Multiple regression - information criteria for large data bases

November 14, 2023

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$$\hat{\sigma}^2 = s^2 = \frac{||Y - X\hat{\beta}_{LS}||^2}{n - p} = \frac{RSS}{n - p}$$

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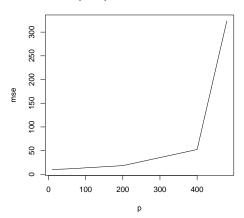
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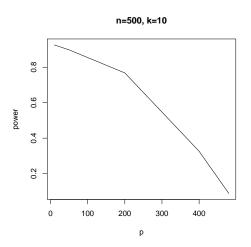
But $(X'X)^{-1}$ has the inverse Wishart distribution and the expected values of the elements on the diagonal are equal to $\frac{n}{n-p-1}$ and become very large as p approaches n.

Inflation of MSE

n=500, k=10, MSE on first 10 coefficients



Loss of Power



Model selection

Model selection in multiple regression - identification of important variables

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Also, RSS is not a good measure of the prediction error.

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 $RSS = ||Y - \hat{Y}||^2$ measures the fit in the training sample, i.e. it depends on the specific realization of the noise term ϵ - this is overfitting. PE measures the fit with respect to the true expected value of Y, which indeed is an indication of predictive properties for different noise terms.

Prediction error

Fact 1:

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Proof:

$$E(\hat{y}_i - y_i)^2 = E((\hat{y}_i - \mu_i) - (y_i - \mu_i))^2$$

= $E(\hat{y}_i - \mu_i)^2 + \sigma^2 - 2Cov(\hat{y}_i, y_i) = PE_i - 2Cov(\hat{y}_i, y_i)$

Prediction error for a linear operator

If
$$\hat{Y} = M_{n \times n} Y$$
 then

$$\sum_{i=1}^{n} Cov(\hat{y}_i, y_i) = Tr(Cov(MY, Y)) = Tr(MCov(Y, Y)) = \sigma^2 Tr(M)$$

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$$PE = E(RSS) + 2\sigma^2 Tr(M)$$

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$$M = X(X'X)^{-1}X'$$

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Leave-one-out cross-validation:

$$CV = \sum_{i=1}^{n} (Y_i - \hat{Y}[i])^2 = \sum_{i=1}^{n} \left(\frac{Y_i - \hat{Y}_i}{1 - M_{ii}}\right)^2$$

Akaike Information Criterion

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$$AIC(M_k) = \ln L(X, \hat{\theta}_{MLE}) - k$$

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$$L(Y|X, \beta, \sigma) = \left(\frac{1}{\sqrt{2\pi}\sigma}\right)^n e^{\frac{-||Y-X\beta||^2}{2\sigma^2}}$$

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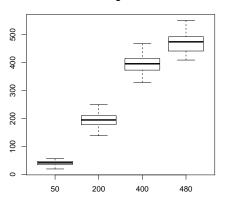
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Maximizing AIC corresponds to minimizing $RSS + 2\sigma^2 k$

Properties of AIC (1)

In our example AIC identifies the true model among 5 models with different dimensions, p = 500, k = 10.

diff in aic between a given and a true model



Can we use AIC to select variables in large data bases?

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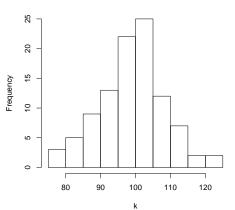
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More complicated heuristics: genetic algorithms, simulated annealing etc.

bigstep - R library with many different search strategies, optimizing a variety of model selection criteria; p = 500, k = 10.

Histogram of the number of selected variables



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In our simulations $\hat{k}\approx 100$ due to additional disturbance by the sample correlations between columns of the design matrix and using the form of AIC with unknown σ



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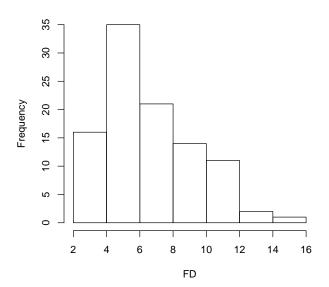
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Thus we expect to see on average $p_0 * 0.013 = 490 * 0.013 \approx 6.5$ false discoveries

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Accuracy of approximation: for p = 500

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Here the expected number of false discoveries is smaller than 1 and decreases with p

Modified BIC

In mBIC (Bogdan et al. 2004) the penalty depends on p and n,

$$mBIC = RSS + \sigma^2 k \left(\log n + 2 \log \left(\frac{p}{C} \right) \right) ,$$

where C is the prior expected number of nonzero regression coefficients. In the lack of the prior knowledge the value C=4 is suggested. It is motivated by controlling FWER.

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mBIC2 (Żak-Szatkowska and Bogdan (CSDA, 2011), Frommlet et al. (2011))

$$mBIC2 := RSS + \sigma^2(k \log(n) + 2k \log(p/4) - 2\log(k!)$$
.

The last relaxing term comes from the BH correction :

$$\Phi^{-1}\left(1-rac{ilpha}{2p}
ight)=\sqrt{2\log(p/i)}(1+o_p)$$

$$\sum_{i=1}^{k} 2\log(p/i) = 2k\log p - 2\log(k!)$$

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- Simulation scenario: β_i equally distributed between 0.27 and 0.66

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- 4. False positive correlation with a causal SNP<0.9

