

02409 Multivariate Statistics

Lecture J, November 10 2025

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(1-3) 60%

Clustering 4 groups

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Groups

28

16

1

Factor 1 [41%]

Factor 3 [19%]

V. De Geneve

Agenda

- Analysis in practice in the ANOVA and ANCOVA situation
- Sequential hypothesis testing in practise
- Revisiting influence diagnostics
- Introduction to the Multivariate General Linear Model
 - Hotellings T^2

Example: Low Birth Weight

Data for 189 child births. `bwt` is the birth weight in grams. Contains additional information, eg. racial group `race`:

```
> lbw <- read.delim("Data/lbw.txt")
```

```
> by(lbw$bwt, lbw$race, summary)
```

```
lbw$race: black
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1135	2370	2849	2720	3057	3860

```
-----  
lbw$race: other
```

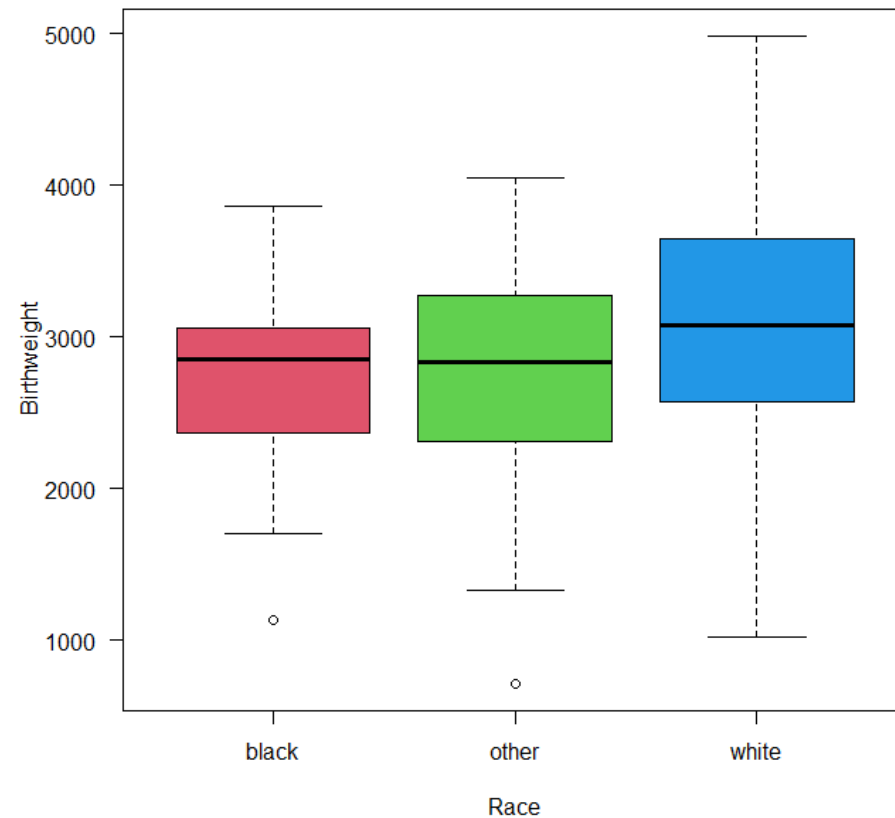
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
709	2313	2835	2804	3274	4054

```
-----  
lbw$race: white
```

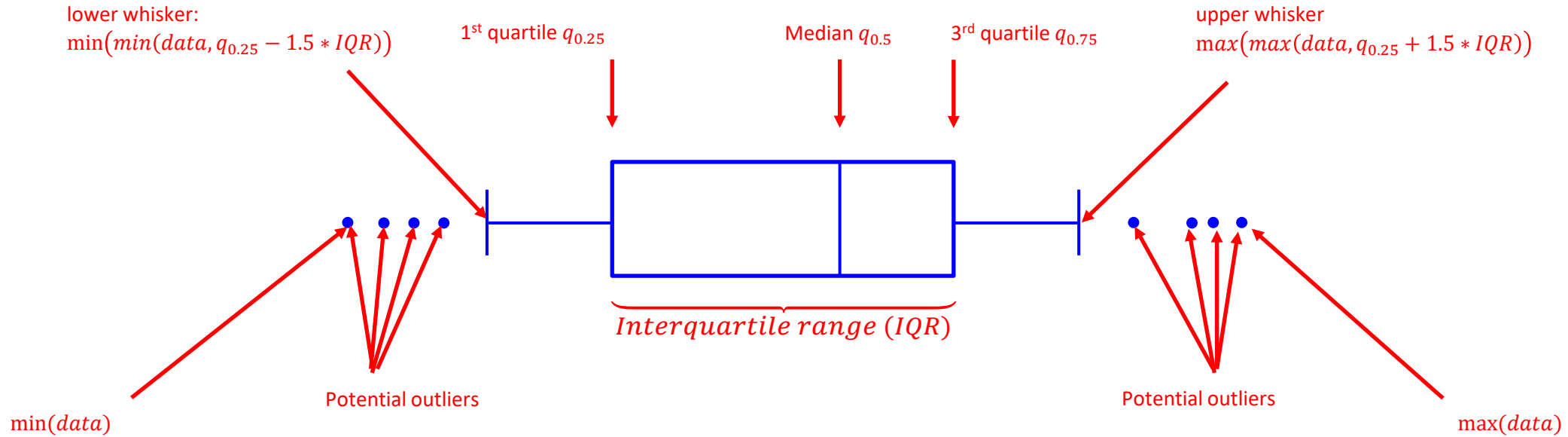
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1021	2585	3076	3103	3651	4990

Example: Low Birth Weight

```
boxplot(bwt ~ race, data = lbw, xlab = 'Race', ylab = 'Birthweight',  
las = 1, col = 2:4)
```



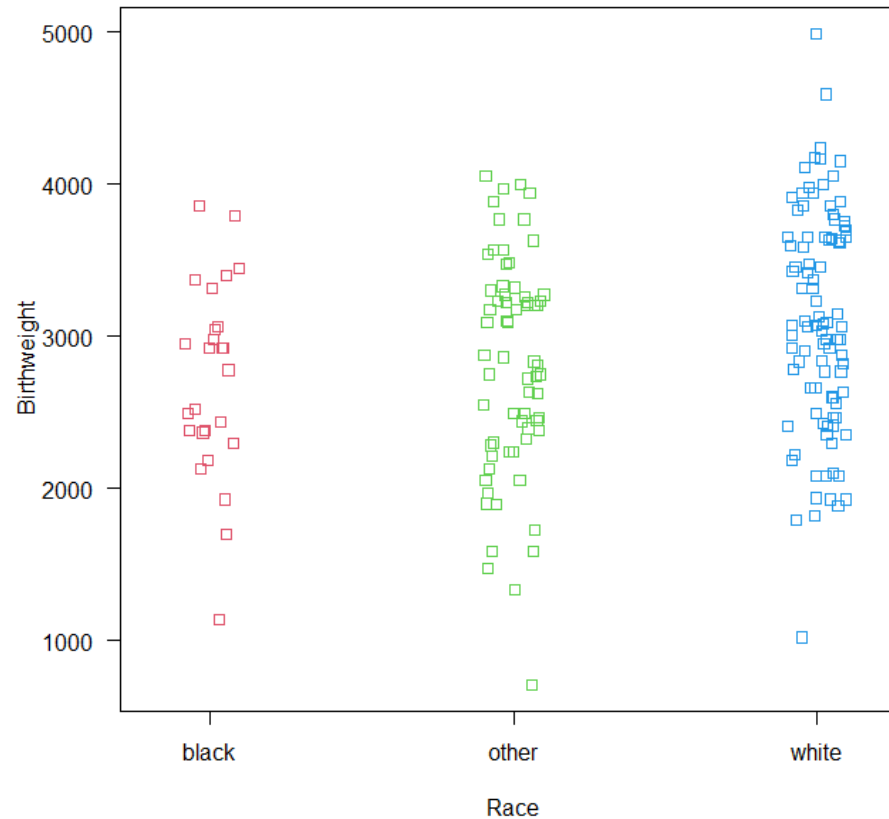
The Box Plot



Displays locality, spread and skewness of data

Example: Low Birth Weight

```
stripchart(bwt ~ race, data = lbw, vertical = TRUE, xlab = "Race",  
ylab = "Birthweight", method = "jitter", las = 1, col = 2:4)
```



Example: Low Birth Weight

- **Statistical model:**

Let Y_{gi} be the birthweight of observation i within racial group g :

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

- One-way **AN**alysis **Of VA**riance (ANOVA).
- Only one hypothesis to test in one-way ANOVA:

$$H_0: \mu_1 = \dots = \mu_k$$

Test sequence:

$$\begin{array}{c} H \\ \downarrow \\ H_0 \end{array}$$

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

- Factor dummy-coding:

$$X_{black,i} = \begin{cases} 1 & \text{if } race_i = "black" \\ 0 & \text{if } race_i \neq "black" \end{cases}; \quad X_{other,i} = \begin{cases} 1 & \text{if } race_i = "other" \\ 0 & \text{if } race_i \neq "other" \end{cases}; \quad X_{white,i} = \begin{cases} 1 & \text{if } race_i = "white" \\ 0 & \text{if } race_i \neq "white" \end{cases}$$

- $X = (X_{black}; X_{other}; X_{white}), \theta = \begin{pmatrix} \mu_{black} \\ \mu_{other} \\ \mu_{white} \end{pmatrix}:$

$$Y_i = \mu_{black}X_{black,i} + \mu_{other}X_{other,i} + \mu_{white}X_{white,i} + \varepsilon_i, \quad i = 1, \dots, 189$$

$$Y = X\theta + \varepsilon$$

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

- Note that $X_{black} + X_{other} + X_{white} = \mathbf{1}$.
- Alternative dummy-coding: $Z_{other} = X_{other} - X_{black}$; $Z_{white} = X_{white} - X_{black}$;
- $\tilde{X} = (\mathbf{1}; Z_{other}; Z_{white})$ spans the same subspace $M \subset \mathbb{R}^{189}$ as X .

For testing, use \tilde{X} rather than X .

- $Y_i = \alpha \mathbf{1}_i + \delta_{other} Z_{other,i} + \delta_{white} Z_{white,i} + \varepsilon_i, \quad i = 1, \dots, 189$

$$Y = \tilde{X}\delta + \varepsilon$$

H_0 translates into

$$H'_0: \delta_{other} = \delta_{white} = 0$$

$$M_0 = \text{V}(\mathbf{1}) \subset M = \text{V}(X) = \text{V}(\tilde{X})$$

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

```
> model1<-lm(bwt ~ race, data = lbw)
```

```
> anova(model1)
```

Analysis of Variance Table

Response: bwt

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
race	2	5048361	2524181	4.949	0.008052 **
Residuals	186	94866938	510037		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

- Data supports association of birth weight with racial group (p=0.008).

Comparisons of nested models with the anova function

```
> model2<-lm(bwt ~ 1, data = lbw)
```

```
> anova(model2,model1)
```

```
Analysis of Variance Table
```

```
Model 1: bwt ~ 1
```

```
Model 2: bwt ~ race
```

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	188	99915299				
2	186	94866938	2	5048361	4.949	0.008052 **

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Compare to the previous slide. Note that `anova` labels the simplest model (1st argument) 'model 1'.

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

```
> summary(model1)
```

```
Call:
```

```
lm(formula = bwt ~ race, data = lbw)
```

```
Residuals:
```

Min	1Q	Median	3Q	Max
-2095.01	-503.01	-13.01	526.99	1886.99

```
Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2719.69	140.06	19.418	<2e-16 ***
raceother	84.32	165.01	0.511	0.6100
racewhite	383.32	157.89	2.428	0.0161 *

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 714.2 on 186 degrees of freedom
```

```
Multiple R-squared:  0.05053,    Adjusted R-squared:  0.04032
```

```
F-statistic: 4.949 on 2 and 186 DF,  p-value: 0.008052
```

Individual p-values for
 δ_{other} , δ_{white}



Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

Confidence intervals:

```
> tab <- cbind(coef(summary(model1))[ , 1:2], "Lower" = confint(model1)[ , 1],  
+             "Upper" = confint(model1)[ , 2])  
> data.frame(round(tab, 2),  
+            "p-value" = format.pval(coef(summary(model1))[ , 4],  
+            digits = 3, eps = 1e-3))
```

	Estimate	Std..Error	Lower	Upper	p.value
(Intercept)	2719.69	140.06	2443.38	2996.00	<0.001
raceother	84.32	165.01	-241.22	409.86	0.6100
racewhite	383.32	157.89	71.83	694.81	0.0161

- Good for testing, less good for illustrating group means.

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

Confidence intervals for group means:

For confidence intervals, use X rather than \tilde{X} .

