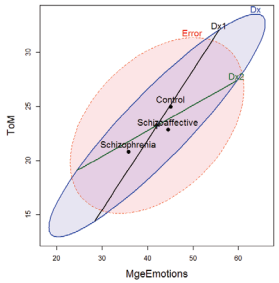

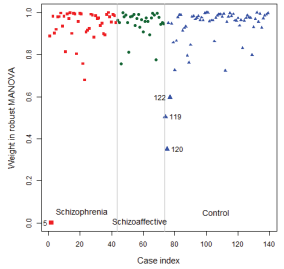

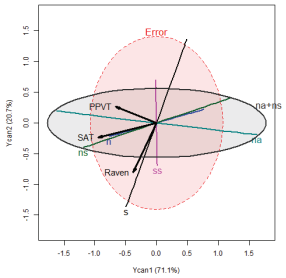

Visualizing Linear Models: An R Bag of Tricks Session 3: Examples & Extensions

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SCS Short Course
Oct. 2020

Today's topics

- Manova examples
  - Distinguishing among psychiatric groups
  - Robust MLMs
- Multivariate regression
  - PA tests & ability
  - Canonical correlation
  - MANCOVA & homogeneity of regression
- Homogeneity of variance

Ex: Neuro- & Social-Cognitive measures in psychiatric groups

- A study by Leah Hartman @York examined whether patients classified as 'schizophrenic' or 'schizoaffective' (on DSM-IV) could be distinguished from a normal, control sample on standardized tests in the following domains:
  - Neuro-Cognitive: processing speed, attention, verbal learning, visual learning, problem solving
  - Social-cognitive: managing emotions, theory of mind, externalizing bias, personalizing bias
- Research questions → MANOVA contrasts
  - Analyze neuro-cog (NC) and social-cog (SC) separately
  - Do the two psychiatric groups differ from the controls?
  - Do the psychiatric groups differ from each other?

See: Friendly & Sigal (2017), Graphical Methods for Multivariate Linear Models in Psychological Research: An R Tutorial *The Quantitative Methods for Psychology, 13*, 20-45, http://dx.doi.org/10.20982/tqmp.13.1.p020

Neuro-cognitive measures

```
library(heplots)
library(candisc)
data(NeuroCog, package="heplots")

# fit the MANOVA model, test hypotheses
NC.mlm <- lm(cbind(Speed, Attention, Memory, Verbal, Visual,ProbSolv) ~ Dx,
             data=NeuroCog)
Anova(NC.mlm)


Type II MANOVA Tests: Pillai test statistic
   Df test stat approx F num Df den Df    Pr(>F)
Dx  2    0.2992   6.8902     12    470 1.562e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So, the groups differ. But how?
What about the research hypotheses? →

```
> contrasts(NeuroCog$Dx)
                  [,1] [,2]
Schizophrenia    -0.5    1
Schizoaffective -0.5   -1
Control           1.0    0
```

Neuro-cognitive measures

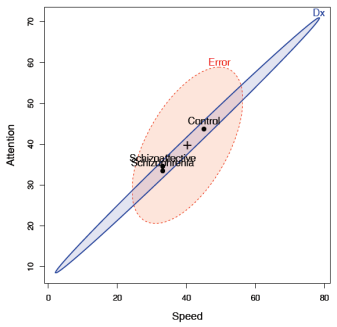
A simple result: Control ≠ (Schizophrenia ≈ Schizoaffective)

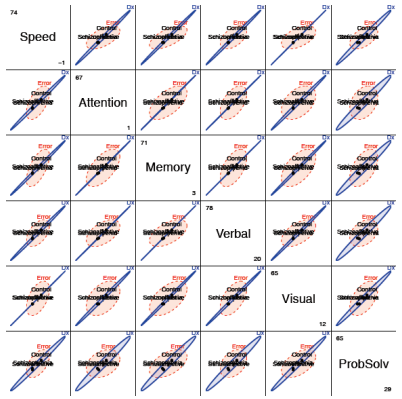
```
> print(linearHypothesis(NC.mlm, "Dx1"), SSP=FALSE)

Multivariate Tests:
                 Df test stat approx F num Df den Df  Pr(>F)
Pillai            1     0.289     15.9      6    234 2.8e-15 ***
Wilks             1     0.711     15.9      6    234 2.8e-15 ***
Hotelling-Lawley  1     0.407     15.9      6    234 2.8e-15 ***
Roy               1     0.407     15.9      6    234 2.8e-15 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> print(linearHypothesis(NC.mlm, "Dx2"), SSP=FALSE)

