

Visualizing Linear Models: An R Bag of Tricks Session 2: Multivariate Models

Michael Friendly
SCS Short Course
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<https://friendly.github.io/VisMLM-course/>

Today's topics

- Brief review of the GLM & MLM $\mathbf{Y} = \mathbf{X} \mathbf{B} + \mathcal{E}$
 $(n \times p) \quad (n \times q) \quad (q \times p) \quad (n \times p)$
- Data ellipses
 - sufficient visual summaries
- HE plot framework
 - H & E matrices/ellipses
 - Discriminant/canonical views
- Example: Penguins data
- Checking assumptions

One-way MANOVA

- p responses, 1 “factor” (IV), g groups
 - $H_0: \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2 = \dots = \boldsymbol{\mu}_g$
 - $H_1: \text{at least one group centroid is different}$
- Assumptions:
 - Independent groups, independent observations
 - Responses are independent, multivariate normal w/in each group
 - Pop. within-group covariance matrices are **equal** across groups
 - $H_0: \boldsymbol{\Sigma}_1 = \boldsymbol{\Sigma}_2 = \dots = \boldsymbol{\Sigma}_g$
 - ($\boldsymbol{\Sigma}$ estimated by $\mathbf{S} = \mathbf{E} / df_e$)
 - tested by e.g., Box’s test, `heplots::boxM`
 - $\rightarrow \mathbf{y}_{ij} (p \times 1) \sim N(\boldsymbol{\mu}_j, \boldsymbol{\Sigma})$

One-way ANOVA vs. MANOVA

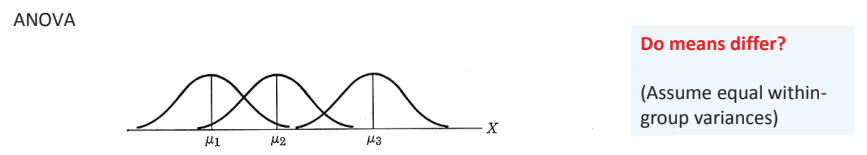


Figure 8.1. The simple anova situation, when the differences among the populations are “real.”
source: Cooley & Lohnes ((1971)

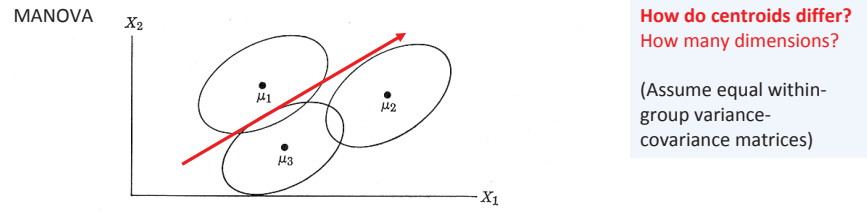
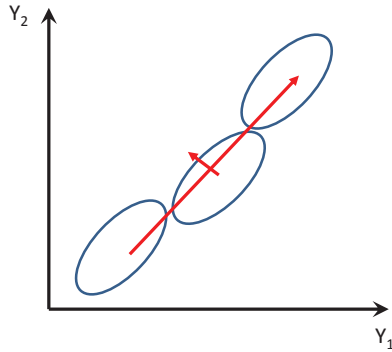


Figure 8.2. The simple manova situation, when the differences among the populations are “real.”

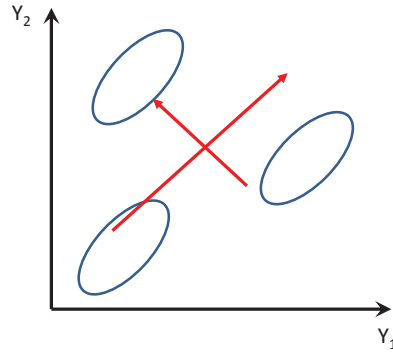
Response dimensions

Means on Y_1 and Y_2 are nearly perfectly correlated



Only 1 dimension required to understand the group effect

Means on Y_1 and Y_2 have a low correlation



Two different aspects are reflected in group means

5

GLM: the design matrix (X)

- In the full GLM, the design matrix (X) may consist of:

- A constant, 1 , for the intercept (usually implicit)
- Quantitative regressors: age, income, education
- Transformed regressors: vage , $\log(\text{income})$
- Polynomial terms: age^2 , age^3 , ...
- Categorical predictors ("factors", class variables): treatment (control, drug A, drug B), sex
- Interactions: $\text{treatment} * \text{sex}$, $\text{age} * \text{sex}$

Model formulae in R define $y \sim X$:

```
prestige ~ income + education           # 2 main effects
prestige ~ income * education           # + interaction
prestige ~ income + education + women + type # 4 main effects
prestige ~ education + poly(women, 2) + log(income)*type
```

6

Univariate linear model

- Model
$$\mathbf{y} = \mathbf{X} \boldsymbol{\beta} + \boldsymbol{\epsilon}$$

$(n \times 1)$ $(n \times q)$ $(1 \times q)$ $(n \times 1)$ $(n \times q) = (x_1, x_2, \dots, x_q)$
matrix of predictors, factors, ...

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \dots + \beta_q x_{iq} + \epsilon_i$$

- Sums of squares

$$SS_{\text{Tot}} = \sum_{i,j} (y_{i,j} - \bar{y}_i)^2 + \sum_{i,j} (y_{i,j} - \hat{y}_i)^2$$

$$= SS_H + SS_E$$

- Hypothesis tests

$$F = \frac{SS_H / df_H}{SS_E / df_E} = \frac{MS_H}{MS_E}$$

How big is hypothesis variation relative to error variation?

↑
mean square is a variance estimate

7

Least squares: SS_T and SS_E

In simple linear regression,

$$y_i = b_0 + b_1 x_i + e_i$$

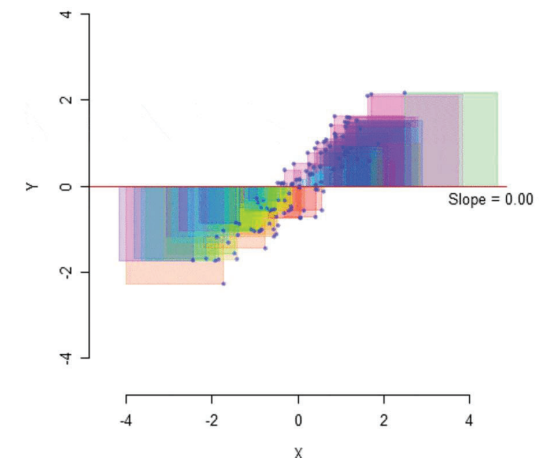
the intercept b_0 & slope b_1 are values that minimize the SS_E (or MS_E)

$$SS_E = \sum e_i^2 = \sum (y_i - \hat{y}_i)^2$$

SS_T is that value when $b_1=0$

b_1	MS_E
.00	1.0
.89	0.2

Average of Squared Errors = 1.00



8

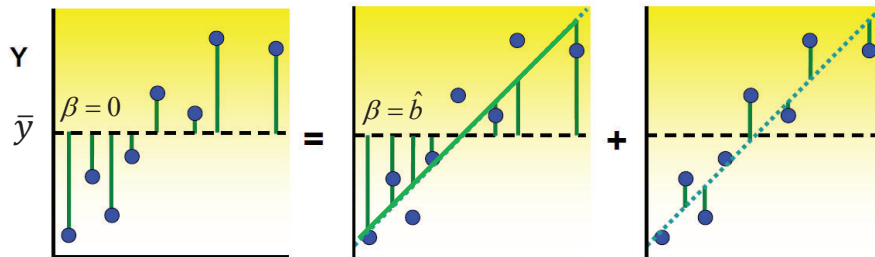
Regression: Visualizing $SS_T = SS_H + SS_E$

Total variance (SS_T) = Regression variance (SS_H) + Residual variance (SS_E)

$$\sum_i (y_i - \bar{y})^2$$

$$\sum_i (\hat{y}_i - \bar{y})^2$$

$$\sum_i (y_i - \hat{y}_i)^2$$



F test: How much better is the fitted regression line ($\beta = \hat{\beta}$) than the flat line ($\beta = 0$)?