```
> modella<-lm(bwt ~ race-1, data = lbw)
>
> tab <- cbind(coef(summary(modella))[ , 1:2], "Lower" = confint(modella)[ , 1],
+             "Upper" = confint(modella)[ , 2])
> data.frame(round(tab, 2))
```

	Estimate	Std..Error	Lower	Upper
raceblack	2719.69	140.06	2443.38	2996.00
raceother	2804.01	87.25	2631.89	2976.14
racewhite	3103.01	72.89	2959.21	3246.81

- No p-values; they are not relevant here, as we are testing that group means are 0.
- Relations:

$$\begin{pmatrix} \alpha \\ \delta_o \\ \delta_w \end{pmatrix} = \frac{1}{3} \begin{pmatrix} 1 & 1 & 1 \\ -3 & 3 & 0 \\ -3 & 0 & 3 \end{pmatrix} \begin{pmatrix} \mu_b \\ \mu_o \\ \mu_w \end{pmatrix}; \quad \begin{pmatrix} \mu_b \\ \mu_o \\ \mu_w \end{pmatrix} = \frac{1}{3} \begin{pmatrix} 3 & -1 & 1 \\ 3 & 2 & -1 \\ 3 & -1 & 2 \end{pmatrix} \begin{pmatrix} \alpha \\ \delta_o \\ \delta_w \end{pmatrix}$$

- One could have retained the coding and used the formula $V(A\hat{\delta}) = AV(\hat{\delta})A^T$ instead with A as above.

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

- Model assumptions:
 - Normality of residuals;
 - Variance homogeneity; same σ^2 in each group;
 - Independence;
 - Same mean within each group.

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

Independence:

- Context. Here:
 - No siblings among children (same mothers);
 - No siblings among mothers (related mothers);

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

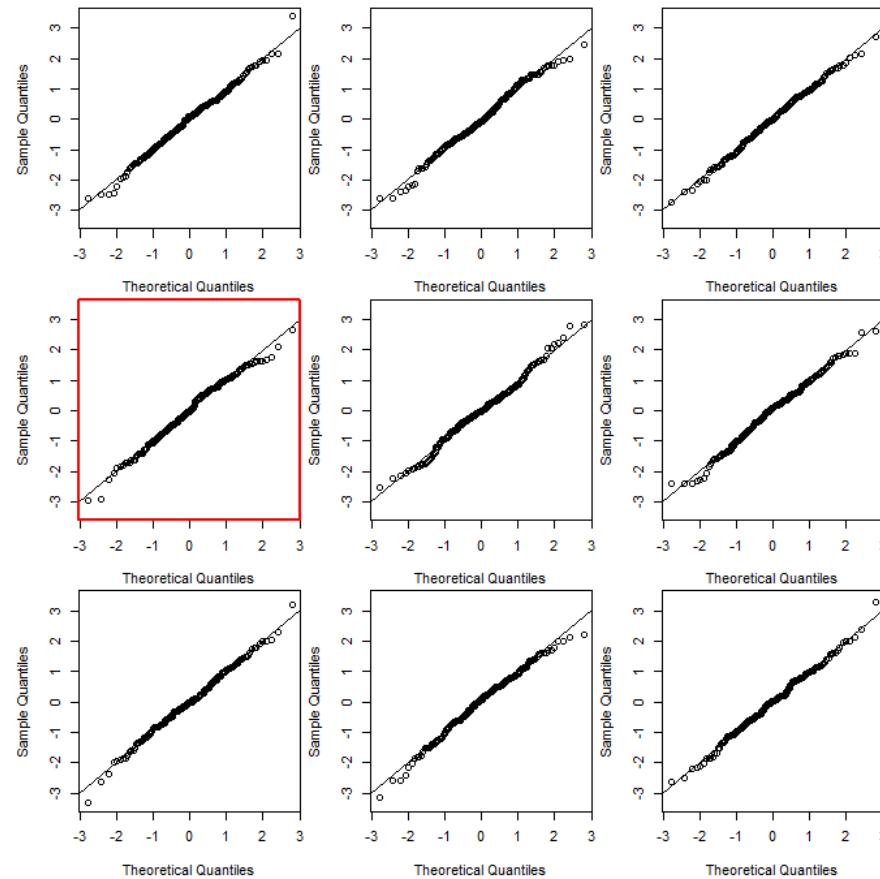
Normality: QQ-plot.

How does one recognize a good QQplot with the EBT?

```
qqwrap <- function(x, y, ...) {qqnorm(y, main="", ...)
                                abline(a=0, b=1)}
wallyplot(model1, FUN=qqwrap)
```

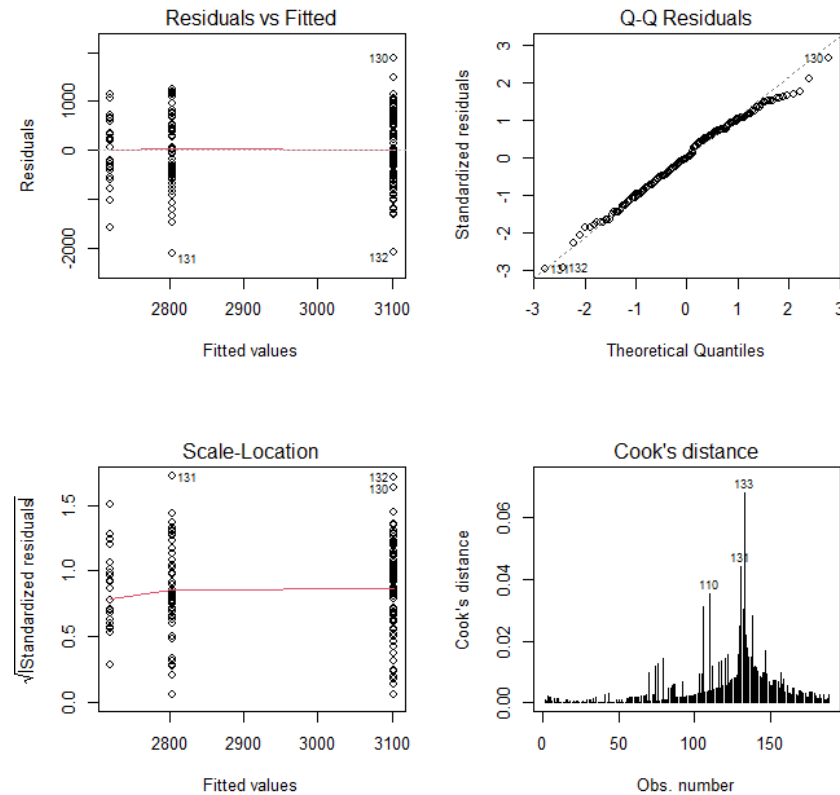
Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$



Example: Low Birth Weight

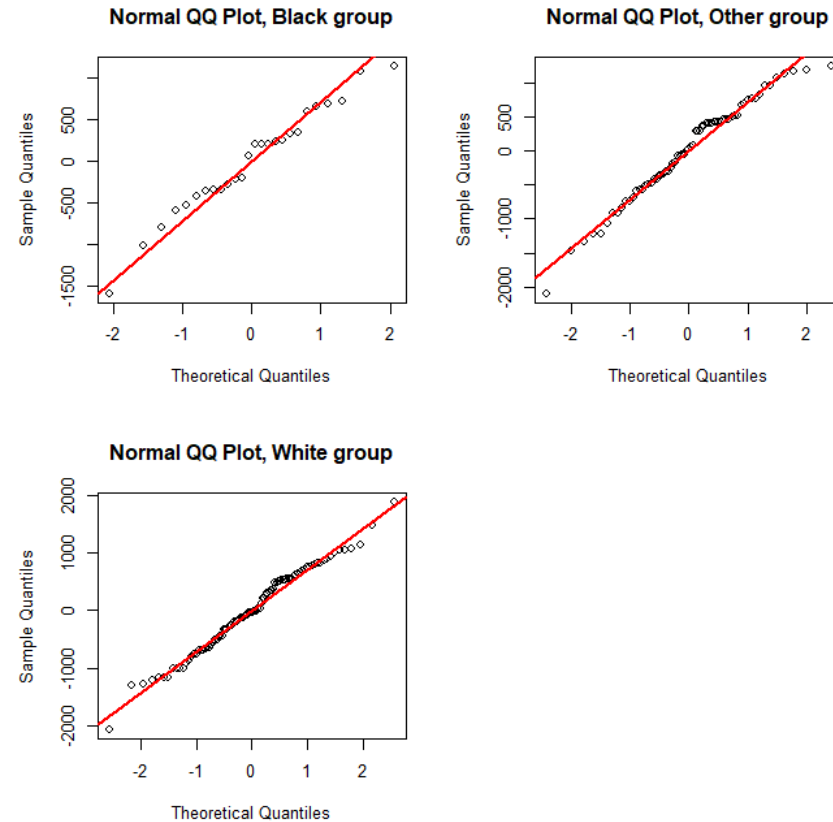
$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$



Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

- Same mean within each group:



Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

Variance homogeneity:

- Testable with a numeric test!

$$Q = \frac{L(\hat{\mu}, \hat{\sigma}^2)}{L(\hat{\mu}, \hat{\sigma}_1^2, \dots, \hat{\sigma}_k^2)} = \frac{(2\pi)^{-N/2} \hat{\sigma}^{2-N/2} \exp\left(-\frac{1}{2\hat{\sigma}^2} (N-k)\hat{\sigma}^2\right)}{\prod_{i=1}^k (2\pi)^{-n_i/2} \hat{\sigma}_i^{2-n_i/2} \exp\left(-\frac{1}{2\hat{\sigma}_i^2} (n_i-1)\hat{\sigma}_i^2\right)} = \frac{\prod_{i=1}^k \hat{\sigma}_i^{2n_i/2}}{\hat{\sigma}^{2N/2}},$$

$$-2\log Q = N\log(\hat{\sigma}^2) - \sum_{i=1}^k n_i \log(\hat{\sigma}_i^2).$$

- Bartlett's test:

$$\chi^2 = \frac{(N-k)\log(\hat{\sigma}^2) - \sum_{i=1}^k (n_i-1)\log(\hat{\sigma}_i^2)}{1 + \frac{1}{3(k-1)}\left(\sum_{i=1}^k \frac{1}{n_i-1} - \frac{1}{N-k}\right)} \underset{as}{\sim} \chi^2(k-1)$$

- Large values of n_1, \dots, n_k : $\chi^2 \approx -2\log Q$.

In a multivariate setting: Theorem 4.32, apply it with $p = 1$.

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

- Bartlett's test in **R**:

```
> bartlett.test(bwt~race, data=lbw)
```

```
Bartlett test of homogeneity of variances
```

```
data: bwt by race
```

```
Bartlett's K-squared = 0.65601, df = 2, p-value = 0.7204
```

- Data supports equal variances (p=0.72)

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

- Model assumptions fulfilled
- Significantly different means in the groups
- But we only know that the three means are significantly different, not how they differ.

Post hoc analysis: Pairwise comparisons

A multiple comparisons element: In general $m = k(k - 1)/2$ comparisons. Probability that one of them is significant by chance under $H_0 \approx 1 - (1 - \alpha)^m$. For $k = 3$ we get 0.14.

One solution: lower the test level from α to α/m ; Then $1 - \left(1 - \frac{\alpha}{m}\right)^m \approx 1 - \left(1 - m \cdot \frac{\alpha}{m}\right) = \alpha$.

Similar: Multiply the p-values by m , and use the original test level:

Bonferroni correction

Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

Post hoc analysis: Pairwise comparisons

```
> pairwise.t.test(lbw$bwt, lbw$race, p.adj = "none")
```

Pairwise comparisons using t tests with pooled SD

```
data: lbw$bwt and lbw$race
```

```
      black  other  
other 0.6100 -  
white 0.0161 0.0093
```


Example: Low Birth Weight

$$Y_{gi} = \mu_g + \varepsilon_{gi}, \quad \varepsilon_{gi} \sim N(0, \sigma^2), \quad i = 1, \dots, n_g, \quad g = 1, \dots, k.$$

Post hoc analysis: Pairwise comparisons

```
> pairwise.t.test(lbw$bwt, lbw$race, p.adj = "bonferroni")
```

Pairwise comparisons using t tests with pooled SD

data: lbw\$bwt and lbw\$race

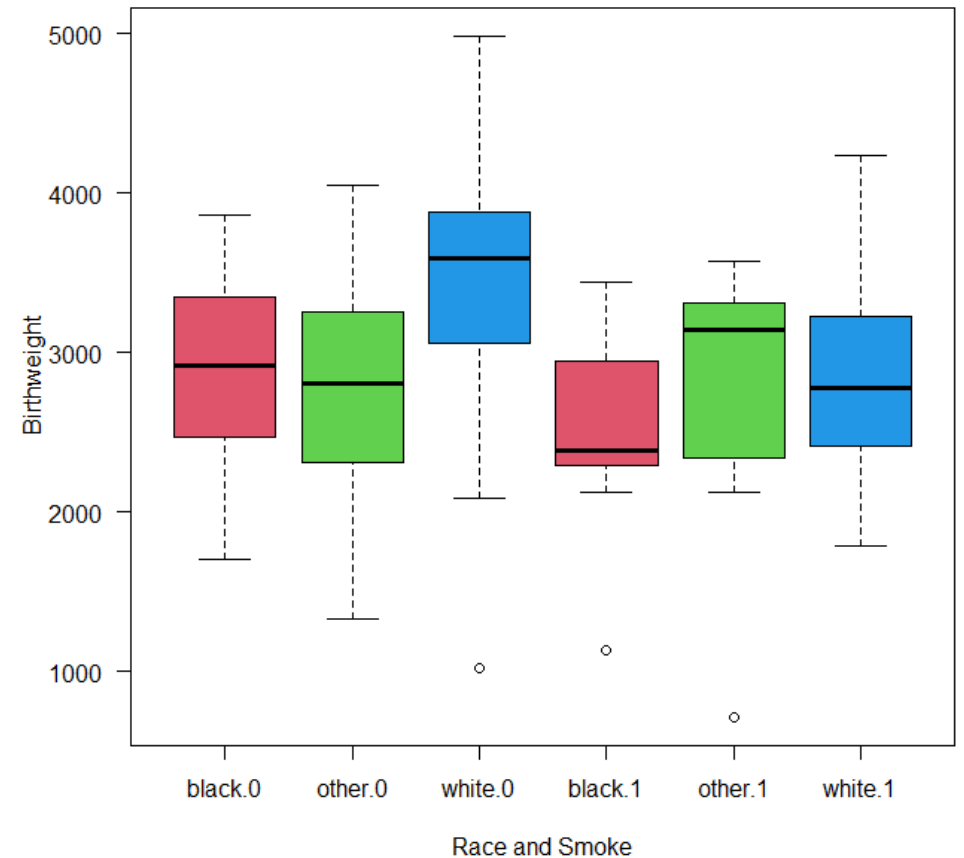
	black	other
other	1.000	-
white	0.048	0.028

P value adjustment method: bonferroni

Example: Low Birth Weight

Let us now, on top of `race` (3 levels), introduce the factor `smoking` (2 levels), indicating whether the mother as been smoking during prenanacy.

```
boxplot(bwt ~ race*smoke, data=lbw,  
        xlab = 'Race and Smoke',  
        ylab = 'Birthweight',  
        las = 1, col = 2:4)
```



Example: Low Birth Weight

Model:

$$Y_{rsi} = \alpha_{rs} + \varepsilon_{rsi}, i = 1, \dots, n_{rs}$$

Two-sided analysis of variance.

Dimension of corresponding subspace: 6 (6 = 3x2 groups).

Formulation through dummy coding appropriate for testing:

$$Y_{rsi} = \alpha + \beta_r + \gamma_s + \delta_{rs} + \varepsilon_{rsi}, i = 1, \dots, n_{rs}$$

```
> lbw$smoke <- as.factor(lbw$smoke)
> model1 <- lm(bwt ~ race + smoke + race:smoke, data = lbw)
```

Example: Low Birth Weight

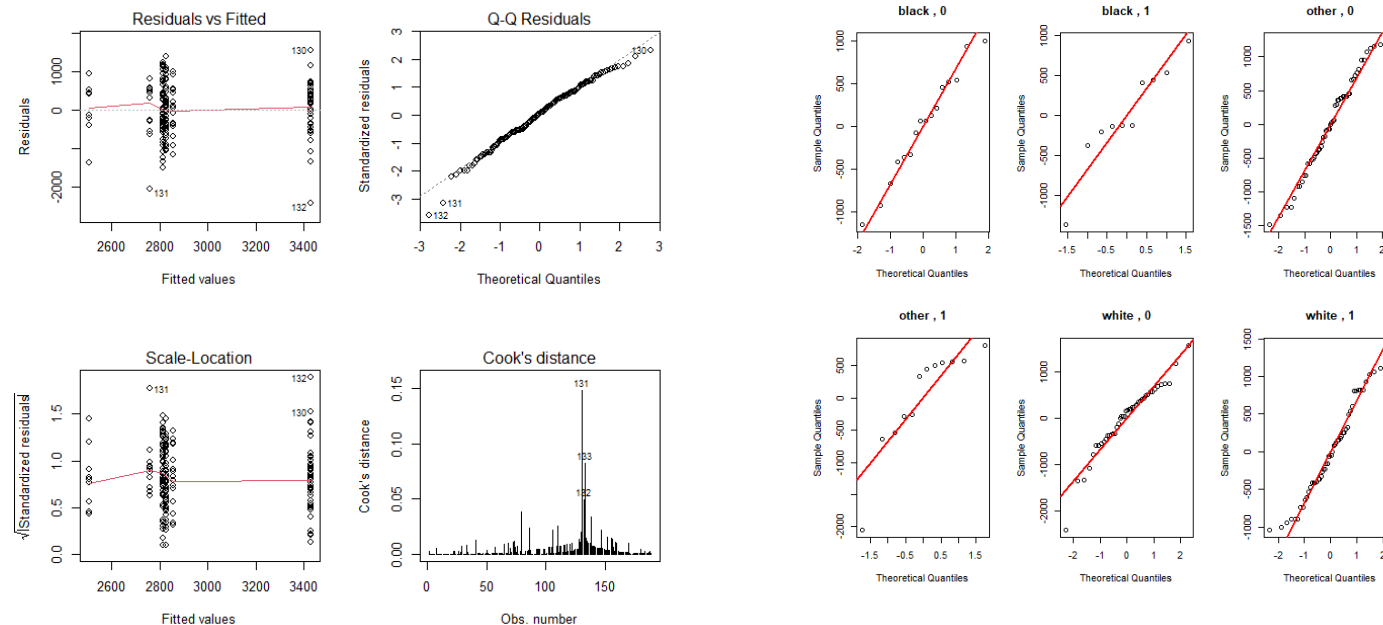
Model control:

```
> lbw2<-lbw; lbw2$group<-paste(lbw$race,"",lbw$smoke)
> bartlett.test(bwt ~ group, data=lbw2)
```

Bartlett test of homogeneity of variances

data: bwt by group

Bartlett's K-squared = 2.0061, df = 5, p-value = 0.8483



Formula objects in R

- Used as argument for analytic routines (eg. `lm`), plotting functions and more.
- Of the form $x \sim y$; corresponds to

$$x = \begin{cases} \alpha + \beta y + \varepsilon & \text{if } y \text{ is numeric} \\ \alpha_y + \varepsilon & \text{if } y \text{ is a factor} \end{cases}$$

- Dummy-coding of factors equates this.

Formula objects in R

- Operators and relations in formulas: \sim , $+$, $:$, $*$, $-$, $^$, I .
- " \sim " separates response from explanatory variables
- " $+$ " indicates additive effects; *bwt~race + smoke*
- " $:$ " indicates interaction effects; the *crossing* of factors:

$$x:y = \begin{cases} \text{a factor with a level for each combination of } x \text{ and } y & \text{if } x, y \text{ factors} \\ \text{a numeric factor for each level of } x \text{ regressing data with that level on } y & \text{if } x \text{ factor, } y \text{ numeric} \\ \text{the numeric variable } xy & \text{if } x, y \text{ numeric} \end{cases}$$

- " $*$ " indicates interaction and main effects; ie. $x * y = x + y + x:y$
- " $^$ " indicates adding main effects and lower order interaction terms:

$$(x + y + z)^2 = x + x + z + x:y + x:z + y:z, \quad (x + y + z)^3 = x + x + z + x:y + x:z + y:z + x:y:z$$

- " $-$ " indicates negative selection; $(x + y + z)^2 - y:z = x + x + z + x:y + x:z$, $y \sim x - 1$ removes constant term from the model.
- " I " overrides the formula calculus, and allows you to do calculations within the formula: $y \sim x + I(x^2)$.

Example: Low Birth Weight

- 3 equivalent model formulations:

```
modell1 <- lm(bwt ~ race + smoke + race:smoke, data = lbw)
modell1 <- lm(bwt ~ race*smoke, data = lbw)
modell1 <- lm(bwt ~ (race+smoke)^2, data = lbw)
```

```
> summary(modell1)
```

Call:

```
lm(formula = bwt ~ race + smoke + race:smoke, data = lbw)
```

Residuals:


Min	1Q	Median	3Q	Max
-2407.75	-417.38	31.25	462.50	1561.25

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2854.50	170.84	16.708	< 2e-16 ***
raceother	-40.26	194.11	-0.207	0.83591
racewhite	574.25	199.50	2.878	0.00447 **
smoke1	-350.50	275.47	-1.272	0.20486
raceother:smoke1	293.43	351.13	0.836	0.40443
racewhite:smoke1	-250.87	309.00	-0.812	0.41792

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

$\dim(M) = 6$: 6 parameters



Example: Low Birth Weight

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2854.50	170.84	16.708	< 2e-16 ***
raceother	-40.26	194.11	-0.207	0.83591
racewhite	574.25	199.50	2.878	0.00447 **
smoke1	-350.50	275.47	-1.272	0.20486
raceother:smoke1	293.43	351.13	0.836	0.40443
racewhite:smoke1	-250.87	309.00	-0.812	0.41792

Estimated birth weight in the groups:

	Race		
Smoke	Black	Other	White
0	2850.50	2850.50 -40.26 = 2814.24	2850.50 +574.25 =3428.75
1	2850.50 -350.50 =2504.00	2850 -40.26 -350.50 +293.43 =2757.17	2850 +574.25 -350.50 -250.87 =2827.38

Example: Low Birth Weight

- Different dummy coding for description:

```
> modell1a <- lm(bwt ~ race:smoke-1, data = lbw)
> summary(modell1a)
```

Call:

```
lm(formula = bwt ~ race:smoke - 1, data = lbw)
```

Residuals:

Min	1Q	Median	3Q	Max
-2407.75	-417.38	31.25	462.50	1561.25

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
raceblack:smoke0	2854.50	170.84	16.71	<2e-16 ***
raceother:smoke0	2814.24	92.15	30.54	<2e-16 ***
racewhite:smoke0	3428.75	103.02	33.28	<2e-16 ***
raceblack:smoke1	2504.00	216.10	11.59	<2e-16 ***
raceother:smoke1	2757.17	197.27	13.98	<2e-16 ***
racewhite:smoke1	2827.38	94.77	29.84	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Example: Low Birth Weight

- Model 1:

$$M_1: Y_{rsi} = \alpha + \beta_r + \gamma_s + \delta_{rs} + \varepsilon_{rsi}, i = 1, \dots, n_{rs}$$

- We want to compare to the simpler additive model :

$$M_2: Y_{rsi} = \alpha + \beta_r + \gamma_s + \varepsilon_{rsi}, i = 1, \dots, n_{rs}$$

- I.e. we wish to test if the two interaction parameter δ_{rs} can be set to 0.

Example: Low Birth Weight

- Hypotheses in two-way ANOVA:

H_2 : Additive hypothesis ($\delta_{rs} = 0$) :

$$M_2: \mu_{rsi} = \alpha + \beta_r + \gamma_s$$

H_{31} : No effect of smoking ($\gamma_s = 0$):

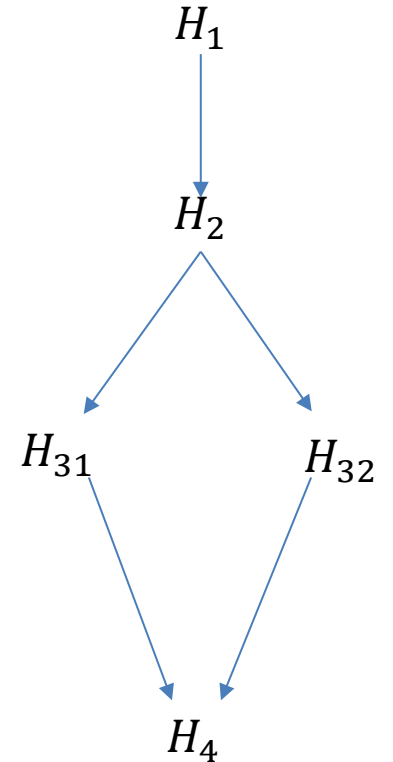
$$M_{31}: \mu_{rsi} = \alpha + \beta_r$$

H_{32} : No effect of race ($\beta_r = 0$):

$$M_{32}: \mu_{rsi} = \alpha + \gamma_s$$

H_4 : No effect of neither smoking nor race ($\beta_r = 0$ or $\gamma_s = 0$):

$$M_4: \mu_{rsi} = \alpha$$



Sequential Testing

- **Backwards Selection.**

Start with a saturated model, evaluate it and simplify it, moving downwards in the test graph.

- **(Forwards selection.**

Start with the simplest model, and complicate it, moving upwards in the test tree.)

- Problem with forward selection: Simpler but **WRONG**. Until the test for the final model, ALL models in tests are wrong, and test values more or less arbitrary!
- **Always use backwards selection.** In complicated test graphs, use forward selection from the final model for completion (sensitivity analysis), **after** backwards selection.

Example: Low Birth Weight

```
> drop1(model1, test="F")  
Single term deletions
```

Model:

```
bwt ~ race + smoke + race:smoke  
              Df Sum of Sq      RSS      AIC F value Pr(>F)  
<none>                85459758 2473.1  
race:smoke    2      2108643 87568401 2473.7   2.2577 0.1075
```

We accept H_2 ($p=0.11$).

```
> model2<-update(model1, ~.-race:smoke)  
> drop1(model2, test="F")  
Single term deletions
```

Model:

```
bwt ~ race + smoke  
              Df Sum of Sq      RSS      AIC F value      Pr(>F)  
<none>                87568401 2473.7  
race      2      8749453 96317854 2487.7   9.2422 0.0001494 ***  
smoke     1      7298537 94866938 2486.9  15.4191 0.0001214 ***
```

No terms are significant at the 5% test level, and the analysis stops here.

Example: Low Birth Weight

Summary of analysis:

```
> data.frame(round(tab, 2),  
+             "p-value" = format.pval(coef(summary(model2))[ , 4],  
+             digits = 3, eps = 1e-3))
```

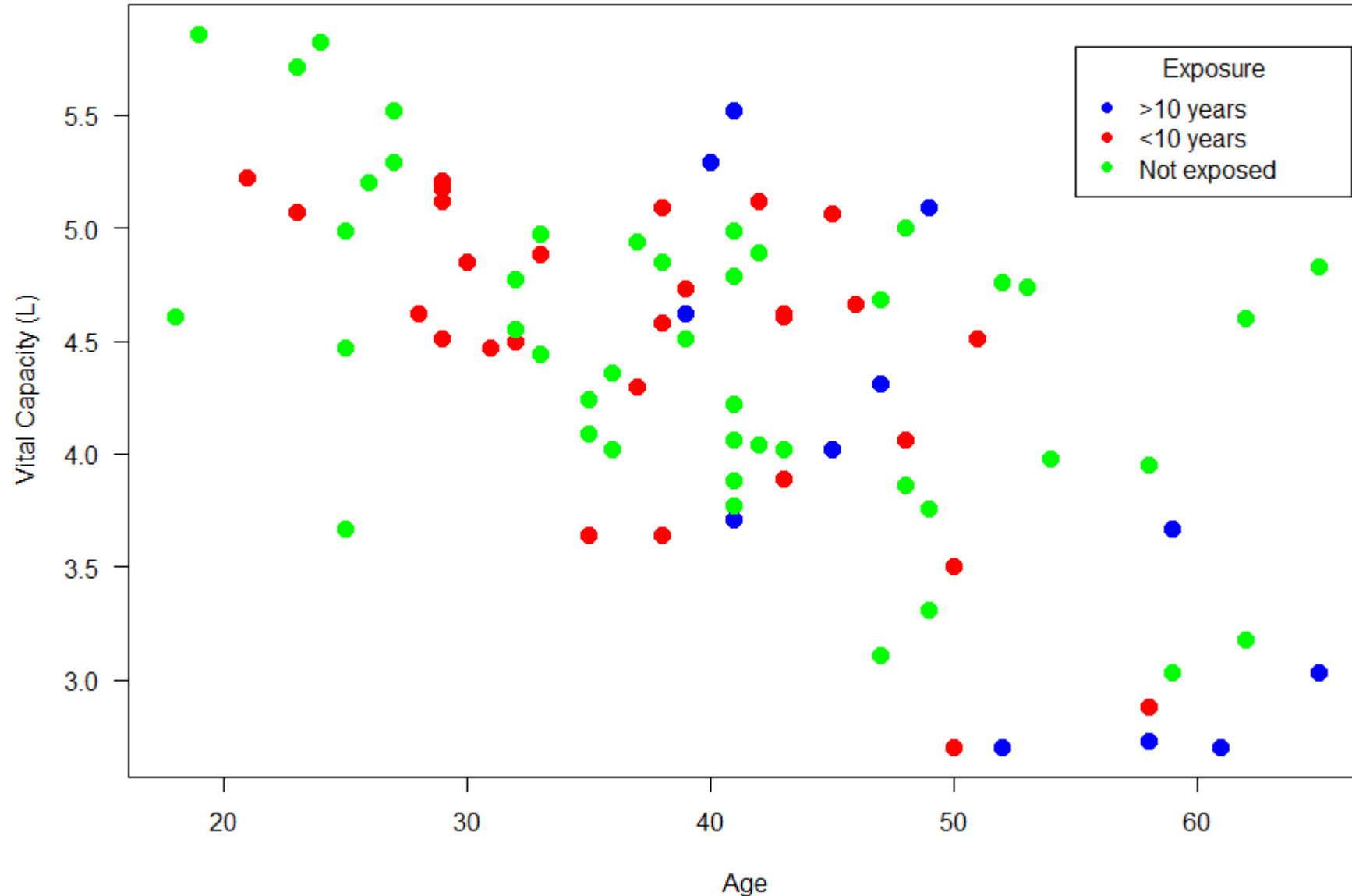
	Estimate	Std..Error	Lower	Upper	p.value
(Intercept)	2884.32	141.29	2517.43	3163.07	< 0.001
raceother	-3.64	160.54	-423.24	313.08	0.98193
racewhite	450.54	153.07	180.63	752.52	0.00366
smoke1	-428.03	109.00	-894.02	-212.98	< 0.001

- For two mothers of the **same race** where one is a smoker and the other nonsmoker, the birth weight of the smoker's baby will on average be 428g less than for the nonsmoker. The difference could be as much as 894g or as little as 213g, based on a 95% CI.
- For two mothers with the **same smoking status** where one belongs the black group and the other belongs to the white group, the birth weight of the baby for the mother that belongs to the black group will on average be 451g less than the baby if the mother belonging to the white group. The difference could be as much as 753g or as little as 181g, based on a 95% CI.

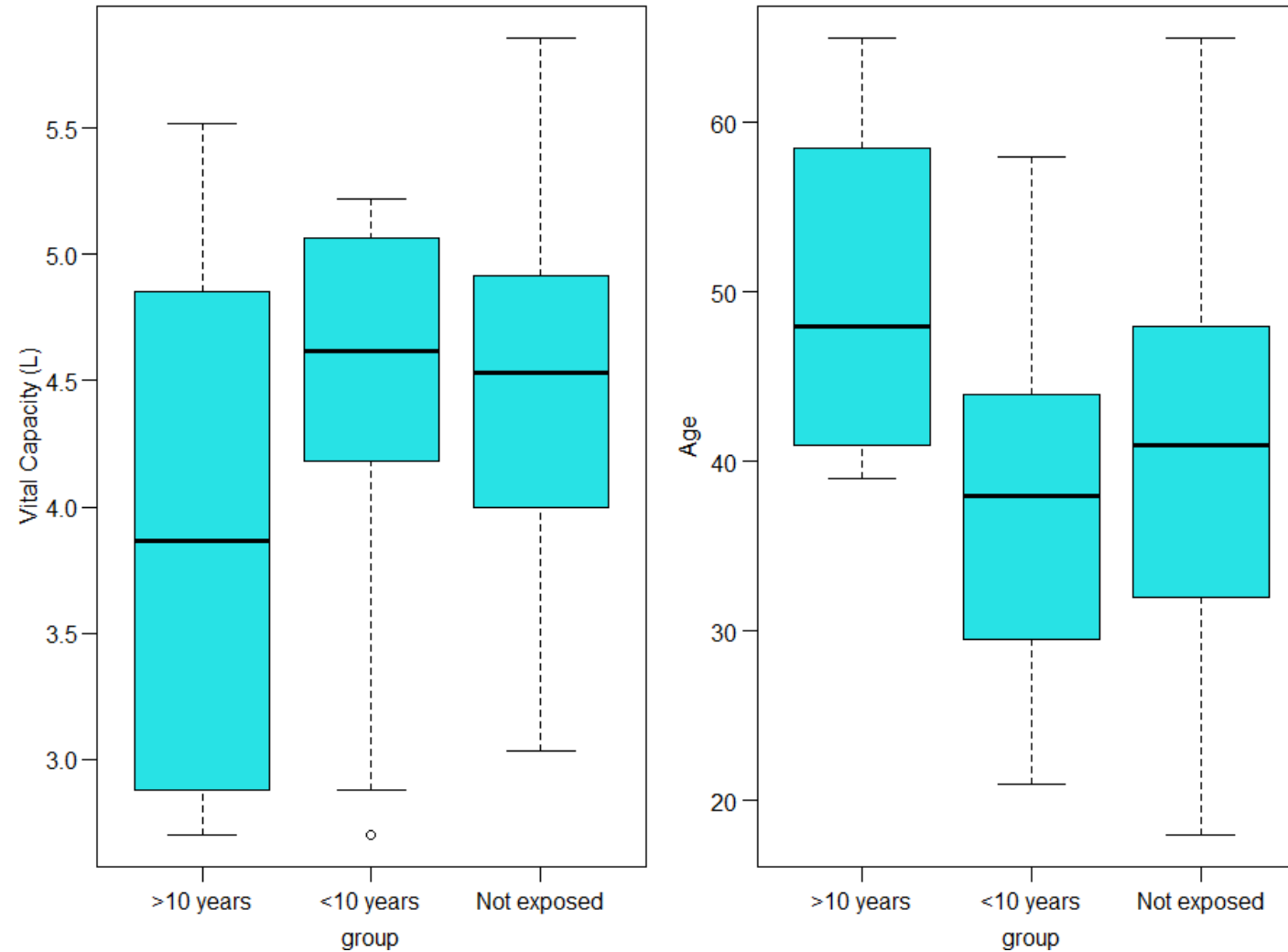
Example: Vital Capacity and Cadmium

- Data from a study of the effect of exposure to cadmium on the vital capacity. *Armitage & G Berry: Statistical methods in medical research. 2nd ed. Blackwell 1987.*
- *Vital capacity* is the maximum amount of air a person can expel from the lungs after a maximum inhalation.
- Measurements of vital capacity (L), age and exposure to cadmium (> 10 years, < 10 years, not exposed).

Example: Vital Capacity and Cadmium

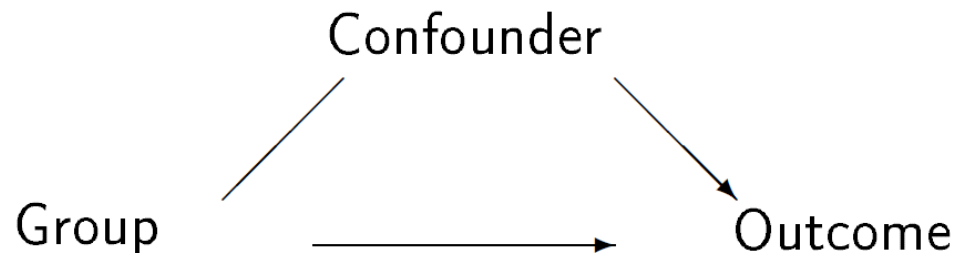
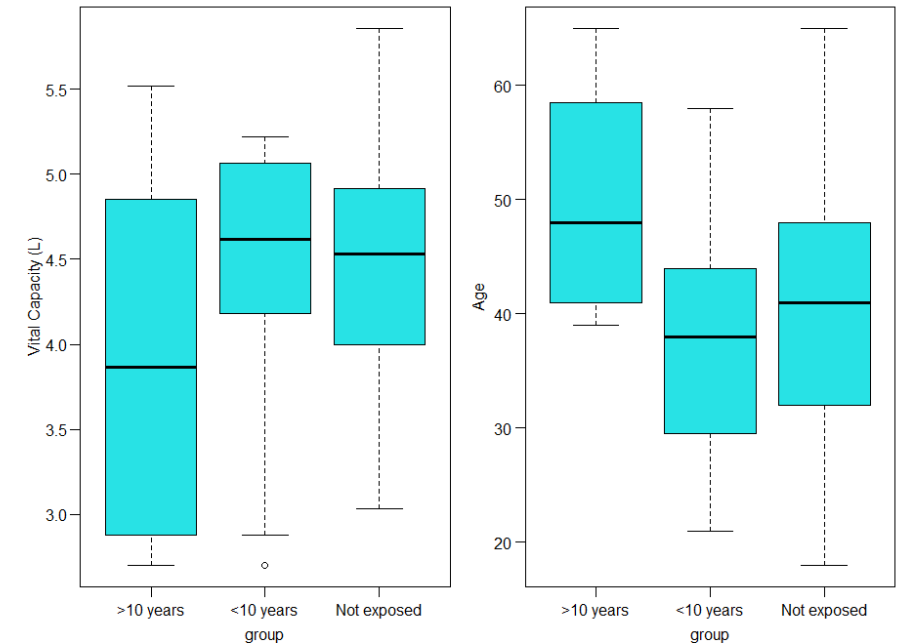


Example: Vital Capacity and Cadmium

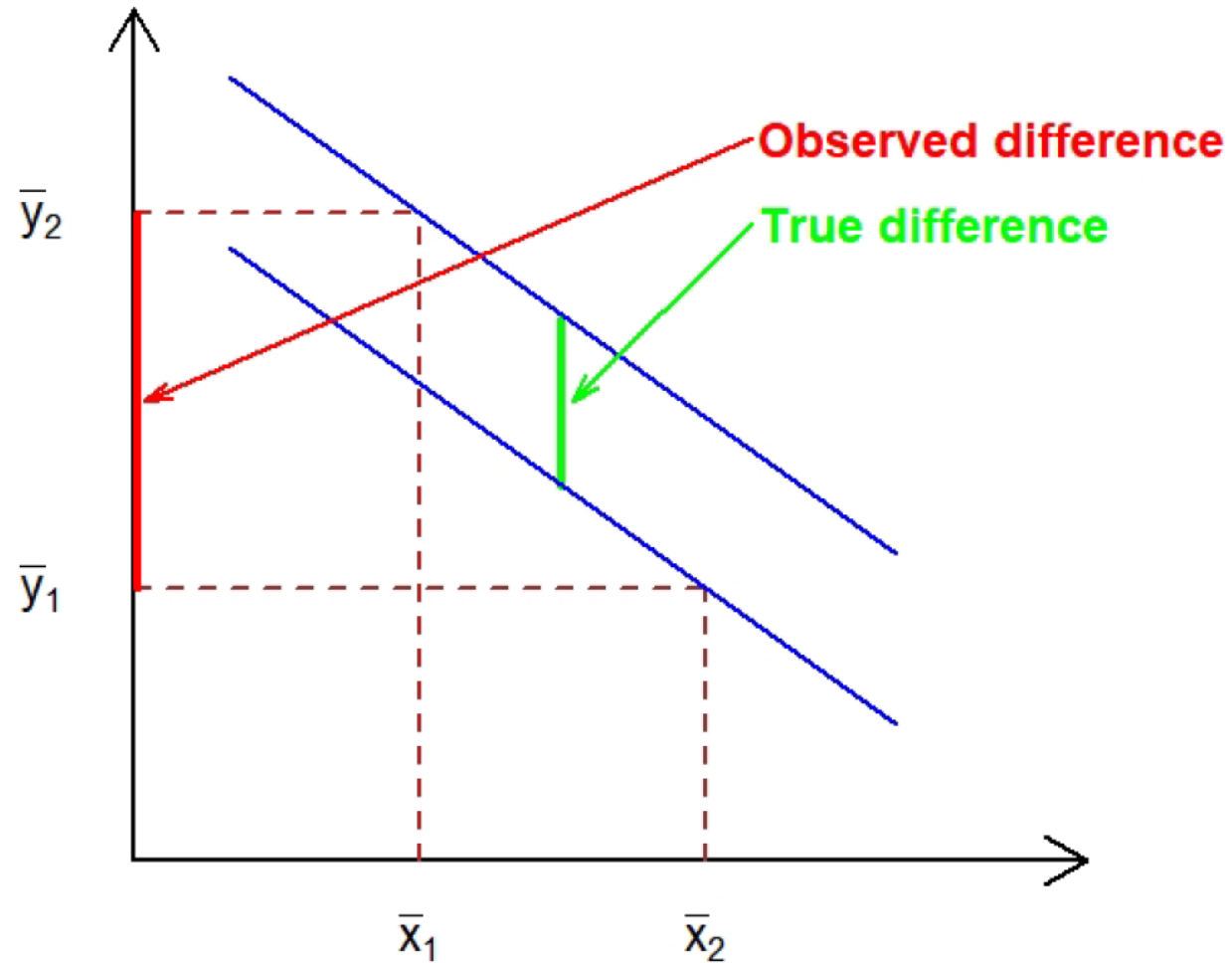


Confounding

- Comparing groups that are not quite comparable (e.g. cadmium exposure).
- Confounder: A variable that
 - Has an effect on the outcome.
 - Is associated to group (different ages in groups)
- This can cause **bias**.

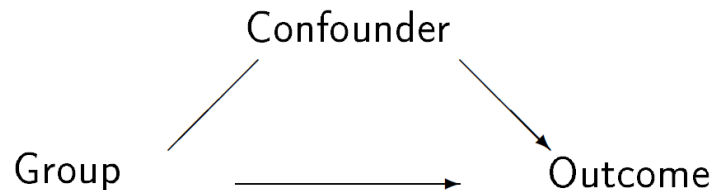


Confounding



Confounding

- Handling confounders:
Include the skew covariate in the model.
- We will answer a different question:
Instead of “Is the vital capacity associated with exposure to cadmium?”, we will investigate
“Is the vital capacity, corrected for age,
associated with exposure to cadmium?”



Example: Vital Capacity and Cadmium

- Model for Vital capacity, dummy-coding the exposure factor:

$$Y_i = \beta_0 + \beta_{<10}X_{<10,i} + \beta_{\geq 10}X_{\geq 10,i} + \beta_{age}X_{age,i} + \varepsilon_i, \quad i = 1, \dots, 84$$

```
CADdata$expo[CADdata$group==3] <- 1
```

```
CADdata$expo[CADdata$group==2] <- 2
```

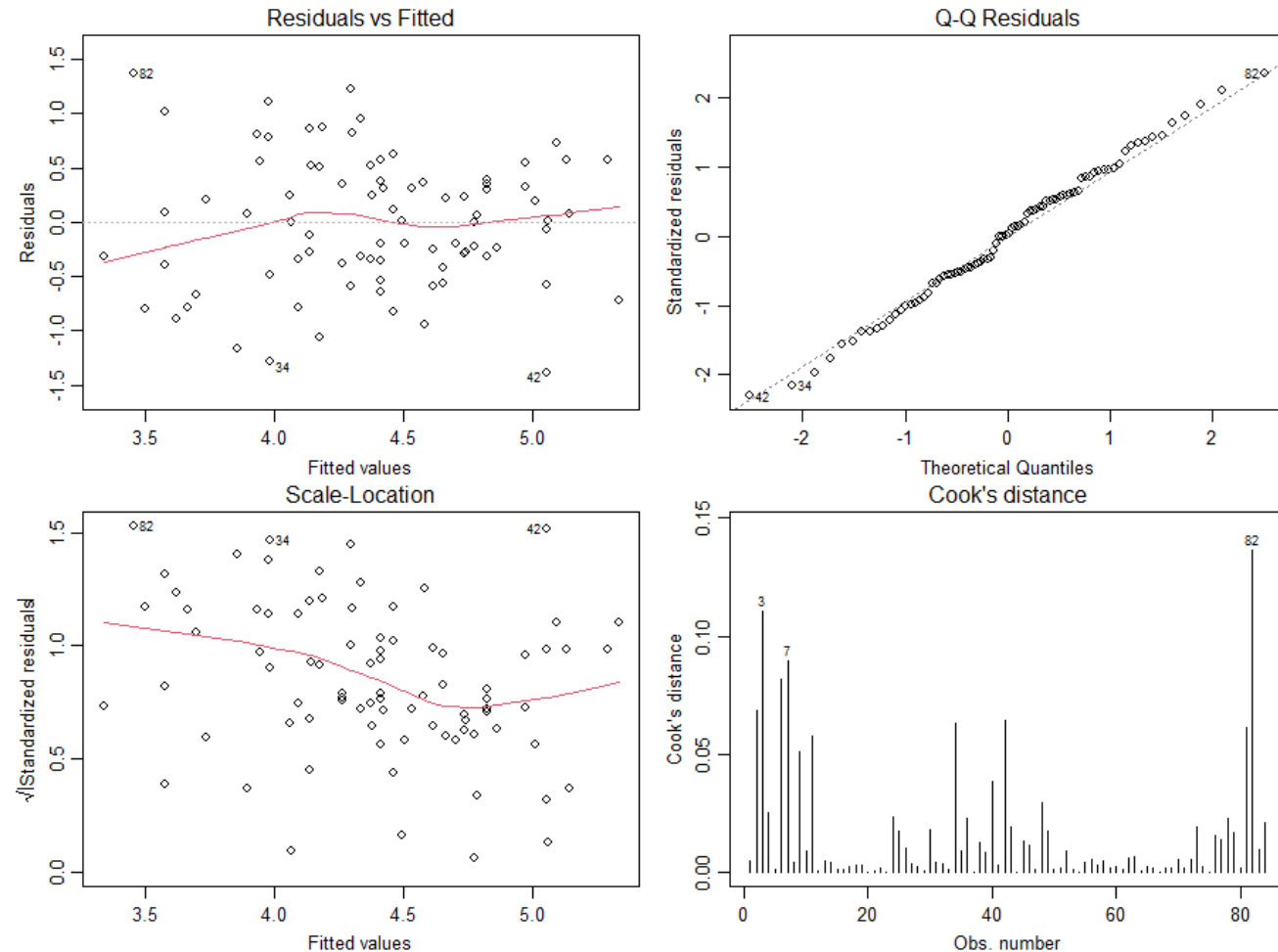
```
CADdata$expo[CADdata$group==1] <- 3
```

