

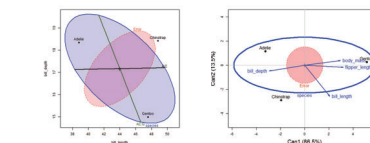
## Visualizing Linear Models: An R Bag of Tricks Session 2: Multivariate Models

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

## Today's topics

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



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## One-way ANOVA vs. MANOVA

ANOVA



Figure 8.1. The simple anova situation, when the differences among the populations are "real."

source: Cooley & Lohnes ((1971))

Do means differ?

(Assume equal within-group variances)

MANOVA

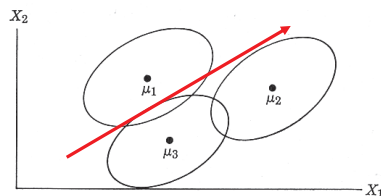


Figure 8.2. The simple manova situation, when the differences among the populations are "real."

How do centroids differ?  
How many dimensions?

(Assume equal within-group variance-covariance matrices)

## 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(income)
  - Polynomial terms: age<sup>2</sup>, age<sup>3</sup>, ...
  - Categorical predictors ("factors", class variables): treatment (control, drug A, drug B), sex
  - Interactions: treatment \* sex, age \* 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
```

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## Univariate linear model

- Model  $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}$   
 $(n \times 1) \quad (n \times q) \quad (1 \times q) \quad (n \times 1)$   
 $\mathbf{X} = (\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_q)$   
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

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

$$= SS_H + SS_E$$

- Hypothesis tests

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

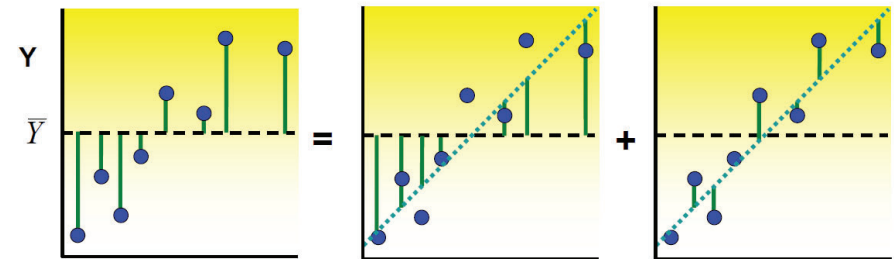
How big is **hypothesis** variation relative to **error** variation?

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## Regression: Visualizing $SS_T = SS_H + SS_E$

$$\text{Total variance} = \text{Regression variance} + \text{Residual variance}$$

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

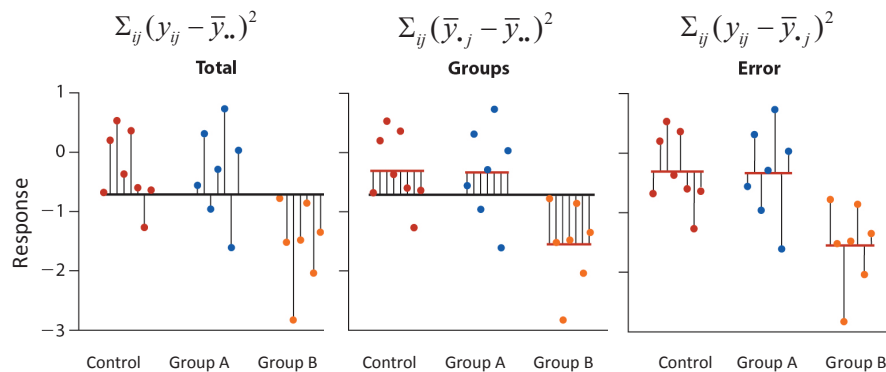


F test: How much better is the fitted regression line ( $\beta = \delta$ ) than the flat line ( $\beta = 0$ ) ?

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## ANOVA: Visualizing $SS_T = SS_H + SS_E$

$$\text{Total variance} = \text{Between group variance} + \text{Within group variance}$$



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

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## Multivariate linear model