9

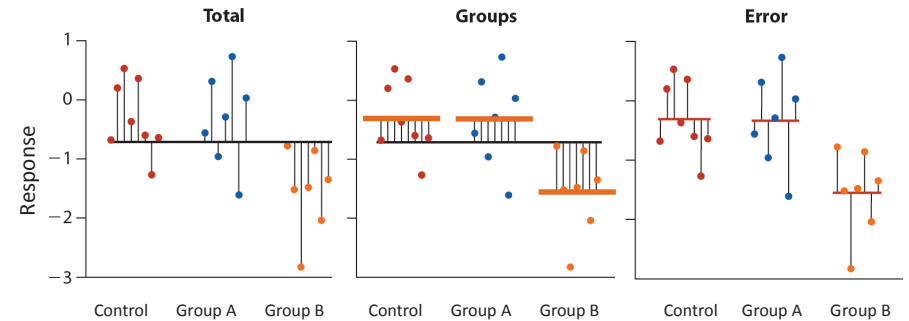
ANOVA: Visualizing $SS_T = SS_H + SS_E$

Total variance = Between group variance + Within group variance

$$\sum_{ij} (y_{ij} - \bar{y}_{..})^2$$

$$\sum_{ij} (\bar{y}_{.j} - \bar{y}_{..})^2$$

$$\sum_{ij} (y_{ij} - \bar{y}_{.j})^2$$



F test: How much better is the groups model than the model ignoring groups?

10

Which means differ?

- In ANOVA, when a factor is significant, follow-up to find **which means differ**
- Post-hoc tests:
 - all-pairwise comparisons
 - all treatments vs. control group
- Need to correct for multiple testing– control family-wise error rate
 - Bonferroni: $\alpha_i = \alpha_{FW} / k$ [too conservative]
 - Tukey pairwise: “honestly significant difference”
 - many others: Dunnett’s test, Sidak, FDR, ...

11

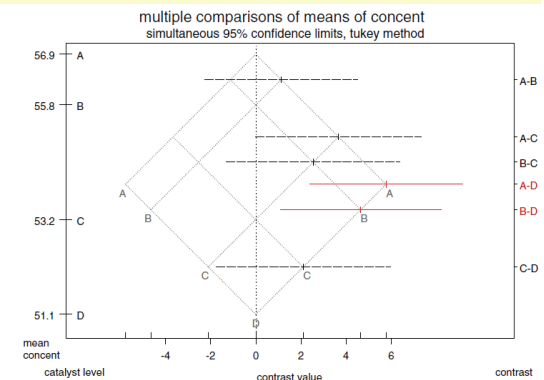
Plotting multiple comparisons

HH: `mmcp1ot()` – the mean-mean multiple comparison plot shows multiple comparisons or contrasts for any linear model

```
library(HH)
catalystm.lm <- lm(concent ~ catalyst, data=catalystm)
catalystm.mmc <- mmc(catalystm.lm, linfct = mcp(catalyst = "Tukey"))
mmcplot(catalystm.mmc)
```

Construction:

- plot means, \bar{y}_i , \bar{y}_j on grid
- rotate 45°
- horizontal axis shows: $\bar{y}_i - \bar{y}_j$
- SE determined by MC method
- signif. comparisons **highlighted**



Contrasts: planned comparisons

- Better to test specific, **planned** comparisons, rather than all-pairwise
- A **contrast** is a weighted sum, L , of the means, with weights, \mathbf{c} , that sum to zero

$$L = \mathbf{c}' \boldsymbol{\mu} = \sum c_i \mu_i \quad \text{such that} \quad \sum c_i = 0$$

$$\begin{array}{l}
 r=4 \\
 \text{groups}
 \end{array}
 \quad
 \begin{array}{l}
 L_1 = (\mu_1 + \mu_2) - (\mu_3 + \mu_4) \rightarrow \mathbf{c}_1 = (1 \ 1 \ -1 \ -1)' \\
 L_2 = \mu_1 - \mu_2 \rightarrow \mathbf{c}_2 = (1 \ -1 \ 0 \ 0)' \\
 L_3 = \mu_3 - \mu_4 \rightarrow \mathbf{c}_3 = (0 \ 0 \ 1 \ -1)'
 \end{array}$$

- In words: average of one subset of groups vs. another subset
- Any $r-1$ **linearly independent** contrasts \rightarrow same overall test
- A priori** contrasts can be tested w/o adjusting α

13

The \mathbf{X} matrix for a factor can be represented by a set of $r-1$ contrasts, combined with the unit vector

$$\mathbf{X}_{(r \times r)} = (\mathbf{1}, \mathbf{C}) \quad \mathbf{X} = \begin{pmatrix} 1 & 1 & 1 & 0 \\ 1 & 1 & -1 & 0 \\ 1 & -1 & 0 & 1 \\ 1 & -1 & 0 & -1 \end{pmatrix}$$

c1 c2 c3

Some **special contrasts**:

Deviation contrasts

$$\mathbf{C} = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -1 & -1 & -1 \end{pmatrix}$$

each treatment vs control or baseline [not orthogonal]

Helmert contrasts

$$\mathbf{C} = \begin{pmatrix} 3 & 0 & 0 \\ -1 & 2 & 0 \\ -1 & -1 & 1 \\ -1 & -1 & -1 \end{pmatrix}$$

ordered treatments: each vs all the rest [always orthogonal]

Polynomial contrasts

$$\mathbf{C} = \begin{pmatrix} -3 & 1 & -1 \\ -1 & -1 & 3 \\ 1 & -1 & -3 \\ 3 & 1 & 1 \end{pmatrix}$$

lin quad cubic

quantitative treatment levels [orthogonal]

14

Using contrasts in R

- R has 4 basic functions for generating contrasts for a factor
 - Dummy** coding, aka "reference level", "treatment" contrasts
 - Deviation** coding, aka "sum-to-zero" constraints
 - Polynomial** contrasts for an ordered/quantitative factor
 - Helmert** contrasts for ordered factor comparisons
- Defaults are set separately for **unordered** and **ordered** factors
- Define your own by assigning a matrix to `contrasts(myfactor) <- cmat`
- These affect the **tests of coefficients**, but not overall tests

```

> contr.treatment(4)
 2 3 4
1 0 0 0
2 1 0 0
3 0 1 0
4 0 0 1

> contr.sum(4)
[,1] [,2] [,3]
1 1 0 0
2 0 1 0
3 0 0 1
4 -1 -1 -1

> contr.poly(4)
      .L .Q .C
[1,] -0.6708 0.5 -0.2236
[2,] -0.2236 -0.5 0.6708
[3,] 0.2236 -0.5 -0.6708
[4,] 0.6708 0.5 0.2236
    
```

```

> options("contrasts")
$contrasts
  unordered      ordered
"contr.treatment" "contr.poly"
    
```

```

> contr.helmert(4)
[,1] [,2] [,3]
1 -1 -1 -1
2 1 -1 -1
3 0 2 -1
4 0 0 3
    
```

15

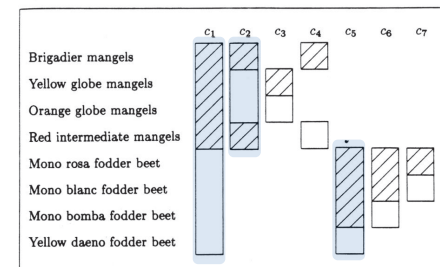
See: http://www.ats.ucla.edu/stat/r/library/contrast_coding.htm

Nested dichotomies

- Orthogonal contrasts can always be generated as **nested dichotomies**
- They correspond to **independent** research questions
- Sums of squares **decompose** the overall effect

$$SS_A = SS_{c_1} + SS_{c_2} + \dots + SS_{c_{(r-1)}}$$

$c_1 =$ mangels vs beets $c_2 =$ globe mangels vs other $c_3 =$ mono beets vs yellow



Treatment		c1	c2	c3	c4	c5	c6	c7
Brigadier mangels	μ_1	1	1	0	1	0	0	0
Yellow globe mangels	μ_2	1	-1	1	0	0	0	0
Orange globe mangels	μ_3	1	-1	-1	0	0	0	0
Red intermediate mangels	μ_4	1	1	0	-1	0	0	0
Mono rosa fodder beet	μ_5	-1	0	0	0	1	1	1
Mono blanc fodder beet	μ_6	-1	0	0	0	1	1	-1
Mono bomba fodder beet	μ_7	-1	0	0	0	1	-2	0
Yellow daeno fodder beet	μ_7	-1	0	0	0	-3	0	0

