Model Selection

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Model selection

- Regression problems often have many predictors
- The number of possible models increase rapidly with number of predictors
- Even if we one of these models is "correct", how do we find it?

Why does it matter?

- One solution could be to use all the predictors
- This is technically a valid model
- Unfortunately this usually leads to unnecessarily high prediction error
- Alternative: find "smallest" model for which F-test comparing to full model is accepted
- This leads to multiple testing, inflated Type I error probability (and no obvious fix)
- Model selection is usually based on some alternative criteria developed specifically for that purpose

Underfitting vs overfitting: the bias-variance trade-off

- The basic problem in model selection is the familiar bias-variance trade-off problem
- Underfitting leads to biased coefficient estimates
- Overfitting leads to coefficient estimates with higher variance
- Formally, suppose we fit the two models

$$E(\mathbf{y}) = \mathbf{X}_1 \beta_1$$

$$E(\mathbf{y}) = \mathbf{X}_1 \beta_1 + \mathbf{X}_2 \beta_2 = \mathbf{X} \beta$$

- If the second model is correct, then $\hat{\beta}_1^{(1)}$ obtained by fitting the first model will be *biased* for β_1 in general
- If the first model is correct, then $\hat{\beta}_1^{(2)}$ obtained by fitting the second model will be unbiased for β_1
- However, in that case, $\hat{\beta}_1^{(2)}$ will have higher variance than $\hat{\beta}_1^{(1)}$ in general; i.e., for any vector **u**,

$$V\left(\mathbf{u}^{T}\hat{\beta}_{1}^{(2)}\right) \geq V\left(\mathbf{u}^{T}\hat{\beta}_{1}^{(1)}\right)$$

• Proof: exercise

Model selection criteria

- Overly simple and overly complex models are both bad
- Best model usually lies somewhere in the middle
- How do we find this ideal model?
- Most common approach: some model-selection criterion measuring overall quality of a model
- To be useful, such a criterion must punish both overly simple and overly complex models
- Once criterion is determined, fit a number of different models and choose the best (details later)
- We will first discuss some possible criteria

Coefficient of determination

• The simplest model quality measure is R^2

$$R^{2} = \frac{T^{2} - S^{2}}{T^{2}} = \frac{\frac{T^{2}}{n} - \frac{S^{2}}{n}}{\frac{T^{2}}{n}}$$

- Always increases when more predictors are added (does not penalize complexity)
- Can compare models of same size, but not generally useful for model selection
- Possible alternative: Adjusted R^2 (substitute unbiased estimators of σ^2)

$$R_{adj}^{2} = \frac{\frac{T^{2}}{n-1} - \frac{S^{2}}{n-p}}{\frac{T^{2}}{n-1}} = 1 - \frac{n-1}{n-p}(1-R^{2})$$

- Maximizing R^2 equivalent to minimizing SSE (or $\hat{\sigma}^2_{MLE})$
- Maximizing R^2_{adj} equivalent to minimizing unbiased $\hat{\sigma}^2$
- Other than simplicity of interpretation, no particular justification

Cross-validation SSE

- Use cross-validation to directly assess prediction error
- Define

$$T_p^2 = \sum_{i=1}^n \left(y_i - \bar{y}_{(-i)} \right)^2$$

and

$$S_p^2 = \sum_{i=1}^n (y_i - \hat{y}_{i(-i)})^2 = \sum_{i=1}^n \left(\frac{e_i}{1 - h_i}\right)^2$$

• The predictive R^2 is defined as

$$R_p^2 = \frac{T_p^2 - S_p^2}{T_p^2}$$

- Equivalently, minimize predictive sum of squares S_p^2 (often abbreviated as PRESS)

Directly estimating bias and variance

- More sophisticated approaches attempt to directly estimate bias and variance
- Suppose true expected value of y_i is μ_i
- Total mean squared error of a model fit is

$$MSE = E \sum_{i} (\hat{y}_{i} - \mu_{i})^{2} = \sum_{i} \left[(E\hat{y}_{i} - \mu_{i})^{2} + V(\hat{y}_{i}) \right]$$

- The first term is the "bias sum of squares" BSS (equals zero if no bias)
- The second term simplifies to

$$\sum_{i} V(\hat{y}_i) = \sigma^2 \sum_{i} \mathbf{x}_i^T (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{x}_i = \sigma^2 \sum_{i} h_i = p\sigma^2$$