```
CADdata$expo<-as.factor(CADdata$expo)
```

```
Model1<-lm(vitcap ~ expo + age, data = CADdata)
```

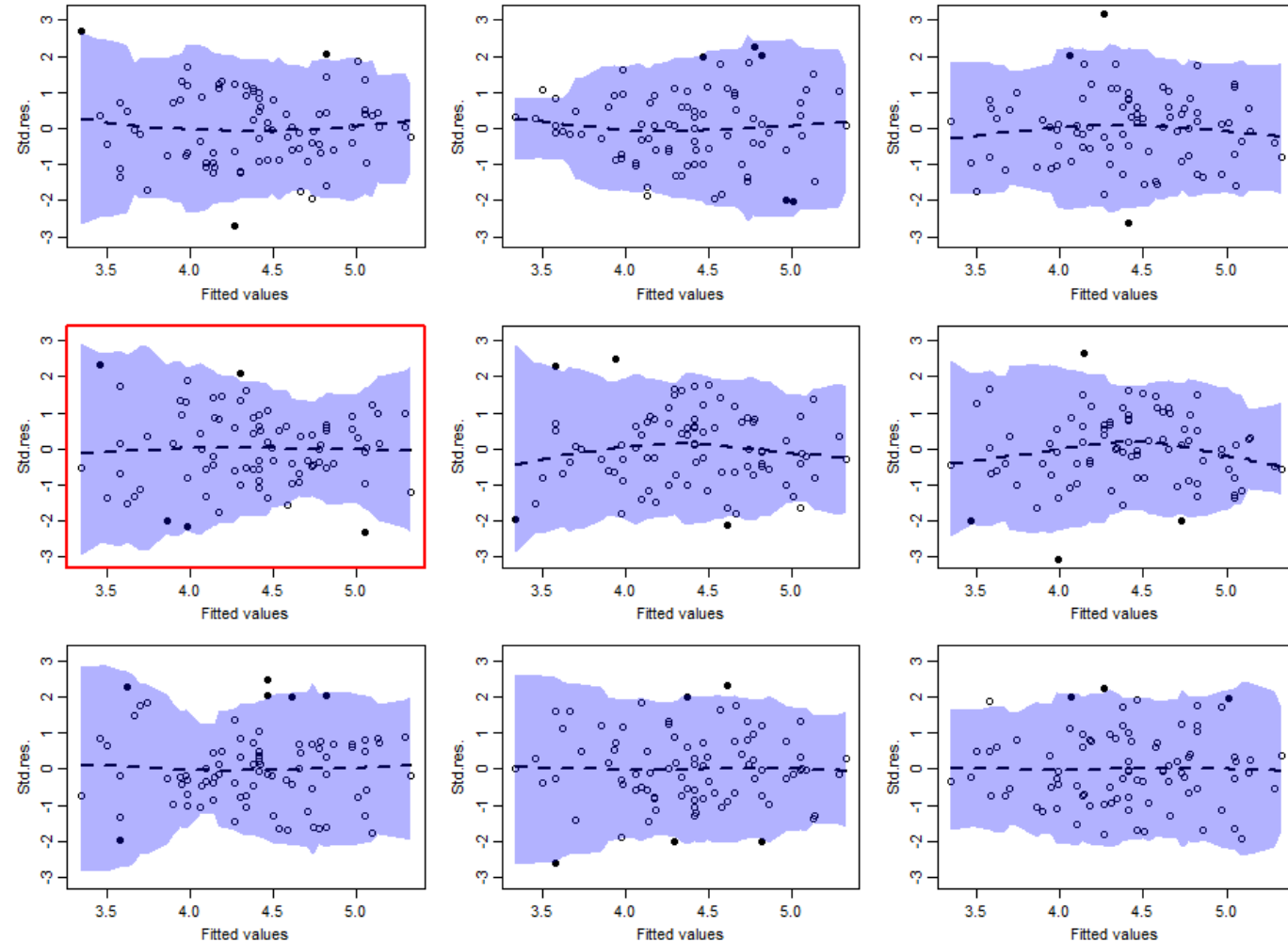
Example: Vital Capacity and Cadmium

- Model control:



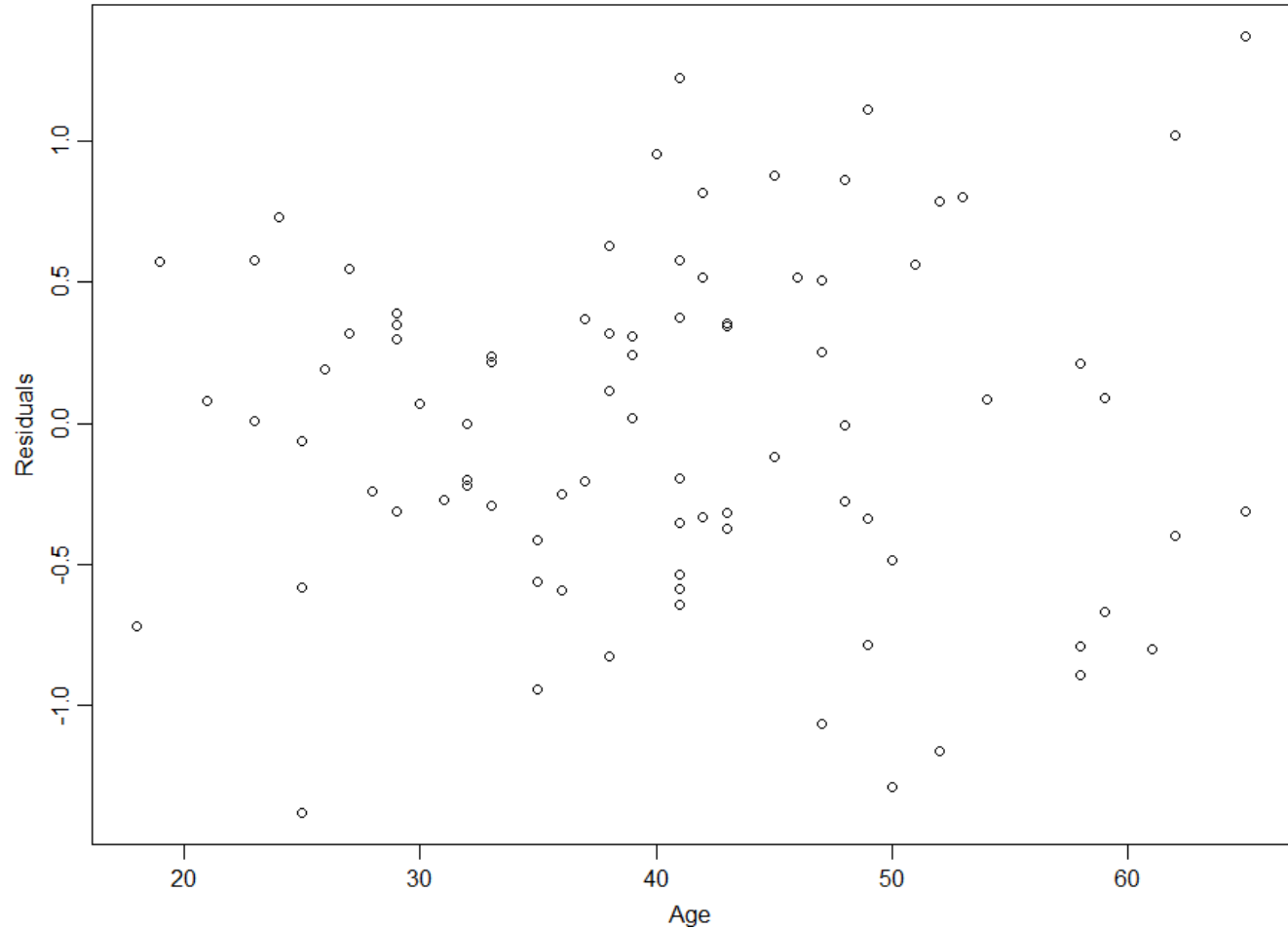
Example: Vital Capacity and Cadmium

wallyplot(model1)



Example: Vital Capacity and Cadmium

- Residuals vs. Age:



Example: Vital Capacity and Cadmium

- Further investigating curvature

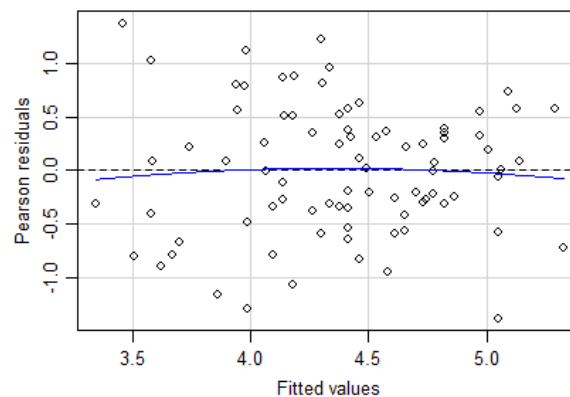
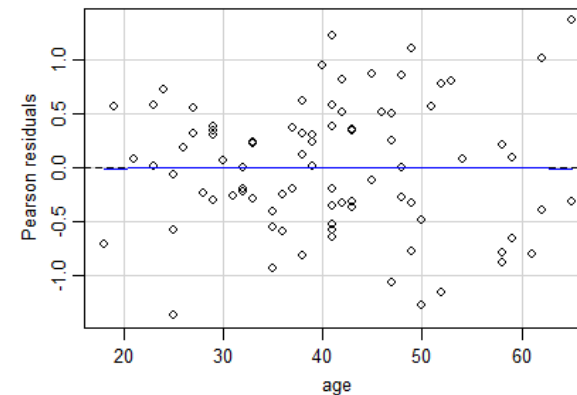
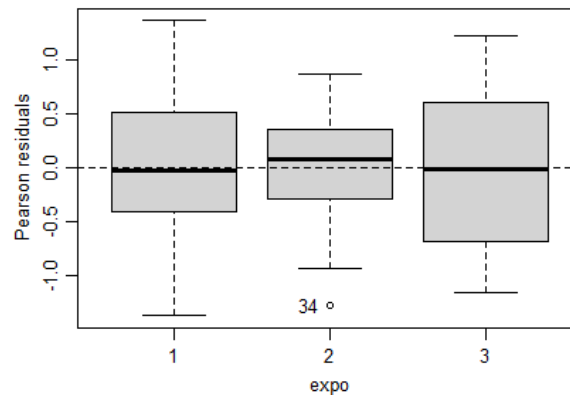
```
> residualPlots(model1)
```

```
Test stat Pr(>|Test stat|)
```

```
expo
```

```
age -0.0535 0.9575
```

```
Tukey test -0.3918 0.6952
```



Example: Vital Capacity and Cadmium

- Model control went well.