16

Multivariate linear model

• Model $\mathbf{Y} = \mathbf{X} \mathbf{B} + \mathcal{E}$

$(n \times p)$ $(n \times q)$ $(q \times p)$ $(n \times p)$

$\mathbf{Y} = (y_1, y_2, \dots, y_p)$
matrix of p responses

• Sums of squares & cross-products

$$\mathbf{SSP}_T = (\hat{\mathbf{Y}}' \hat{\mathbf{Y}} - n \bar{y} \bar{y}') + \mathcal{E}' \mathcal{E}$$

$(p \times p)$

$$= \mathbf{SSP}_H + \mathbf{SSP}_E = \mathbf{H} + \mathbf{E}$$

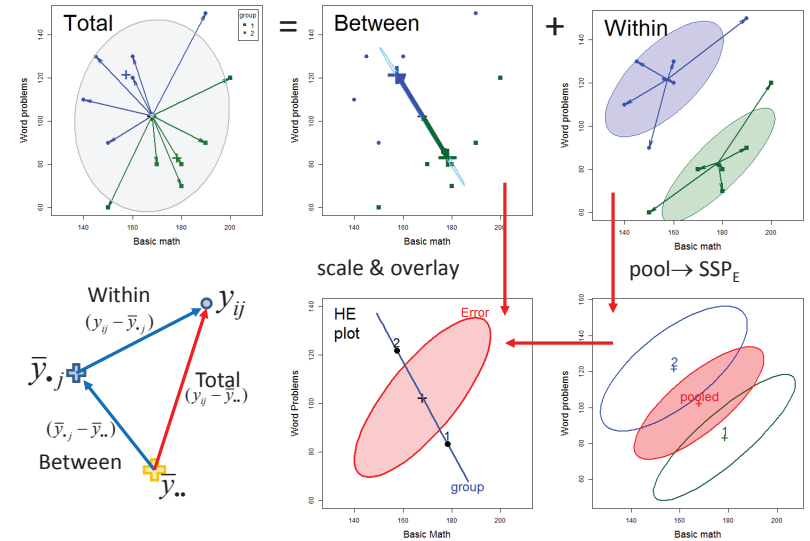
• Hypothesis tests

- Eigenvalues $\lambda_i, i=1:p$ of $\mathbf{H} \mathbf{E}^{-1}$
- Wilks' Λ , Pillai & Hotelling trace, Roy's test
- how many dimensions (aspects of responses)?

How big is **hypothesis** variation relative to **error** variation?

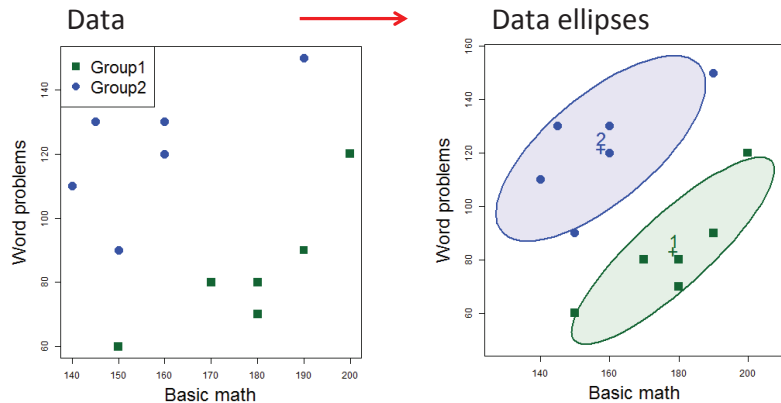
Ah, but there are up to $s = \min(p, df_H)$ dimensions of size

Visualizing $\mathbf{SSP}_T = \mathbf{SSP}_H + \mathbf{SSP}_E$



Data ellipsoids

The data ellipsoid is a **sufficient visual summary** for multivariate location & scatter, just as (\bar{y}, \mathbf{S}) are sufficient for (μ, Σ)



Data ellipsoids: definitions

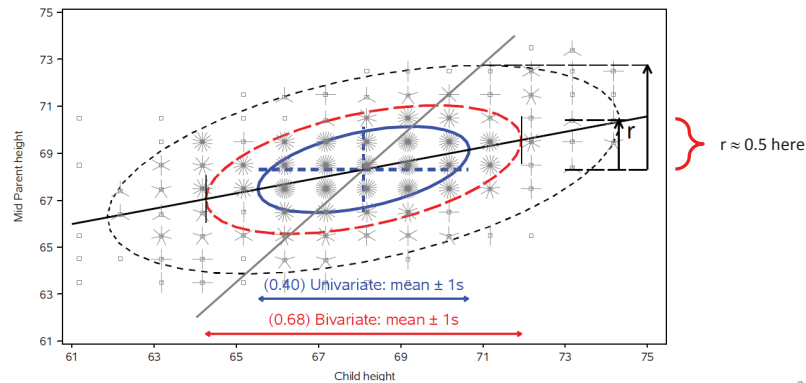
- For a p -dimensional multivariate sample, $\mathbf{Y}_{N \times p}$, the sample mean vector, \bar{y} , and sample covariance matrix, \mathbf{S} , are **minimally sufficient statistics** under classical (gaussian) assumptions.
- These can be represented visually by the p -dimensional **data ellipsoid**, \mathcal{E}_c of size ("radius") c centered at \bar{y} ,

$$\mathcal{E}_c(\bar{y}, \mathbf{S}) := \{ \mathbf{y} : (\mathbf{y} - \bar{y})^T \mathbf{S}^{-1} (\mathbf{y} - \bar{y}) \leq c^2 \} \quad \text{or,} \quad D_M^2(\mathbf{y}) \leq c^2$$

- \rightarrow an ellipsoid centered at the means whose size & shape reflects variances & covariances
- We consider this a **minimally sufficient visual summary** of multivariate location and scatter.

Data ellipsoids: properties

- Ellipsoid boundary: Mahalanobis $D_M^2(y_i) \sim \chi_p^2$
 - $p=2$: shadows generalize univariate **confidence intervals**
 - eccentricity: precision; **visual estimate** of correlation



21

The HE plot framework

- Hypothesis-Error (HE) plots
 - Visualize multivariate tests in the MLM
 - Linear hypotheses--- lower-dimensional ellipsoids
 - Extension: HE plot matrices
- Canonical displays
 - low-dimensional multivariate juicers
 - shows data in the space of maximal effects
- Covariance ellipsoids
 - visualize tests of homogeneity of covariance matrices
- For all: **robust** methods are available or good research projects!

22

HE plot framework: Trivial example

Two groups of middle-school students are taught algebra by instructors using different methods, and then tested on:

- BM**: basic math problems (7 * 23 - 2 * 9 = ?)
- WP**: word problems ("a train travels at 23 mph for 7 hours, but for 2 hours ...")

Do the groups differ on (BM, WP) by a multivariate test?
If so, how ???

```
> data(mathscore, package="heplots")
> mod <- lm(cbind(BM, WP) ~ group, data=mathscore)
> Anova(mod)
```

```
Type II MANOVA Tests: Pillai test statistic
Df test stat approx F num Df den Df Pr(>F)
group 1 0.86518 28.878 2 9 0.0001213 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

23

Follow along

The R script ([mathscore-ex.R](#)) for this example is linked on the course page. Download and open in R Studio to follow along.

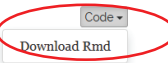
- Examples:
 - Math scores: Simple demo of MLMs [mathscore-simple.R](#)
 - Math scores: HE plot examples [mathscore-ex.R](#) | [mathscore-ex.html](#)
 - Penguins data: [Multivariate EDA vignette](#)
 - Diabetes data: [heplots and candisc examples vignette](#)
- HW: explore other examples

The script was run with `knitr` (ctrl+shift+K) in R Studio to create the HTML output ([mathscore-ex.html](#))

The **Code** button there allows you do download the R code and comments

Math scores: HE plot examples

Michael Friendly



(R notebooks are a simple way to turn R scripts into finished documents)

24

Why do multivariate tests?

Could do univariate ANOVAs (or t-tests) on each response variable (BM, WP)