• On the other hand

$$E(RSS) = E\sum_{i} (y_i - \hat{y}_i)^2 = E(\mathbf{y}^T (\mathbf{I} - \mathbf{H})\mathbf{y})$$

- This equals $(n-p)\sigma^2$ when \hat{y}_i -s are unbiased
- If \hat{y}_i -s are biased, it can be shown that this term equals $BSS + (n-p)\sigma^2$
- This gives the following estimator of MSE (up to unknown σ^2)

$$RSS - (n-p)\sigma^2 + p\sigma^2 = RSS + (2p-n)\sigma^2$$

Mallow's C_p

• Dividing by σ^2 on both sides, this gives Mallow's C_p criterion

$$C_p = \frac{RSS}{\sigma^2} + 2p - n$$

- This requires an estimate of σ^2
- It is customary to use $\hat{\sigma}^2$ from the largest model
- If model has no bias, then $C_p \approx p$ (exact for largest model by definition)
- An alternative expression for C_p is (exercise)

$$C_p = (p_f - p)(F - 1) + p$$

• where

 $-p_f$ is the number of coefficients in the largest model (used to estimate σ^2)

- F is the F-statistic comparing the model being evaluated with the largest model

- Again, if the model is "correct", then $F\approx 1,$ so $C_p\approx p$

Likelihood based criterion

• A more general approach is to prefer models that improve the expected log-likelihood

$$E\sum_{i}\log P_{\hat{\theta}}(y_i)$$

- Here the expectation is over two independent sets of the true distribution of ${\bf y}$
- One set of **y** is used to estimate $\hat{\theta}$
- Akaike showed that

$$-2E\sum_{i}\log P_{\hat{\theta}}(y_i) \approx -2E(\text{loglik}) + 2p$$

• Here loglik is the maximized log-likelihood for the fitted model

Akaike Information Criterion

• This suggests the Akaike Information Criterion (AIC)

$$AIC = -2loglik + 2p$$

• For linear models, this is equivalent to (up to a constant)

$$AIC = n \log RSS + 2p$$

- An advantage of AIC over C_p is that it does not require an estimate of σ^2
- It is also applicable more generally (e.g., for GLMs)

Bayesian Information Criterion

• A similar criterion is the Bayesian Information Criterion (BIC)

$$BIC = -2loglik + p \log n$$

- As suggested by its name, this is derived using a Bayesian approach
- The complexity penalty for BIC is higher (except for small n), so favours simpler models

Example: SLID data — comparing pre-determined set of models

```
SLID2 <- transform(na.omit(SLID), log.wages = log(wages), edu.sq = education<sup>2</sup>)
SLID2 <- SLID2[c("log.wages", "sex", "edu.sq", "age", "language")]
str(SLID2)
'data.frame': 3987 obs. of 5 variables:
$ log.wages: num 2.36 2.4 2.88 2.64 2.1 ...
$ sex : Factor w/ 2 levels "Female", "Male": 2 2 2 1 2 1 1 1 2 2 ...
$ edu.sq : num 225 174 196 256 225 ...
$ age : int 40 19 46 50 31 30 61 46 43 17 ...
$ language : Factor w/ 3 levels "English", "French", ..: 1 1 3 1 1 1 3 1 1 ...</pre>
```

```
fm <- list()
fm[["S+E+A"]] <- lm(log.wages ~ sex + edu.sq + poly(age, 2), data = SLID2)
fm[["S+E+A+L"]] <- lm(log.wages ~ sex + edu.sq + poly(age, 2) + language, data = SLID2)
fm[["+ SE"]] <- update(fm[[2]], . ~ . + sex:edu.sq)
fm[["+ SA"]] <- update(fm[[2]], . ~ . + sex:poly(age, 2))
fm[["+ EA"]] <- update(fm[[2]], . ~ . + edu.sq:poly(age, 2))
fm[["(S+E+A)^2"]] <- update(fm[[2]], . ~ . + (sex + edu.sq + poly(age, 2))^2)
fm[["(S+E+A)^2"]] <- update(fm[[2]], . ~ . + (sex + edu.sq + poly(age, 2))^2)
fm[["(S+E+A+L)^2"]] <- update(fm[[2]], . ~ . + (sex + edu.sq + poly(age, 2) + language)^2)
fm[["(S+E+A)^3"]] <- update(fm[[2]], . ~ . + (sex + edu.sq + poly(age, 2))^3)
fm[["(S+E+A+L)^3"]] <- update(fm[[2]], . ~ . + (sex + edu.sq + poly(age, 2))^3)
fm[["(S+E+A+L)^3"]] <- update(fm[[2]], . ~ . + (sex + edu.sq + poly(age, 2))^3)
models <- factor(names(fm), levels = names(fm))</pre>
```

