

# Linear Regression

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# Model Building: Overview

# Model-Building Steps

- ▶ Data collection and processing
- ▶ Exploratory data analysis
- ▶ Preliminary model investigation
- ▶ Model selection
- ▶ Model diagnostics and validation

# Case Study: Surgical Unit

A hospital surgical unit was interested in predicting survival times of patients (in days, ascertained in a follow-up study) undergoing a particular type of liver operation. 108 such patients were randomly selected for this study. The following variables were measured for each patient: blood clotting score, prognostic index, enzyme function test score, liver function test score, age (in years), gender (male or female) and history of alcohol use (none, moderate or severe). We use half of the data to build the model (**training data**) and use the other half to perform model validation (**validation data**) later.

hold out data

# **Model Building: Exploratory Data Analysis**

# Exploratory Data Analysis

- ▶ Type of each variable: 

定量  
quantity

 or 

定性  
quantity
- ▶ Distribution of each variable: symmetric or skewed? outliers?
- 定量 ▶ Quantitative: histogram, boxplot, summary statistics, etc.
- 定性 ▶ Qualitative: pie chart, frequency table, etc.
- ▶ Relationships among variables:
  - ▶ scatter plot matrix, correlation matrix, side-by-side box plots
  - ▶ nonlinear pattern? clusters? outliers?

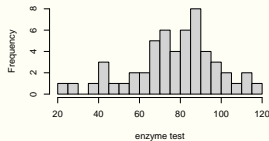
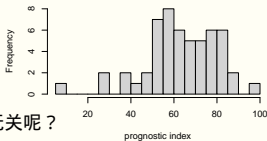
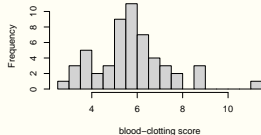
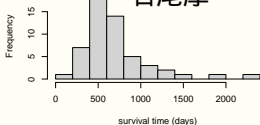


Figure: Histograms of quantitative variables

right-skewed=可以用log(y)来fix  
右尾厚

其实是用boxcox  
搞一个合适的 $\lambda$   
使得 $\text{trans}(Y) \sim X$   
的 $\text{residual} = Y - \hat{Y}$   
最像normal

response variable

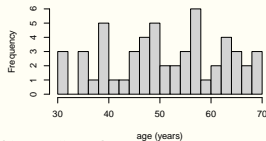
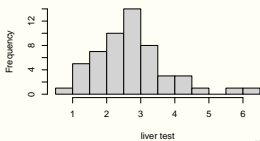


根据经验  
right-skewed的Y  
的 $\lambda$ 常常接近0  
就是  
trans=log的时候  
见PPTweek3P26

但是  
这个事情为什么与X无关呢？

其实有关  
当X不是normal  
Y很自然不是normal  
e也可以是normal  
但根据经验，  
往往log就可以了，  
不过分析的时候，  
logY~N，

不能作为做log的理由，要用boxcox的 $\lambda$ 最可能是0（or非常接近）作理由



```

panel.cor <- function(x, y){
  #usr <- par("usr")
  #on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r <- round(cor(x, y, use="complete.obs"), 2)
  txt <- paste0("R = ", r)
  cex.cor <- 0.8/strwidth(txt)
  text(0.5, 0.5, txt,
       cex = cex.cor * r)
}

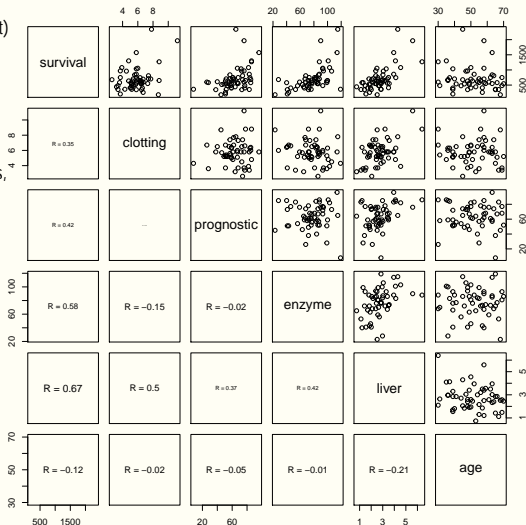
```

**Figure:** Scatter plot matrix of quantitative variables

```

pairs(~weight+waist+hip
+height+age, data=diabetes,
lower.panel = panel.cor)

```





定性

Figure: Pie charts of qualitative variables

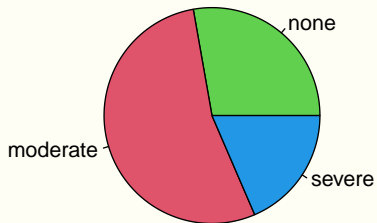
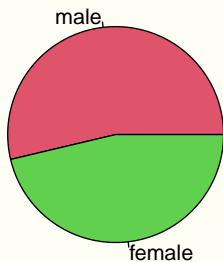


Figure: Side-by-side pie charts

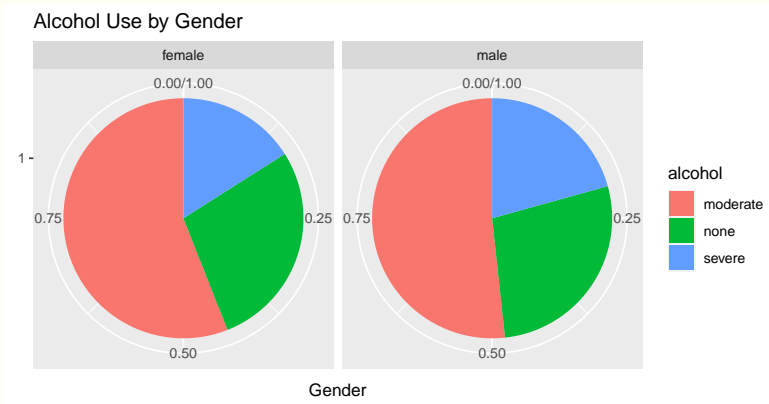
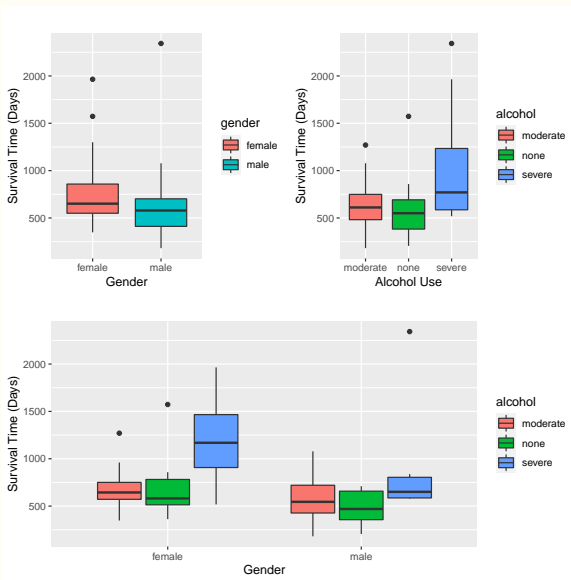