```
> Anova(lm(BM ~ group, data=mathscore))
Anova Table (Type II tests)

Response: BM
      Sum Sq Df F value Pr(>F)
group    1302  1  4.24  0.066 .
Residuals 3071 10
```

```
> Anova(lm(WP ~ group, data=mathscore))
Anova Table (Type II tests)

Response: WP
      Sum Sq Df F value Pr(>F)
group    4408  1  10.4  0.009 **
Residuals 4217 10
```

From this, might conclude that:

- Groups don't differ on Basic Math score ✘
- Groups are significantly different on Word problems ✔

Multivariate tests:

- Do not require correcting for multiple tests (e.g., Bonferroni)
- Combine evidence from multiple response variables ("pooling strength")
- Show how the multivariate responses are jointly related to the predictors
 - How many aspects (dimensions?)

Why do multivariate tests?

Overall test is highly significant:

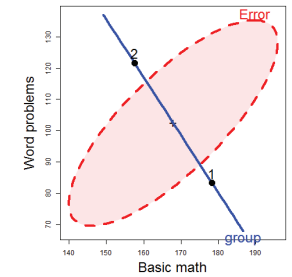
- Combines the evidence for all predictors ✔
- Takes response correlations into account ✔

```
> mod <- lm(cbind(BM, WP) ~ group, data=mathscore)
> Anova(mod)
```

```
Type II MANOVA Tests: Pillai test statistic
      Df test stat approx F num Df den Df Pr(>F)
group  1  0.86518  28.878  2  9 0.0001213 ***
```

Visual test of significance (Roy's test)

- The H ellipse projects outside the E ellipse iff the effect is significant.

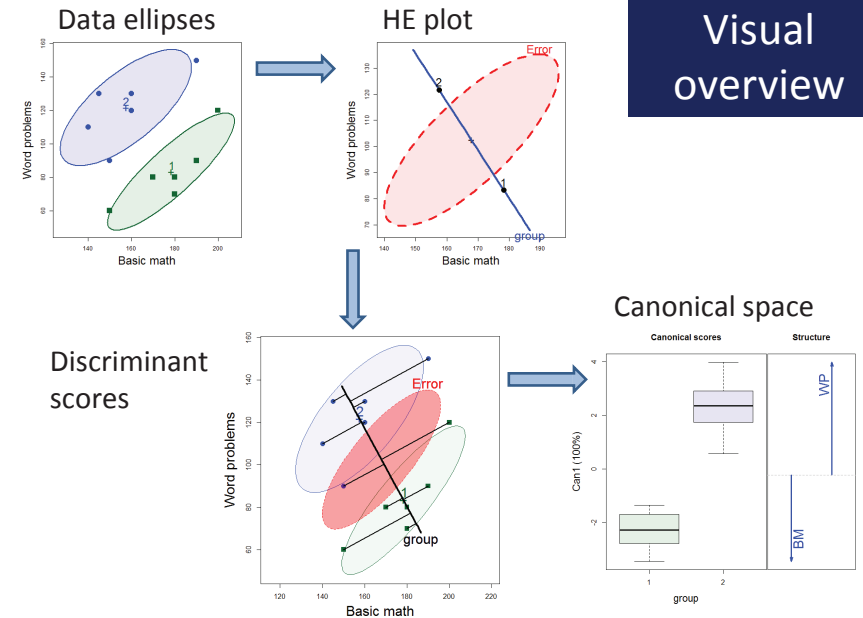
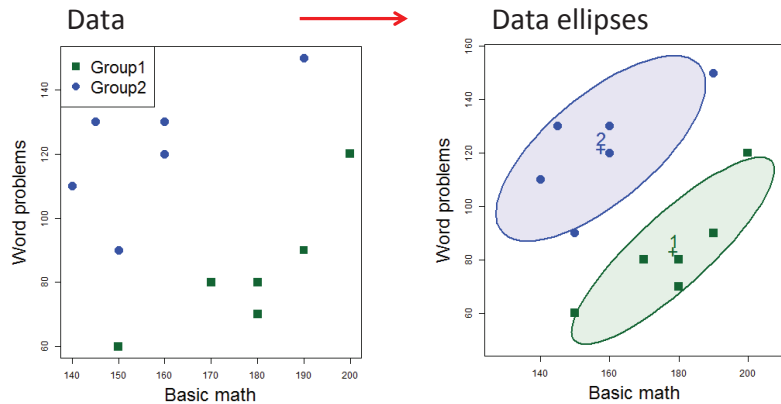


HE plot provides an interpretation:

- Group 1 > Group 2 on Basic Math, but worse on Word Problems
- Group 2 > Group 1 on Word Problems, but worse on Basic Math
- BM & WP are + correlated w/in groups

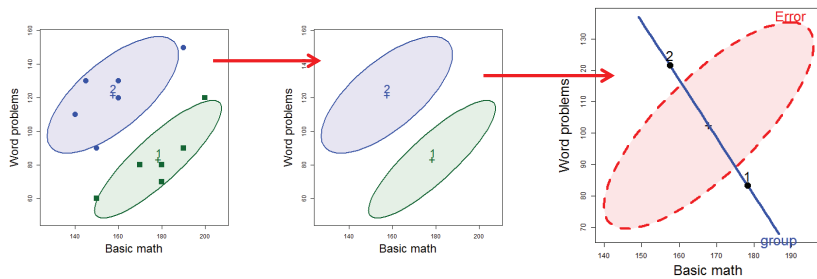
HE plot framework: Visual overview

The data ellipsoid is a sufficient visual summary for multivariate location & scatter, just as (\bar{y}, S) are sufficient for (μ, Σ)



Visual overview

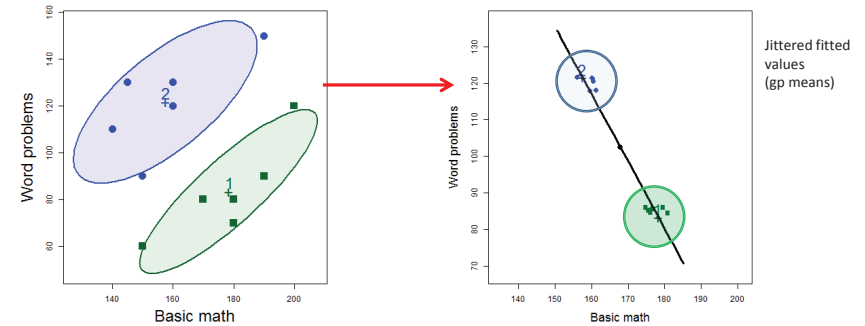
Data → Data ellipses → HE plot



- Differences between group means are shown by the **H** ellipse— data ellipsoid of the **fitted** values (w/ 1 df, degenerates to a line)
 - Direction shows relation of groups to response variables
 - Size shows “how big is H relative to E”
- Variation within groups is reflected in the **E** ellipsoid-- data ellipsoid of the **residuals**
 - Direction: residual (partial) correlation between BM & WP
 - Size/shape: residual variance

29

The H ellipse

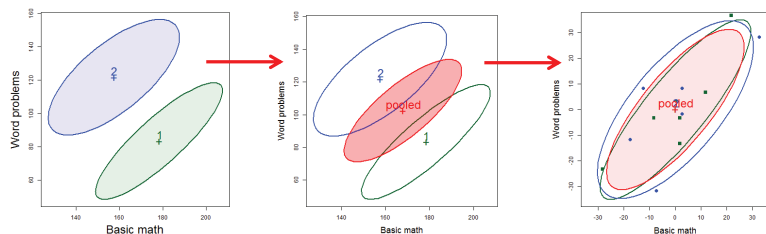


- The **H** ellipse is the data ellipse of the fitted values (group means, here)
 - The **H** matrix is the sum of squares and crossproducts of the fitted values, corrected for the grand mean

$$\mathbf{H} = (\hat{\mathbf{Y}}' \hat{\mathbf{Y}} - n \bar{y} \bar{y}')$$

30

The E ellipse



- The **E** ellipse is the data ellipse of the residuals
 - What you get when you subtract the group means from all observations, shifting them to the grand means.
 - E** matrix called the “within-group **pooled** covariance matrix”

$$\mathbf{E} = (\hat{\mathbf{Y}} - \bar{\mathbf{Y}})' (\hat{\mathbf{Y}} - \bar{\mathbf{Y}}) = \mathcal{E}' \mathcal{E}$$

31

H & E in numbers

The **H** and **E** matrices are calculated in the `car::Anova()` function and saved as the **SSP** and **SSPE** components, used in the statistical tests.

