Model checking and model selection

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Model checking and model selection

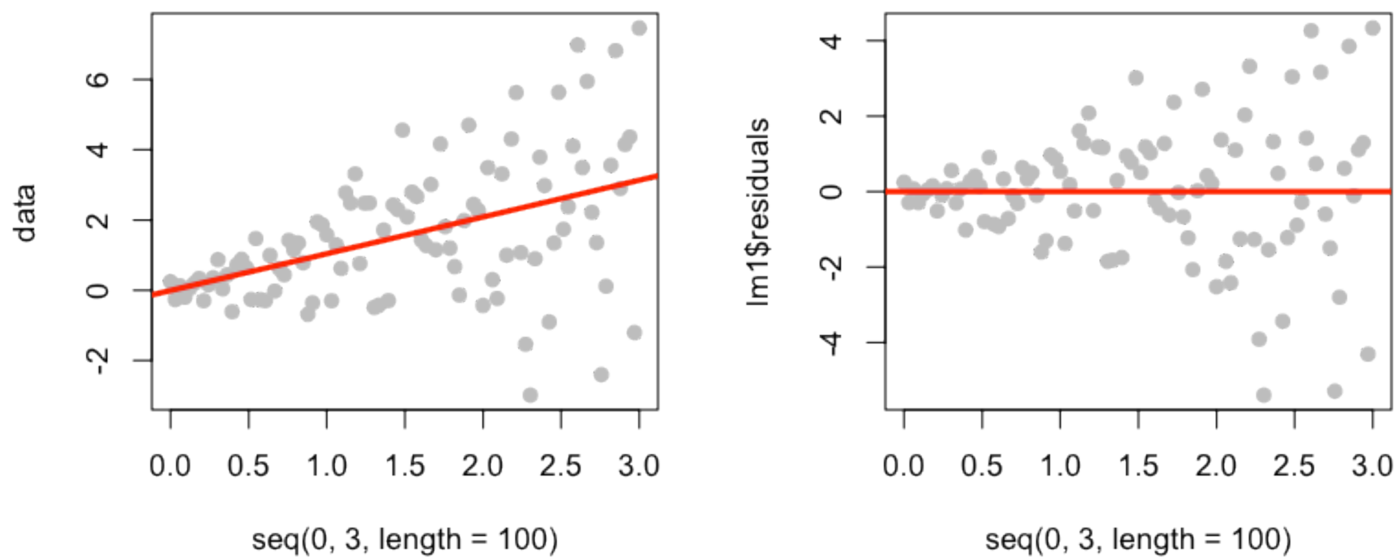
- Sometimes model checking/selection not allowed
- Often it can lead to problems
    - Overfitting
    - Overtesting
    - Biased inference
- *But* you don't want to miss something obvious

Linear regression - basic assumptions

- Variance is constant
- You are summarizing a linear trend
- You have all the right terms in the model
- There are no big outliers

Model checking - constant variance

```
set.seed(3433); par(mfrow=c(1,2))
data <- rnorm(100,mean=seq(0,3,length=100),sd=seq(0.1,3,length=100))
lm1 <- lm(data ~ seq(0,3,length=100))
plot(seq(0,3,length=100),data,pch=19,col="grey"); abline(lm1,col="red",lwd=3)
plot(seq(0,3,length=100),lm1$residuals,,pch=19,col="grey"); abline(c(0,0),col="red",lwd=3)
```



What to do

- See if another variable explains the increased variance
- Use the *vcovHC* {sandwich} variance estimators (if n is big)