Multivariate Tests:
                 Df test stat approx F num Df den Df Pr(>F)
Pillai            1     0.006    0.249      6    234   0.96
Wilks             1     0.994    0.249      6    234   0.96
Hotelling-Lawley  1     0.006    0.249      6    234   0.96
Roy               1     0.006    0.249      6    234   0.96
```


Visualize me: in data space

```
# Bivariate view for any 2 responses:
heplot(NC.mlm, var=1:2, ...)
```

```
# HE plot matrix: for all responses
pairs(NC.mlm, ...)
```

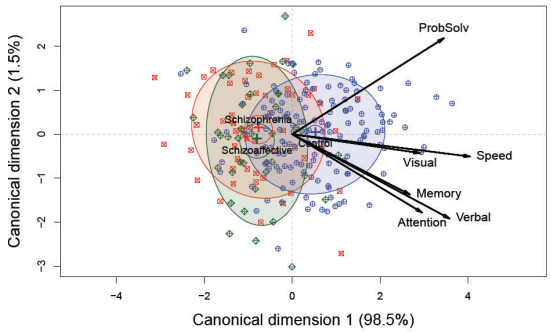




Wow! All neuro-cog measures highly correlated in group means!
Only 1 dim. of **H** variation

Visualize me: in canonical space

- As with biplot, we can visualize MLM hypothesis variation for *all* responses by projecting $\boldsymbol{H}$ and $\boldsymbol{E}$ into low-rank space.
- Canonical projection: $\boldsymbol{Y}_{n\times p} \mapsto \boldsymbol{Z}_{n\times s} = \boldsymbol{Y}\boldsymbol{E}^{-1/2}\boldsymbol{V}$, where $\boldsymbol{V}$ = eigenvectors of $\boldsymbol{H}\boldsymbol{E}^{-1}$.
- This is the view that maximally discriminates among groups, ie max. $\boldsymbol{H}$ wrt $\boldsymbol{E}$!



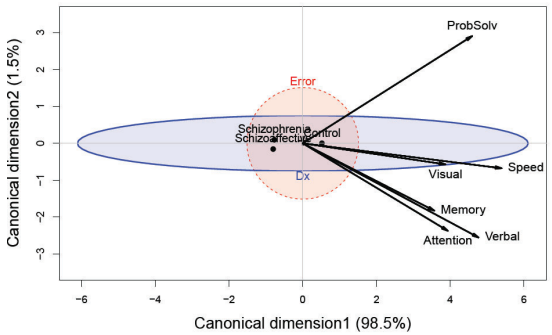
Very simple interpretation

Can1: normal vs. others
All vars highly correlated;

Can2: only 1.5%, NS; but perhaps suggestive

Visualize me: canonical HE plots

- Canonical HE plot is just the HE plot of canonical scores, $(\boldsymbol{z}_1, \boldsymbol{z}_2)$ in 2D,
- or, $\boldsymbol{z}_1, \boldsymbol{z}_2, \boldsymbol{z}_3$, in 3D.
- As in biplot, we add vectors to show relations of the $\boldsymbol{y}_j$ response variables to the canonical variates.
- variable vectors here are structure coefficients = correlations of variables with canonical scores.



The multivariate “juicer”

Shows just group means, H ellipse & E ellipse

Variable vectors offer interpretation of Can dimensions.

Social cognitive measures

- These measures deal with the person's perception and cognitive processing of emotions of others
  - Scales: managing emotions, theory of mind, externalizing bias, personalizing bias
- Questions:
  - Do these differentiate normal from patient groups?
  - Can they distinguish between schizophrenic & schizoaffective
  - If so, this could be a major finding.

Social cognitive measures

```
> data(SocialCog, package="heplots")
> SC.mlm <-  lm(cbind(MgeEmotions,ToM, ExtBias, PersBias) ~ Dx,
             data=SocialCog)
> Anova(SC.mlm)

Type II MANOVA Tests: Pillai test statistic
   Df test stat approx F num Df den Df  Pr(>F)
Dx  2     0.212     3.97      8    268 0.00018 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

✓

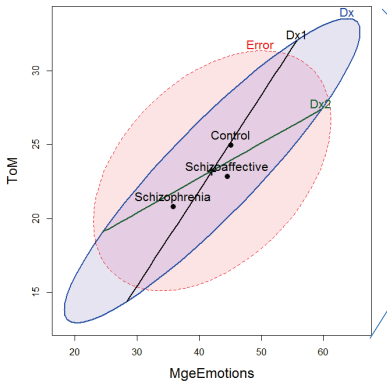
Test contrasts: Dx1 = Normal vs. Patient; Dx2 = Schizo vs. Schizoaffective

```
> print(linearHypothesis(SC.mlm, "Dx1"), SSP=FALSE)
Multivariate Tests:
               Df test stat approx F num Df den Df   Pr(>F)
Pillai          1    0.1355    5.212      4    133 0.000624 ***

> print(linearHypothesis(SC.mlm, "Dx2"), SSP=FALSE)
Multivariate Tests:
               Df test stat approx F num Df den Df Pr(>F)
Pillai          1    0.0697    2.493      4    133 0.0461 *
```