Figure: Side-by-side box plots



# **Model Building: Preliminary Fit**

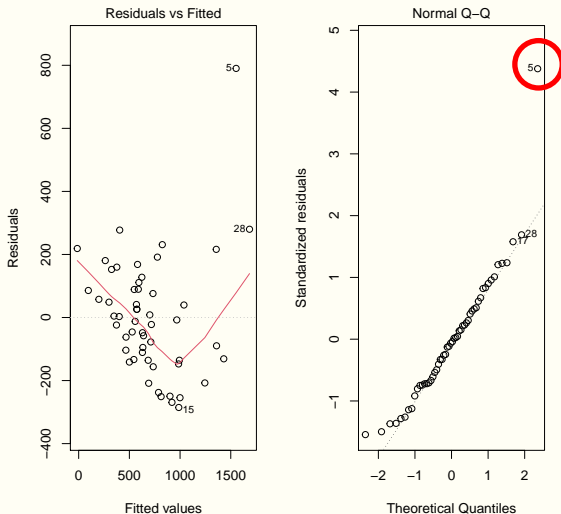
# Preliminary Model Fitting

- ▶ Residual plots based on initial fits:
  - ▶ nonlinearity? departure from Normality? nonconstant error variance?  
? log transformation
  - ▶ transformations needed?
  - ▶ interaction terms and/or high-order power terms?
- ▶ The goal is to decide on:
  - ▶ Functional forms in which variables should enter the model;
  - ▶ Potential pool of  $X$  variables to be considered in subsequent analysis;
- ▶ This process should be aided by prior knowledge and domain expertise if available.

## Surgical Unit: First-Order Model

Fit a first-order model with survival time as response, and blood clotting score, prognostic index, enzyme function test score, liver function test score, age, gender (male or female) and history of alcohol use (none, moderate or severe) as  $X$  variables. Note that, gender and alcohol use should be treated as factors.

There appears to be non-linearity in regression relation. Residual Q-Q plot indicates outliers on the right tail.



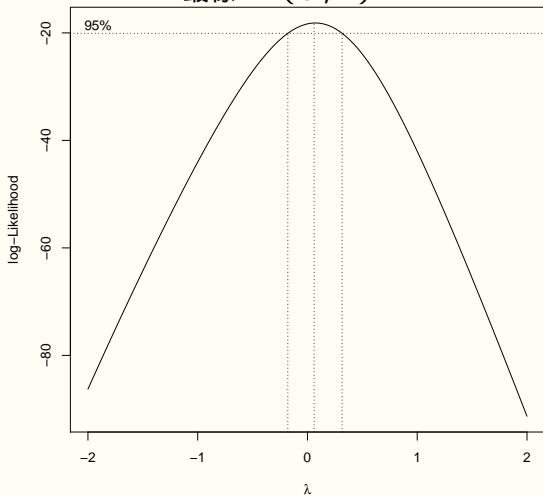
Box-cox procedure suggests logarithm transformation of the response variable.

Linear Regression 第一步

做个transform of Y ,

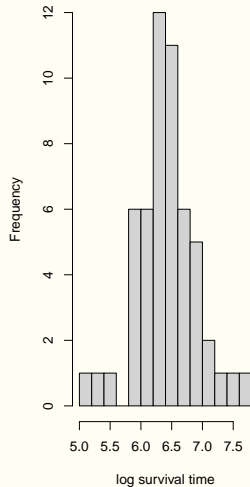
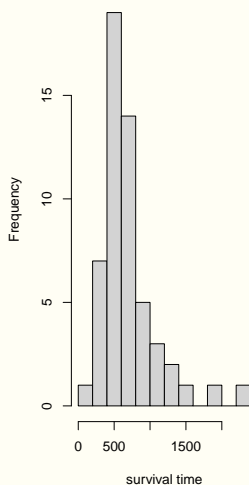
使得回归后的residual=Y-hatY