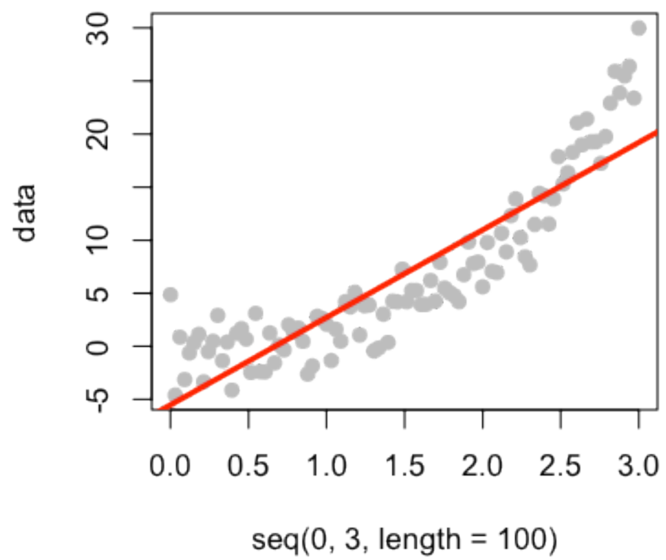
Using the sandwich estimate

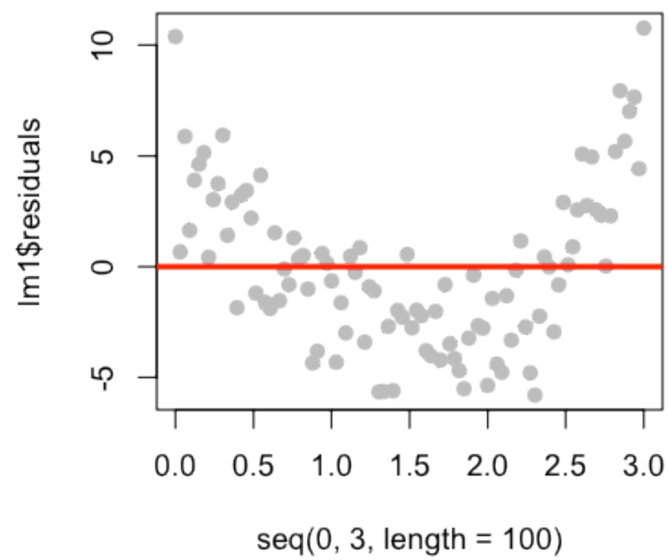
```
set.seed(3433); par(mfrow=c(1,2)); data <- rnorm(100,mean=seq(0,3,length=100),sd=seq(0.1,3,length=1
lm1 <- lm(data ~ seq(0,3,length=100))
vcovHC(lm1)
summary(lm1)$cov.unscaled
```

```
                        (Intercept) seq(0, 3, length = 100)
(Intercept)                 0.03941                -0.01960
seq(0, 3, length = 100)    -0.01960                 0.01307
```

Model checking - linear trend

```
set.seed(3433); par(mfrow=c(1,2))
data <- rnorm(100,mean=seq(0,3,length=100)^3,sd=2)
lm1 <- lm(data ~ seq(0,3,length=100))
plot(seq(0,3,length=100),data,pch=19,col="grey"); abline(lm1,col="red",lwd=3)
plot(seq(0,3,length=100),lm1$residuals,,pch=19,col="grey"); abline(c(0,0),col="red",lwd=3)
```





What to do

- Use Poisson regression (if it looks exponential/multiplicative)
- Use a data transformation (e.g. take the log)
- Smooth the data/fit a nonlinear trend (next week's lectures)
- Use linear regression anyway
  - Interpret as the linear trend between the variables
  - Use the *vcovHC* {sandwich} variance estimators (if n is big)