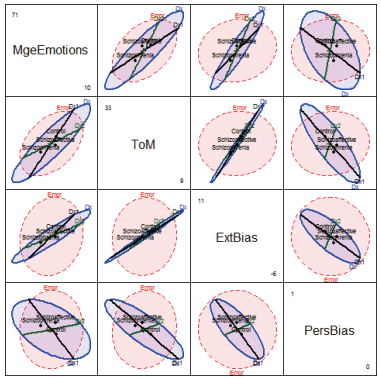
✓ ✓

Visualize me: data space

```
heplot(SC.mlm,
hypotheses=list("Dx1", "Dx2"),...)
```




```
pairs(SC.mlm,
hypotheses=list("Dx1", "Dx2"),...)
```

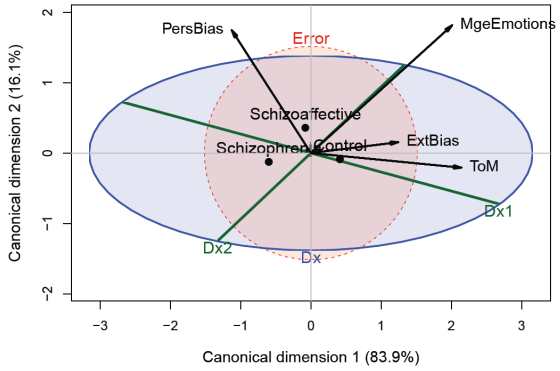


The groups are ordered Schizo < ScAffective < Control on these measures

One of these vars is not like the others!

Visualize me: canonical space

Contrasts:
Dx1 : Control vs. patients. Controls > patients on MgeEmotions, ExtBias, ToM
Dx2 : Schizo vs. schizoaffective.



Can1: group order

Can2: Schizoaffective vs. others

Model checking & remedies

- The MLM assumes residuals are multivariate normal
  - → Squared Mahalanobis distances

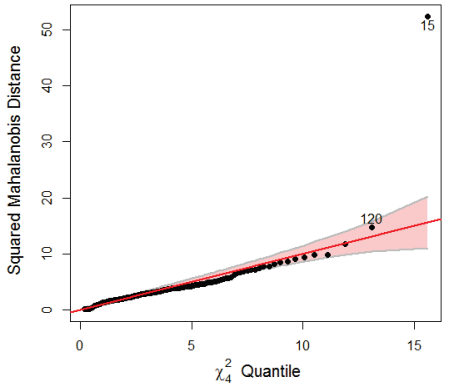
$$D^2_M(\mathbf{y}_i) = (\mathbf{y}_i - \bar{\mathbf{y}})^T \mathbf{S}^{-1} (\mathbf{y}_i - \bar{\mathbf{y}}) \sim \chi^2_p \text{ with p d.f.}$$

  - → a quantile – quantile plot of ordered $D^2_M(\mathbf{y}_i)$ vs. quantiles of χ^2_p should plot as straight line
  - Outliers are readily apparent
  - plots: heplots::cqplot()
- Influence plots
  - mvinfluence::influence() calculates multivariate analogs of influence measures

Social cog: cqplot

`heplots::cqplot()` creates a chi-square QQ plot from a MLM

```
cqplot(SC.mlm, id.n=2)
```



One observation appears as an extreme outlier.

This was a case w/ ExtBias = -33, but valid range = (-10, +10)

Refitting w/o case 15:
Overall & DX1 tests still OK ☺
Dx2 test: *p*=0.074, now NS ☹

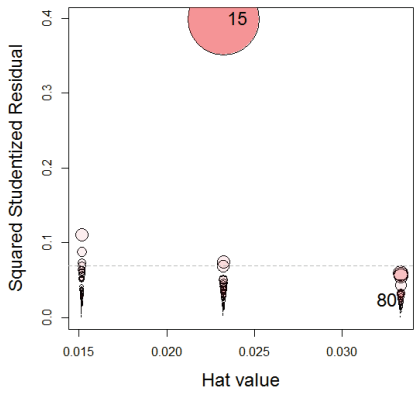
Social cog: Influence

mvinfluence::influencePlot() creates a multivariate analog of an influence plot

```
>library(mvinfluence)
>influencePlot(SC.mlm, …)

   H      Q      CookD  L      R
15 0.0233 0.3985 0.4202 0.0238 0.4080
80 0.0333 0.0233 0.0352 0.0345 0.0241
```

