

Visualizing Linear Models: An R Bag of Tricks

Session 3: Examples & Extensions

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

2

Today's topics

- MANOVA examples
 - Distinguishing among psychiatric groups
 - Robust MLMs: down-weighting outliers
- Multivariate regression
 - PA tests & ability
 - Canonical correlation
 - MANCOVA & homogeneity of regression
- Homogeneity of (co)variance
 - Visualizing Box's M test

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/qmp.13.1.p020>

3

Schizophrenia symptoms: Hallucinations, disorganized thinking, delusions, ...
Schizoaffective disorder combines symptoms of schizophrenia with mood disorder (bipolar or depression)



4

Neuro-cognitive measures

Data

```
> car::some(NeuroCog)
  dx Speed Attention Memory Verbal Visual ProbSolv SocialCog Age Sex
14 Schizophrenia 19 9 19 33 24 39 28 44 Female
88 Schizoaffective 27 44 24 33 26 31 36 53 Female
105 Schizoaffective 23 41 42 48 46 29 50 52 Female
114 Schizoaffective 41 53 47 39 30 50 63 32 Female
130 Control 44 25 21 37 32 43 29 43 Female
165 Control 35 35 43 53 57 37 40 30 Male
194 Control 47 40 53 53 40 45 49 55 Female

diagnostic group ----- neuro-cognitive measures ----- ignored --
```

Questions:

- Do the diagnostic groups differ **collectively** on the neuro-cognitive measures?
- How do group differences relate to **research hypotheses**?
- How many **dimensions** (aspects) are reflected in the differences among means?

5

Neuro-cognitive measures: MANOVA

```
library(heplots); library(car)
data(NeuroCog, package="heplots")

# fit the MANOVA model
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
```

Dx1: Control – (Schiz + SchizAff)/2 = 0

7

Neuro-cognitive measures: Analyses

- Could do a series of univariate ANOVAs

```
car::Anova(NC.mlm1 <- lm(Speed ~ Dx, data=NeuroCog))
car::Anova(NC.mlm2 <- lm(Attention ~ Dx, data=NeuroCog))
car::Anova(NC.mlm3 <- lm(Memory ~ Dx, data=NeuroCog))
...
```

- Better: MANOVA test for **all 7 responses together**

```
Anova(NC.mlm = lm(cbind(Speed, Attention, Memory, ...) ~ Dx, data=SocialCog))
```

- Research hypotheses: test contrasts

```
Dx1: Control – (Schiz + SchizAff)/2 = 0 → lnearHypotheses(NC.mlm, "Dx1")
Dx2: Schiz – SchAff = 0 → lnearHypotheses(NC.mlm, "Dx2")
```

- Dimensions:

```
NC.can <- candisc(NC.mlm); plot(NC.can)
Canonical HE plot → heplot(NC.can)
```

- Tech note: `anova()` in base R vs. `car::Anova`

- `anova()` uses only Type 1 (sequential) tests, rarely useful; doesn't handle MLM well
- `car::Anova()` provides Type 2, 3 (partial) tests; give sensible results for MLMs
- `car::linearHypotheses()` gives univariate and multivariate tests of contrasts

