Set S04 - Model comparison

STAT 401 (Engineering) - Iowa State University

April 24, 2017

Comparing nested models

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How do we compare non-nested models?

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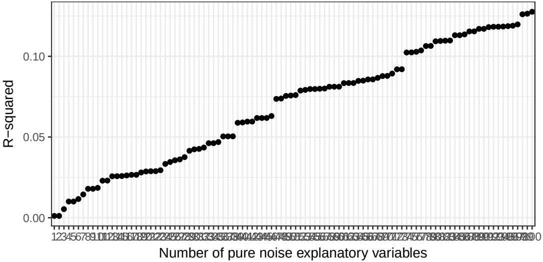

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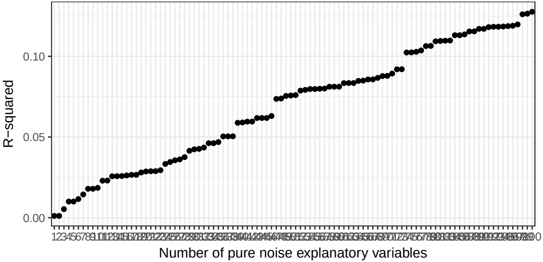

For this reason, sometimes R^2 is reported with a subscript that indicates the number of βs in the model.

Adjusted R-squared

One way to remedy this is to use "adjusted R^2" which can be calculated using the formula

$$\overline{R}^2 = 1 - \frac{(1 - R^2)(n-1)}{n-p-1}$$

where

- R^2 is the unadjusted R^2
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The idea with adjusted R^2 is that it only increases if the inclusion of a new explanatory variable is more than one would expect to see by chance.

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- AIC: $-2\log L(\hat{\theta}_{MLE}) + 2p$
- BIC: $-2\log L(\hat{\theta}_{MLE}) + p\log(n)$
- AICc: $-2\log L(\hat{\theta}_{MLE}) + 2p(p+1)/(n-p-1)$

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There are a number of alternatives that also modify the "fit" component:

- DIC: $-2\log L(E[\theta|y]) + 2p_D$ (effective number of parameters)
- BPIC: $-2\log p(\tilde{y}|E[\theta|y]) + 2p_D$
- $\vdots$

Obtaining AIC/BIC in R

```
lm1 <- lm(Fertility ~ . , data = swiss)
AIC(lm1)
```

```
[1] 326.0716
```

```
BIC(lm1)
```

```
[1] 339.0226
```

```
lm2 <- update(lm1, . ~ . -Examination)
AIC(lm1, lm2)
```

```
    df      AIC
lm1  7 326.0716
lm2  6 325.2408
```

```
BIC(lm1, lm2)
```

```
    df      BIC
lm1  7 339.0226
lm2  6 336.3417
```

Obtaining AICc in R

```
AICcmodavg::AICc(lm1)

[1] 328.9434

AICcmodavg::AICc(lm2)

[1] 327.3408

sme::AICc(lm1)

[1] 328.9434

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```

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This integral provides a natural penalty for increased number of parameters. BIC is an asymptotic approximation to $p(y|M_j)$.

Bayes Factors in R

```
library("bayess")
m <- BayesReg(swiss$Fertility, swiss[,-1])
```

```
          PostMean PostStError Log10bf EvidAgaH0
Intercept  70.1426      1.0339
x1         -3.7865      1.5463  0.4357       (*)
x2         -1.9939      1.9614 -0.6087
x3         -8.1123      1.7043  3.3083    (****)
x4          4.2062      1.4240  0.9664      (**)
x5          3.0389      1.0767  0.8215      (**)


Posterior Mean of Sigma2: 50.2438
Posterior StError of Sigma2: 71.877
```

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Bayesian model averaging

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$$p(\mu|y) = \sum_{j=1}^{J} p(\mu|M_j, y)p(M_j|y)$$

and model averaging for an unknown predictive value $\tilde{y}$ is

$$p(\tilde{y}|y) = \sum_{j=1}^{J} p(\tilde{y}|M_j, y)p(M_j|y).$$

AIC model averaging

You can also perform AIC model averaging using Akaike weights:

$$w_j = \frac{e^{-\Delta_j}/2}{\sum_{i=1}^{J} e^{-\Delta_i}/2}$$

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Since there is no notion of a posterior distribution, we calculate an estimate and standard error of quantities of interest. For example, a model averaged mean estimate is

$$\hat{\mu} = \sum_{j=1}^{J} \hat{\mu}_j w_j.$$

Step-wise model selection

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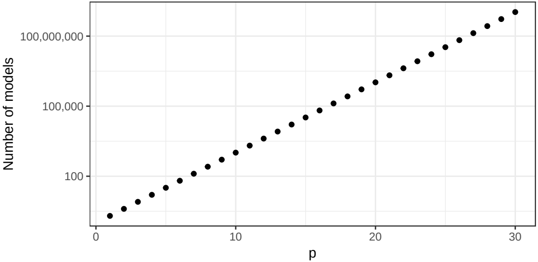
Once you have chosen a criteria, a common approach is to choose the model that optimizes that criteria. But in regression problems there are 2^p models to consider which is often too many to enumerate. An alternative is to use a stepwise selection procedure that compares all *neighboring* models.



Stepwise selection in R