Case 15 stands out as hugely influential

The 3 columns of circles correspond to the 3 groups



Robust MLMs

- Robust methods for univariate LMs are now well-developed and implemented
  - → proper SEs, CIs and hypothesis tests
- Analogous methods for multivariate LMs are a current hot research topic
- The heplots package now provides `robmlm()` for the fully general MLM (MANOVA, MMReg)
  - Uses simple M-estimator via IRLS
  - Weights: calculated from Mahalanobis D^2, a robust covariance estimator and weight function, $\psi(D^2)$

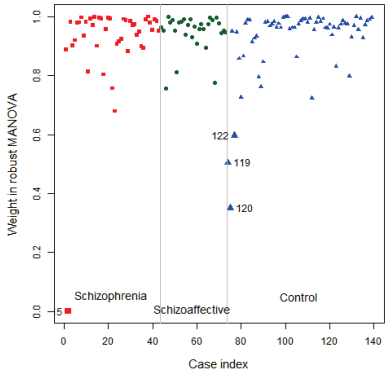
$$D^2 = (\mathbf{Y} - \bar{\mathbf{Y}})^T \mathbf{S}^{-1}_{\text{robust}} (\mathbf{Y} - \bar{\mathbf{Y}}) \sim \chi^2_p$$

  - Downside: SEs, *p*-values only approximate

Robust MLMs

```
SC.rlm <- robmlm(cbind( MgeEmotions, ToM, ExtBias, PersBias) ~ Dx,
          data=SocialCog)
```

Observation weights



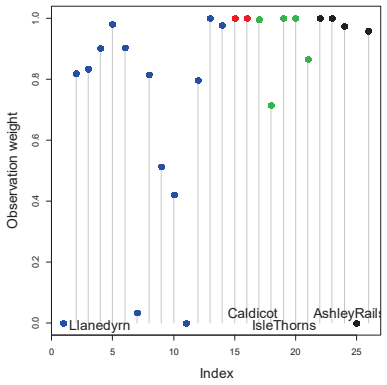
Approx test of Dx2 in robust model

```
> print(linearHypothesis(SC.rlm, "Dx2"), SSP=FALSE)

Multivariate Tests:
          Df test stat approx F num Df den Df Pr(>F)
Pillai  1     0.069     2.44      4    132   0.05 *
Wilks   1     0.931     2.44      4    132   0.05 *
 …
```

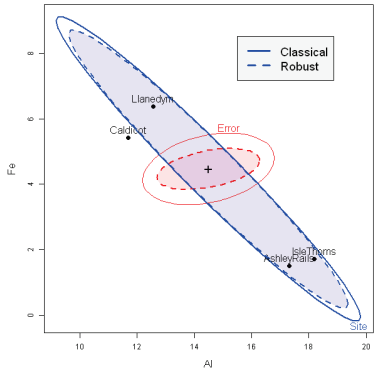

Robust MLMs: Pottery data

```
> pottery.mod <- lm(cbind(Al,Fe,Mg,Ca,Na)~Site, data=Pottery)
> pottery.rmod <- robmlm(cbind(Al,Fe,Mg,Ca,Na)~Site, data=Pottery)
```

Observation weights



overlaid HE plots



MMRA example: PA tasks & ability

- Rohwer data from Timm (1975)
- How well do paired associate (PA) tasks predict performance on measures of aptitude & achievement in kindergarten children?
  - Samples: 69 children in two groups (schools): 'Lo' | 'Hi' SES
  - Outcomes (Y):
    - Scholastic aptitude test (SAT)
    - Peabody picture vocabulary test (PPVT)
    - Raven progressive matrices (Raven)
  - Predictors (X): Scores (0—40) on PA tasks where the stimuli were:
    - named (n), still (s), named-still (ns), named-action (na), sentence-still (ss)

```
> data("Rohwer", package="heplots")
> car::some(Rohwer, n=5)
   group SES SAT PPVT Raven n  s ns na ss
8      1  Lo   8   68     8 0  0 10 19 14
9      1  Lo  49   74    11 0  0  7 16 13
17     1  Lo  19   66    13 7 12 21 35 27
52     2  Hi  38   66    14 0  0  3 16 11
66     2  Hi   8   55    16 4  7 19 20 13
```

```
> Rohwer2 <- subset(Rohwer, subset=SES=="HI")
```

