

STAT 538 LEC. # 7

Model Choice

Say measure (Y, X_1, \dots, X_m) for n subjects.

Data acquisition may have been “fishing expedition” - don’t necessarily believe all m predictors are relevant.

May seek a final model including only m^* of the predictors (or equivalently, set $m - m^*$ of the regression coefficients to zero).

First, a more focussed question. How to compare *two* models.

but also consider interactions, possibly quadratic effects - end up with p coefficients/parameters

Comparing 2 models

Likelihood Ratio Test (LRT)

Data D, Model M_0 (p_0 params) nested within M_1 (p_1 params).

If M_0 true, $\hat{\theta}_0 > \hat{\theta}_1$

$$2 \left\{ l_1(\hat{\theta}_1; D) - l_0(\hat{\theta}_0; D) \right\} \stackrel{\text{approx}}{\sim} \chi^2_{p_1 - p_0}$$

$$= D_0 - D_1$$

Usual hypothesis testing implementation and interpretation.

can be more reliable than
comparing $\frac{\beta_j - 0}{SE(\hat{\beta}_j)}$ to $N(0, 1)$

Wald test

saturated model terms cancel

Akaike

?IC

An Information Criterion (AIC)

No requirement that competing models be nested.

Choose the one maximizing

maximized log-likelihood under i th model $\rightarrow l_i(\hat{\theta}_i; D) - 2p_i$,
i.e., notion of *complexity penalty*. p again # parameters in i th model

Motivated as a measure of *predictive performance*.

Bayesian Information Criterion (BIC)

Again no nesting requirement.

Choose the model maximizing

$$l_i(\hat{\theta}_i; D) - \boxed{\{(1/2) \log n\} p_i},$$

was I with
AIC

i.e., bigger complexity penalty than AIC, especially for large samples.

Rationale: Bayesian - somewhat crude approximation to choosing the model for which $Pr(\text{Model } i \text{ is true} | \text{Data}=D)$ is largest.

Practical Difference - YES

x_j should be in the model yes

Say comparing M_0 and M_1 , nested, with $p_1 = p_0 + 1$. Choose M_1 if $2\{l_1(\hat{\theta}_1; D) - l_0(\hat{\theta}_0; D)\} > c$.

LRT: $c = \chi^2_1$ quantile, i.e.,

$$c = \begin{cases} 2.71 & 10\% \text{ sig.}, \\ 3.84 & \underline{5\% \text{ sig.}}, \\ 6.63 & 1\% \text{ sig.} \end{cases}$$

liberal

AIC: $c = 2$.

BIC: $c = \log n$, i.e.,

conservative

$$c = \begin{cases} \underline{4.6} & \text{if } n = 100, \\ 6.2 & \text{if } n = 500, \\ 6.9 & \text{if } n = 1000. \end{cases}$$

Comparing all possible models

?IC can compare any collection of models.

There are 2^m subsets of m predictor variables.

Fitting 2^{10} models may be tolerable. $\leftarrow \approx 1000$

Fitting 2^{20} models may not be. $\leftarrow 1000000$

Situation worse if want to consider possibilities of ‘curved’ effects and/or interactions.

e.g. interactions: m physical variables, but $m + m(m - 1)/2$ possible predictors for inclusion/exclusion.

Motivates stepwise procedures. Search for models with high values of criterion function without evaluating all possible models.

one of many stepwise implementations -
details differ

stepAIC() in R (part of MASS library)

Iterative scheme.

From current model, consider all possible ‘one-term deletions’
(backward) AND/OR ‘one-term additions (forward).’

Of these, the new model is the one with the best improvement in
AIC (or BIC).

Iterate this scheme until no such changes improve AIC.

Practical, but no guarantee of global max.

$y = \begin{cases} 1 & \text{'low'} \\ 0 & \text{'normal'} \end{cases}$ birthweight $n=189$

8 predictors of various types

Stepwise Example (low birthweight dataset)

```
fit0 <- glm(low ~ ., family=binomial, data=bwt)
```

starting model

```
fit1 <- stepAIC(fit0, ~.)
```

scope }

changing initial model

```
fit2 <- stepAIC(fit0, ~.^2 + I(scale(age)^2) +  
I(scale(lwt)^2) )
```

↓ some?

```
fit3 <- stepAIC(fit1, ~.^2 + I(scale(age)^2) +  
I(scale(lwt)^2) )
```

```
> summary(fit0)
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.82302	1.24471	0.661	0.50848
age	-0.03723	0.03870	-0.962	0.33602
lwt	-0.01565	0.00708	-2.211	0.02705 *
raceblack	1.19241	0.53597	2.225	0.02609 *
raceother	0.74069	0.46174	1.604	0.10869
smokeTRUE	0.75553	0.42502	1.778	0.07546 .
ptdTRUE	1.34376	0.48062	2.796	0.00518 **
htTRUE	1.91317	0.72074	2.654	0.00794 **
uiTRUE	0.68019	0.46434	1.465	0.14296
ftv1	-0.43638	0.47939	-0.910	0.36268
ftv2+	0.17901	0.45638	0.392	0.69488
---	trimester visits to physician			

Residual deviance: 195.48 on 178 degrees of freedom

AIC: 217.48

```
> fit1$anova  
Stepwise Model Path
```

Analysis of Deviance Table

Initial Model:

```
low ~ age + lwt + race + smoke + ptd + ht + ui + ftv
```

Final Model:

```
low ~ lwt + race + smoke + ptd + ht + ui
```

D + 2 # params

Step	Df	Deviance	Resid. Df	Resid. Dev	AIC
1			178	195.4755	217.4755
2	- ftv	2	1.358185	180	196.8337
3	- age	1	1.017866	181	197.8516