```
> math.aov <- Anova(math.mod)
> (H <- math.aov$SSP)
$group
      BM      WP
BM 1302.1 -2395.8
WP -2395.8  4408.3
```

Direct calculation: $\mathbf{H} = (\hat{\mathbf{Y}}' \hat{\mathbf{Y}} - n \bar{y} \bar{y}')$

```
> fit <- fitted(math.mod)
> ybar <- colMeans(mathscore[,2:3])
> n <- nrow(mathscore)
> crossprod(fit) - n*outer(ybar, ybar)
      BM      WP
BM 1302.1 -2395.8
WP -2395.8  4408.3
```

```
> fit
      BM      WP
1 178.33  83.333
2 178.33  83.333
3 178.33  83.333
4 178.33  83.333
5 178.33  83.333
6 178.33  83.333
7 157.50 121.667
8 157.50 121.667
9 157.50 121.667
10 157.50 121.667
11 157.50 121.667
12 157.50 121.667
```

32

H & E in numbers

```
> (E <- math.aov$SSPE)
      BM      WP
BM 3070.8 2808.3
WP 2808.3 4216.7
```

Direct calculation: $\mathbf{E} = (\hat{\mathbf{Y}} - \bar{\mathbf{Y}})'(\hat{\mathbf{Y}} - \bar{\mathbf{Y}}) = \mathcal{E}'\mathcal{E}$

```
> resid <- residuals(math.mod)
> crossprod(resid)
      BM      WP
BM 3070.8 2808.3
WP 2808.3 4216.7
```

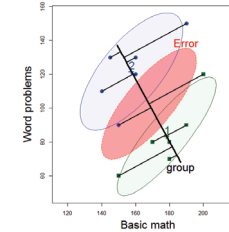
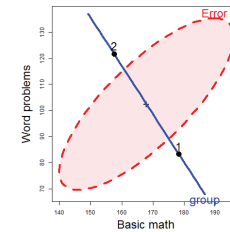
```
> cor(resid)
      BM      WP
BM 1.00 0.78
WP 0.78 1.00
```

```
> resid
      BM      WP
1  11.667  6.667
2  -8.333 -3.333
3   1.667 -3.333
4  21.667 36.667
5 -28.333 -23.333
6   1.667 -13.333
7   2.500 -1.667
8  32.500 28.333
9  -7.500 -31.667
10  2.500  8.333
11 -17.500 -11.667
12 -12.500  8.333
```

33

Discriminant analysis

- MANOVA and linear discriminant analysis (LDA) are intimately related and differ mainly in perspective:
 - MANOVA: Do means of groups on 2+ responses differ?
 - LDA: Find weighted sums of responses that best discriminate groups
- In both cases,
 - Group differences are represented by the **H** matrix; residuals: **E** matrix
 - Test statistics based on eigenvalues of \mathbf{HE}^{-1}
 - Discriminant weights are eigenvectors of \mathbf{HE}^{-1}



34

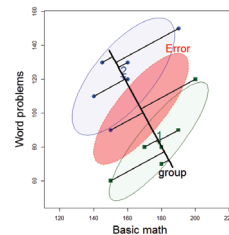
Discriminant analysis

- For 2 groups,
 - the discriminant axis is the line joining the two group centroids,
 - discriminant scores are the projections of observations on this line.
- MASS:lda() does this analysis

```
> (mod.lda <- MASS::lda(group ~ ., mathscore))
```

```
Group means:
      BM      WP
1 178.3  83.33
2 157.5 121.67
```

```
Coefficients of linear discriminants:
      LD1
BM -0.08350
WP  0.07527
```

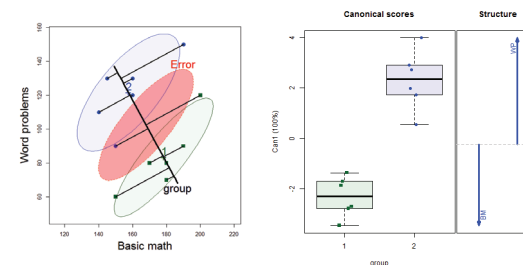


The canonical dimension is $\text{Can1} = 0.075 \text{ WP} - 0.083 \text{ BM}$, a contrast between the two tests

35

Canonical space

- The HE plot view shows the data in **data** space
- Easier to see effects by projecting scores to **canonical** space – the best-discriminating axes.
- For a 1 df effect, there is only one canonical dimension
 - Arrows show the relative size & direction of discriminant weights



```
library(candisc)
mod.can <- candisc(math.mod)
plot(mod.can)
```

36

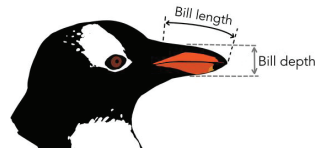
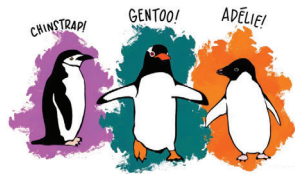
Penguin data

- Data on 3 species of penguins, measured on 3 Antarctic islands

- How does penguin "size" differ by species, island, ... ?



```
> library(palmerpenguins)
> peng <- penguins %>% rename(...) %>% ... # clean up names, etc.
> peng[sample(1:333, 5), ]
# A tibble: 5 x 8
  species island  bill_length bill_depth flipper_length body_mass sex  year
<fct> <fct> <dbl> <dbl> <int> <int> <fct> <int>
1 Chinstrap Dream 58 17.8 181 3700 f 2007
2 Adelle Torgersen 39.6 17.2 196 3550 f 2008
3 Gentoo Biscoe 46.2 14.1 217 4375 f 2009
4 Chinstrap Dream 49 19.5 210 3950 m 2008
5 Gentoo Biscoe 50.4 15.7 222 5750 m 2009
```

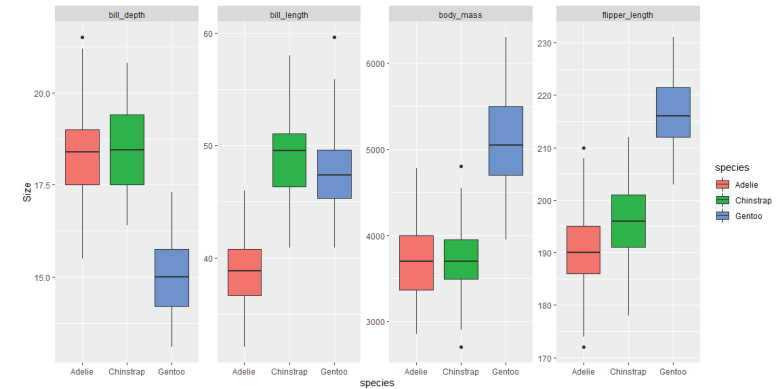


37

Penguins: Multivariate EDA

Boxplots by grouping variables (factors) are often useful for an initial overview

- Can show multiple variables, but hard for >1 factor.
- What is the pattern here?



38

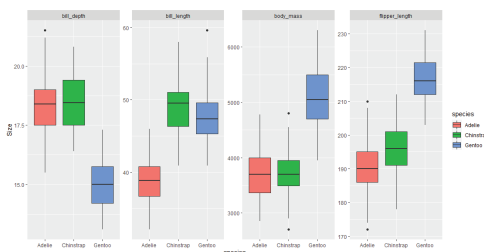
Penguins: Multivariate EDA

Boxplots by grouping variables (factors) are often useful for an initial overview

- Need to reshape data from wide to long format