Having a group factor makes the analysis more complicated (MANCOVA)

Start with analysis of the Hi SES group

Why not univariate models?

```
rohwer.mod1 <- lm(SAT   ~ n + s + ns + na + ss, data = Rohwer2)
rohwer.mod2 <- lm(PPVT  ~ n + s + ns + na + ss, data = Rohwer2)
rohwer.mod3 <- lm(Raven ~ n + s + ns + na + ss, data = Rohwer2)

library(stargazer)
stargazer(rohwer.mod1, rohwer.mod2, rohwer.mod3, type="text", …)
```

```
Univariate regression models for Rohwer data
=================================================================
                                Dependent variable:
                            ----------------------------
                                SAT         PPVT      Raven
-----------------------------------------------------------------
n                             3.26*        0.07       0.06
s                              3.00        0.37      0.49**
ns                          -5.86***      -0.37      -0.16
na                          5.67***       1.52*      0.12
ss                           -0.62        0.41      -0.12
-----------------------------------------------------------------
R2                            0.56        0.35       0.31
F Statistic (df = 5; 26)    6.54***      2.85*      2.32
=================================================================
Note:                     *p<0.05; **p<0.01; ***p<0.001
```

Results are disappointing

- Only model for SAT highly signif.
- Only a few coefs. signif. ≠0

MANOVA tests

```
> rohwer.mlm <- lm(cbind(SAT, PPVT, Raven) ~ n + s + ns + na + ss, data=Rohwer2)
> Anova(rohwer.mlm)

Type II MANOVA Tests: Pillai test statistic
   Df test stat approx F num Df den Df Pr(>F)
n   1     0.202     2.02      3     24 0.1376
s   1     0.310     3.59      3     24 0.0284 *
ns  1     0.358     4.46      3     24 0.0126 *
na  1     0.465     6.96      3     24 0.0016 **
ss  1     0.089     0.78      3     24 0.5173
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Much better!

Multivariate tests:
- pool evidence for all Ys
- take correlations of Ys into account

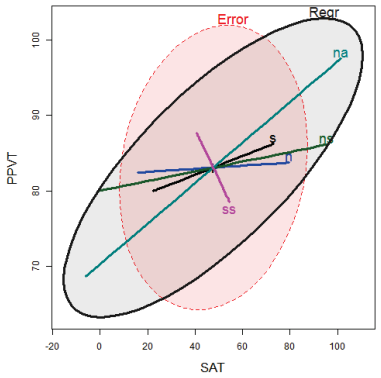
Can also test overall hypothesis, H_0: **B** = **0** (all coefs = 0)

```
> print(linearHypothesis(rohwer.mlm,
+                        c("n", "s", "ns", "na", "ss")), SSP=FALSE)

Multivariate Tests:
                 Df test stat approx F num Df den Df   Pr(>F)
Pillai            5    1.0386    2.753     15  78.00 0.001912 **
Wilks             5    0.2431    2.974     15  66.65 0.001154 **
Hotelling-Lawley  5    2.0615    3.115     15  68.00 0.000697 ***
Roy               5    1.4654    7.620      5  26.00 0.000160 ***
```

Strongly reject H_0 by all criteria

Visualize me!

```
cols <-  c("red", "blue", "black", "darkgreen", "darkcyan", "magenta", "gray20")
hyp <- list("Regr" = c("n", "s", "ns", "na", "ss"))   # Test of B = 0
heplot(rohwer.mlm,
       hypotheses = hyp,
       fill=TRUE, fill.alpha=0.1, col=cols,lwd=c(1,3))
```



Each predictor gives a 1 df test -> $\mathbf{H}_i$ ellipse is a line
E here is a 3D ellipsoid (rank(**E**) = min(p,q))

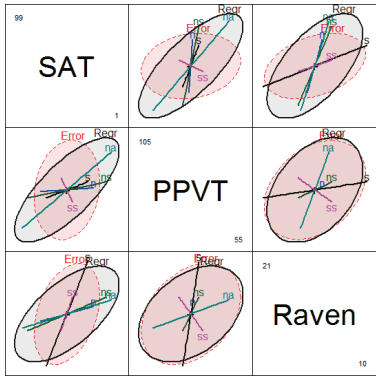
Interpretation:

- Any **H** ellipse that protrudes outside **E** ellipse is significant by Roy's test
- Length of each $\mathbf{H}_i$ line ≈ strength of association
- Orientation of each $\mathbf{H}_i$ line shows relation of X_i to the two Y_j responses shown.

pairs.mlm() plot

View all pairwise HE plots