```
> summary(modell)
```

```
Call:
```

```
lm(formula = vitcap ~ expo + age, data = CADdata)
```

```
Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.044917	0.268025	22.554	< 2e-16 ***
expo2	-0.070198	0.148669	-0.472	0.638
expo3	-0.116935	0.209236	-0.559	0.578
age	-0.039775	0.006322	-6.291	1.57e-08 ***

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 0.6127 on 80 degrees of freedom
```

```
Multiple R-squared:  0.3696,    Adjusted R-squared:  0.3459
```

```
F-statistic: 15.63 on 3 and 80 DF,  p-value: 4.323e-08
```

```
> drop1(modell,test="F")
```

```
Single term deletions
```

```
Model:
```

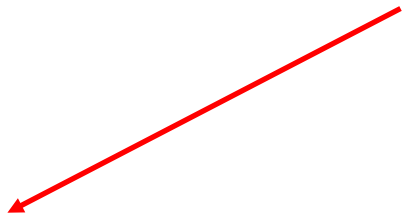
```
vitcap ~ expo + age
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>			30.035	-78.391		
expo	2	0.1617	30.196	-81.940	0.2153	0.8067
age	1	14.8589	44.894	-46.628	39.5781	1.572e-08 ***

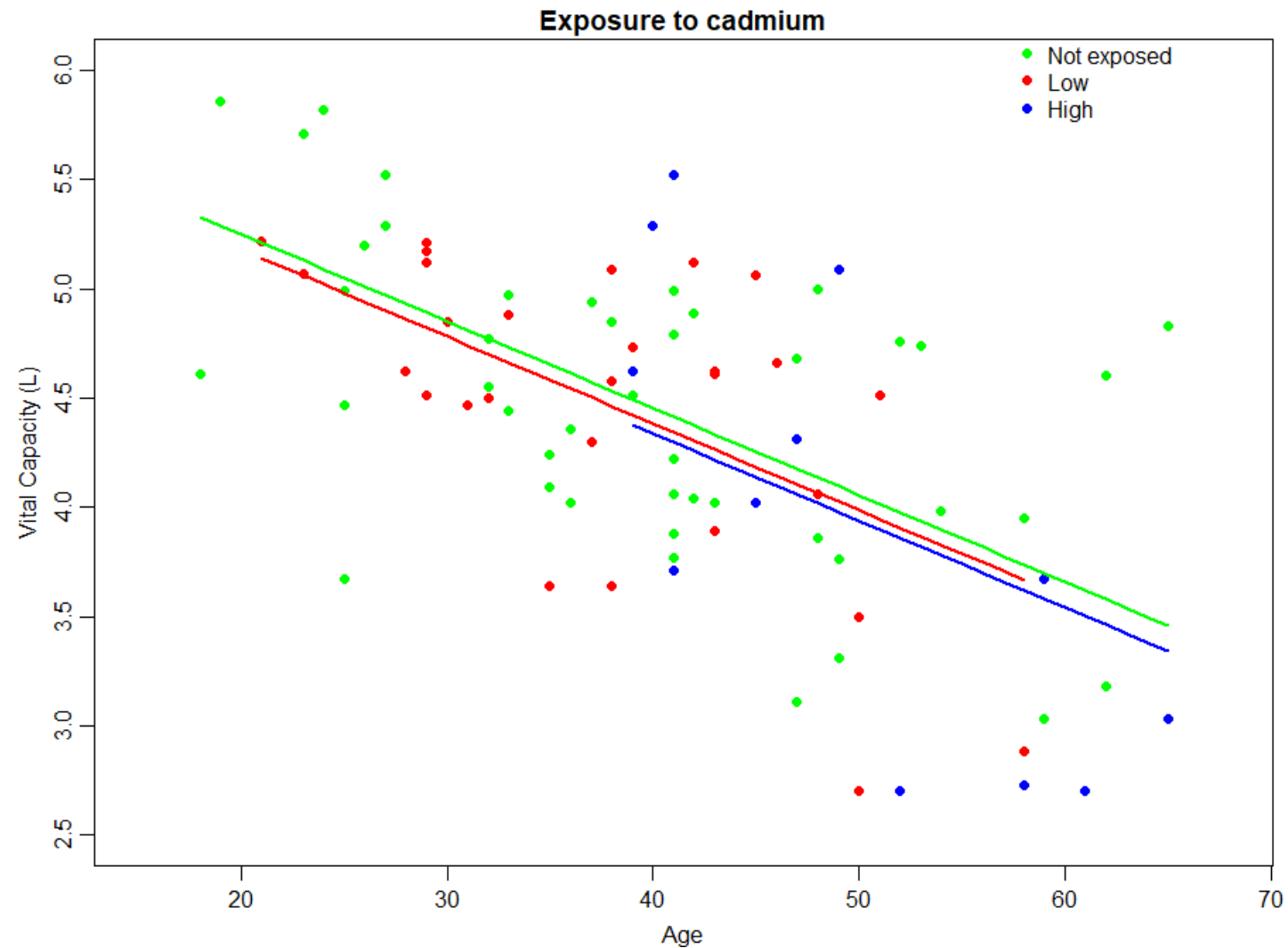
```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**When correcting for age,
exposure to cadmium does NOT
seem to be significant in model 1**



Example: Vital Capacity and Cadmium



Example: Vital Capacity and Cadmium

- The vital capacity decreases with -0.04 L per year.
- Is it reasonable that the vital capacity decreases with the same rate in all three exposure groups?
- Allow different slopes in the three groups → Include an interaction between age and group.

```
> model2 <- lm(vitcap ~ age + expo + age:expo, data = CADdata)
> summary(model2)
```

```
Call:
lm(formula = vitcap ~ age + expo + age:expo, data = CADdata)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	5.680291	0.313426	18.123	< 2e-16	***
age	-0.030613	0.007547	-4.056	0.000117	***
expo2	0.549740	0.575884	0.955	0.342728	
expo3	2.503148	1.041842	2.403	0.018655	*
age:expo2	-0.015919	0.014547	-1.094	0.277170	
age:expo3	-0.054498	0.021070	-2.587	0.011554	*

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

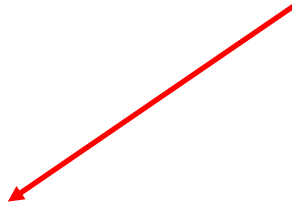
```
> drop1(model2, test = "F")
Single term deletions
```

Model:

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)	
<none>			27.535	-81.689			
age:expo	2	2.4995	30.035	-78.391	3.5402	0.03376	*

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

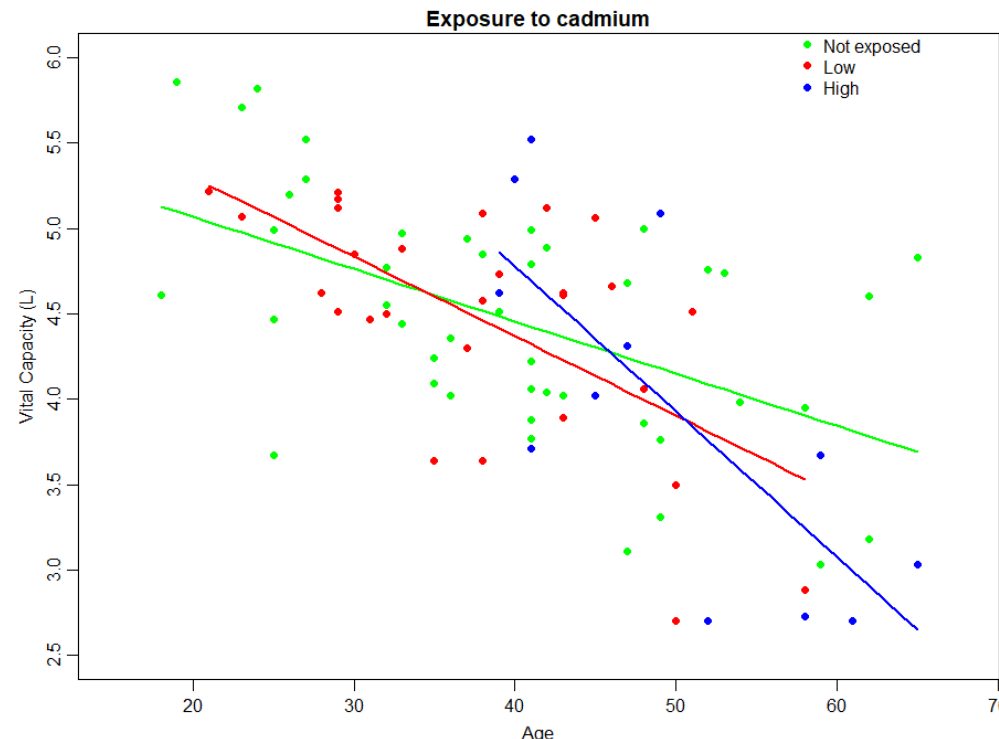
**When correcting for age,
exposure to cadmium IS
significant in model 2**



Example: Vital Capacity and Cadmium

- Redoing dummy coding for easy plotting:

```
> model2B<-lm(vitcap ~ 0 + expo + age:expo,  
              data = CADdata)  
> my.coef <- coef(model2B)  
> my.coef  
      expo1      expo2      expo3  expo1:age  expo2:age  expo3:age  
5.68029060 6.23003098 8.18343838 -0.03061267 -0.04653201 -0.08511099
```



- The model control of model 1 did not reveal anything problematic.
- Yet, the conclusion was turned upside down by the addition of an interaction.
- You may not see the need for an interaction unless you investigate it.

Model Diagnostics Revisited

- With h_{ii} the *leverage* of observation i , the diagonal element of $P_M = X(X^T X)^{-1}X^T$:

$$h_{ii} = X_i(X^T X)^{-1}X_i^T;$$

$$e_i = Y_i - \hat{Y}_i,$$

a representation of Cooks Distance is

$$D_i = \frac{e_i^2}{p\hat{\sigma}^2} \frac{h_{ii}}{(1 - h_{ii})^2}$$

Note that Cook's distance is high when both the leverage h_{ii} and the (squared) residual e_i^2 is high.

Model Diagnostics Revisited

- Assume no constant term, and that all explanatory variables are mean-centered

$$h_{ii} = X_i(X^T X)^{-1} X_i^T = \|X_i\|_{(X^T X)^{-1}}^2$$

is a distance measure in the feature space wrt. The variation of the features. High leverage means far away from the average in the feature space.