6

Neuro-cognitive measures: Contrasts

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)
```

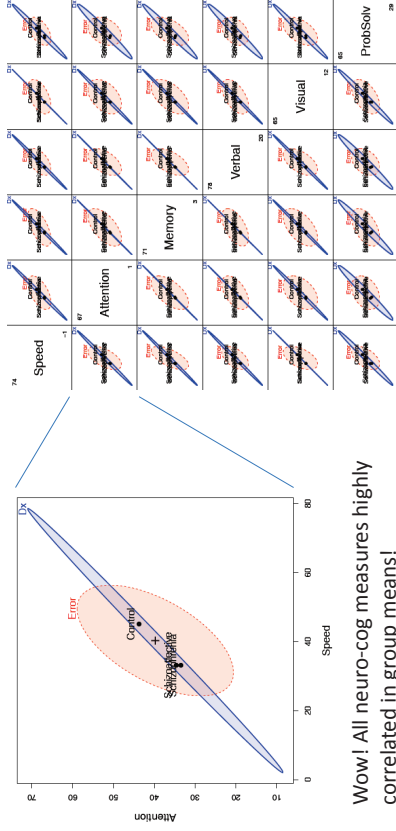
Multivariate Tests:	Df	test stat	approx F	num Df	den Df	Pr(>F)
Pillai	1	0.006	0.249	6	234	0.96
Wilks	1	0.994	0.249	6	234	0.96
Hotelling-Lawley	1	0.006	0.249	6	234	0.96
Roy	1	0.006	0.249	6	234	0.96

8

Visualize me: in data space

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

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

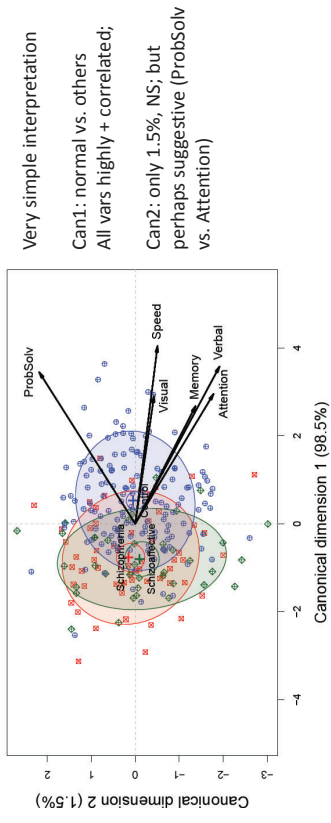


Wow! All neuro-cog measures highly correlated in group means!
Only 1 dim. of H variation

9

Visualize me: in canonical space

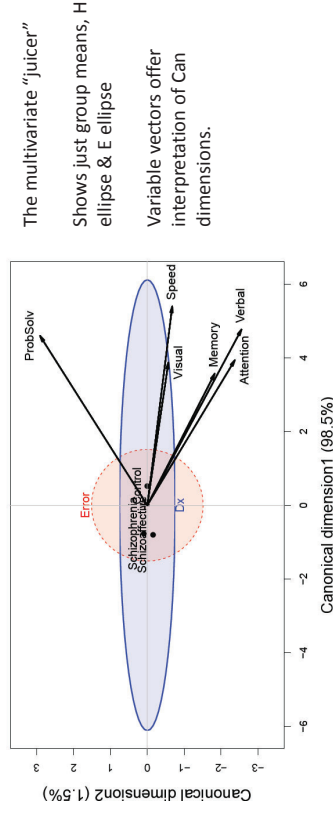
- As with biplot, we can visualize MLM hypothesis variation for *all* responses by projecting H and E into low-rank space.
- Canonical projection: $Y_{n \times p} \mapsto Z_{n \times s} = YE^{-1/2}V$, where $V =$ eigenvectors of HE^{-1} .
- This is the view that maximally discriminates among groups,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



10

Visualize me: canonical HE plots

- Canonical HE plot is just the HE plot of canonical scores, (z_1, z_2) in 2D, or z_1, z_2, z_3 in 3D.
- As in biplot, we add vectors to show relations of the y_i response variables to the canonical variates.
- variable vectors here are **structure coefficients** = correlations of variables with canonical scores.



11

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.

12

Social cognitive measures

Data

```
> car::some(SocialCog)
      Dx MgeEmotions ToM ExtBias PersBias
24  Schizophrenia    32  18    -2    1.00
58  Schizophrenia    32  17     4    0.92
69  Schizophrenia    52  23     2    0.80
85  Schizoaffective    28  12    -5    1.00
99  Schizoaffective    40  22     1    0.36
111 Schizoaffective    51  23     6    0.91
124 Control          51  24    -5    1.00
155 Control          57  28     1    0.30
168 Control          47  32     0    0.77
216 Control          64  31     3    0.69
```

diagnostic group ----- social-cognitive measures -----

Analyses

Standard MANOVA test:

Anova(SC.m1m = lm(cbind(...) ~ DX, data=SocialCog)

Test contrasts:

```
linearHypotheses(SC.m1m, "Dx1")
linearHypotheses(SC.m1m, "Dx2")
```

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

13

Social cognitive measures

```
> data(SocialCog, package="heplots")
> SC.m1m <- lm(cbind(MgeEmotions,ToM, ExtBias, PersBias) ~ Dx,
data=SocialCog)
> Anova(SC.m1m)

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

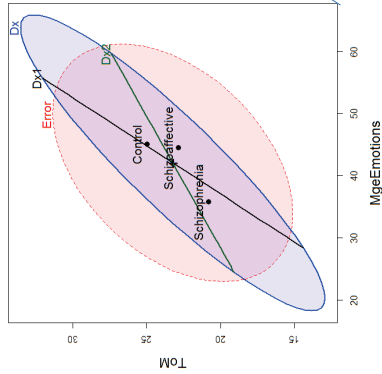
```
> print(linearHypothesis(SC.m1m, "Dx1"), SSP=FALSE)
Multivariate Tests:
Df test stat approx F num Df den Df Pr(>F)
Pillai 1 0.1355 5.212 4 133 0.000624 ***

> print(linearHypothesis(SC.m1m, "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 *
```

14

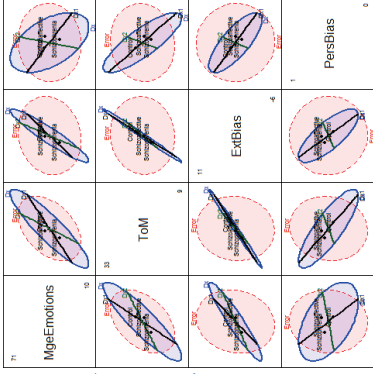
Visualize me: data space

```
heplot(SC.m1m,
hypotheses=List("Dx1", "Dx2"),...)
```



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

```
pairs(SC.m1m,
hypotheses=List("Dx1", "Dx2"),...)
```



One of these vars is not like the others!

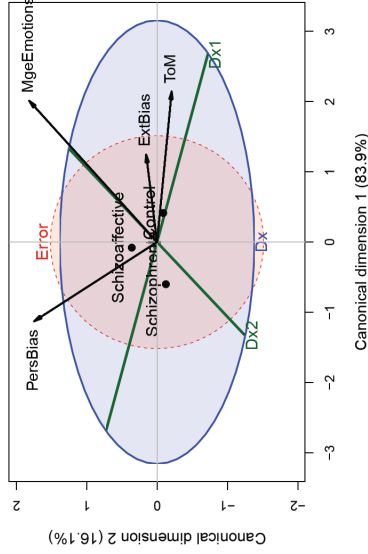
15

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

Dx1 suggests ≈ spacing
Schizo < SCAff < Control

16

Model checking & remedies

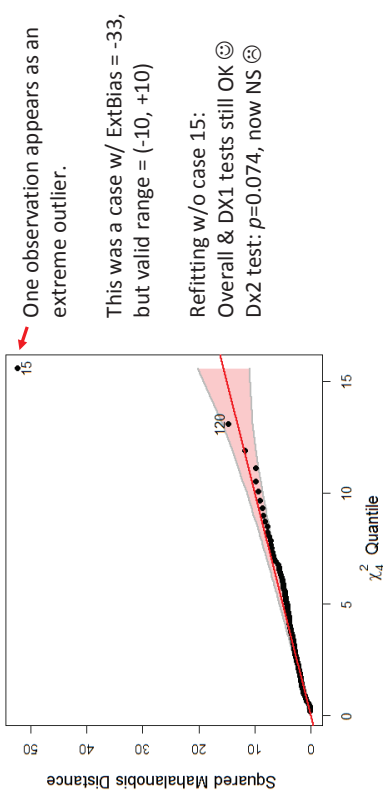
- The MLM assumes residuals are multivariate normal
 - Squared Mahalanobis distances
 - $D^2_M(\mathbf{y}_i) = (\mathbf{y}_i - \bar{\mathbf{y}})^T \mathbf{S}^{-1}(\mathbf{y}_i - \bar{\mathbf{y}}) \sim \chi^2_p$ with p d.f.
 - a quantile – quantile plot of ordered $D^2_M(\mathbf{y}_i)$ vs. quantiles of 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