- Model  $\mathbf{Y} = \mathbf{X}\mathbf{B} + \mathcal{E}$   
 $(n \times p) \quad (n \times q) \quad (q \times p) \quad (n \times p)$   
 $\mathbf{Y} = (\mathbf{y}_1, \mathbf{y}_2, \dots, \mathbf{y}_p)$   
matrix of  $p$  responses

- Sums of squares & cross-products

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

$$= SSP_H + SSP_E = \mathbf{H} + \mathbf{E}$$

- Hypothesis tests

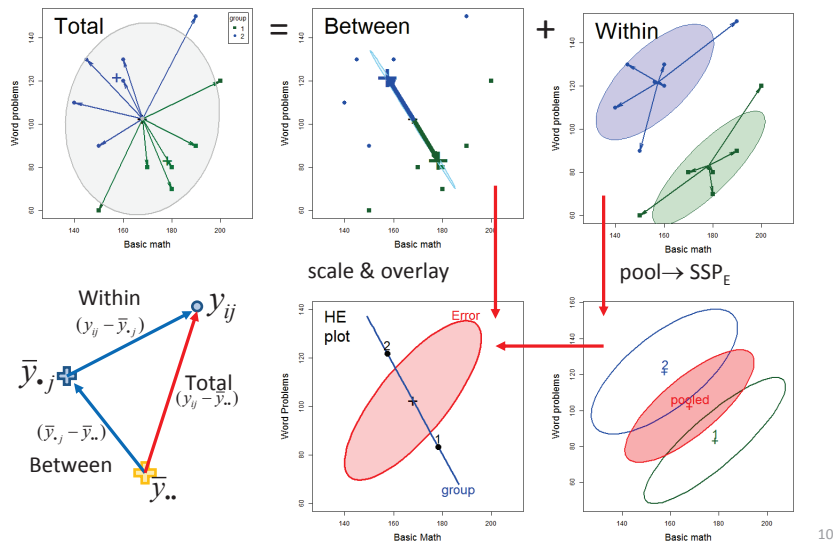
- Eigenvalues  $\lambda_i, i=1:p$  of  $\mathbf{H} \mathbf{E}^{-1}$
- Wilks'  $\Lambda$ , Pillai & Hotelling trace, Roy's test
- how many dimensions (aspects of responses)?

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

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

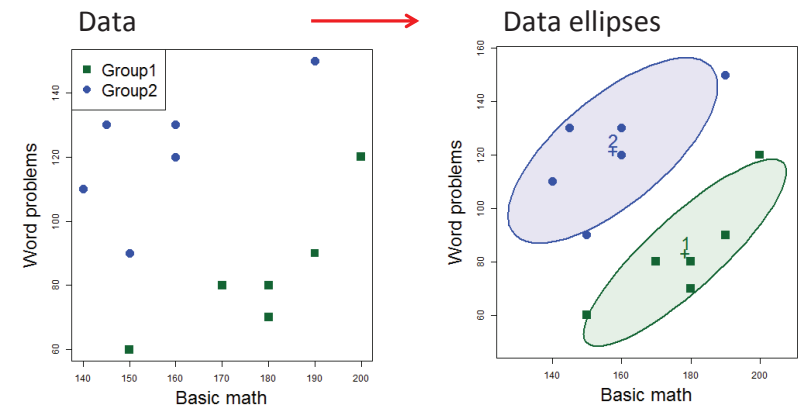
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## Visualizing $SSP_T = SSP_H + SSP_E$



## Data ellipsoids

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



## Data ellipsoids: definitions

- For a  $p$ -dimensional multivariate sample,  $\mathbf{Y}_{N \times p}$ , the sample mean vector,  $\bar{\mathbf{y}}$ , 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  $\bar{\mathbf{y}}$ ,

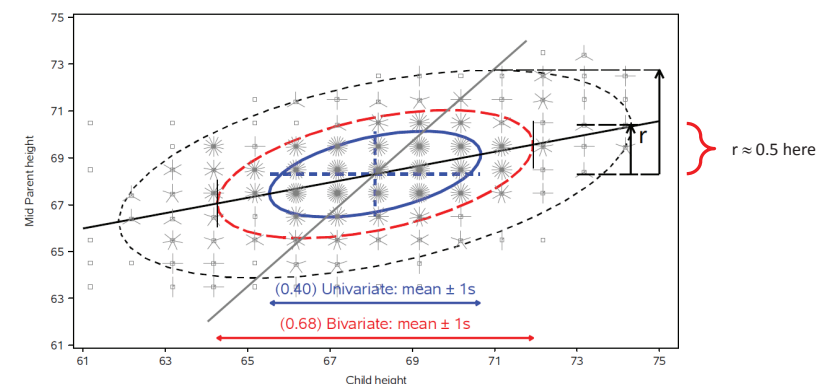
$$\mathcal{E}_c(\bar{\mathbf{y}}, \mathbf{S}) := \{\mathbf{y} : (\mathbf{y} - \bar{\mathbf{y}})^T \mathbf{S}^{-1} (\mathbf{y} - \bar{\mathbf{y}}) \leq c^2\} \quad \text{or,} \quad D_M^2(\mathbf{y}) \leq c^2$$

- 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.

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## Data ellipsoids: properties

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



## 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!

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## 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

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## 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.

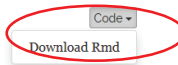
- Examples:
    - Math scores: Simple demo of MLMs [mathscore-simple.R](#)
    - Math scores: HE plot examples [mathscore-ex.R](#) || [mathscore-ex.html](#)
    - Penguins data: Multivariate EDA vignette
    - Diabetes data: [heplots and candisc examples vignette](#)
- HW: explore other examples

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 to 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)

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## 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)
```