```
peng_long <- peng |> # convert wide to long format
  tidyr::gather(Measure, Size, bill_length:body_mass)

ggplot(peng_long, aes(x=species, y=Size, fill=species)) +
  geom_boxplot() +
  facet_wrap(~ Measure, scales="free_y", nrow=1)
```



39

PCA & Biplots

- For multivariate data, often want to view the data in a low-D space that shows the most **total variance**
- PCA: finds weighted sums of variables which are:
 - Uncorrelated
 - Account for maximum variance
 - How many dimensions are necessary?
- A biplot is a 2D (or 3D) plot of the largest PCA dimensions
 - Vectors** in this plot show the original data variables
 - Points** in this plot show the observations
 - Data ellipses here show within group relations

40

PCA animation

PCA:

- PC1 is the direction along which points have max. variance
- Equivalently, the perp. deviations from the line have min. residual SS

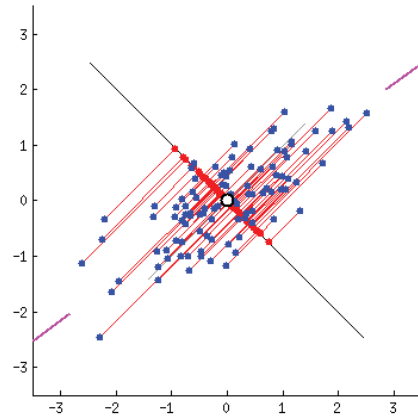
PCA by springs

- Imagine each pt connected to a possible PC1 line by springs
- Force \sim deviation²

Forces balance, naturally seek the min. residual SS position.

Voila, QED!

- A visual proof



PCA

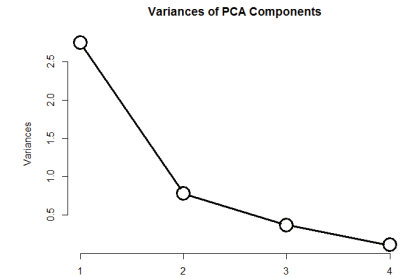
```
peng.pca <- prcomp (~ bill_length + bill_depth + flipper_length + body_mass,
  data=peng,
  na.action=na.omit,
  scale. = TRUE)
screplot(peng.pca, type = "line", lwd=3, cex=3,
  main="Variances of PCA Components")
```

```
> summary(peng.pca)
Importance of components:
          PC1  PC2  PC3  PC4
Standard deviation  1.657 0.882 0.6072 0.328
Proportion of Variance 0.686 0.195 0.0922 0.027
Cumulative Proportion 0.686 0.881 0.9730 1.000
```

2D: 88.1 %

3D: 97.3 %

See: <https://rpubs.com/friendly/penguin-biplots> for details



42

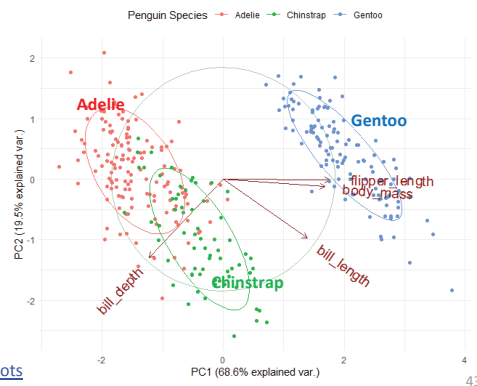
Biplot

```
library(ggbiplot)
ggbiplot(peng.pca, obs.scale = 1, var.scale = 1,
  groups = peng$species,
  ellipse = TRUE, circle = TRUE) +
  scale_color_discrete(name = 'Penguin Species')
```

PC1, PC2 \sim 88.1% of variance

- PC1: largely flipper length & body mass: "penguin size"
- PC2 (& PC1): relates to "bill shape"

Easy to characterize the species in terms of these variables



See: <https://rpubs.com/friendly/penguin-biplots>

43

Penguins: MANOVA

Assume the goal is to determine whether/how the penguins differ in "size" by species

- A MLM tests all 4 size variables together: \sim species
- Could also use other factors: \sim species + sex + island

```
> peng.mod0 <- lm(cbind(bill_length, bill_depth, flipper_length, body_mass) ~ species,
  data=peng)
> Anova(peng.mod0)

Type II MANOVA Tests: Pillai test statistic
Df test stat approx F num Df den Df Pr(>F)
species 2 1.64 371 8 656 <2e-16 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

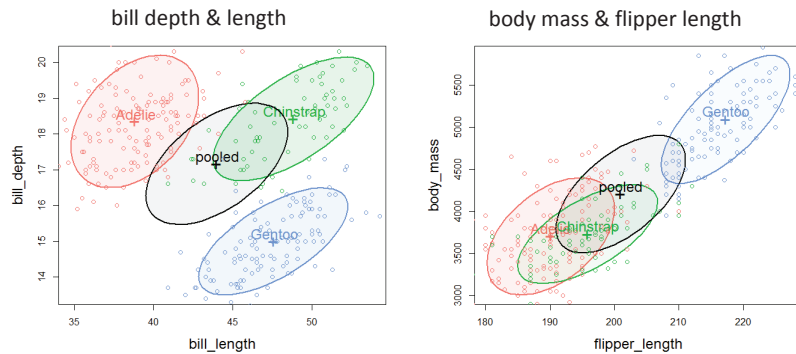
Yet, we are left to understand the nature of this effect wrt. the size variables.

See: <https://rpubs.com/friendly/penguin-manova> for details

44

Penguins: view data ellipses

Data ellipses in 2D provide a good start for pairwise relations



- group means **negatively** correlated
- within group correlation > 0

45

HE plot details

- **E** ellipse reflects within-group error (co)variation
 - Size: E / df_e set to cover 68%, an analog of $\bar{y} \pm 1$ std
 - Shift to grand mean for direct comparison with **H**
- **H** ellipse reflects (co)variation of group means
 - **effect size** scaling, uses H/df_e to put this on the same scale as the **E** ellipse. Analog of effect size in univariate designs.
 - **significance** (“evidence”) scaling: uses $H/\lambda_\alpha df_e$.
 - The **H** ellipse protrudes outside the **E** ellipse somewhere, *iff* an effect is significant (Roy’s largest root test) at $p < \alpha$

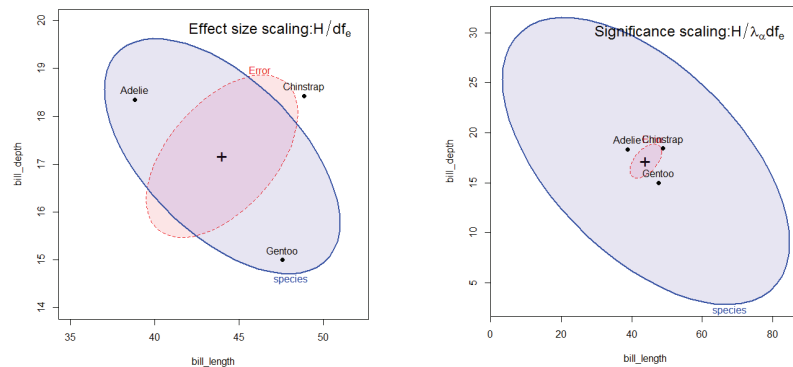


46

Penguins: HE plots

Orientation of the **H** ellipse reflects **negative** correlation of the species means: species with larger bill depth have smaller bill length (bill “shape”?)

E ellipse: **within species**, larger bill length → larger bill depth



heplot(peng.mod0, size="effect")

heplot(peng.mod0, size="evidence")

47

Contrasts

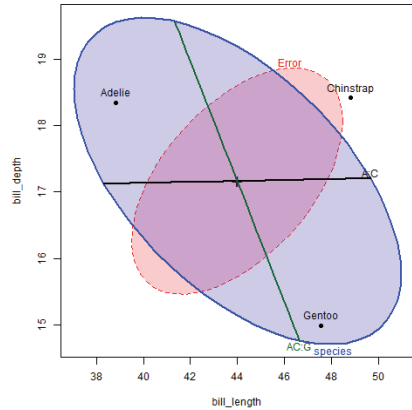
- In linear models, any effect of $df_h > 1$ can be partitioned into df_h separate 1 df tests of contrasts
 - If orthogonal, $H = H_1 + H_2 + \dots H_{dfh}$ -- accounts for total effect
 - Tested as a linear hypothesis, e.g., $x_1 - (x_2 + x_3)/2 = 0$
 - Each H_i has rank=1, so appears as a line in HE plots
- Assume we want to compare the species as two contrasts:
 - Do Adelie differ from Chinstrap?
 - Do Gentoo penguins differ from the other two?

```
> contrasts(peng$species) <- matrix(c(1, -1, 0, -1, -1, -2), 3, 2)
> contrasts(peng$species)
      [,1] [,2]
Adelie    1   -1
Chinstrap -1   -1
Gentoo    0    2
```

48

Contrasts

```
hyp <- list("A:C"="species1", "AC:G"="species2") # give names to contrasts
heplot(peng.mod0, fill=TRUE, fill.alpha=0.2,
       hypotheses=hyp, size="effect")
```



Result is very clear:

- Adelle & Chinstrap differ only in bill length
- Gentoo differ from other two – longer, but less deep bills (bill shape)

Both of these are large effects!