17

Social cog: cqplot

`heplots::cqplotO` creates a chi-square QQ plot from a MLM

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



18

Social cog: Influence

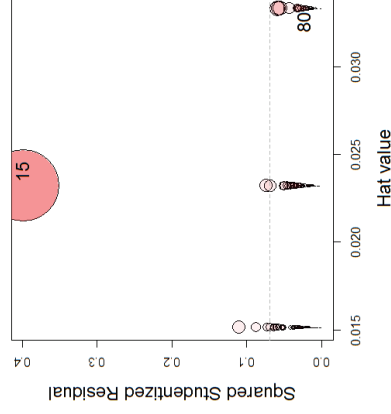
`mvinfluence::influencePlot()` creates a multivariate analog of an influence plot

```
>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



19

Robust MLMs

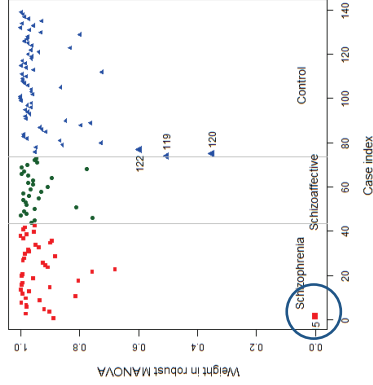
- Robust methods for univariate LM are now well-developed and implemented
 - proper SEs, CIs and hypothesis tests
 - Analogous methods for multivariate LMs are a current hot research topic
 - The heplots package now provides `robmlm()` for the fully general MLM (MANOVA, MMReg)
 - Uses simple M-estimator via IRLS
 - Weights: calculated from Mahalanobis D^2 , a robust covariance estimator and weight function, $\psi(D^2)$
- $$D^2 = (\mathbf{Y} - \bar{\mathbf{Y}})^T \mathbf{S}_{\text{robust}}^{-1} (\mathbf{Y} - \bar{\mathbf{Y}}) \sim \chi^2_p$$
- Downside: SEs, p -values only approximate

20

Robust MLMs

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

Observation weights



Approx test of Dx2 in robust model

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

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

Robust MLMs: Pottery data

- Chemical composition of ancient pottery found at four sites in Great Britain
 - Sites: AshleyRails, Caldicot, IsleThorns, Llanedynrn
 - Measures: Al Fe Mg Ca Na
- Analyses:
 - standard MANOVA `lm(cbind(Al, Fe, Mg, ...) ~ Site, data=Pottery)`
 - robust MANOVA `robmlm(cbind(Al, Fe, Mg, ...) ~ Site, data=Pottery)`

```
> car::some(Pottery)
```

Data:

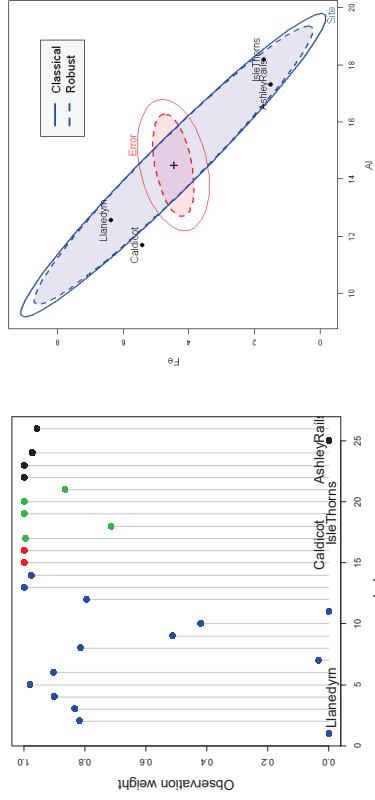
	Site	Al	Fe	Mg	Ca	Na
2	Llanedynrn	13.8	7.08	3.43	0.12	0.17
14	Llanedynrn	12.5	6.44	3.94	0.22	0.23
17	IsleThorns	18.3	1.28	0.67	0.03	0.03
18	IsleThorns	15.8	2.39	0.63	0.01	0.04
21	IsleThorns	20.8	1.51	0.72	0.07	0.10
22	AshleyRails	17.7	1.12	0.56	0.06	0.06
23	AshleyRails	18.3	1.14	0.67	0.06	0.05

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)
```