	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)
```

	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?)

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# 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

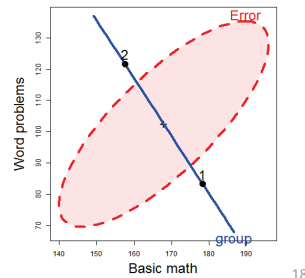
	Df test	stat	approx F	num Df	den Df	Pr(>F)
group	1	0.86518	28.878	2	9	0.0001213 ***

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:

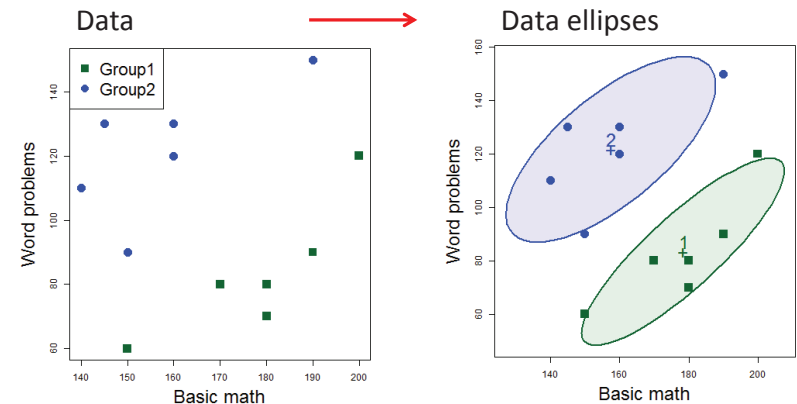
- Group 1 > Group 2 on Basic Math, but worse on Word Problems
- Group 2 > Group 1 on Word Problems, but worse on Basic Math
- BM & WP are + correlated w/in groups



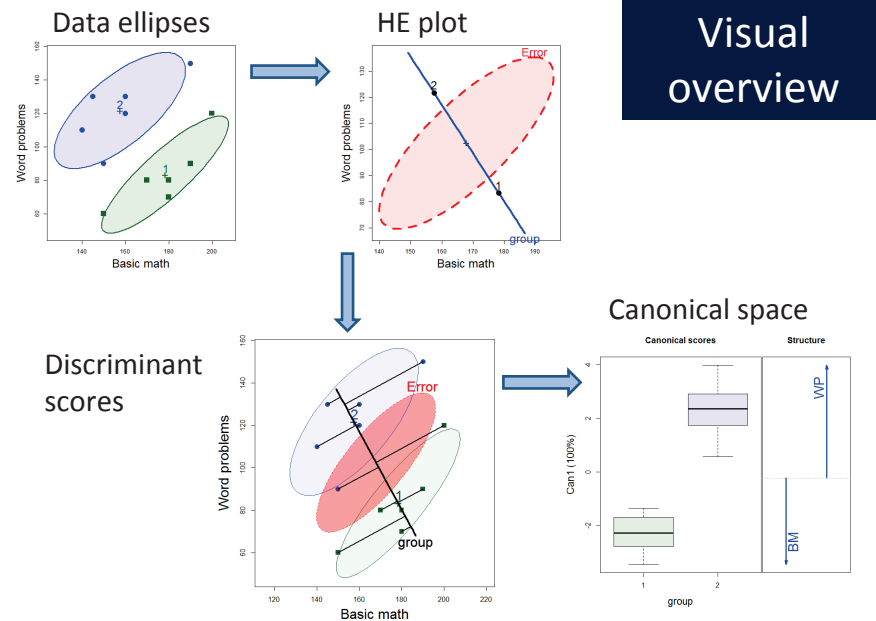
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# HE plot framework: Visual overview

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

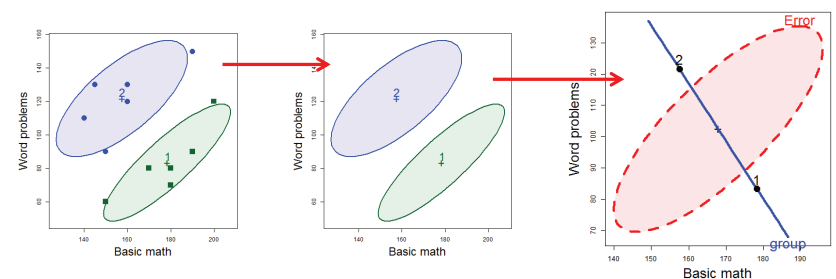


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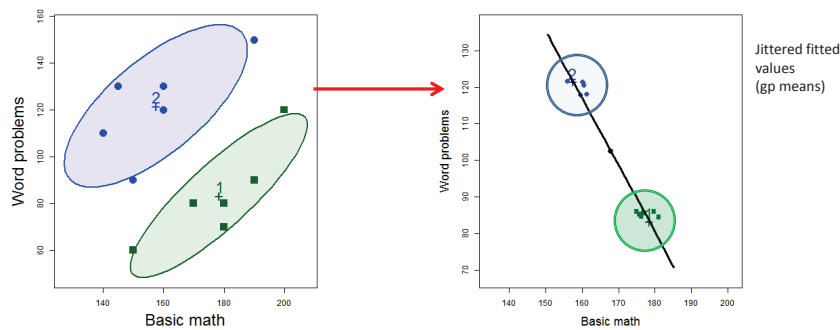