最像  $\sim N(0, \dots)$

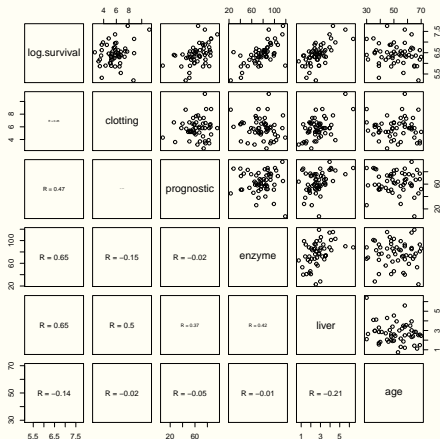


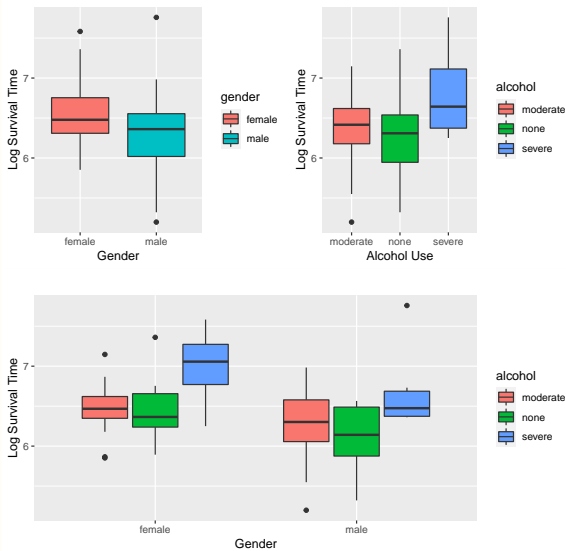


# Surgical Unit: Log-Transformation

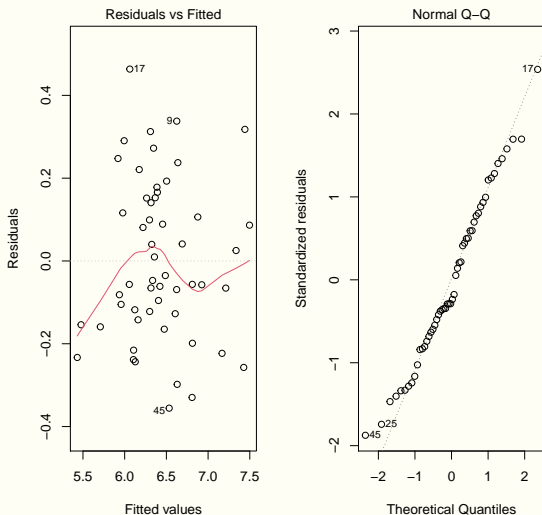


No obvious nonlinearity between log-survival-time and the quantitative X variables:





Fit the first-order model with log-survival-time as response: model assumptions appear to hold better.



Based on these preliminary fits, we decided to:

- ▶ use log-survival-time as the response variable;
- ▶ not include any interaction terms: this could be further examined by plotting residuals versus various interaction terms (e.g., those involving significant predictors).

Next, we should examine whether all predictors are needed or a subset of them is adequate in explaining log-survival-time  $\implies$

## **model selection**

# Bias-Variance Trade-off

# Correct Models vs. Good Models

- ▶ Correct models are those that contain all important  $X$  variables  $\implies$  little model bias.
- ▶ However, a correct model is not necessarily a good model because it may include too many nuisance variables  $\implies$  large sampling variability and overfitting.
- ▶ A good model should contain all important  $X$  variables (correct: little bias), and at the same time it should have few nuisance variables (simple: small variability)  $\implies$  achieves *bias-variance trade-off*.

## Example

$$Y = 1 + 2X_1 + 3X_2 + \epsilon$$

correct model=有显著变量(+垃圾变量)的model

- ▶ Any model contains  $(X_1, X_2)$  is a correct model, e.g.,  
 $\{X_1, x_2\}, \{X_1, X_2, X_1 X_2\}, \vee \{X_1, X_2, X_1^2, X_2^2\}, \{X_1, X_2, X_3, X_4, X_5\}$ .
  - ▶ These models have unbiased estimates.
  - ▶ However, some of them may have very large model variance such that the estimates behave erratically with even very small perturbation of the data.
- ▶ The models  $\{X_1\}$  or  $\{X_2\}$  both have an important  $X$  variable omitted and thus have substantial model bias.



In the following:

- ▶ Assume the response vector  $\mathbf{Y}$  has  $\text{Var}(\mathbf{Y}) = \sigma^2 \mathbf{I}_n$ .
- ▶ Let  $\boldsymbol{\mu} = E(\mathbf{Y})$  denote the mean of the response vector.
- ▶ Let  $\mathbb{M} = \mathbb{M}(X_1, \dots, X_{p-1})$  denote an arbitrary model (**not necessarily** a correct model) and  $\mathbf{X}$  denote its corresponding design matrix.
- ▶ Let  $H(\mathbf{X}) = \mathbf{X}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T$  be the hat matrix and  $\hat{\mathbf{Y}} = \hat{\mathbf{Y}}(\mathbf{X}) = H(\mathbf{X})\mathbf{Y}$  be the fitted values vector.

Note that,  $\mathbb{M}$  being a correct model means that there exists a vector  $\boldsymbol{\beta}$  such that  $\boldsymbol{\mu} = \mathbf{X}\boldsymbol{\beta}$ .

# Model Variance

- ▶ The (in-sample) variance of  $\mathbb{M}$  is the overall variances of the fitted values:

$$\text{Var}_{in}(\mathbb{M}) := \sum_{i=1}^n \text{Var}(\hat{Y}_i) = \text{Tr}(\text{Var}(\hat{\mathbf{Y}})) = \sigma^2 \text{Tr}(H(\mathbf{X})) = p\sigma^2$$

- ▶ Therefore, larger models always have larger variances, whether they are correct or not.

# Model Bias

- ▶ The (in-sample) bias of  $\mathbb{M}$  is the overall biases of the fitted

values:

model不是correct model的时候，会有in sample bias

当我们没有include所有important的X的时候，会出现in sample bias

$$bias_{in}(\mathbb{M}) := \|E(\hat{\mathbf{Y}}) - E(\mathbf{Y})\|_2 = \|(H(\mathbf{X}) - \mathbf{I})\boldsymbol{\mu}\|_2$$

- ▶ Model bias depends on how well the column space  $\langle \mathbf{X} \rangle$

$\boldsymbol{\mu} = E\mathbf{Y}$

approximates the mean response vector  $\boldsymbol{\mu}$ :

$(\mathbf{I} - H(\mathbf{X}))\boldsymbol{\mu}$

column space

$C(\mathbf{X}) := \text{span}(\text{col}(\mathbf{X}))$

$\text{span}(\text{col}(\mathbf{X}))$ 的正交补空间

$$\boldsymbol{\mu} = E(\mathbf{Y}) = \boldsymbol{\mu}_X + \boldsymbol{\mu}_{X^\perp}, \quad \boldsymbol{\mu}_X \in \langle \mathbf{X} \rangle, \quad \boldsymbol{\mu}_{X^\perp} \in \langle \mathbf{X} \rangle^\perp$$

symmetric 对称  
idempotent 幂等

$$(H(\mathbf{X}) - \mathbf{I})\boldsymbol{\mu} = -\boldsymbol{\mu}_{X^\perp}, \quad bias_{in}^2(\mathbb{M}) = \boldsymbol{\mu}^T (\mathbf{I} - H(\mathbf{X}))\boldsymbol{\mu} = \|\boldsymbol{\mu}_{X^\perp}\|_2^2$$

- ▶ If  $\mathbb{M}$  is a correct model, then  $bias_{in}(\mathbb{M}) = 0$  because:

$$\boldsymbol{\mu} = E(\mathbf{Y}) = \mathbf{X}\boldsymbol{\beta} \in \langle \mathbf{X} \rangle, \quad \text{so,} \quad \boldsymbol{\mu}_{X^\perp} = \mathbf{0}$$

# Mean-Squared-Estimation-Error

有时候也叫"mse", 不是MSE=mean sum of squared error!