residual E ellipse shrinks a lot

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
9	1	Lo	49	74	11	0	0	7	16
17	1	Lo	19	66	13	7	12	21	35
52	2	Hi	38	66	14	0	0	3	16
66	2	Hi	8	55	16	4	7	19	20

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

Start with analysis of the Hi SES group

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

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		

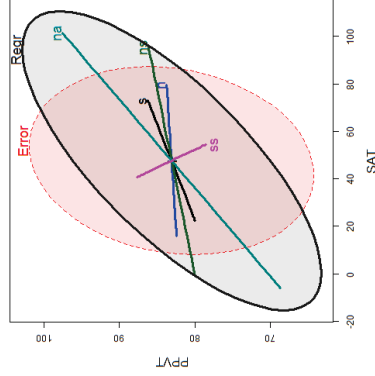
Results are disappointing

- Only model for SAT highly signif.
- Only a few coeffs. signif. $\neq 0$

25

Visualize me!

```
cols <- c("red", "blue", "black", "darkgreen", "darkcyan", "magenta", "gray20")
hyp <- list("regr" = c("n", "s", "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 $\rightarrow H_i$ ellipse is a line
 E here is a 3D ellipsoid ($\text{rank}(E) = \min(p, q)$)

Interpretation:

- Any H ellipse that protrudes outside E ellipse is significant by Roy's test
- Length of each H_i line \approx strength of association
- Orientation of each H_i line shows relation of X_i to the two Y_j responses shown.

27

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 Y_s
 - take correlations of Y_s into account

Can also test overall hypothesis, $H_0: B = 0$ (all coeffs = 0)

```
> print(lmearhypothesis(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 ***				

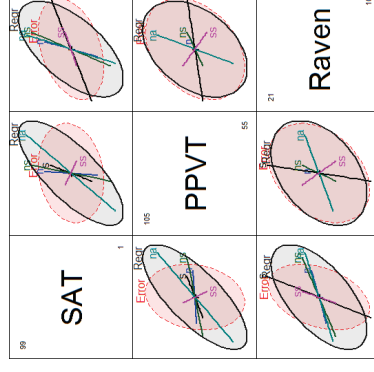
Strongly reject H_0 by all criteria

26

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

28

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

	CanR	CanRSQ	Eigen percent	cum	scree
1	0.7710	0.5944	1.4654	71.080	71.080
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

29

MANCOVA & homogeneity of regression

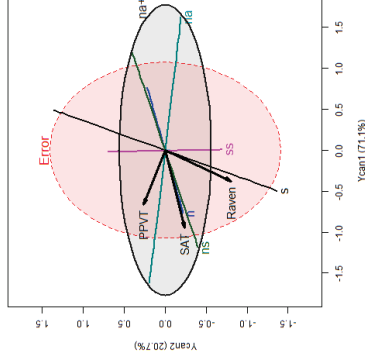
- With a group variable (SES) can test differences in means (intercepts)
 - rohwer.mod <- lm(cbind(SAT, PPVT, Raven) ~ SES + n + s + ns + na + ss, data=Rohwer)
 - This assumes that slopes (B) are the same for both groups (homogeneity of regression)
- Can test for equal slopes by adding interactions of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