# Data → Data ellipses → HE plot



- Differences between group means are shown by the **H** ellipsoid-- 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

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## The H ellipse

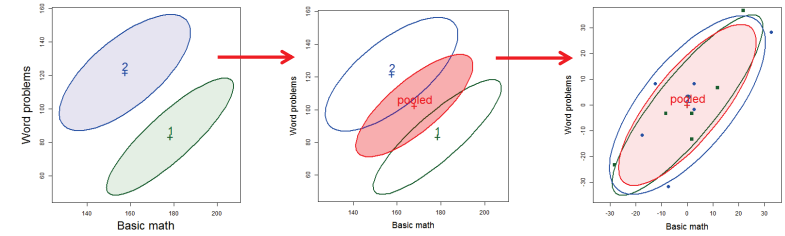


- The **H** ellipse is the data ellipse of the fitted values (group means, here)
  - The **H** matrix is the sum of squares and crossproducts of the fitted values, corrected for the grand mean

$$\mathbf{H} = (\hat{\mathbf{Y}}'\hat{\mathbf{Y}} - n\bar{y}\bar{y}')^2$$

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## 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”

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

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## 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:  $\mathbf{H} = (\hat{\mathbf{Y}}'\hat{\mathbf{Y}} - n\bar{y}\bar{y}')^2$