## ► Mean squared estimation error (msee) of $\hat{Y}_i$ :

$$\begin{aligned}
 \text{"mean"} & \quad E[(\hat{\theta} - \theta)^2] \\
 \text{est.err} & \quad \downarrow \\
 \text{squared} & \quad \downarrow \\
 msee_i(\mathbb{M}) & := E((\hat{Y}_i - \mu_i)^2) \\
 & = E[(\hat{Y}_i - \text{Ehat}Y_i + \text{Ehat}Y_i - \mu_i)^2] \\
 & = E[(\hat{Y}_i - \text{Ehat}Y_i)^2] + \underbrace{E[(\text{Ehat}Y_i - \mu_i)^2]}_{=0} + 2(\text{Ehat}Y_i - \mu_i)E(\hat{Y}_i - \text{Ehat}Y_i) \\
 & = E[(\hat{\theta} - \text{Ehat}\theta + \text{Ehat}\theta - \theta)^2] \\
 & = E[(\hat{\theta} - \text{Ehat}\theta)^2] + (\text{Ehat}\theta - \theta)^2 + 2(\text{Ehat}\theta - \theta)E(\hat{\theta} - \text{Ehat}\theta) \\
 & = E[(\hat{\theta} - \text{Ehat}\theta)^2] + (\text{Ehat}\theta - \theta)^2 = \text{Var}(\hat{\theta}) + \text{bias}(\hat{\theta})^2 \\
 & = \text{Var}(\hat{Y}_i) + (\text{E}(\hat{Y}_i) - \mu_i)^2 \\
 & \quad \text{bias}(\text{hat}Y_i)^2
 \end{aligned}$$

## ► The (in-sample) msee of $\mathbb{M}$ equals model variance plus

squared model bias:

对不同的 $\text{hat}Y_i$ ,  $\mu_i$ 是不同的 (由所有 significant 的  $X_i$  决定, 这些  $X_i$  不一定在我们的 model 里面)

$$msee_{in}(\mathbb{M}) := \sum_{i=1}^n msee_i(\mathbb{M})$$

这里有tradeoff

minimize msee 可以是我们的 goal

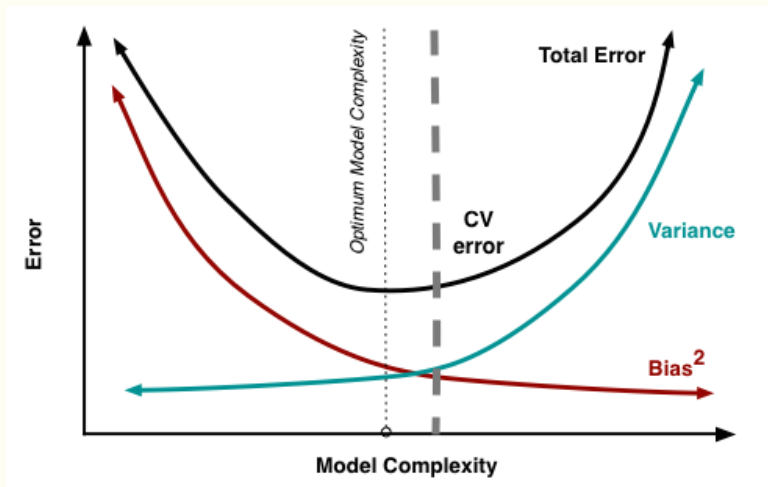
$$= \text{Var}_{in}(\mathbb{M}) + \text{bias}_{in}^2(\mathbb{M})$$

$$= p\sigma^2 + \|\mu_{X^\perp}\|_2^2$$

p 越大

线性空间 dim 越大  
正交补空间 dim 越小  
无法解释的  $\mu$  越少

# Bias-Variance Trade-off



## $E(SSE)$ of a Model

- ▶  $SSE = \mathbf{e}^T \mathbf{e} = \mathbf{Y}^T (\mathbf{I} - H(\mathbf{X})) \mathbf{Y}$ , is a measure of *goodness-of-fit* of the model to the **observed data**  $\mathbf{Y}$ .
- ▶  $E(SSE)$  is affected by three factors: (i) model complexity  $p$ ;  
(ii) error variance  $\sigma^2$ ; (iii) and model bias  $bias_{in}$ .

$$\begin{aligned} E(SSE) &= E(\text{Tr}((\mathbf{I} - H(\mathbf{X}))\mathbf{Y}\mathbf{Y}^T)) = \text{Tr}((\mathbf{I} - H(\mathbf{X}))E(\mathbf{Y}\mathbf{Y}^T)) \\ &= \text{Tr}((\mathbf{I} - H(\mathbf{X}))(\sigma^2 \mathbf{I} + \boldsymbol{\mu}\boldsymbol{\mu}^T)) \\ &= (n - p)\sigma^2 + \boldsymbol{\mu}^T (\mathbf{I} - H(\mathbf{X}))\boldsymbol{\mu} \\ &= (n - p)\sigma^2 + bias_{in}^2 \geq (n - p)\sigma^2 \end{aligned}$$

$p$ 越大， $E(SSE)$ 一定越小，所以minimize  $E(SSE)$ 不是我们的goal

- ▶ If  $\mathbb{M}$  is a correct model, then  $bias_{in}(\mathbb{M}) = 0$  and thus  $E(SSE) = (n - p)\sigma^2$  and  $E(MSE) = \sigma^2$ .
- ▶ If  $\mathbb{M}$  is an incorrect model, i.e.,  $\mu = E(\mathbf{Y}) \notin \langle \mathbf{X} \rangle$ , then  $E(SSE) > (n - p)\sigma^2$  and  $E(MSE) > \sigma^2$ .

# Summary

- ▶ Larger models have larger variances.
- ▶ Model bias depends on how well the column space of its design matrix approximates the mean response vector.
- ▶ For two correct models, the larger model has a smaller  $E(SSE)$ , but a larger variance and thus a larger overall mean-squared-estimation-error. So it tends to *overfit* the observed data.
- ▶ Incorrect models have larger  $E(SSE)$  than correct models of the same size, so they tend to *underfit* the observed data.