31

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

30

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

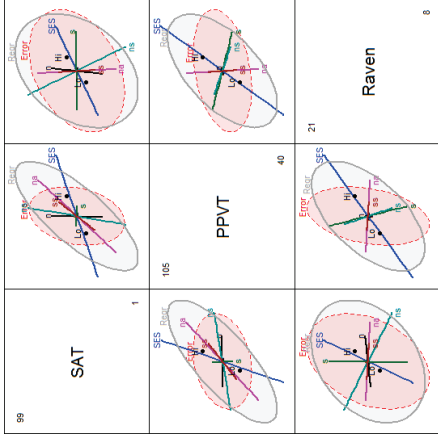
	Df	test stat	approx F	num Df	den Df	Pr(>F)	SES: diff in means
SES	1	0.379	12.18	3	60	2.5e-06 ***	
n	1	0.040	0.84	3	60	0.4773	
s	1	0.093	2.04	3	60	0.1173	
ns	1	0.193	4.78	3	60	0.0047 **	
na	1	0.231	6.02	3	60	0.0012 **	
ss	1	0.050	1.05	3	60	0.3770	

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

32

Visualize effects

```
pairs(rohwer.mod1,
      hypotheselist("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

33

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 ???
```

34

Test interactions

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

I use a '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

35

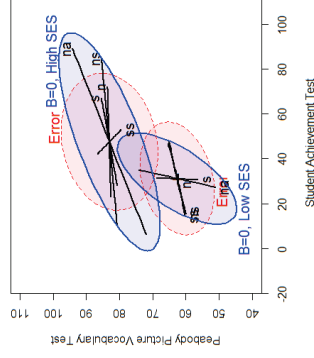
Fit separate models

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

For SAT & PPVT:

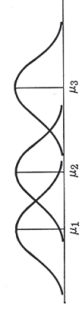
- means higher for Hi SES
- within-group covariance larger for Hi SES
- slopes of predictors smaller for Hi SES
→ SAT more important for this group.



36

Homogeneity of (co)variances

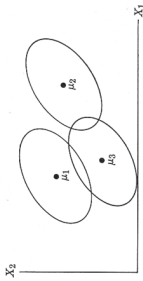
- ANOVA assumes equality of residual variances



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

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

- MANOVA: assumes equality of covariance matrices



$$\Sigma_1 = \Sigma_2 = \dots = \Sigma_g$$

Box's M test: $M = (N - g) \ln |\mathbf{S}_P| - \sum_{i=1}^g (n_i - 1) \ln |\mathbf{S}_i|$
 $-2 \ln(M) \sim \chi^2_{df}$

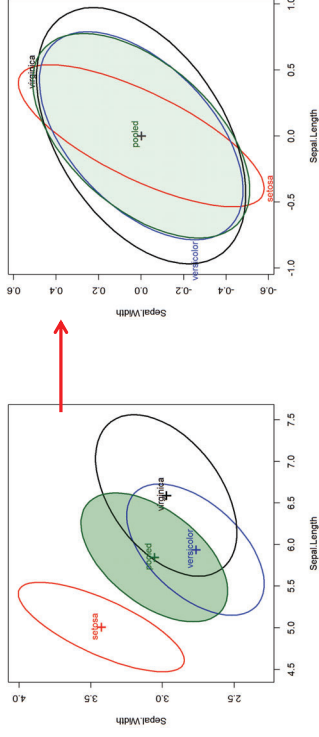
See: <http://www.datavis.ca/papers/EqCov-TAS.pdf>