```
> 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
```

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## 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

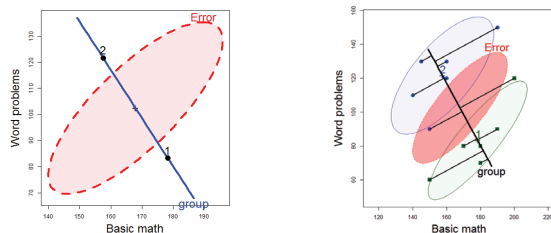
```
> cor(resid)
      BM      WP
BM 1.00 0.78
WP 0.78 1.00
```

```
> 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
```

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## 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  $HE^{-1}$
  - Discriminant weights are eigenvectors of  $HE^{-1}$



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## 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

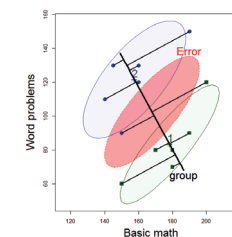
```
> (mod.lda <- MASS::lda(group ~ ., mathscore))
```

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

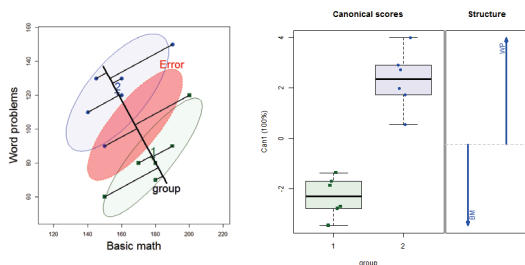


The canonical dimension is  $Can1 = 0.075 WP - 0.083 BM$ , a contrast between the two tests

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## 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)
```

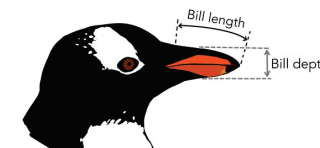
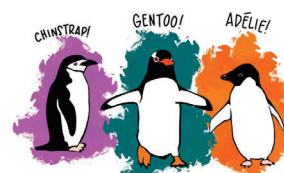
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## Penguin data

- 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 Adelie 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
```

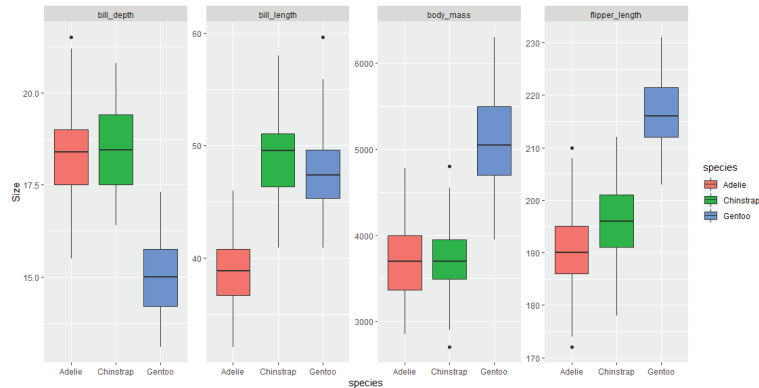


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## Penguins: Multivariate EDA

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?



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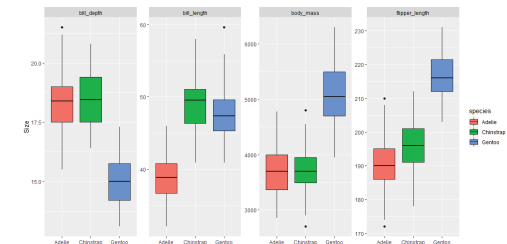
## Penguins: Multivariate EDA

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

- Need to reshape data from wide to long format