# Model Selection: Overview

# Full Model vs. Candidate Model

- ▶ *Full model*: The model that contains all  $P - 1$  potential  $X$  variables in the pool.
  - ▶ **Assume the full model is a correct model.**
- ▶ *Candidate model*: A model that contains a subset of  $p - 1$   $X$  variables with  $1 \leq p \leq P$ .
- ▶ The goal is to choose good model(s) (subset(s) of  $X$  variables) that balances bias and variance.

# Key Components for Model Selection

- ▶ **Criterion to compare models:**

- ▶  $R_a^2, C_p, AIC_p, BIC_p, Press_p$ , etc.

- ▶ **Procedure to search for good model(s):**

- ▶ *Best subset selection*: Exhaustive search; Applicable when the number of potential  $X$  variables is not too big ;
  - ▶ *Stepwise regression*: Greedy search; The number of potential  $X$  variables can be large;

# Surgical Unit

If clotting ( $X_1$ ), prognostic ( $X_2$ ), enzyme ( $X_3$ ), liver ( $X_4$ ) form the potential pool of  $X$  variables, then there are 16 sub-models.

none model	选: p	intercept	X1	X2	X3	X4	sse	R^2	R^2_a	大	小	小	小	cp值可以小于p的
										Cp	aic	bic	press	
	1	1	0	0	0	0	12.805	0.000	0.000	151.569	-75.716	-73.727	13.292	
	2	1	0	0	1	0	7.334	0.427	0.416	66.518	-103.811	-99.833	8.329	The full model p Cp p by definition
	2	1	0	0	0	1	7.408	0.421	0.410	67.696	-103.268	-99.290	8.024	
	2	1	0	1	0	0	9.974	0.221	0.206	108.469	-87.205	-83.227	10.738	
	2	1	1	0	0	0	12.028	0.061	0.043	141.093	-77.096	-73.118	13.508	
	3	1	0	1	1	0	4.313	0.663	0.650	20.523	-130.479	-124.512	5.066	
	3	1	0	0	1	1	5.132	0.599	0.583	33.536	-121.089	-115.122	6.123	
	3	1	1	0	1	0	5.783	0.548	0.531	43.873	-114.644	-108.677	6.989	不同criteria 不一定选中 同一个model
	3	1	0	1	0	1	6.620	0.483	0.463	57.175	-107.342	-101.375	7.474	
	3	1	1	0	0	1	7.299	0.430	0.408	67.961	-102.070	-96.103	8.472	
	3	1	1	1	0	0	9.437	0.263	0.234	101.937	-88.194	-82.227	11.055	
	4	1	1	1	1	0	3.109	0.757	0.743*	3.388*	-146.161*	-138.205*	3.914*	
	4	1	0	1	1	1	3.615	0.718	0.701	11.434	-138.011	-130.055	4.598	
	4	1	1	0	1	1	4.970	0.612	0.589	32.960	-120.823	-112.867	6.209	
	4	1	1	1	0	1	6.568	0.487	0.456	58.358	-105.763	-97.807	7.902	
full model	5	1	1	1	1	1	3.084	0.759*	0.739	5.000	-144.587	-134.642	4.069	

The full model p  
Cp p  
by definition

不同criteria  
不一定选中  
同一个model

# Model Selection: Criteria

## Mallows' $C_p$ Criterion

For full model:

$$C_p = (SSE_p) / \hat{\sigma}^2 - (n - 2p) = (n - p) - (n - 2p) = p$$

$$C_p := \frac{SSE_p}{\hat{\sigma}^2} - (n - 2p)$$

- ▶  $n$  : sample size
- ▶  $p$ : number of regression coefficients in the candidate model
- ▶  $SSE_p$ : error sum of squares of the candidate model
- ▶  $\hat{\sigma}^2$ : an unbiased estimator of the error variance  $\sigma^2$ :

need assumption

that full model is correct


$$\hat{\sigma}^2 = MSE_{\text{full model}} = SSE_{\text{full}} / (n - p)$$

## Mallows' $C_p$ : Interpretation

Let  $\mathbb{M} = \mathbb{M}(X_1, \dots, X_{p-1})$  denote the candidate model, then

$$\begin{aligned} E(C_p(\mathbb{M})) &\approx \frac{E(\text{SSE}(\mathbb{M}))}{\sigma^2} - (n - 2p) \\ E[\text{SSE}(\mathbb{M})/\hat{\sigma}^2] - (n - 2p) &= \frac{(n - p)\sigma^2 + \text{bias}_{in}^2(\mathbb{M})}{\sigma^2} - (n - 2p) \\ \text{这里用了一个非常不对的近似} & \\ E[\text{SSE}(\mathbb{M})/\hat{\sigma}^2] &= \frac{p\sigma^2 + \text{bias}_{in}^2(\mathbb{M})}{\sigma^2} \\ E(\text{SSE}(\mathbb{M}))/\sigma^2 &= \frac{\text{Var}_{in}(\mathbb{M}) + \text{bias}_{in}^2(\mathbb{M})}{\sigma^2} = \frac{\text{mse}_{in}(\mathbb{M})}{\sigma^2} \\ \text{考试不可用这个} & \end{aligned}$$

So  $C_p$  can be viewed as an <sup>very rough</sup> estimator of the overall mean-squared-estimation-error divided by the error variance.