37

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, ...)
```



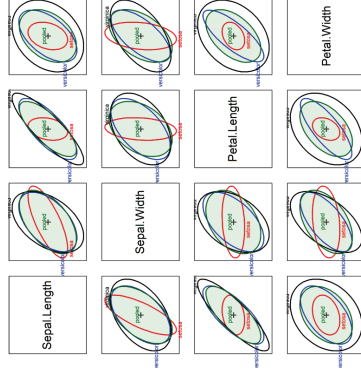
38

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)

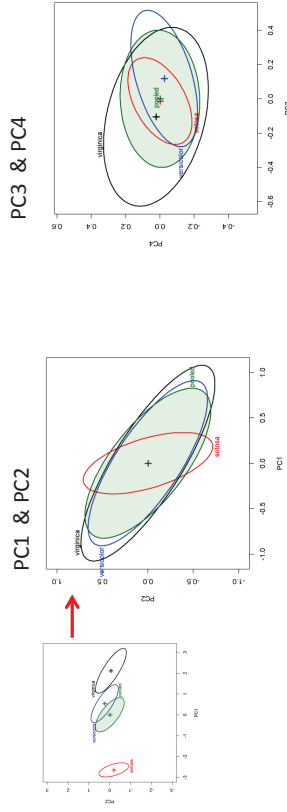


39

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.



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

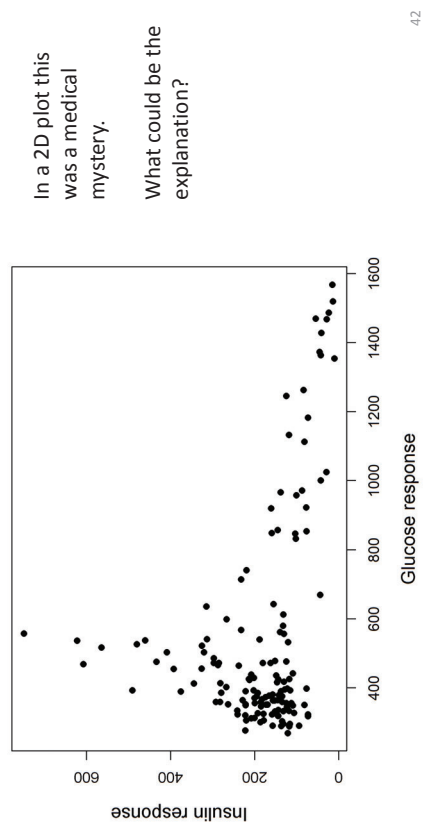
```
covEllipses(iris.pca$x, iris$Species, center=TRUE,
variables=3:4, ...)
```

40

Visualizing Box's M test

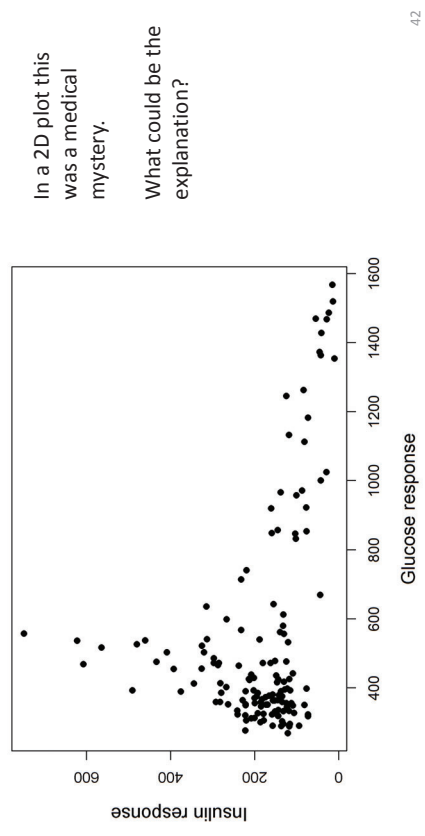
Box's test is based on a comparison of the log $|S_p|$ relative to log $|S_p|$: **plot them!**

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



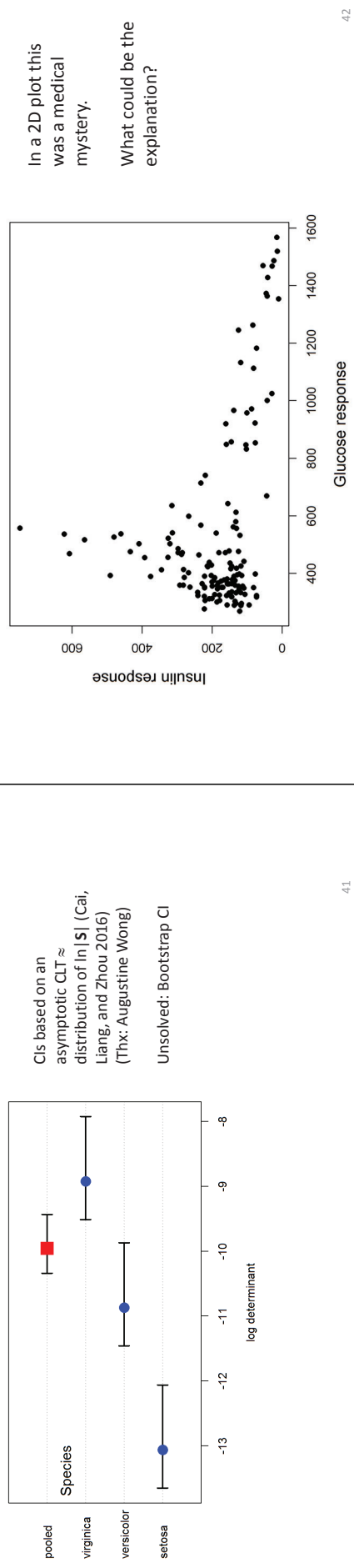
Diabetes data: 2D mystery