```
peng_long <- peng %>%
  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)
```



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## 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

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## PCA

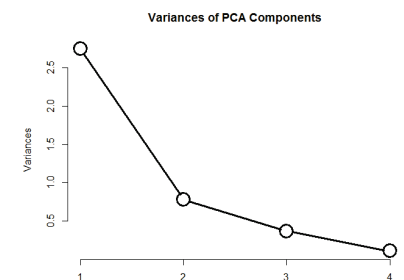
```
peng.pca <- prcomp (~ bill_length + bill_depth + flipper_length + body_mass,
  data=peng,
  na.action=na.omit,
  scale. = TRUE)

screeplot(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



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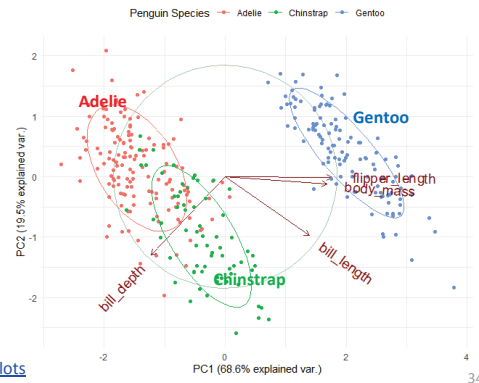
## Biplot

```
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 ~ 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>

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## 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: **~ species**
- Could also use other factors: **~ species + island + sex**

```
> 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
```

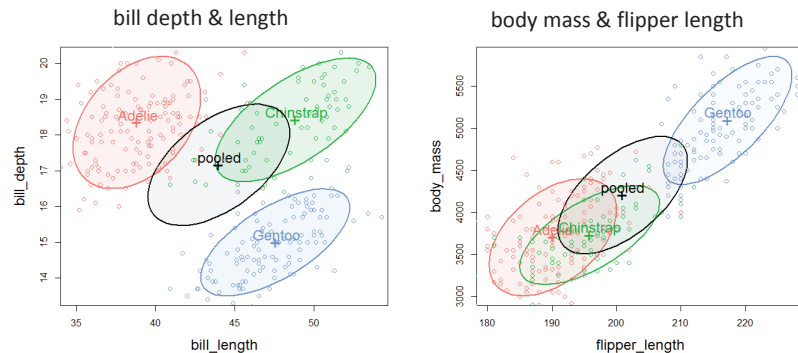
Yet, we are left to understand the nature of this effect wrt. the size variables.

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

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## Penguins: view data ellipses

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



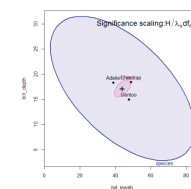
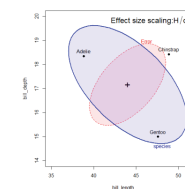
- group means negatively correlated
- within group correlation > 0

- group means positively correlated
- within group correlation > 0

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## 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  $p < \alpha$

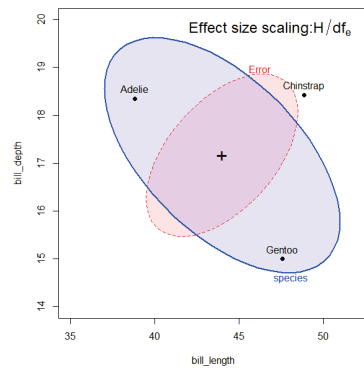


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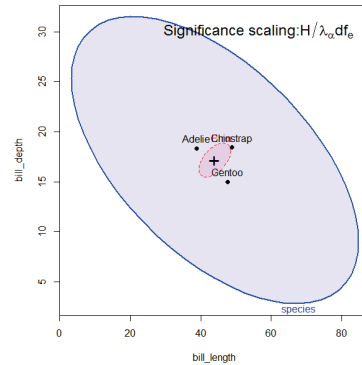
## Penguins: HE plots

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")

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## Contrasts

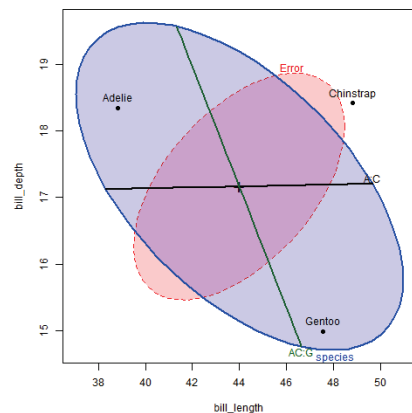
- In linear models, any effect of  $df_h > 1$  can be partitioned into  $df_h$  separate 1 df tests of contrasts
  - If orthogonal,  $H = H_1 + H_2 + \dots H_{dfh}$  -- accounts for total effect
  - Tested as a linear hypothesis, e.g.,  $x_1 - (x_2 + x_3)/2 = 0$
  - Each  $H_i$  has rank=1, so appears 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
```