## How to Use $C_p$ ?

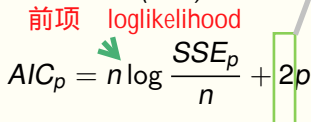
- ▶ If a model has no bias, i.e., a correct model, then  $E(C_p) \approx p$ ;  
Otherwise  $E(C_p)$  tends to be larger than  $p$ .
- ▶ When  $C_p$  is plotted against  $p$ , then models with little bias will tend to fall near the diagonal line  $C_p = p$ .
- ▶ On the other hand, models with substantial bias will tend to fall considerably above this line.
- ▶ Look for models with (i) the  $C_p$  value not far above  $p$  and (ii) less X variables  $\implies$  small bias and small variance



# $AIC_p$ and $BIC_p$ Criteria

- Akaike's information criterion (AIC): SSE

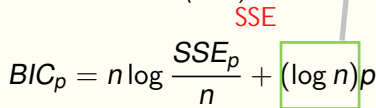
前项      loglikelihood

$$AIC_p = n \log \frac{SSE_p}{n} + 2p$$


n>8时  
AIC会选更大的p  
更注重拟合效果

- Bayesian information criterion (BIC):

SSE

$$BIC_p = n \log \frac{SSE_p}{n} + (\log n)p$$


n>8时  
BIC会选跟小的p  
更注重模型正确性

- How to use: Look for models with small AIC (BIC)

当candidate models里有  
correct model, BIC基本以概率1选中正确的model

## $AIC_p$ and $BIC_p$ : Interpretation

- ▶ The first term:  $n \log \frac{SSE_p}{n}$  reflects the *goodness-of-fit* of the model to the **observed data**:
  - ▶ decreases by adding more  $X$  variables into the model
- ▶ The second term,  $2p$  for AIC and  $(\log n)p$  for BIC, reflects model complexity:
  - ▶ increases by adding more  $X$  variables into the model
  - ▶ If  $n \geq 8$ , then  $\log n > 2$  and BIC puts more penalty on model complexity and tends to choose smaller models than AIC.

- ▶ Overly simplified models have small model complexity ( $p$ ), but they tend to have large  $SSE$  (underfitting, high bias).
- ▶ Overly complicated models may have a small  $SSE$ , but they have large model complexity (overfitting, high variance).
- ▶ By minimizing AIC (or BIC), we are trying to find a model that balances between model complexity and the goodness-of-fit.

Predicted residual sum of squares ( $Press_p$ ):

$$Press_p = \sum_{i=1}^n (Y_i - \widehat{Y}_{i(i)})^2.$$

- 第*i*个case  
里面没有X<sub>i</sub>  
预测的Y =
- ▶  $Y_i$  is the observed response of the *i*th case.
  - ▶  $\widehat{Y}_{i(i)}$  is the predicted value for the *i*th case obtained by fitting the model only using  $n - 1$  cases excluding case *i*.
  - ▶  $Press_p$  is also known as leave-one-out-cross-validation (LOOCV).
  - ▶ Models with small  $Press_p$  are considered good in terms of predictive ability.

$h_{ii}=1$  可以取到

iff 列向量  $P_i$  在  $\lambda=0$  的地方都是 0

$0 \leq h_{ii} \leq 1$

$h_{ii}=0$  可以取到

iff 列向量  $P_i$  在  $\lambda=1$  的地方都是 0

## Press<sub>p</sub>: Calculation

$$h_{ii} = e_i' H e_i = e_i' P' \text{capital} \lambda P e_i = P_i' \text{capital} \lambda P_i$$

$$\leq ||P_i||_2^2 = 1$$

$$\text{又 } P_i' \text{capital} \lambda P_i = \sum_{j \in \text{supp}(\lambda)} P_{ij}^2 \geq 0 [\text{not all } \lambda=0, \text{ some } =1]$$

Press<sub>p</sub> can be calculated without actually performing  $n$  regressions

because the deleted residual for the  $i$ th case:

$$\underline{d_i} := Y_i - \widehat{Y}_{i(i)} = \frac{e_i}{1 - h_{ii}}, \quad i = 1, \dots, n.$$

when fitting using all  $n$  cases

where  $e_i$  =  $Y_i - \widehat{Y}_i$  is the residual of the  $i$ th case and  $h_{ii}$  is the  $i$ th

diagonal element of the hat matrix  $H$ , both from the regression fit

using **all**  $n$  cases. So

Hat matrix  $H$  cannot be trace zero ! so this inequation can never become equation !

$$\text{Press}_p = \sum_{i=1}^n \frac{(Y_i - \widehat{Y}_i)^2}{(1 - h_{ii})^2} \cdot \text{>SSE}$$

计算的时候用的是这个式子

# Surgical Unit: Full Model

```
lm(formula = log(Y) ~ X1 + X2 + X3 + X4, data = data.o)
```

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 3.851933 0.266263 14.467 < 2e-16 \*\*\*

X1 0.083739 0.028834 2.904 0.00551 \*\*

X2 0.012671 0.002315 5.474 1.50e-06 \*\*\*

X3 0.015627 0.002100 7.440 1.38e-09 \*\*\*

X4 0.032056 0.051466 0.623 0.53627

Residual standard error: 0.2509 on 49 degrees of freedom

Multiple R-squared: 0.7591, Adjusted R-squared: 0.7395

F-statistic: 38.61 on 4 and 49 DF, p-value: 1.398e-14

Analysis of Variance Table

Df Sum Sq Mean Sq F value Pr(>F)

X1 1 0.7770 0.7770 12.3443 0.0009618 \*\*\*

X2 1 2.5904 2.5904 41.1565 5.341e-08 \*\*\*

X3 1 6.3286 6.3286 100.5490 1.838e-13 \*\*\*

X4 1 0.0244 0.0244 0.3879 0.5362698

Residuals 49 3.0841 0.0629

- ▶ Full model has  $P = 5$  and

$$SSE = 3.0841, \quad MSE = 0.0629, \quad R^2 = 0.7591, \quad R_a^2 = 0.7395$$

- ▶ By definition, for the full model,  $C_P = P = 5$
- ▶ Sample size  $n = 54$ , so for the full model:

$$AIC_P = 54 \log(3.0841/54) + 2 \times 5 = -144.5871 \text{ and}$$

$$BIC_P = 54 \log(3.0841/54) + \log(54) \times 5 = -134.6422$$

- ▶  $Press_p = 4.069$

```
> e.f=fit.f$residuals ## residuals
```

```
influence > h.f=influence(fit.f)$hat ## diagonals of hat matrix
```

```
> press.f= sum(e.f^2/(1-h.f)^2) ## calculate press
```

R code for  $Press_p$

# Model Selection: Stepwise Regression



# Model Search Procedures

- ▶ The number of possible models,  $2^{P-1}$ , grows very fast with the number potential  $X$  variables  $P - 1$ .
- ▶ Evaluating every possible model can be computationally infeasible even for moderate  $P$ .
- ▶ A variety of search procedures have been developed to efficiently search for the “best” model(s) in the model space.
  - ▶ *Stepwise regression procedures* Greedy Strategy
  - ▶ *Best subsets algorithms*: Not applicable when the pool of potential  $X$  variables is large.