Model checking - missing covariate

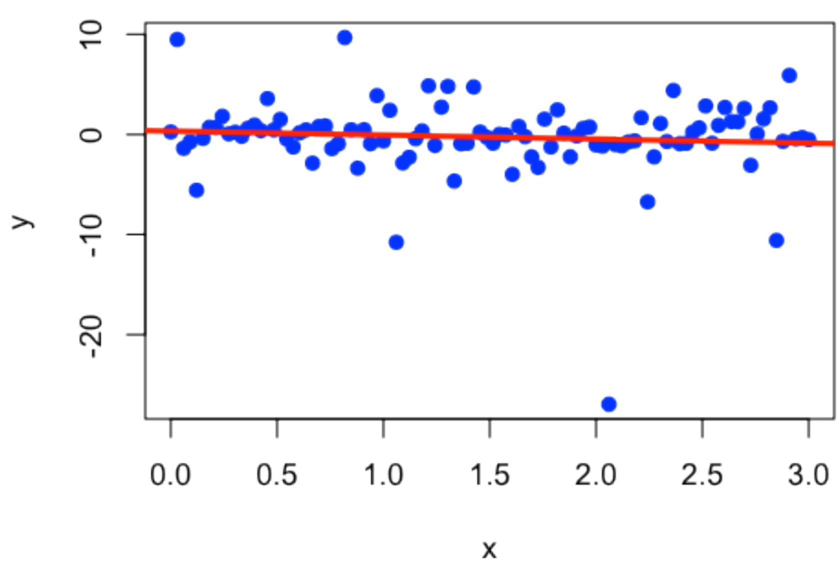
```
set.seed(3433); par(mfrow=c(1,3)); z <- rep(c(-0.5,0.5),50)
data <- rnorm(100,mean=(seq(0,3,length=100) + z),sd=seq(0.1,3,length=100))
lm1 <- lm(data ~ seq(0,3,length=100))
plot(seq(0,3,length=100),data,pch=19,col=((z>0)+3)); abline(lm1,col="red",lwd=3)
plot(seq(0,3,length=100),lm1$residuals,pch=19,col=((z>0)+3)); abline(c(0,0),col="red",lwd=3)
boxplot(lm1$residuals ~ z,col = ((z>0)+3) )
```

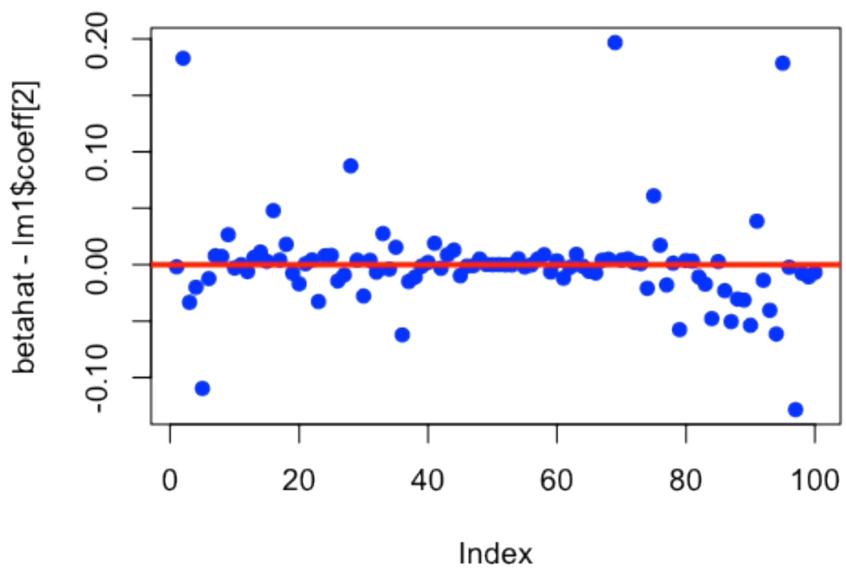
What to do

- Use exploratory analysis to identify other variables to include
- Use the *vcovHC* {sandwich} variance estimators (if n is big)
- Report unexplained patterns in the data

Model checking - outliers

```
set.seed(343); par(mfrow=c(1,2)); betahat <- rep(NA,100)
x <- seq(0,3,length=100); y <- rcauchy(100); lm1 <- lm(y ~ x)
plot(x,y,pch=19,col="blue"); abline(lm1,col="red",lwd=3)
for(i in 1:length(data)){betahat[i] <- lm(y[-i] ~ x[-i])$coeff[2]}
plot(betahat - lm1$coeff[2],col="blue",pch=19); abline(c(0,0),col="red",lwd=3)
```