Together, they are the entire species effect!

49

Other models

```
peng.mod2 <- lm(cbind(bill_length, bill_depth, flipper_length, body_mass) ~ species + sex, data=peng)
Anova(peng.mod2)
```

Type II MANOVA Tests: Pillai test statistic

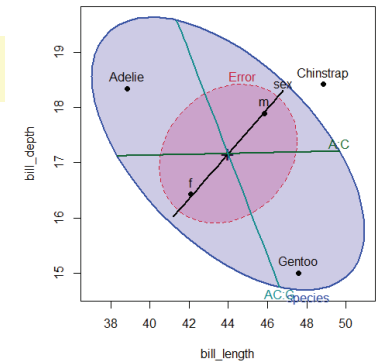
	Df	test stat	approx F	num Df	den Df	Pr(>F)
species	2	1.65480	391.89	8	654	< 2.2e-16 ***
sex	1	0.64004	144.91	4	326	< 2.2e-16 ***

```
heplot(peng.mod2, fill=TRUE, fill.alpha=0.2,
       hypotheses=hyp)
```

Effect of sex: male penguins have larger bills

Adding sex reduces E variances
→ Effect of species now more pronounced

Each 1 df effect plots as a line



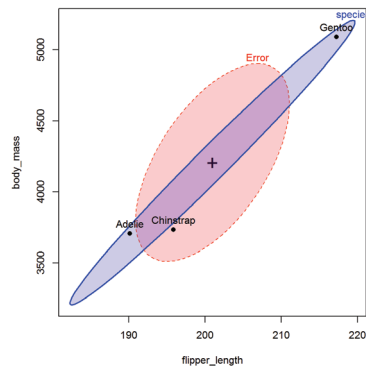
Other HE plots

- 2D: can plot any pair of responses in data space
- pairs.mlm(): all pairwise 2D views
- heplot3d(): plots in 3D, can rotate, spin, zoom, ...

```
heplot(peng.mod0, variables=3:4,
       fill=TRUE, fill.alpha=0.2, size="effect")
```

Interpretation:

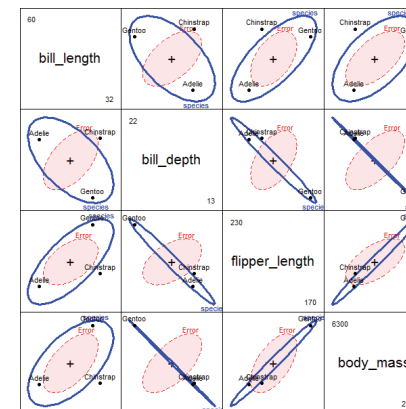
- major axis of the H ellipse measures "penguin size"
- Gentoo are the Big Birds in this story!



49

HE Pairs plots

The pairs() method for mlm objects gives all pairwise HE plots in a scatterplot matrix format.



```
pairs(peng.mod0, size="effect",
      fill=c(TRUE, FALSE))
```

Something new here:

- avg. bill depth is negatively correlated with "size" variables – larger penguin species have smaller bill depths (curvature?)
- correlation of avg. bill depth with body mass nearly -1

52

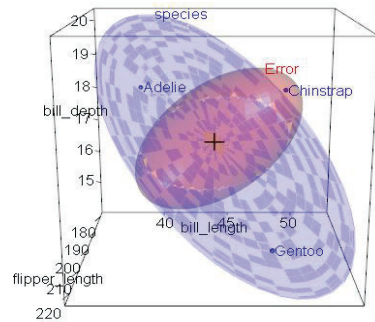
heplot3d()

3D HE plots can show other features

```
heplot3d(peng.mod0, size="effect")
```

The H ellipsoid here is flat (2D), because the species effect has 2 df

In this 3D view, the 3 species form a triangle, suggesting some further interpretation, not seen in 2D views



53

Canonical view

- 4 response variables, but only $s=\min(q, dfh)=2$ dimensions.
 - Here, both dimensions are significant
 - Can1 accounts for 86.5% of between-species variance
 - Can 2 accounts for the rest: 13.5%

```
> library(candisc)
> (peng.can <- candisc(peng.mod0))
```

Canonical Discriminant Analysis for species:

	CanRsq	Eigenvalue	Difference	Percent	Cumulative
1	0.938	15.03	12.7	86.5	86.5
2	0.700	2.34	12.7	13.5	100.0

Test of H0: The canonical correlations in the current row and all that follow are zero

	LR test	stat	approx	F	numDF	denDF	Pr(> F)
1		0.0187		516	8	654	<2e-16 ***
2		0.2997		255	3	328	<2e-16 ***

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

54

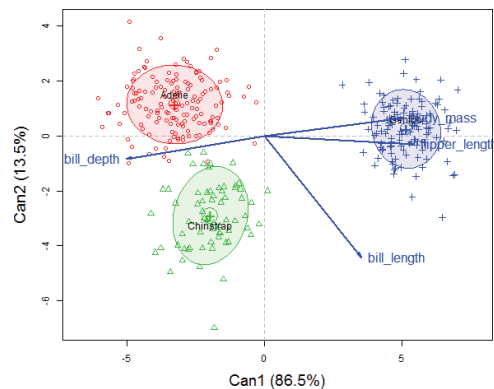
Canonical view

The plot() method for candisc objects shows points for observations and vector for variables

```
plot(peng.can, ellipse = TRUE ... ) #plot CAN scores with ellipses
```

Can1: largely body mass & flipper length, that separate Gentoo from (Adelie, Chinstrap)

Can2: bill length distinguishes Chinstrap from others.



Canonical HE plot

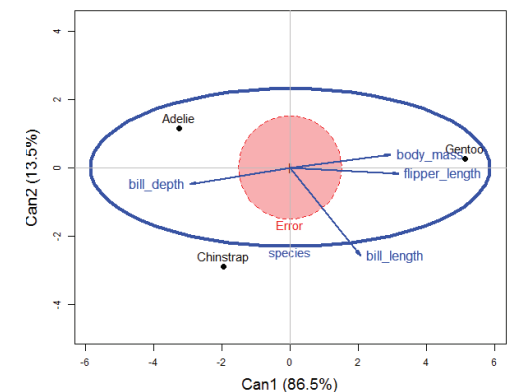
```
heplot(peng.can, size="effect", fill=c(TRUE, FALSE))
```

Here is the **entire** effect of species shown in one HE plot

In CAN space, residuals are uncorrelated: $E = \text{circle}$

Size of H shows the total effect of species

Variable vectors show how the groups are discriminated.



56

Checking assumptions

- Assumptions in the MLM extend those in univariate models
 - Linearity: Each y_i is linearly related to all x s
 - Constant variance matrices of residuals

$$S_1 = S_2 = \dots = S_g \quad \left. \vphantom{S_1 = S_2 = \dots = S_g} \right\} \epsilon_i \sim \text{MVN}(\mathbf{0}, \Sigma)$$
 - Residuals are multivariate normal
- In addition, need to check
 - No multivariate outliers
 - No multicollinearity among predictors

57

Checking assumptions

- Linearity: plot each y_i against each x_j
 - quantitative x_j : `plot(y_i ~ x_j) + loess smooth`
 - factor: boxplots
- Constant variance
 - visual: plot data ellipses for each group
 - `heplots::covEllipses(data, group=, ...)`
 - univariate-- levene test: `heplots::leveneTests()`
 - multivariate-- Box M test: $H_0 : \Sigma_1 = \Sigma_2 = \dots = \Sigma_g$
 - `res <- heplots::boxM(); plot(res)`
- Multivariate outliers
 - Mahalanobis $D^2(\mathbf{y}_i) \sim \chi^2_p$: outlier if `prob(χ^2_p) < .01`
 - Chisquare QQ plot: `plot D^2(y_i) vs. χ^2_p quantiles: cqplot()`

58

Constant variance: Visual

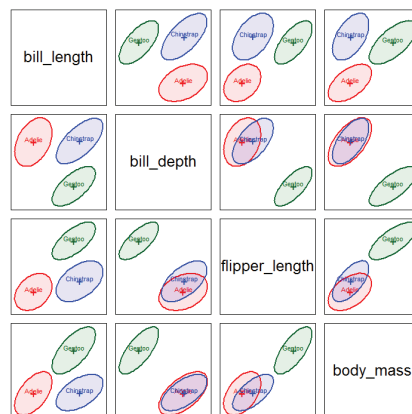
`heplots::covEllipses()` plots the data ellipses for each group, for 2+ variables
Are the sizes and shapes & orientations \cong the same in all panels?