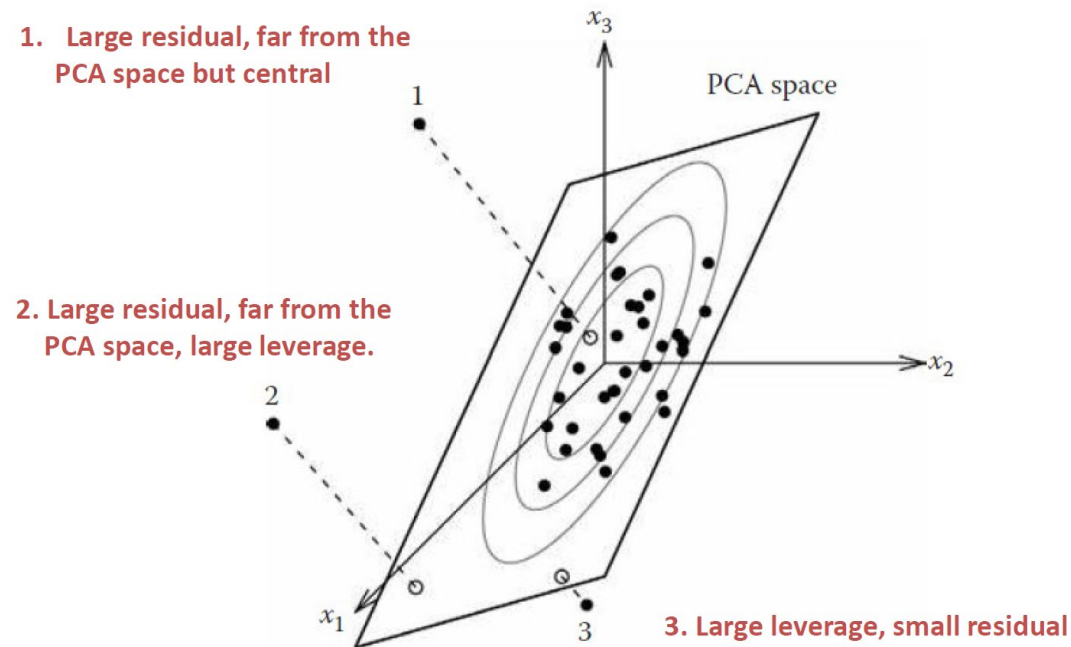
with

$$D_i = \frac{e_i^2}{p\hat{\sigma}^2} \frac{h_{ii}}{(1 - h_{ii})^2}$$

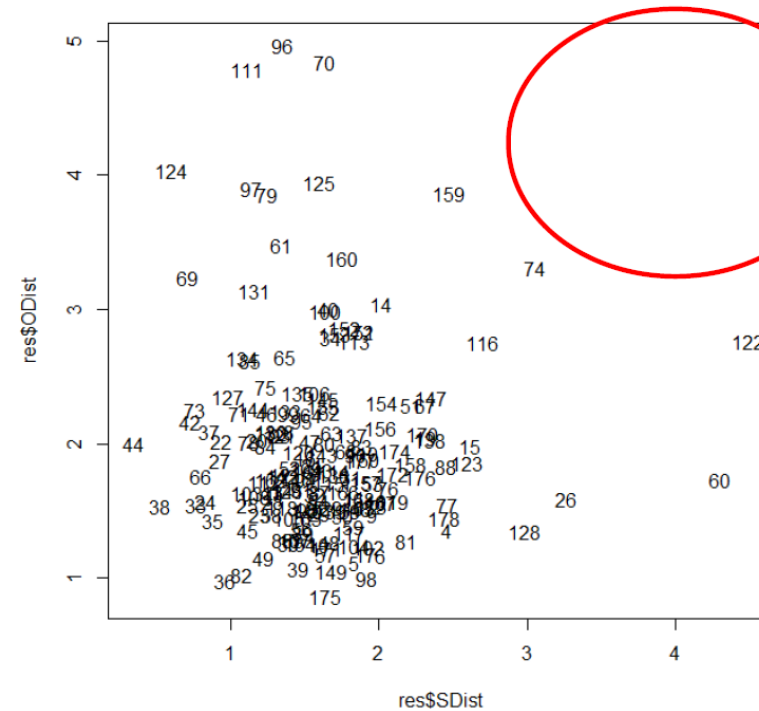
Cook's distance is high when both the leverage h_{ii} and the (squared) residual e_i^2 is high. Conforms with the criteria for problematic data in PCA analysis:

Model Diagnostics Revisited

Diagnostic Plots – Residuals and Leverage



Points corresponding to large values of Cooks distance



Model Diagnostics Revisited

- DFFITS: Studentized DFFIT (Difference in Fit).

$$DFFIT_i = \hat{y}_i - \hat{y}(i)_i$$
$$DFFITS_i = \frac{\hat{y}_i - \hat{y}(i)_i}{\sigma_{(i)}\sqrt{h_{ii}}}$$

DFFITS is a measure similar to Cooks distance and may be converted to it.

- DFBETAS – Studentised DFBETA.

$$DFBETAS_j = \frac{\hat{\theta}_j - \hat{\theta}(i)_j}{\sigma_{(i)}\sqrt{(X^T X)^{-1}_{jj}}}$$

For each observation i , the set of DFBETAS measures the effect on parameter estimation of removing that observations in standard errors.

Model Diagnostics Revisited

- **Multicollinearity:** Can seriously inflate the variance of parameter estimates due to $X^T X$ being close to singular.

Definition 3.15

We define the *tolerance (TOL)* and the *variance inflation (VIF)* as

$$\begin{aligned} \text{TOL}_i &= 1 - R^2(x_i | \text{all other } x\text{-variables}) \\ \text{VIF}_i &= \frac{1}{\text{TOL}_i} \end{aligned}$$

As a rule of thumb, $\text{TOL} < 0.1$ or equivalently $\text{VIF} > 10$ indicates a multicollinearity problem.

Definition 3.16

We define the *condition number* as the square root of the largest eigenvalue of $\mathbf{x}\mathbf{x}^T$ divided by the smallest. The condition number should be below 15. If it is above 30, it is a matter of serious concern.

- Best method to handle it: Be careful when modeling.

INTRODUCTION TO MULTIVARIATE ANALYSIS OF VARIANCE

Hotelling's T-Square in the One-Sample Case

We consider independent random variables X_1, \dots, X_n , with $X_i \sim N_p(\mu, \Sigma)$, $i = 1, \dots, n$.

Parameter estimates:

$$\hat{\mu} = \bar{X} = \frac{1}{n} \sum_{i=1}^n X_i \sim N_p \left(\mu, \frac{1}{n} \Sigma \right)$$

$$\hat{\Sigma} = S = \frac{1}{n-1} \sum_{i=1}^n (X_i - \bar{X})(X_i - \bar{X})^T \sim W \left(n-1, \frac{1}{n-1} \Sigma \right)$$

Suppose that we wish to test the hypothesis

$$H_0: \mu = \mu_0 \text{ against } H_1: \mu \neq \mu_0$$

Hotelling's T-Square in the One-Sample Case

||| Theorem 4.2

We will use the notation

$$T^2 = n(\bar{X} - \mu_0)^T \mathbf{S}^{-1}(\bar{X} - \mu_0),$$

where \bar{X} , μ_0 and \mathbf{S} are as stated in the introduction to this section. Then the critical area for a ratio test of H_0 against H_1 at level α is

$$C = \{x_1, \dots, x_n \mid \frac{n-p}{(n-1)p} t^2 > F(p, n-p)_{1-\alpha}\},$$

where t^2 is the observed value of T^2 .

Hotelling's T-Square in the One-Sample Case

EXAMPLE . At the Laboratory of Heating- and Climate-technique, DTU, one has measured the following in an experiment

- i) the height in cm.
- ii) evaporation loss in g/m^2 skin during a 3 hour periode
- iii) mean temperature in $^{\circ}\text{C}$. This temperature is found by measuring the skin temperature at 14 different locations every minute for 5 minutes (same locations every time). The mean temperature is then an average of all $14 \times 5 = 70$ measurements,

on 16 men and 16 women. '

Hotelling's T-Square in the One-Sample Case

We use the notation

$$\bar{\mathbf{X}} = \frac{1}{n} \sum_{i=1}^n \mathbf{X}_i \in N_p(\boldsymbol{\mu}, \frac{1}{n} \boldsymbol{\Sigma})$$

$$\bar{\mathbf{Y}} = \frac{1}{m} \sum_{i=1}^m \mathbf{Y}_i \in N_p(\boldsymbol{\nu}, \frac{1}{m} \boldsymbol{\Sigma})$$

$$\mathbf{S}_1 = \frac{1}{n-1} \sum_{i=1}^n (\mathbf{X}_i - \bar{\mathbf{X}})(\mathbf{X}_i - \bar{\mathbf{X}})^T$$

$$\mathbf{S}_2 = \frac{1}{m-1} \sum_{i=1}^m (\mathbf{Y}_i - \bar{\mathbf{Y}})(\mathbf{Y}_i - \bar{\mathbf{Y}})^T$$

$$\mathbf{S} = \frac{(n-1)\mathbf{S}_1 + (m-1)\mathbf{S}_2}{n+m-2} \in W(n+m-2, \frac{1}{n+m-2} \boldsymbol{\Sigma})$$

Hotelling's T-Square in the One-Sample Case

||| Theorem 4.9

We use the same notation as given above. Now, let

$$T^2 = \frac{nm}{n+m}(\bar{X} - \bar{Y})^T S^{-1}(\bar{X} - \bar{Y}).$$

Then the critical region for a test of H_0 against H_1 at level α is equal to

$$C = \{x_1, \dots, x_n, y_1, \dots, y_m \mid \frac{n+m-p-1}{(n+m-2)p} t^2 > F(p, n+m-p-1)_{1-\alpha}\}$$

Here t^2 is the observed value of T^2 .

Hotelling's T-Square in the One Sample Case

```
> heatclimate<-read.table("Data/heatclimate.txt",header=T, sep=" ")
```

```
> heatclimate$sex<-as.factor(heatclimate$sex)
```

```
> summary(heatclimate)
```

sex	height	evap	temp
f:16	Min. :157.0	Min. :12.60	Min. :31.90
m:16	1st Qu.:166.2	1st Qu.:18.48	1st Qu.:33.20
	Median :173.0	Median :20.75	Median :33.55
	Mean :172.9	Mean :22.49	Mean :33.52
	3rd Qu.:180.0	3rd Qu.:25.65	3rd Qu.:33.90
	Max. :190.0	Max. :45.40	Max. :34.80

- We want to compare the multivariate data for males and females. We will disregard the height.

Hotelling's T-Square in the One Sample Case

```
> X<-as.matrix(heatclimate[heatclimate$sex=="f",3:4])
> Y<-as.matrix(heatclimate[heatclimate$sex=="m",3:4])
> n<-dim(X)[1]
> m<-dim(Y)[1]
> p<-dim(X)[2]
> Xbar<-colMeans(X)
> Ybar<-colMeans(Y)
>
> Xbar2<-matrix(rep(Xbar,16),ncol=p,byrow=T)
> Ybar2<-matrix(rep(Ybar,16),ncol=p,byrow=T)
>
> S1<-t(X-Xbar2)%*(X-Xbar2)/(n-1)
> S2<-t(Y-Ybar2)%*(Y-Ybar2)/(m-1)
>
> S<-((n-1)*S1+(m-1)*S2)/(n+m-2)
> S
```

```
      evap      temp
evap 45.5081250 -0.3004167
temp -0.3004167  0.2985000
```

Hotelling's T-Square in the One Sample Case

```
> T2<-(n*m/(n+m))*t(Xbar-Ybar)%*%solve(S)%*%(Xbar-Ybar)
> T2
      [,1]
[1,] 4.612128
> ((n+m-p-1)/((n+m-2)*p))*T2
      [,1]
[1,] 2.229195
> 1-pf(((n+m-p-1)/((n+m-2)*p))*T2,p,n+n-p+1)
      [,1]
[1,] 0.1245838
```

The data supports that males and females have the same measurements ($p=0.12$).

Exercises

- Exam 2007 problem 8,
- Exam 2008 problem 3 (disregard pin 3.7)
- Exercise 4.3 (disregard task 5)
- Exercise 5.1