Reaven & Miller (1968) found a peculiar “horse shoe” result in analysis of data on the relationship of blood glucose levels and production of insulin in patients with varying degrees of hyperglycemia



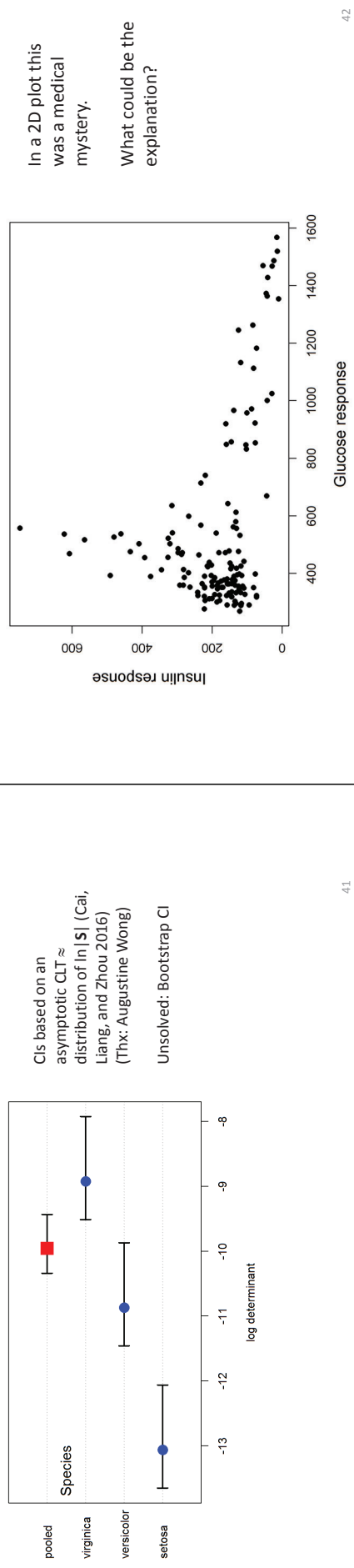
Diabetes data: 3D clarity

Using the first 3D computer graphics system (PRIM-9) they rotated the data in 3-space until a hypothesis was suggested.



Diabetes data: Ellipses

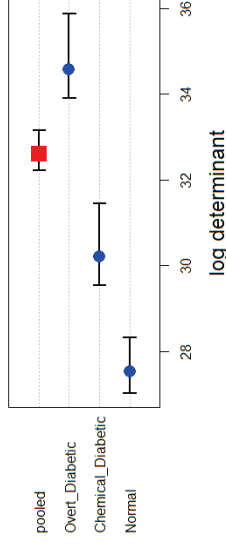
The pairwise data ellipses show visual summaries of the data. The differences in correlation and variances are dramatic here



Box's M test

```
diab.boxm <- boxM(Diabetes[,2:5], Diabetes$group)
diab.boxm
##
## Box's M-test for Homogeneity of Covariance Matrices
##
## data: Diabetes[, 2:5]
## Chi-Sq (approx.) = 383, df = 20, p-value <2e-16
plot(diab.boxm)
```

All pairs differ!



45

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 $|\mathbf{S}_i|$

46