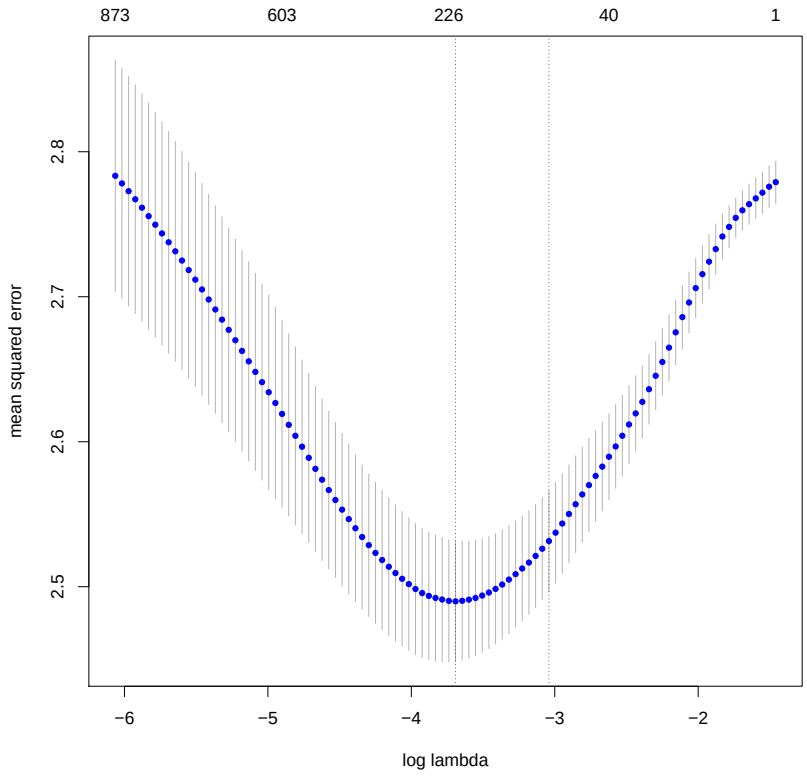


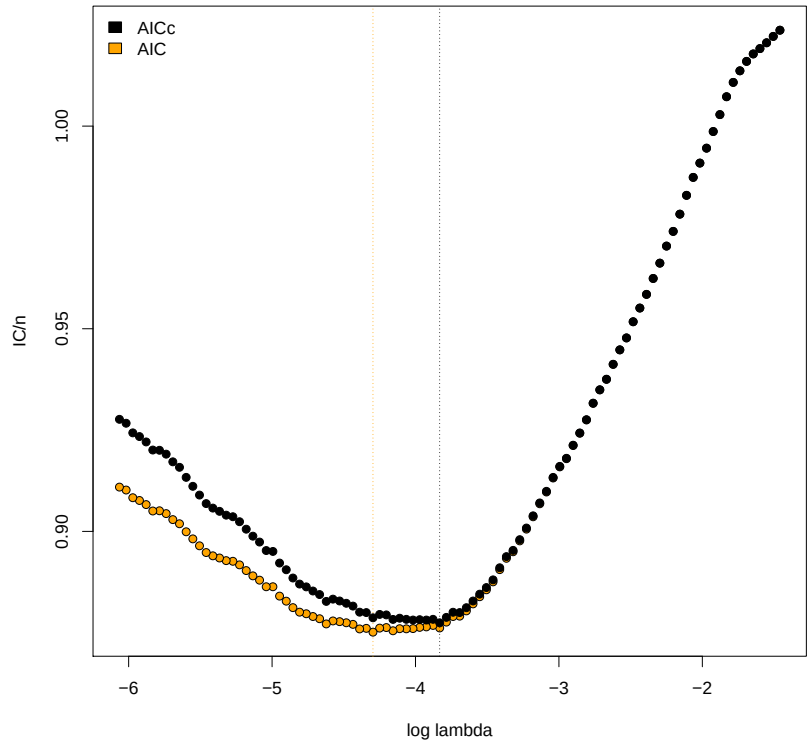
And it is the default for `coef.gamlr`

```
B <- coef(spender)[-1,]
B[c(which.min(B),which.max(B))]
```

```
    cursormania.com shopyourbargain.com
          -0.998143             1.294246
```