```
> fit2$anova
```

bigger slope

Stepwise Model Path

Analysis of Deviance Table

Initial Model:

```
low ~ age + lwt + race + smoke + ptd + ht + ui + ftv
```

Final Model:

```
low ~ age + lwt + smoke + ptd + ht + ui + ftv + age:ftv +  
smoke:ui
```

Step	Df	Deviance	Resid. Df	Resid. Dev	AIC
1			178	195.4755	217.4755
2 + age:ftv	2	12.474896	176	183.0006	209.0006
3 + smoke:ui	1	3.056805	175	179.9438	207.9438
4 - race	2	3.129586	177	183.0734	207.0734

```
> fit3$anova
```

Stepwise Model Path

Analysis of Deviance Table

Initial Model:

low ~ lwt + race + smoke + ptd + ht + ui

6 predictors

Final Model:

low ~ lwt + race + smoke + ptd + ht + ui

final model can depend on the
initial model - can't expect to
find the global

Step Df Deviance Resid. Df Resid. Dev

1

181 197.8516 213.8516

AIC

minimum

```
> summary(fit2)
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.582374	1.421613	-0.410	0.682057
age	0.075539	0.053967	1.400	0.161599
lwt	-0.020373	0.007497	-2.717	0.006580 **
smokeTRUE	0.780044	0.420385	1.856	0.063518 .
ptdTRUE	1.560317	0.497001	3.139	0.001693 **
htTRUE	2.065696	0.748743	2.759	0.005800 **
uiTRUE	1.818530	0.667555	2.724	0.006446 **
ftv1	2.921088	2.285774	1.278	0.201270
ftv2+	9.244907	2.661497	3.474	0.000514 ***
age:ftv1	-0.161824	0.096819	-1.671	0.094642 .
age:ftv2+	-0.411033	0.119144	-3.450	0.000561 ***
smokeTRUE:uiTRUE	-1.916675	0.973097	-1.970	0.048877 *
Residual deviance:	183.07	on 177 degrees of freedom		
AIC:	207.07			

Now - try the same stepwise procedures using BIC.

```
> fit1a <- stepAIC(fit0, ~., k=log(nrow(bwt)))  
> fit1a$anova  
Initial Model: main effects only scope replacing default k=2  
low ~ age + lwt + race + smoke + ptd + ht + ui + ftv  
Final Model:  
low ~ lwt + ptd + ht ↗ BIC being more conservative
```

Step	Df	Deviance	Resid. Df	Resid. Dev	AIC
1			178	195.4755	253.1347
2	- ftv	2 1.358185	180	196.8337	244.0094
3	- age	1 1.017866	181	197.8516	239.7855
4	- race	2 7.614209	183	205.4658	236.9163
5	- smoke	1 2.046576	184	207.5124	233.7211
6	- ui	1 2.611024	185	210.1234	231.0904

```
> fit2a <- stepAIC(fit0, ~.^2 + I(scale(age)^2) +  
+ I(scale(lwt)^2), k=log(nrow(bwt)))
```

```
> fit2a$anova
```

Initial Model:

low ~ age + lwt + race + smoke + ptd + ht + ui + ftv

Final Model:

low ~ lwt + ptd + ht

BIC

Step	Df	Deviance	Resid. Df	Resid. Dev	AIC
1			178	195.4755	253.1347
2	- ftv	2 1.358185	180	196.8337	244.0094
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More purely empirical model comparison?

CROSS-VALIDATION

- Randomly split data into *training* (T) and *validation* (V) cases.
- Fit model to (X_T, Y_T) data.
- Use the fitted model to generate predictions Y_V^* given X_V .

How close is Y_V^* to the actual Y_V ?

One formalization - pick the model M for which

$$\log f_M(y_V | x_V, \hat{\theta}_T)$$

is largest.

Biggest model doesn't necessarily win.

Sensitivity to random split?

k-fold cross-validation

Randomly split cases into k blocks: (Y_j, X_j) , $j = 1, \dots, k$.

Let $(Y_{(j)}, X_{(j)})$ denote all data except (Y_j, X_j) .

Do cross-validation k times, each time with $k - 1$ blocks as training data, one block as validation data.

Aggregate results. For instance choose model for which

$$\sum_{j=1}^k \log f_M(y_j | x_j, \hat{\theta}_{(j)})$$

is largest.

Ex.: Compare our AIC and BIC champions.

```
### randomly assign 189 subjects to five blocks
ind <- sample( c(rep(1,38), rep(2,38), rep(3,38),
                 rep(4,38), rep(5,37)) )

for (i in 1:5) {
  ### fit models to all but i-th block
  m0 <- glm(low~age+lwt+smoke+ptd+ht+ui+ftv+age:ftv+smoke:ui,
             family=binomial, data=bwt, subset=(ind!=i) )
  m1 <- glm(low~lwt+ptd+ht, AIC
             family=binomial, data=bwt, subset=(ind!=i) )

  ### predicted prob(Y=1) for i-th block
  ftpr0[ind==i] <- predict(m0, newdata=bwt,
                           type="response") [ind==i]
  ftpr1[ind==i] <- predict(m1, ...)
```

```

### predictive log-likelihoods and magnitude of diff.

> predll0 <- sum(as.numeric(bwt$low)*log(ftpr0) +
+                  (1-as.numeric(bwt$low))*log(1-ftpr0))
> predll1 <- sum(as.numeric(bwt$low)*log(ftpr1) +
+                  (1-as.numeric(bwt$low))*log(1-ftpr1))

> c(predll0, predll1)
-341.5994 -274.8250

> exp((predll0-predll1)/189)
0.7023638

```

HUGE preference for second (smaller, BIC-champ.) model. Why?