```
pairs(rohwer.mlm, hypotheses=hyp, col=cols, fill=TRUE, fill.alpha=0.1, …)
```



Can now understand more subtle aspects

SAT is best predicted overall, but relation with PA tests varies
The na & ns tasks are strongest for SAT

Raven is weakly predicted

Canonical correlations

For quantitative (X, Y) data, canonical correlation analysis is an alternative to MMRA
It finds the weighted sums of the Y variables most highly correlated with the Xs

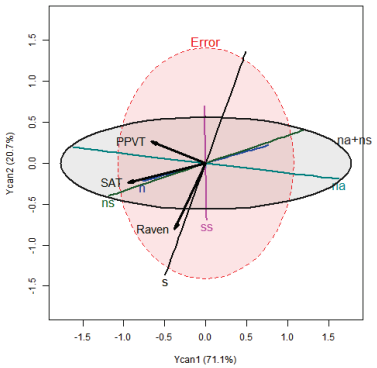
```
> X <- Rohwer2[, 6:10] # X variables for High SES students
> Y <- Rohwer2[, 3:5]  # Y variables for High SES students
> (cc <- cancor(X, Y, set.names=c("PA", "Ability")))

Canonical correlation analysis of:
         5   PA  variables:  n, s, ns, na, ss
  with   3   Ability  variables:  SAT, PPVT, Raven

    CanR CanRSQ  Eigen percent    cum                              scree
1 0.7710 0.5944 1.4654  71.080  71.08 ********************************
2 0.5465 0.2987 0.4259  20.659  91.74 *********
3 0.3815 0.1455 0.1703   8.261 100.00 ***

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

     CanR LR test stat approx F numDF  denDF  Pr(> F)
1 0.77096      0.24307   2.9738    15 66.655 0.001154 **
2 0.54652      0.59926   1.8237     8 50.000 0.094538 .
3 0.38147      0.85448   1.4759     3 26.000 0.244178
```

Two dimensions acct for 91.7% of (X,Y) association

Only Can1 is significant

Visualize CCA in HE plot

```
cols <-  c("red", "blue", "black", "darkgreen", "darkcyan",
           "magenta", "gray20")
heplot(cc, hypotheses=list("na+ns"=c("na", "ns")),
       fill = TRUE, fill.alpha=0.1, col=cols,
       label.pos = c(3, rep(1,5), .1),
       cex=1.4, var.cex=1.25, var.lwd=3, var.col="black")
```



Residuals are uncorrelated in canonical space

H ellipses for X terms same as in ordinary HE plots – outside **E** ellipse *iff* signif. by Roy's test

Variable vectors for Ys: correlations with canonical variables Ycan1, Ycan2

- SAT & PPVT: mainly Ycan1
- Raven: more aligned with Ycan2

MANCOVA & homogeneity of regression

- With a group variable (SES) can test differences in means (intercepts)
  - rohwer.mod <- lm(cbind(SAT, PPVT, Raven) ~ SES + n + s + ns + na + ss, data=Rohwer)
  - This assumes that slopes (B) are the same for both groups (homogeneity of regression)
- Can test for equal slopes by adding interactions of SES with Xs
  - rohwer.mod1 <- lm(cbind(SAT, PPVT, Raven) ~ SES * (n + s + ns + na + ss))
- Or, fit separate models for each group

```
rohwer.ses1 <- lm(cbind(SAT, PPVT, Raven) ~ n + s + ns + na + ss,
                  data = Rohwer, subset = SES == "Hi")
rohwer.ses2 <- lm(cbind(SAT, PPVT, Raven) ~ n + s + ns + na + ss,
                  data = Rohwer, subset = SES == "Lo")
```

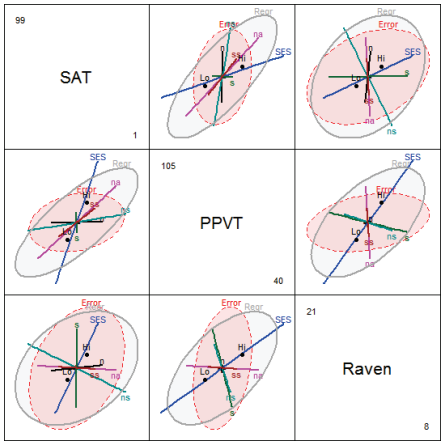

MANCOVA

Fit the MANCOVA model & test hypotheses

```
> rohwer.mod <- lm(cbind(SAT, PPVT, Raven) ~ SES + n + s + ns + na + ss,
+                  data=Rohwer)
> Anova(rohwer.mod)