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What to do

- If outliers are experimental mistakes -remove and document them
- If they are real - consider reporting how sensitive your estimate is to the outliers
- Consider using a robust linear model fit like *rlm* {MASS}

Robust linear modeling

```
set.seed(343); x <- seq(0,3,length=100); y <- rcauchy(100);
lm1 <- lm(y ~ x); rlm1 <- rlm(y ~ x)
lm1$coeff
```

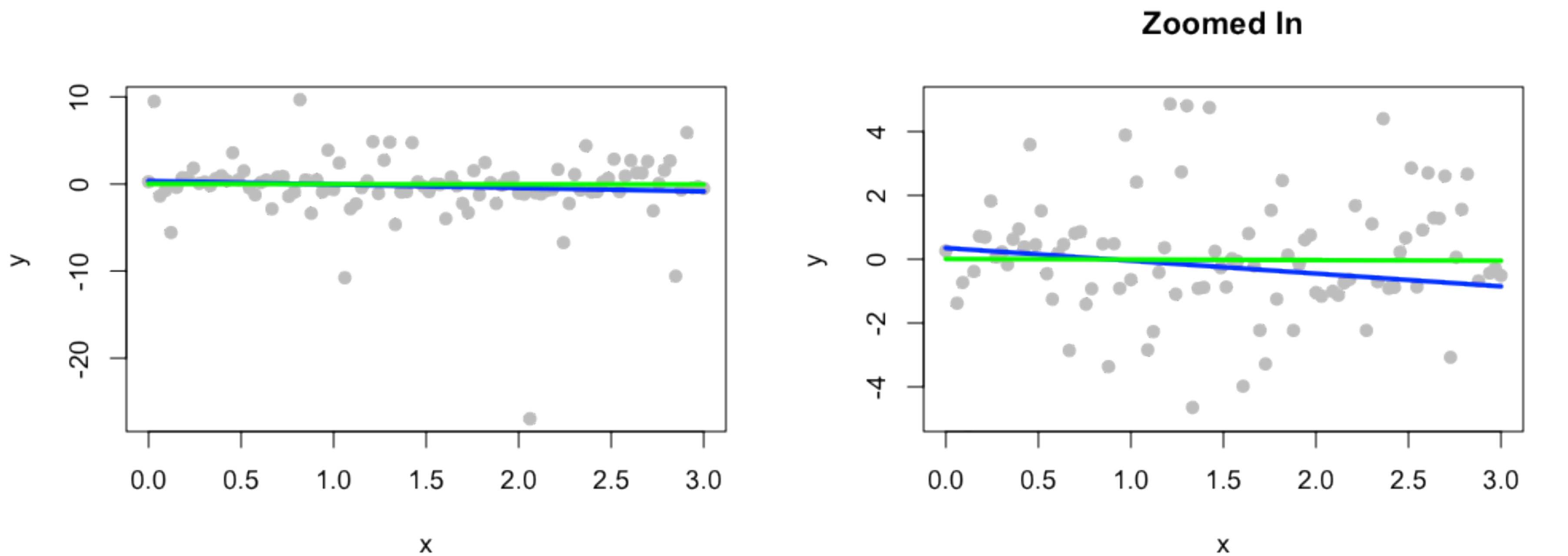
```
(Intercept)           x
     0.3523     -0.4011
```

```
rlm1$coeff
```

```
(Intercept)           x
   0.008527   -0.017892
```