Approximately true, w/ some differences

- Gentoo looks a bit smaller
- Adelie: correlations \sim differ?

This might be good enough

```
covEllipses(peng[,3:6],
             group = peng$species,
             variables=1:4, # all pairs
             fill=TRUE, fill.alpha=0.1,
             pooled=FALSE)
```

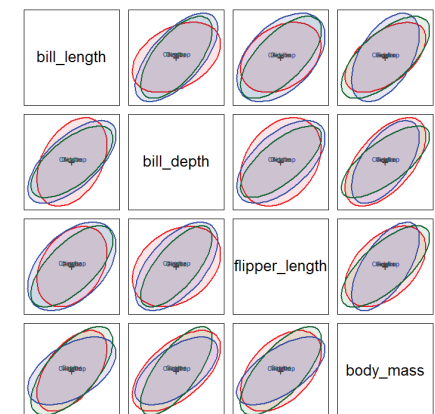


59

Constant variance: Visual

This is easier to judge if all groups are centered at the grand mean in each panel

```
covEllipses(peng[,3:6],
             group = peng$species,
             variables=1:4,
             center=TRUE,
             fill=TRUE, fill.alpha=0.1,
             pooled=FALSE)
```



60

Constant variance: statistical tests

Levene tests for each response variable separately:

```
> hep1ots::leveneTests(peng[,3:6], group=peng$species)
Levene's Tests for Homogeneity of Variance (center = median)
```

	df1	df2	F value	Pr(>F)
bill_length	2	330	2.29	0.1033
bill_depth	2	330	1.91	0.1494
flipper_length	2	330	0.44	0.6426
body_mass	2	330	5.13	0.0064 **

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

Box's M test: all responses together – equal variances & correlations !

```
> hep1ots::boxM(peng[,3:6], group = peng$species)
```

Box's M-test for Homogeneity of Covariance Matrices

data: peng[, 3:6]
Chi-Sq (approx.) = 75, df = 20, p-value = 3e-08

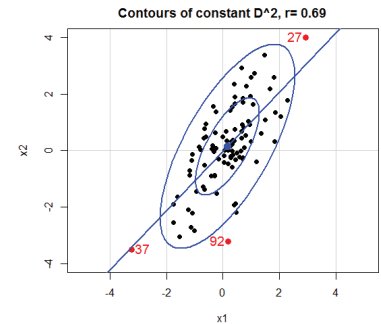
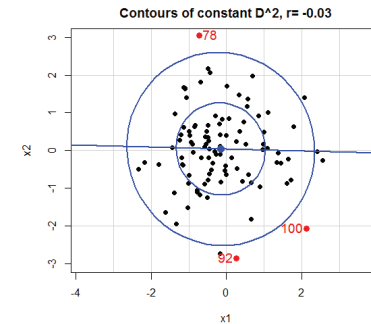
NB: Box's M test is highly sensitive to small differences; use $\alpha = 0.001$

Multivariate normality: $z^2 \rightarrow D^2$

For MVN & outliers, Mahalanobis D^2 generalizes z scores

- 1 variable: $z_i = (x_i - \bar{x})/s \sim N(0,1)$ or, $z_i^2 \sim \chi^2_{(1)}$
- 2 variables, uncorrelated: squared distance from mean is $D_i^2 = z_{i1}^2 + z_{i2}^2 \sim \chi^2_{(2)}$
- p variables: $D_i^2 =$ Mahalanobis squared distance of x_i from centroid

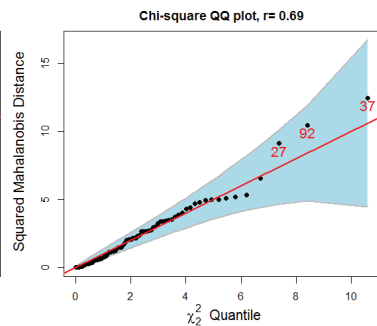
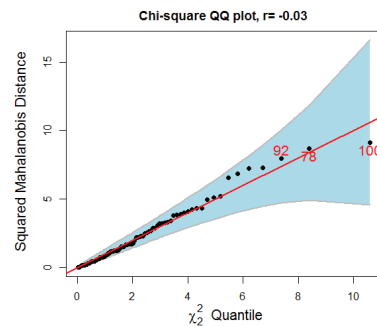
$$D_i^2 = (x_i - \bar{x})^T S^{-1} (x_i - \bar{x}) \sim \chi^2_{(p)}$$



Chi-squared QQ plot

- QQ plot of ordered distances, $D^2_{(i)}$ vs $\chi^2_{(p)}$ quantiles should plot as a 45° line through origin if MVN
- Multivariate outliers: outside the envelope
- Here: both cases check out as OK: no outliers, MVN ✓

```
heplots::cqplot(df, id.n=3)
```



Penguins: MVN & outliers

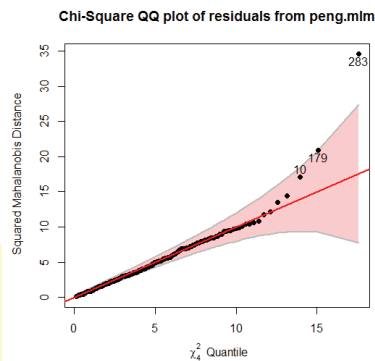


Penguins: MVN & outliers

```
heplots::cqqplot(peng.mlm,
  id.n = 3, conf=0.999)
```

```
Get D2 values
  with rstatix::mahalanobis_distance
Find z-scores
Select outliers (is.outlier==TRUE)
```

```
peng |>
  group_by(species) |>
  mahalanobis_distance(bill_length:body_mass) |>
  tibble::rownames_to_column() |>
  mutate(across(bill_length:body_mass,
    .fns= scale)) |>
  filter(is.outlier == TRUE) |>
  as.data.frame()
```



```
rowname bill_length bill_depth flipper_length body_mass mahal.dist is.outlier
1 283 2.561 0.3225 -1.425 -0.6297 27.76 TRUE
```

66

MVN: Numerical tests

- Shapiro-Wilk test
 - Originally for univariate normality: `stats::shapiro.test()`
 - Multivariate version: `rstatix::mshapiro_test()`

```
peng |>
  select(bill_length : body_mass) |>
  rstatix::mshapiro_test()
```

```
# A tibble: 1 x 2
  statistic p.value
  <dbl>     <dbl>
1 0.978 0.0000484
```

- Mardia test: multivariate skewness & kurtosis

```
res <- MVN::mvn(data = peng[,c(3:6)],
  mvnTest="mardia")
res$multivariateNormality
```

	Test	Statistic	p value	Result
1	Mardia Skewness	127.42	< 0.001	NO
2	Mardia Kurtosis	-2.51	0.0118	NO
3	MVN	<NA>	<NA>	NO

- But: these are overly-sensitive; MLM is relatively robust

67

Summary

- MLM just like univariate LM, but for multiple responses
 - Simultaneous tests – no need for p-value adjustment
 - Take correlations among responses into account
 - Indicates **# of dimensions** of responses
- Data ellipses
 - Summarize bivariate data to show means, variances, correlation
 - MANOVA: shows how groups differ in these
- HE framework
 - Visualize multivariate tests in the MLM
 - Canonical displays show these results in the 2D (or 3D) space that accounts for largest **between-group variance**.
- Checking assumptions: visual tests are often sufficient
 - homogeneity of variances: `heplots::covEllipses()`
 - outliers & MVN: `heplots::cqqplot()`

68