Example: SLID data — R^2 and adjusted R^2

```
R2 <- sapply(fm, function(fit) summary(fit)$r.squared)
adj.R2 <- sapply(fm, function(fit) summary(fit)$adj.r.squared)
dotplot(R2 + adj.R2 ~ models, type = "o", pch = 16)</pre>
```



Example: SLID data — prediction SS

PRESS <- sapply(fm, function(fit) sum((residuals(fit) / (1-hatvalues(fit)))^2))
dotplot(PRESS ~ models, type = "o", pch = 16)</pre>



Example: SLID data — Mallow's C_p

```
sigma.sq <- summary(fm[[9]])$sigma^2 # common 'scale' for all fits
Cp <- sapply(fm, function(fit) extractAIC(fit, scale = sigma.sq)[2])
dotplot(Cp ~ models, type = "o", pch = 16)</pre>
```



Example: SLID data — AIC

```
AIC <- sapply(fm, function(fit) extractAIC(fit)[2])
dotplot(AIC ~ models, type = "o", pch = 16)</pre>
```



Example: SLID data — BIC

```
n <- nrow(SLID2)
BIC <- sapply(fm, function(fit) extractAIC(fit, k = log(n))[2])
dotplot(BIC ~ models, type = "o", pch = 16)</pre>
```



Automatic model selection

- This process still requires us to construct a list of models to consider
- In general, the number of possible models can be large
- With k predictors, there are 2^k additive models, many more with interactions

- How do we select the "best" out of all possible models?
- Two common strategies
 - Best subset selection: exhaustive search of all possible models
 - Stepwise selection: add or drop one term at a time (only benefit: needs less time)

Best subset selection: exhaustive search

t(summary(reg.sub)\$outmat)

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poly(age, 2)2		" "		"*"		"*"	"*"	
languageFrench		11 11						
languageOther		11 11						
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sexMale:languageFrench								
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languageFrench	"*"		"*"			"*"	
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sexMale:edu.sq	"*"	"*"	"*"	"*"	"*"	"*"	"*"
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<pre>sexMale:edu.sq:languageOther</pre>			"*"		"*"	"*"	"*"
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<pre>sexMale:poly(age, 2)1:languageOther</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>sexMale:poly(age, 2)2:languageOther</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>edu.sq:poly(age, 2)1:languageFrench</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>edu.sq:poly(age, 2)2:languageFrench</pre>							
<pre>edu.sq:poly(age, 2)1:languageOther</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>edu.sq:poly(age, 2)2:languageOther</pre>							
	26 (1)	26 (2)	27 (1)	27 (2)	28 (1)	28 (2)	29 (
sexMale	"*"	"*"	"*"	"*"	"*"	"*"	"*"
edu.sq	"*"	"*"	"*"	"*"	"*"	"*"	"*"
poly(age, 2)1	"*"	"*"	"*"	"*"	"*"	"*"	"*"
poly(age, 2)2	"*"	"*"	"*"	"*"	"*"	"*"	"*"
languageFrench						"*"	"*"
languageOther		" "					" "
sexMale:edu.sq	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>sexMale:poly(age, 2)1</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>sexMale:poly(age, 2)2</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
sexMale:languageFrench	"*"	"*"	"*"	"*"	"*"	"*"	"*"