```
d <- data.frame(X = X) %>% mutate(y = 10 * X.1 + 10 * X.2 + 10 * X.3 +
                                           X.4 +      X.5 +      X.6 +
                                      .1 * X.7 + .1 * X.8 + .1 * X.9 +
                                    rnorm(n()))
m <- step(lm(y ~ ., data = d), k = 2, trace=FALSE) # AIC
summary(m)
```

```

Call:
lm(formula = y ~ X.1 + X.2 + X.3 + X.4 + X.5 + X.6 + X.7 + X.8 +
    X.9 + X.12 + X.13 + X.17 + X.21 + X.27 + X.28 + X.30 + X.31 +
    X.34 + X.48 + X.49 + X.61 + X.62 + X.67 + X.71 + X.82 + X.83 +
    X.93, data = d)

Residuals:
     Min       1Q   Median       3Q      Max
-2.68780 -0.67529 -0.02836  0.63979  2.73789

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.05188    0.03106  -1.670 0.095220 .
X.1         10.02987    0.03076 326.076  < 2e-16 ***
X.2         10.02637    0.02999 334.288  < 2e-16 ***
X.3          9.96052    0.03106 320.687  < 2e-16 ***
X.4          0.97607    0.03151  30.973  < 2e-16 ***
X.5          1.05271    0.03187  33.030  < 2e-16 ***
X.6          0.97690    0.02914  33.522  < 2e-16 ***
X.7          0.09115    0.03149   2.895 0.003881 **
X.8          0.11682    0.02966   3.938 8.79e-05 ***
X.9          0.11488    0.03156   3.640 0.000287 ***
X.12        -0.06478    0.03002  -2.158 0.031194 *
```

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All the criterion (and posterior probabilities) are based on some theoretical basis. So you can choose a criterion based on your preferred theoretical basis or based on what your field uses. Often times a criterion is justified based on predictive performance. But then why not just use predictive ability as your criterion?

Assessing predictive performance

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- training data set
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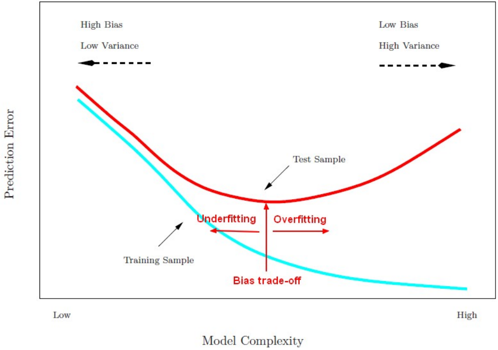
- testing data set

Use the training data set to build your model and then use your testing data set to evaluate the fit.

Overfitting



https://gerardnico.com/wiki/data_mining/overfitting

Example splitting in R

```
d <- data.frame(X = X) %>% mutate(y = 10 * X.1 + 10 * X.2 + 10 * X.3 +
                                           X.4 +      X.5 +      X.6 +
                                      .1 * X.7 + .1 * X.8 + .1 * X.9 +
                                    rnorm(n()),
                                  train = rbinom(n(), 1, 0.5))
train <- d %>% filter(train == 1) %>% dplyr::select(-train)
test <- d %>% filter(train == 0) %>% dplyr::select(-train)

m <- step(lm(y ~ ., data = train), k = log(nrow(train)), trace=FALSE)
m


Call:
lm(formula = y ~ X.1 + X.2 + X.3 + X.4 + X.5 + X.6 + X.8 + X.9 +
    X.42, data = train)

Coefficients:
(Intercept)          X.1          X.2          X.3          X.4          X.5          X.6          X.8
    0.02409     10.02275     10.09242      9.93224      1.02931      0.96461      1.02814      0.10513      0.1
       X.42
   -0.13081


test <- test %>% bind_cols(data.frame(prediction = predict(m, newdata = test)))

# Calculate mean sum of squared errors
with(test, mean((y-prediction)^2))


[1] 1.14051
```

Cross-validation

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Two special cases:

- Leave-one-out cross-validation (LOO-CV)
- k-fold cross validation

Cross-validation in R

```
library(DAAG)
m <- lm(y~., data = d %>% dplyr::select(-train))
cv <- cv.lm(data = d, form.lm = m, m=nrow(d)/5, plotit=FALSE)
```

```
Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq  F value  Pr(>F)
X.1        1 104960  104960 1.04e+05 < 2e-16 ***
X.2        1 114848  114848 1.14e+05 < 2e-16 ***
X.3        1  97843   97843 9.73e+04 < 2e-16 ***
X.4        1   1064    1064 1.06e+03 < 2e-16 ***
X.5        1    992     992 9.87e+02 < 2e-16 ***
X.6        1   1110    1110 1.10e+03 < 2e-16 ***
X.7        1     11      11 1.09e+01 0.00097 ***
X.8        1      2       2 1.51e+00 0.21926
X.9        1      7       7 7.38e+00 0.00673 **
X.10       1      0       0 2.70e-01 0.60023
X.11       1      0       0 4.00e-02 0.84768
X.12       1      0       0 4.00e-01 0.52756
X.13       1      0       0 2.50e-01 0.61982
X.14       1      0       0 1.40e-01 0.71302
X.15       1      1       1 5.20e-01 0.47089
X.16       1      0       0 4.10e-01 0.51996
X.17       1      0       0 1.20e-01 0.72433
X.18       1      4       4 3.97e+00 0.04656 *
X.19       1      1       1 1.14e+00 0.28620
X.20       1      1       1 1.00e+00 0.31700
X.21       1      0       0 1.60e-01 0.69183
X.22       1      0       0 1.50e-01 0.69504
```