Robust linear modeling

```
par(mfrow=c(1,2))
plot(x,y,pch=19,col="grey")
lines(x,lm1$fitted,col="blue",lwd=3); lines(x,rlm1$fitted,col="green",lwd=3)
plot(x,y,pch=19,col="grey",ylim=c(-5,5),main="Zoomed In")
lines(x,lm1$fitted,col="blue",lwd=3); lines(x,rlm1$fitted,col="green",lwd=3)
```



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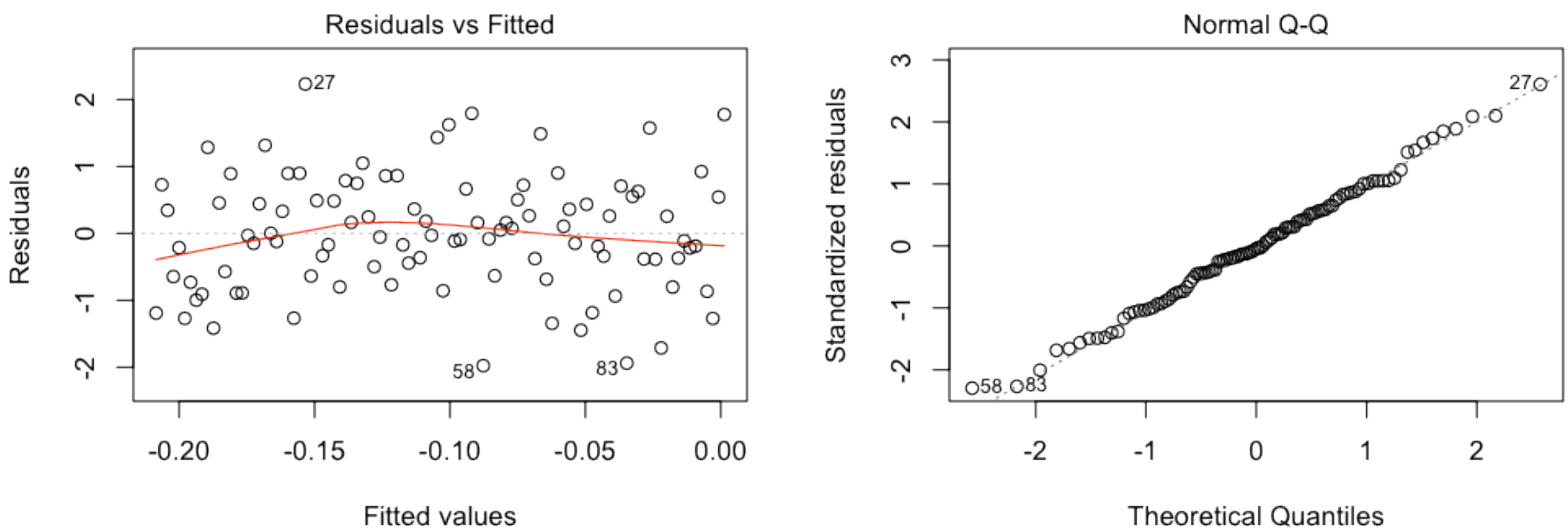
Model checking - default plots

```
set.seed(343); par(mfrow=c(1,2))
x <- seq(0,3,length=100); y <- rnorm(100); lm1 <- lm(y ~ x)
plot(lm1)
```