IC and CV on the Comscore Data



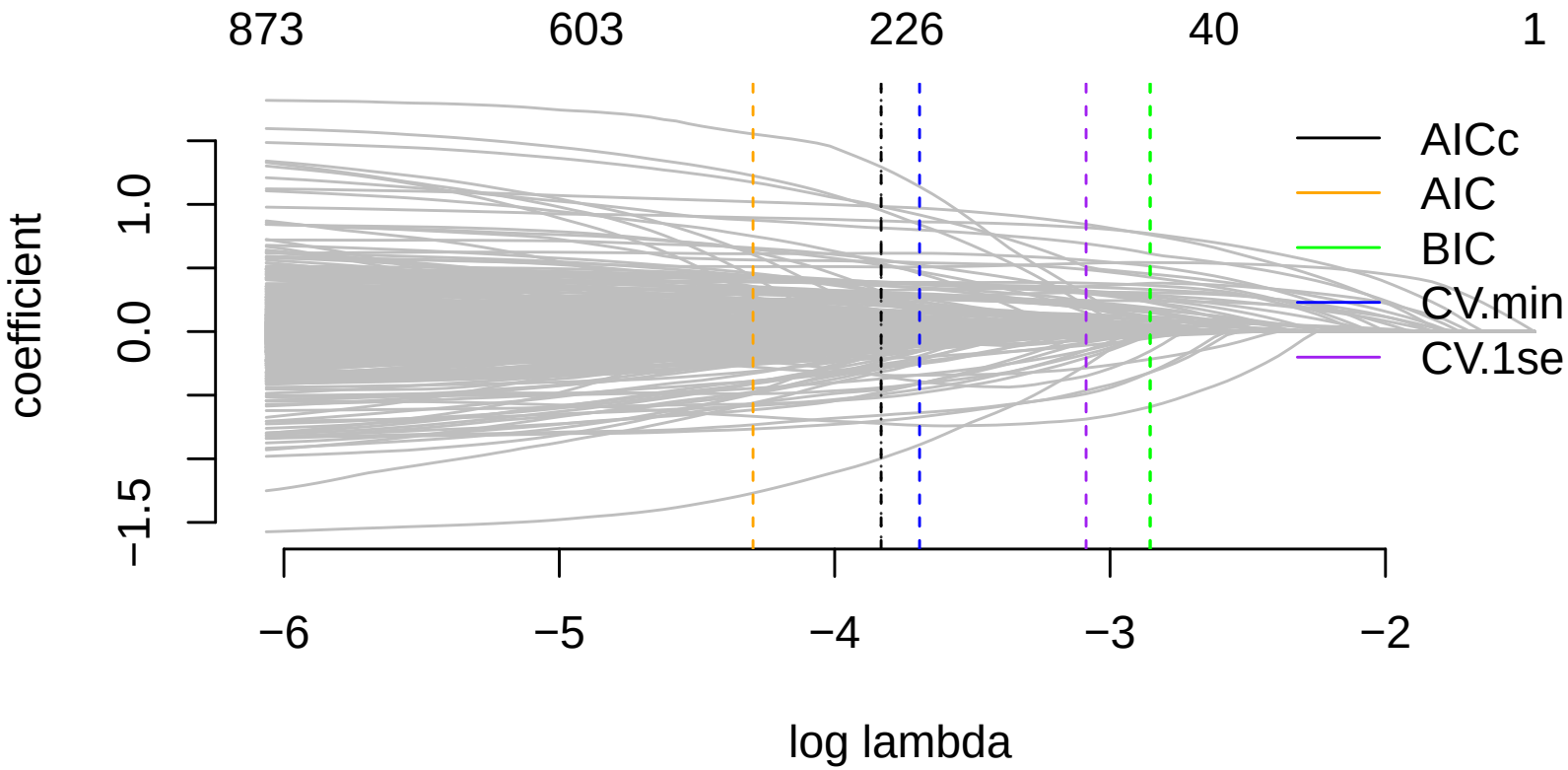


The take home message: AICc curve looks like CV curve.

In practice, BIC works more like the 1se CV rule.

But with big n it chooses too simple models (it underfits).

IC and CV on the Comscore Data



With all of these selection rules, you get a range of answers.

If you have time, do CV. But AICc is fast and stable.

If you are worried about false discovery, tend towards BIC/1se.

Extra Slides: Creating Sparse Design Matrices

For `gamlr`/`glmnet` you need to build your own design matrix i.e., what the `y ~ x1 + x2` formula does for you inside `glm`.

In lecture 2 we saw how to do this with `model.matrix` for dense matrices. The sparse version works the same way.

```
> xdemo <- sparse.model.matrix(~., data=demo)[,-1]
> xdemo[101:105,8:10]  # zeros are not stored

5 x 3 sparse Matrix of class "dgCMatrix"
     regionNE regionS regionW
8463        1       .       .
40          .       .       .
4669        .       .       .
7060        .       1       .
3902        1       .       .
```

Extra Slides: Sparse Factor Designs

Under penalization, factor reference levels now matter!

We're shrinking effects towards zero, which means
every factor effect is shrunk towards the reference level.

My solution is to just get rid of the reference level.

Then every factor level effect is shrunk towards a shared intercept, and only significantly distinct effects get nonzero $\hat{\beta}$.

In particular, code in `naref.R` makes `NA`, R's code for 'missing', the reference level for factors. This has the extra advantage of giving us a framework for missing data...

```
> demo <- naref(demo)
> levels(demo$region)
[1] NA   "MW" "NE" "S"  "W"
```

Extra Slides: Another IC option BIC

The BIC is Deviance $+ \log(n) \times df$.

This *looks* just like AIC, but comes from a very different place.

$BIC \approx -\log \mathbb{P}(M_b|\text{data})$, the 'probability that model b is true'.

$$\mathbb{P}(M_b|\text{data}) = \frac{\mathbb{P}(\text{data}, M_b)}{\mathbb{P}(\text{data})} \propto \underbrace{\mathbb{P}(\text{data}|M_b)}_{\text{LHD}} \underbrace{\mathbb{P}(M_b)}_{\text{prior}}$$

The 'prior' is your probability that a model is true *before* you saw any data. BIC uses a 'unit-info' prior: $\text{N}\left[\hat{\boldsymbol{\beta}}, \frac{2}{n}\text{var}(\hat{\boldsymbol{\beta}})^{-1}\right]$

AICc tries to approximate OOS deviance.

BIC is trying to get at the 'truth'.