<pre>sexMale:languageOther</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
edu.sq:poly(age, 2)1	"*"	"*"	"*"	"*"	"*"	"*"	"*"
edu.sq:poly(age, 2)2	"*"	"*"	"*"	"*"	"*"	"*"	"*"
edu.sq:languageFrench	"*"	"*"	"*"	"*"	"*"	"*"	"*"
edu.sq:languageOther	"*"	"*"	"*"	"*"	"*"	"*"	"*"
poly(age, 2)1:languageFrench	"*"	"*"	"*"	"*"	"*"	"*"	"*"
poly(age, 2)2:languageFrench	"*"		"*"	"*"	"*"	"*"	"*"
poly(age, 2)1:languageOther	"*"	"*"	"*"	"*"	"*"	"*"	"*"
poly(age, 2)2:languageOther			"*"	н	"*"	"*"	"*"
<pre>sexMale:edu.sq:poly(age, 2)1</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>sexMale:edu.sq:poly(age, 2)2</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
sexMale:edu.sq:languageFrench	"*"	"*"	"*"	"*"	"*"	"*"	"*"
sexMale:edu.sq:languageOther	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>sexMale:poly(age, 2)1:languageFrench</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>sexMale:poly(age, 2)2:languageFrench</pre>					" "		" "
<pre>sexMale:poly(age, 2)1:languageOther</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
<pre>sexMale:poly(age, 2)2:languageOther</pre>	"*"	"*"	"*"	"*"	"*"	"*"	"*"
edu.sq:poly(age, 2)1:languageFrench	"*"	"*"	"*"	"*"	"*"	"*"	"*"
edu.sq:poly(age, 2)2:languageFrench		"*"		"*"	"*"		"*"
edu.sq:poly(age, 2)1:languageOther	"*"	"*"	"*"	"*"	"*"	"*"	"*"
edu.sq:poly(age, 2)2:languageOther	"*"	"*"	"*"	"*"	"*"	"*"	"*"
	30 (1)	30 (2)	31 (1)				
sexMale	"*"	"*"	"*"				
edu.sq	"*"	"*"	"*"				
polv(age, 2)1	"*"	"*"	"*"				
polv(age, 2)2	"*"	"*"	"*"				
languageFrench	"*"	"*"	"*"				
languageOther		"*"	"*"				
sexMale:edu.sq	"*"	"*"	"*"				
<pre>sexMale:polv(age, 2)1</pre>	"*"	"*"	"*"				
sexMale:polv(age, 2)2	"*"	"*"	"*"				
sexMale:languageFrench	"*"	"*"	"*"				
sexMale: languageOther	"*"	"*"	"*"				
edu.sg:polv(age, 2)1	"*"	"*"	"*"				
edu.sg:polv(age, 2)2	"*"	"*"	"*"				
edu.sg:languageFrench	"*"	"*"	"*"				
edu.sg:languageOther	"*"	"*"	"*"				
polv(age, 2)1: languageFrench	"*"	"*"	"*"				
poly(age, 2)2:languageFrench	"*"	"*"	"*"				
poly(age, 2)1:languageOther	"*"	"*"	"*"				
poly(age, 2)2:languageOther	"*"	"*"	"*"				
sexMale:edu sg:poly(age 2)1	"*"	"*"	"*"				
sexMale:edu sg:poly(age, 2)?	"*"	"*"	" * "				
sexMale:edu sq:languageFrench	"*"	"*"	" * "				
sexMale:edu sg:languagefter	"*"	"*"	" * "				
sevMale: nolv(age 2)1: languageFrench	" * "	" * "	" * "				
sexMale.nolv(age 2)2.languageFrench	" * "		" * "				
sexMale.nolu(age 2)1.languagef1ellol	"*"	"*"	"*"				
sexMale.poly(age, 2)1.1anguage001101	"* "*"	" <u>*</u> "	"*"				
adu sa noly (age 2)1. language Franch	"*"	" * "	"*"				
edu sacholu(ago 2)2:languageFrench	т П ч П	т Пун					
edu sa poly(age, 2)2.1anguager1ench	т ‼ж‼	- 	т !! ж !!				
odu sa poly (ago 2)2.1 anguageother	т у	- 	т П.¥.II				
euu.sq.pory(age, 2)2.ranguageotner	ጥ	Ŧ	Ŧ				



xyplot(scale(bic) + scale(cp) ~ seq_along(bic), data = summary(reg.sub), grid = TRUE, type = "o", pch = 16)

xyplot(scale(bic) + scale(cp) ~ seq_along(bic), data = summary(reg.sub), grid = TRUE, type = "o", pch = 16, ylim = c(NA, 0.5))



Models ordered by BIC





Handling dummy variables, interactions, etc.