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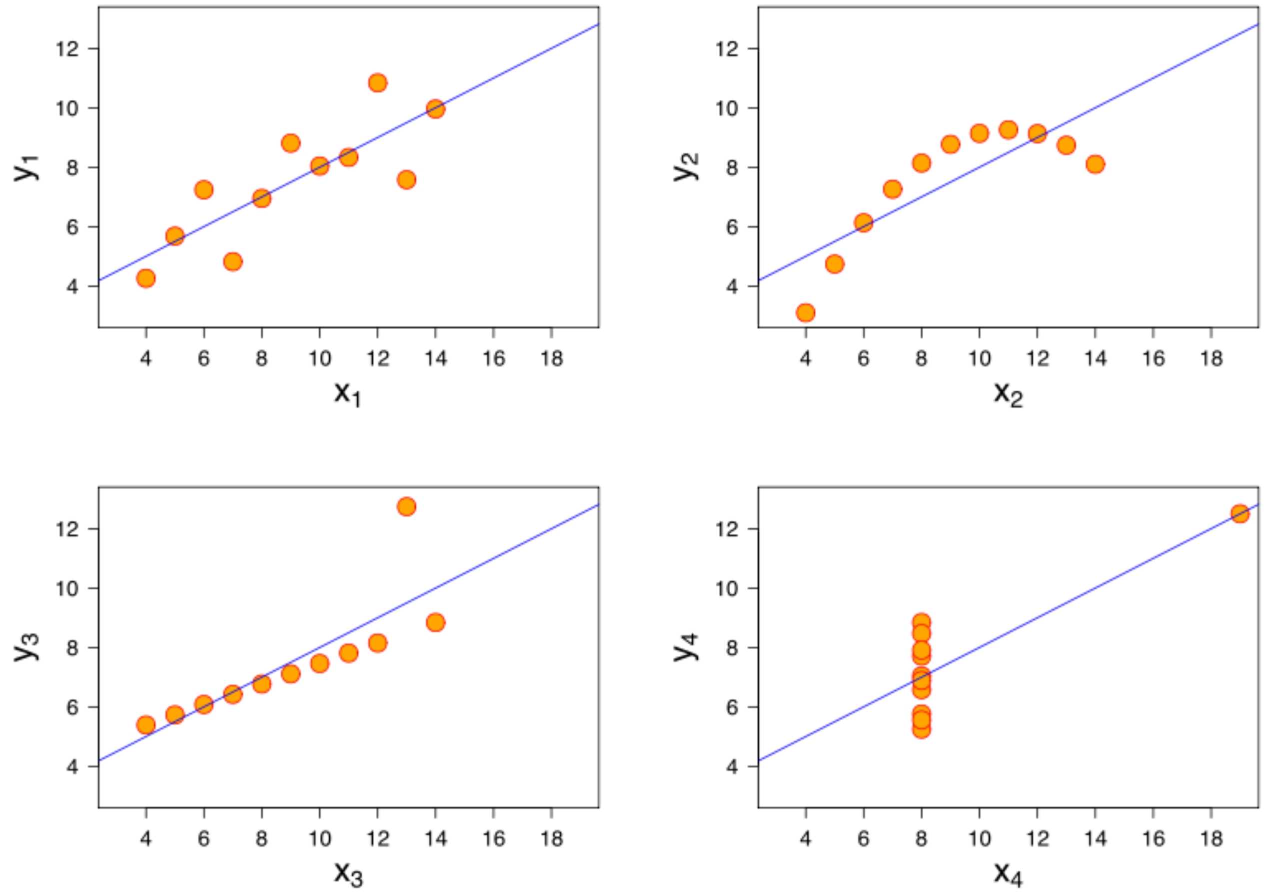
Model checking - deviance

- Commonly reported for GLM's
- Usually compares the model where every point gets its own parameter to the model you are using
- On it's own it doesn't tell you what is wrong
- In large samples the deviance may be big even for "conservative" models
- You can not compare deviances for models with different sample sizes

R^2 may be a bad summary



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Model selection

- Many times you have multiple variables to evaluate
- Options for choosing variables
  - Domain-specific knowledge
  - Exploratory analysis
  - Statistical selection
- There are many statistical selection options
  - Step-wise
  - AIC
  - BIC
  - Modern approaches: Lasso, Ridge-Regression, etc.
- Statistical selection may bias your inference
  - If possible, do selection on a held out sample

Error measures

- R^2 alone isn't enough - more variables = bigger R^2
- Adjusted R^2 is R^2 taking into account the number of estimated parameters
- AIC also penalizes models with more parameters
- BIC does the same, but with a bigger penalty