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## 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:

- Adelie & 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!

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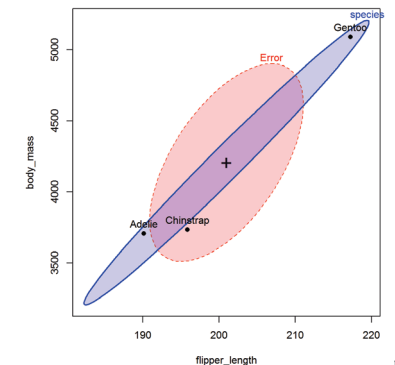
## Other HE plots

- 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:

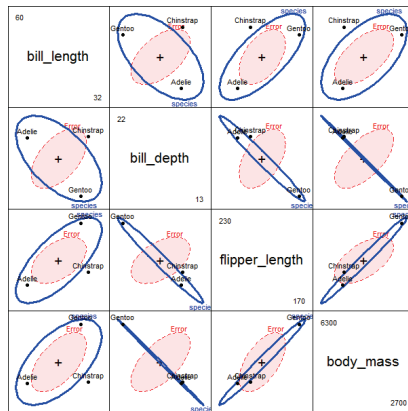
- major axis of the **H** ellipse measures “penguin size”
- Gentoo are the Big Birds in this story!



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## HE Pairs plots

The pairs() method for mlm objects gives a 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

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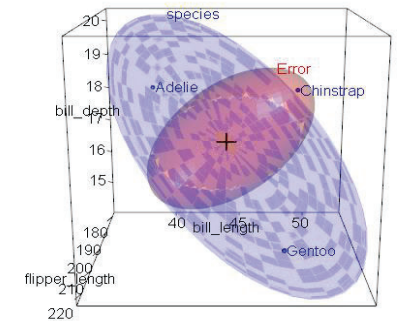
## heplot3d()

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



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## 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

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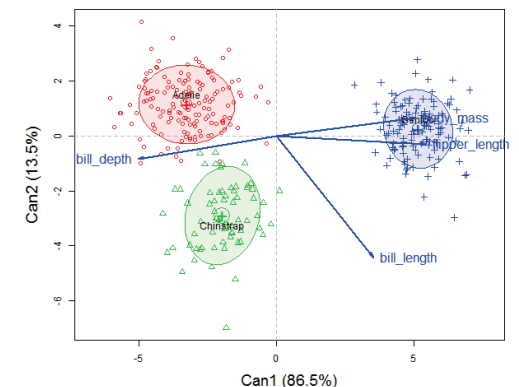
## Canonical view

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

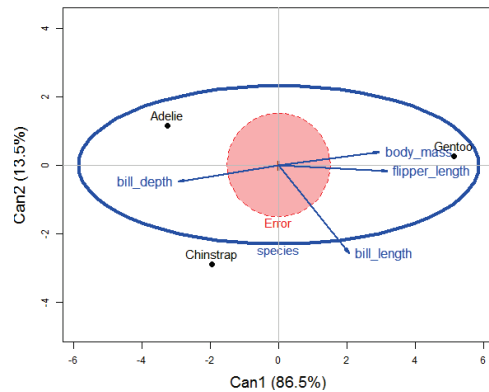
```
heplot(peng.can, size="effect", fill=c(TRUE, FALSE))
```

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

In CAN space, residuals are uncorrelated: **E** = circle

Size of **H** shows the total effect of species

Variable vectors show how the groups are discriminated.



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## 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**.

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