Type II MANOVA Tests: Pillai test statistic
    Df test stat approx F num Df den Df  Pr(>F)
SES  1     0.379    12.18      3     60 2.5e-06 ***
n    1     0.040     0.84      3     60  0.4773
s    1     0.093     2.04      3     60  0.1173
ns   1     0.193     4.78      3     60  0.0047 **
na   1     0.231     6.02      3     60  0.0012 **
ss   1     0.050     1.05      3     60  0.3770
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Visualize effects

```
pairs(rohwer.mod,
      hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")),
      fill=TRUE, fill.alpha=0.1)
```



The SES effect is positive for all Y variables
Hi SES group > Lo SES group

Fit model with interactions

Fit heterogeneous regression model with SES interactions

```
> rohwer.mod1 <- lm(cbind(SAT, PPVT, Raven) ~ SES * (n + s + ns + na + ss),
+                   data=Rohwer)
> Anova(rohwer.mod1)

Type II MANOVA Tests: Pillai test statistic
       Df test stat approx F num Df den Df  Pr(>F)
SES     1     0.391    11.78      3     55 4.5e-06 ***
n       1     0.079     1.57      3     55 0.20638
s       1     0.125     2.62      3     55 0.05952 .
ns      1     0.254     6.25      3     55 0.00100 ***
na      1     0.307     8.11      3     55 0.00015 ***
ss      1     0.060     1.17      3     55 0.32813
SES:n   1     0.072     1.43      3     55 0.24417
SES:s   1     0.099     2.02      3     55 0.12117
SES:ns  1     0.118     2.44      3     55 0.07383 .
SES:na  1     0.148     3.18      3     55 0.03081 *
SES:ss  1     0.057     1.12      3     55 0.35094
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

OK, as expected

Hmm ???

Test interactions

Can test all interactions simultaneously with linearHypothesis()
Do I need any interaction terms?

I use ‘grep’ trick here to find the names of coefficients like ‘SES:’ containing a ‘:’

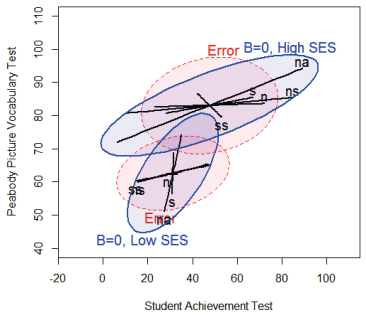
```
> coefs <- rownames(coef(rohwer.mod1))   # store coefficient names in a vector
> print(linearHypothesis(rohwer.mod1,    # only test for interaction effects
+                        coefs[grep(":", coefs)]), SSP=FALSE)

Multivariate Tests:
                 Df test stat approx F num Df den Df  Pr(>F)
Pillai            5    0.4179    1.845     15  171.0 0.03209 *
Wilks             5    0.6236    1.894     15  152.2 0.02769 *
Hotelling-Lawley  5    0.5387    1.927     15  161.0 0.02396 *
Roy               5    0.3846    4.385      5   57.0 0.00191 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Evidence shows that some slopes differ for Hi/Lo SES

Fit separate models

Fitting a model for each group allows all slopes to differ
Also allows within-group covariances to differ

```
rohwer.ses1 <- lm(cbind(SAT, PPVT, Raven) ~ n + s + ns + na + ss,
                  data = Rohwer, subset = SES == "Hi")
rohwer.ses2 <- lm(cbind(SAT, PPVT, Raven) ~ n + s + ns + na + ss,
                  data = Rohwer, subset = SES == "Lo")
```



For SAT & PPVT:

- means higher for Hi SES
- within-group covariance larger for Hi SES
- slopes of predictors smaller for Hi SES
  → SAT more important for this group.

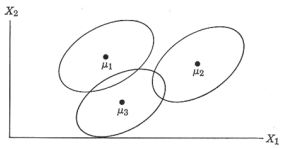
Homogeneity of (co)variances

- ANOVA assumes equality of residual variances

$\sigma_1^2 = \sigma_2^2 = \ldots = \sigma_g^2$

Levine’s test: ANOVA of $z_{ij} = | y_{ij} - \bar{y}_i |$

- MANOVA: assumes equality of covariance matrices



$\Sigma_1 = \Sigma_2 = \ldots = \Sigma_g$

Box’s M test: $M = (N-g)\ln|\mathbf{S}_p| - \sum_{i=1}^{g}(n_i - 1)\ln|\mathbf{S}_i|$