# Stepwise Regression Procedures

Stepwise可以从任何initial model开始

从none model ( 只有intercept term ) 开始=forward stepwise

从full model开始=backward stepwise

- ▶ Use “greedy” search strategies to examine a sequence of models by adding or deleting only one  $X$  variable according to a pre-specified criterion (e.g.,  $AIC$ ) at each search step.
- ▶ Could end up with a *local optimal model* rather than the global “best” model.
- ▶ Commonly used stepwise procedures: *forward stepwise*, *forward selection*, *backward stepwise* and *backward elimination*.

# Forward Stepwise Procedure

Inputs:

- ▶ A model selection criterion, e.g.,  $AIC$ .
- ▶ An initial model  $M_0$ , usually a small model, e.g., the null-model with no  $X$  variable.
- ▶ The pool of potential  $X$  variables  $\mathcal{X}$ .
- ▶ The set of terms that will always be in the model  $\mathcal{X}_0$ , e.g., the intercept term.

Starting from the initial model  $M_0$ , at each step:

- (a) Consider the  $X$  variables in the pool  $X$  that are not currently in the model. Examine the change of the criterion by adding each such variable into the current model. examine "what if Add one in"
- (b) Consider the  $X$  variables that are already in the model but not in the set  $X_0$ . Examine the change of the criterion by dropping each such variable out of the current model. examine "what if Drop one out"
- (c) Choose the operation that improves the criterion the most and update the current model accordingly. Choose adding one in/dropping one out  
iff  
AIC or BIC decreases and decreases most.

Repeat steps (a) – (c) until there is no operation that can improve the criterion anymore.

# Forward Selection and Backward Elimination

- ▶ *Forward selection* is a simplified version of forward stepwise procedure by omitting the considerations of dropping a variable currently in the model at each step.  
Forward selection不考虑在过程中drop
- ▶ *Backward elimination* is the opposite of the forward selection:  
Backward elimination不考虑在过程中add
  - ▶ Start with a “big” initial model, e.g., the full model.
  - ▶ At each step, examine the change of the criterion by dropping a variable currently in the model.
- ▶ *Backward stepwise procedure*: opposite of forward stepwise.  
Forward/Backward stepwise: 过程中既有add又有drop  
区别在初始模型：F是从intercept term开始，B是从Full model开始

# Stepwise Procedures: Comparisons

- ▶ Forward stepwise procedure often works better than forward selection when there is high multicollinearity among the potential  $X$  variables.
- ▶ Backward procedures are not good when the number of potential  $X$  variables is large. Particularly, they are not feasible when  $P > n$ , since then the full model can not be fitted.
- ▶ A commonly used alternative to forward stepwise procedure is to perform one pass of forward selection, followed by one pass of backward elimination.

没有stepBIC() 【可以通过 $k=\log(n)$ 做到，这个时候就BIC】

## stepAIC() Function in R library MASS

- ▶ direction=“both” corresponds to forward stepwise procedure or backward stepwise procedure (depending on the initial model); direction=“forward” corresponds to forward selection; direction=“backward” corresponds to backward elimination.
- ▶ The option scope specifies the potential pool of X variables  
full model 是 upper，不会选择比upper的X variables 之外的X变量了！  
(upper) and the X variables that should always be included in the model (lower). lower model中的每一个X变量都总在model中
- ▶  $k=2$  corresponds to AIC criterion;  $k=\log(n)$  corresponds to BIC criterion.

# Surgical Unit

initial model

```
> fit.0=lm(log(survival)~1, data=data.o) ##initial model, only intercept
> step.aic=stepAIC(fit.0, scope=list(upper=~clotting+prognostic+enzyme+liver+age+gender
+alcohol.mod+alcohol.sev, lower=~1), direction="both", k=2, trace=FALSE)
> step.aic$anova
```

Stepwise Model Path

Analysis of Deviance Table

Initial Model:

log(survival) ~ 1

Final Model:

log(survival) ~ enzyme + prognostic + alcohol.sev + clotting + gender + age

Step		Df	Deviance	Resid. Df	Resid. Dev	AIC
1				53	12.804509	-75.71608
2	+ enzyme	1	5.47078352	52	7.333726	-103.81102
3	+ prognostic	1	3.02085553	51	4.312870	-130.47855
4	+ alcohol.sev	1	1.47089284	50	2.841977	-151.00214
5	+ clotting	1	0.66416961	49	2.177808	-163.37593
6	+ gender	1	0.09659084	48	2.081217	-163.82569
7	+ age	1	0.07688125	47	2.004335	-163.85826

不要show过程

both就是  
stepwise

k=2就是AIC

其实stepwise只有initial model之间的区别

F/B stepwise之间没有本质区别

initial model

maybe only this matters->this dummy v  
can be just  
"severe or not"



# Model Validation

# Model Validation

- ▶ *Internal validation*: Check validity using **the same data** used to fit the model.
- ▶ *External validation*: Check validity using **new data** – either newly collected or a holdout sample.

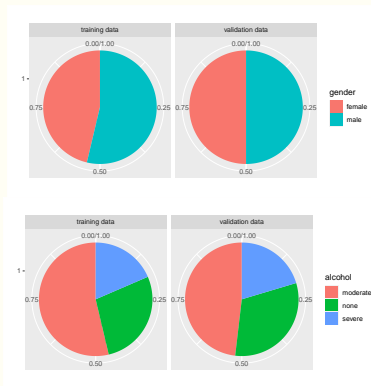
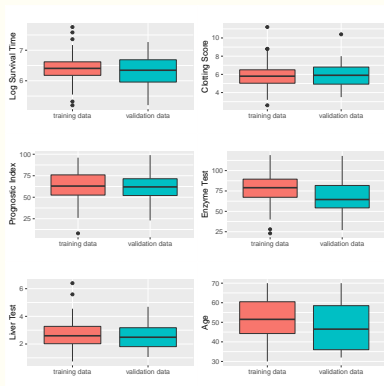
# Training Data vs. Validation Data

When sample size is sufficiently large, an option is to split the data into two sets, a *training data* used to build the model and a *validation data* used to check model validity.

- ▶ Training data should be sufficiently large so that a reliable model can be built from it. Sometimes, the validation data will have to be smaller.
- ▶ Once a final model has been validated and chosen, it is a common practice to use the entire data set to re-fit the final model.