Movie Data

```
download.file("http://www.rossmanchance.com/iscam2/data/movies03RT.txt",destfile="./data/movies.txt
movies <- read.table("./data/movies.txt",sep="\t",header=T,quote="")
head(movies)
```

```
                 X score rating            genre box.office running.time
1 2 Fast 2 Furious  48.9  PG-13 action/adventure     127.15          107
2    28 Days Later  78.2      R           horror      45.06          113
3      A Guy Thing  39.5  PG-13       rom comedy      15.54          101
4      A Man Apart  42.9      R action/adventure      26.25          110
5    A Mighty Wind  79.9  PG-13           comedy      17.78           91
6 Agent Cody Banks  57.9     PG action/adventure      47.81          102
```

http://www.rossmanchance.com/

Model selection - step

```
movies <- movies[,-1]
lm1 <- lm(score ~ .,data=movies)
aicFormula <- step(lm1)
```

```
Start:  AIC=727.5
score ~ rating + genre + box.office + running.time

               Df Sum of Sq   RSS AIC
- genre        12      2575 22132 721
- rating        3        40 19596 722
- running.time  1       237 19793 727
<none>                      19556 728
- box.office    1      3007 22563 746

Step:  AIC=720.8
score ~ rating + box.office + running.time

               Df Sum of Sq   RSS AIC
- rating        3       491 22623 718
<none>                      22132 721
```

Model selection - step

```
aicFormula
```

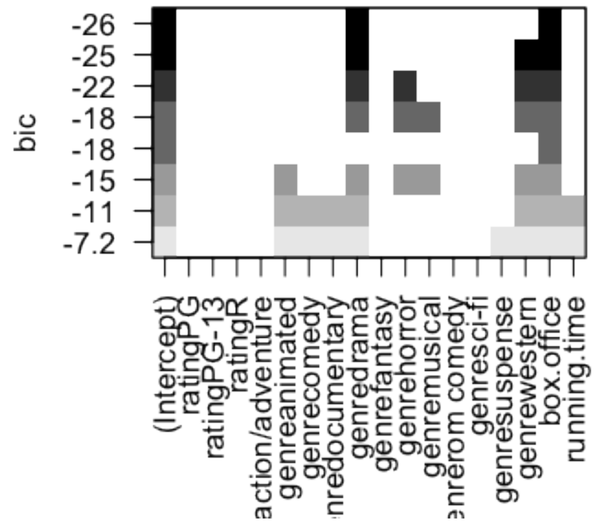
```

Call:
lm(formula = score ~ box.office + running.time, data = movies)

Coefficients:
 (Intercept)    box.office  running.time
     37.2364        0.0824        0.1275
```

Model selection - regsubsets

```
library(leaps);
regSub <- regsubsets(score ~ .,data=movies)
plot(regSub)
```



http://cran.r-project.org/web/packages/leaps/leaps.pdf

Model selection - bic.glm

```
library(BMA)
bicglm1 <- bic.glm(score ~.,data=movies,glm.family="gaussian")
print(bicglm1)
```

```


Call:
bic.glm.formula(f = score ~ ., data = movies, glm.family = "gaussian")



 Posterior probabilities(%):
      rating        genre   box.office running.time
         0.0        100.0        100.0         18.2

 Coefficient posterior expected values:
         (Intercept)                ratingPG             ratingPG-13                 ratingR
              45.263                   0.000                   0.000                   0.000
genreaction/adventure            genreanimated             genrecomedy        genredocumentary
              -0.120                   7.628                   2.077                   8.642
          genredrama             genrefantasy             genrehorror            genremusical
              13.041                   1.504                  -3.458                 -12.255
```

Notes and further resources

- Exploratory/visual analysis is key
- Automatic selection produces an answer - but may bias inference
- You may think about separating the sample into two groups
- The goal is not to get the "causal" model
- Lars package
- Elements of machine learning