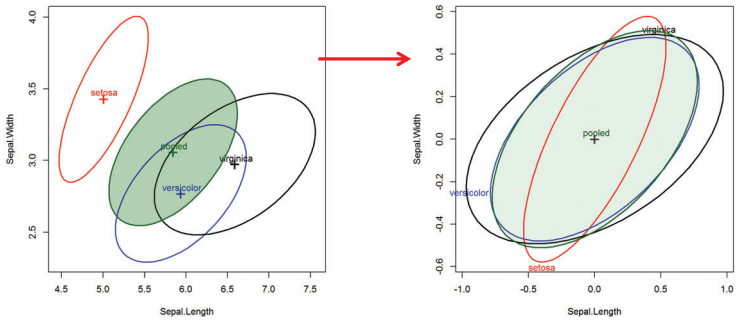
-2 ln(M)~ χ^2_{df}

See: http://www.datavis.ca/papers/EqCov-TAS.pdf

Visualizing covariance matrices

Visualize covariance ellipses in data space
Center to see pure differences in size & shape

```
covEllipses(iris[,1:2], iris$Species, ...)
covEllipses(iris[,1:2], iris$Species, center=TRUE, ...)
```

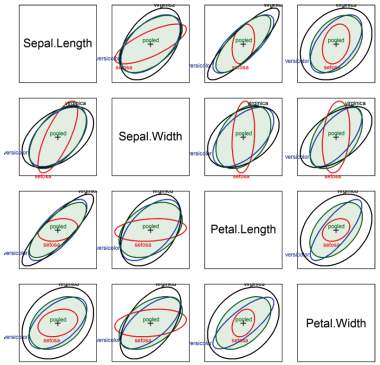


View all pairs

```
covEllipses(iris[,1:4], iris$Species,
    center=TRUE, variables=1:4,  ...)
```

In all cases, setosa stands out as different from the others

- sometimes correlation differs
- sometimes smaller variance(s)

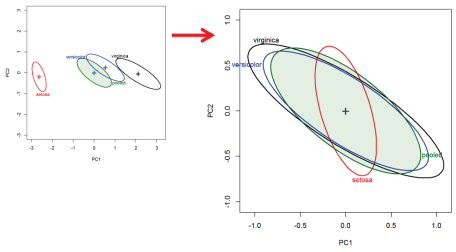


Visualize in PCA space

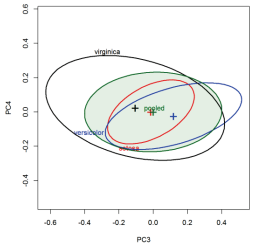
PCA projects the data into an orthogonal space accounting for maximum variance
Covariance ellipses show the differences among groups in this space

Surprisingly, the small dimensions contribute largely to Box's *M* test.

PC1 & PC2



PC3 & PC4



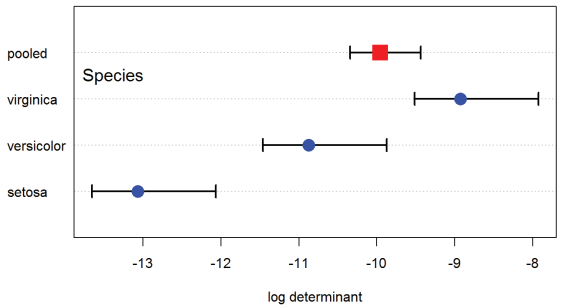

```
iris.pca <- prcomp(iris[,1:4])
covEllipses(iris.pca$x, iris$Species,  ...)
covEllipses(iris.pca$x, iris$Species,  center=TRUE, ...)
```

```
covEllipses(iris.pca$x, iris$Species, center=TRUE,
variables=3:4, ...)
```


Visualizing Box's *M* test

Box's test is based on a comparison of the log $|\mathbf{S}_i|$ relative to log $|\mathbf{S}_p|$: **plot them!**

```
iris.boxm <- boxM(iris[, 1:4], iris[, "Species"])
plot(iris.boxm, gplabel="Species")
```



CIs based on an asymptotic CLT ≈ distribution of $\ln|\mathbf{S}|$ (Cai, Liang, and Zhou 2016) (Thx: Augustine Wong)

Unsolved: Bootstrap CI

Summary

- MANOVA tests of MLMs are easily visualized in HE plots
  - Contrasts among groups can be easily shown
  - Canonical plots show data in 2D/3D space of max. group differences
  - Robust methods can help guard against outliers
- MMRA models
  - Visualize effects of quant. predictors as lines in data space
  - Test & visualize any linear hypothesis
  - Canonical correlations: visualize in 2D/3D of max. (X, Y) correlations
- Homogeneity of covariances
  - Visualize within-group $\mathbf{S}_i$ and pooled $\mathbf{S}_p$ by data ellipses
  - Visualize Box's M test by simple dot plot of $|\mathbf{S}_p|$ and $|\mathbf{S}_i|$