# Surgical Unit: Training Data vs. Validation Data

**Figure:** Distributions of variables in training data ( $n = 54$ ) and validation data ( $n = 54$ )



## Internal Validation by $Press_p$ and $C_p$

$Press_p > SSE$  for sure:

$$Press_p = \sum_i [e_i^2 / (1 - h_{ii})^2] > \sum e_i^2 = SSE$$

- ▶  $Press_p$  is a measure of the predictive ability of the model:

no  
severe  
over-fitting

$Press_p$  not much larger than  $SSE_p$  means there is no severe over-fitting by the model.

- ▶  $C_p \approx p$  indicates little bias in the model, whereas  $C_p \gg p$  indicates substantial model bias.

## External Validation by Mean Squared Prediction Error

$$MSPE_v := \frac{\sum_{j=1}^m (Y_j - \hat{Y}_j)^2}{m},$$

where  $m$  is the sample size of the validation data,  $Y_j$  is the  $j$ th observation in the validation data, and  $\hat{Y}_j$  is the predicted value of the  $j$ th case in the validation data based on the model fitted on the training data.

- ▶  $MSPE_v$  is a measure of the predictive ability of the model.
- ▶  $MSPE_v$  is usually larger than  $SSE/n$ :  $MSPE_v$  not much larger than  $SSE/n$  indicates no severe over-fitting by the model.

# Surgical Unit: Internal Validation

Three “best” models according to various criteria:

- ▶ By  $BIC_p$  and  $Press_p$ : Model 1,  $\log Y \sim X_1, X_2, X_3, X_8$ .
  - ▶  $p = 5$ ,  $SSE_p = 2.178$ ,  $C_p = 5.734$ ,  $Press_p = 2.736$ .
- ▶ By  $C_p$ : Model 2,  $\log Y \sim X_1, X_2, X_3, X_6, X_8$ .
  - ▶  $p = 6$ ,  $SSE_p = 2.081$ ,  $C_p = 5.528$ ,  $Press_p = 2.782$ .
- ▶ By  $R_{a,p}^2$  and  $AIC_p$ : Model 3,  $\log Y \sim X_1, X_2, X_3, X_5, X_6, X_8$ .
  - ▶  $p = 7$ ,  $SSE_p = 2.004$ ,  $C_p = 5.772$ ,  $Press_p = 2.771$ .
- ▶ For all three models,  $Press_p$  and  $SSE_p$  are reasonably close and  $C_p \approx p$ , supporting their validity.

# Surgical Unit: Model 1 External Validation

Training		Validation		
<u>Estimate</u>	<u>Std. Error</u>	<u>Estimate</u>	<u>Std. Error</u>	
(Intercept)	3.853	0.193	3.635	0.289
X1	0.073	0.019	0.096	0.032
X2	0.014	0.002	0.016	0.002
X3	0.015	0.001	0.016	0.002
X8	0.353	0.077	0.186	0.096

sse	mse	R2_a	press	press/n	mspe	
Training	2.178	0.044	0.816	2.736	0.051	--
Validation	3.794	0.077	0.682	--	--	0.077



# Surgical Unit: Model 2 External Validation

Training		Validation		
<u>Estimate</u>	<u>Std. Error</u>	<u>Estimate</u>	<u>Std. Error</u>	
(Intercept)	3.867	0.191	3.614	0.291
X1	0.071	0.019	0.100	0.032
X2	0.014	0.002	0.016	0.002
X3	0.015	0.001	0.015	0.002
X6	0.087	0.058	0.073	0.079
X8	0.363	0.077	0.189	0.097

sse	mse	R2_a	press	press/n	mspe	
Training	2.081	0.043	0.821	2.782	0.052	--
Validation	3.728	0.078	0.682	--	--	0.076

# Surgical Unit: Model 3 External Validation

Training		Validation		
<u>Estimate</u>	<u>Std. Error</u>	<u>Estimate</u>	<u>Std. Error</u>	
(Intercept)	4.054	0.235	3.470	0.347
X1	0.072	0.019	0.099	0.032
X2	0.014	0.002	0.016	0.002
X3	0.015	0.001	0.016	0.002
X5	-0.003	0.003	0.003	0.003
X6	0.087	0.058	0.073	0.079
X8	0.351	0.076	0.193	0.097

sse	mse	R2_a	press	press/n	mspe	
Training	2.004	0.043	0.823	2.771	0.051	--
Validation	3.681	0.078	0.679	--	--	<u>0.079</u>

最大的mspe，估计误差最大

## Surgical Unit: Choice of Final Model

- ▶  $MSPE_v$  of the three models have similar values, indicating that they have similar predictive ability.
- ▶ Model 3 has one estimated regression coefficient changing sign due to relatively large SE of this coefficient.
- ▶ Models 1 and 2 perform similarly in validation.
- ▶ Based on the **principle of parsimony** (“Occam’s Razor”), choose Model 1 as the final model and re-fit Model 1 on all data.

# Surgical Unit: Model 1 Fitted on All Data

```
lm(formula = log(Y) ~ X1 + X2 + X3 + X8, data = rbind(data.o,data.v))
```

```
Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept) 3.756276 0.162825 23.069 < 2e-16 ***
```

```
X1          0.083744 0.016781 4.990 2.46e-06 ***
```

```
X2          0.014988 0.001409 10.641 < 2e-16 ***
```

```
X3          0.015690 0.001134 13.839 < 2e-16 ***
```

```
X8          0.265096 0.060045 4.415 2.50e-05 ***
```

```
Residual standard error: 0.2446 on 103 degrees of freedom
```

```
Multiple R-squared: 0.7642, Adjusted R-squared: 0.755
```

```
F-statistic: 83.45 on 4 and 103 DF, p-value: < 2.2e-16
```

## Analysis of Variance Table

```
Df Sum Sq Mean Sq F value Pr(>F)
```

```
X1          1 1.0809 1.0809 18.064 4.703e-05 ***
```

```
X2          1 6.5415 6.5415 109.322 < 2.2e-16 ***
```

```
X3          1 11.1859 11.1859 186.940 < 2.2e-16 ***
```

```
X8          1 1.1663 1.1663 19.492 2.498e-05 ***
```

```
Residuals 103 6.1632 0.0598
```