- One problem with this approach: considers each column of X separately
- Usually we would keep or drop all columns for a term (factor, polynomial) together
- Similarly, an interaction term usually not meaningful without main effects and lower order interactions

• Such considerations are not automated by regsubsets() and have to be handled manually

Best subset selection: stepwise search

- Stepwise selection methods are greedy algorithms that add or drop one predtctor at a time
- This greatly limits the number of subsets evaluated
- Makes the problem tractable if number of predictors is large
- On the other hand, stepwise methods explore only a fraction of possible subsets
- For many predictors, rarely finds the optimal model
- Forward selection
 - Find best one-variable model
 - Find best two-variable model by adding another variable
 - and so on
- That is, do not look at all two-variable models; only ones that contain the best one-variable model
- Backward selection: start with full model and eliminate variables successively
- Sequential replacement: consider both adding and dropping in each step
- Stepwise selection is supported by regsubsets()
- Also implemented in MASS::stepAIC() and stats::step()

Best subset selection: forward selection



})



Best subset selection: sequential replacement



})





Benefits and drawbacks of automated model selection

- Can quickly survey a large number of potential models
- However, there are many drawbacks to this approach

edu.sq:poly(age, 2)2:languageOther edu.sq:poly(age, 2)1:languageOther edu.sq:poly(age, 2)2:languageFrench

- In fact, automated model selection basically invalidates inference
- This is because all derivations assume that model and hypotheses are prespecified
- As a result, for the model chosen by automated selection
 - Test statistics no longer follow $t \ / \ F$ distributions
 - Standard errors have negative bias, and confidence intervals are falsely narrow
 - *p*-values are falsely small
 - Regression coefficients are biased away from 0

Simulation example: no predictive relationship

- Simulate $V_2, ..., V_{21} \sim$ i.i.d. N(0, 1)
- Simulate independent $V_1 \sim N(0, 1)$
- Regress V_1 on $V_2, ..., V_{21}$
- Select model using stepAIC()

```
library(MASS)
d <- as.data.frame(matrix(rnorm(100 * 21), 100, 21))</pre>
fm.step <- stepAIC(lm(V1 ~ ., data = d), direction = "both", trace = 0)</pre>
summary(fm.step)
Call:
lm(formula = V1 ~ V2 + V3 + V6 + V9 + V13, data = d)
Residuals:
    Min
               1Q
                    Median
                                  ЗQ
                                          Max
-2.20598 -0.59320 -0.05848 0.56056 2.34801
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.03006
                        0.08906 -0.338 0.73645
V2
                        0.09139
                                 1.434 0.15493
            0.13104
VЗ
            -0.16376
                        0.08943 -1.831 0.07026 .
V6
            -0.29802
                        0.10074 -2.958 0.00391 **
                                 1.798 0.07542 .
٧9
             0.15936
                        0.08864
V13
             0.17006
                        0.08214
                                 2.070 0.04116 *
___
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.8665 on 94 degrees of freedom
Multiple R-squared: 0.1932,
                                Adjusted R-squared: 0.1503
F-statistic: 4.501 on 5 and 94 DF, p-value: 0.001011
with(summary(fm.step), pf(fstatistic[1], fstatistic[2], fstatistic[3], lower.tail = FALSE))
     value
0.00101054
## Replicate this experiment
pvals <-
    replicate(100,
    {
        d <- as.data.frame(matrix(rnorm(100 * 21), 100, 21))</pre>
        fm.step <- stepAIC(lm(V1 ~ ., data = d), direction = "both", trace = 0)</pre>
        if (length(coef(fm.step)) > 1)
            with(summary(fm.step), pf(fstatistic[1], fstatistic[2], fstatistic[3], lower.tail = FALSE))
        else 1
   })
sum(pvals < 0.05)</pre>
[1] 84
```

Simulation example: no predictive relationship

```
densityplot(~ pvals)
```



- Results are slightly better when using BIC rather than AIC, but still bad
- Select model using stepAIC(..., k = log(n))

```
pvals <-
    replicate(100,
    {
        d <- as.data.frame(matrix(rnorm(100 * 21), 100, 21))
        fm.step <- stepAIC(lm(V1 ~ ., data = d), direction = "both", trace = 0, k = log(100))
        if (length(coef(fm.step)) > 1)
            with(summary(fm.step), pf(fstatistic[1], fstatistic[2], fstatistic[3], lower.tail = FALSE))
        else 1
    })
sum(pvals < 0.05)
[1] 56
densityplot(~ pvals)</pre>
```



Summary

- Automated model selection has its uses
- However, blindly applying it without thinking about the problem is dangerous
- Many applied studies have no prespecified hypothesis
- Especially in observational studies (e.g., public health and social sciences)
- Model is often chosen by automated selection, but interpreted as if prespecified
- Result: much more than 5% of "significant" results are probably false