

Discriminant Analysis

Discriminant analysis

- ANOVA and MANOVA: predict a (counted/measured) response from group membership.
- Discriminant analysis: predict group membership based on counted/measured variables.
- Covers same ground as logistic regression (and its variations), but emphasis on classifying observed data into correct groups.

... continued

- Does so by searching for linear combination of original variables that best separates data into groups (canonical variables).
- Assumption here that groups are known (for data we have). If trying to “best separate” data into unknown groups, see *cluster analysis*.

Packages

```
library(MASS, exclude = "select")
library(tidyverse)
library(ggrepel)
library(ggbiplot) # this loads plyr (different from dplyr)
library(MVTests) # for Box M test
library(conflicted)
conflict_prefer("arrange", "dplyr")
conflict_prefer("summarize", "dplyr")
conflict_prefer("select", "dplyr")
conflict_prefer("filter", "dplyr")
conflict_prefer("mutate", "dplyr")
conflicts_prefer(dplyr::count)
```

- `ggrepel` allows labelling points on a plot so they don't overwrite each other.
- `ggbiplot` uses `plyr` rather than `dplyr`, which has functions by similar names.

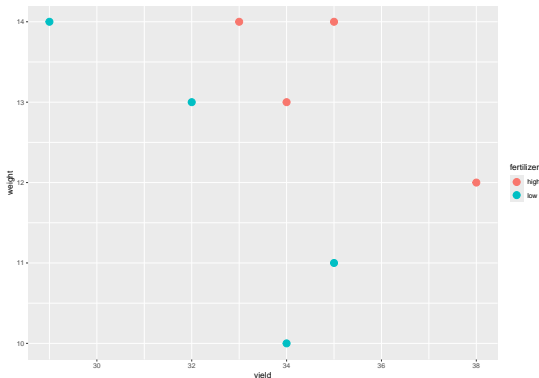
About select

- Both dplyr (in tidyverse) and MASS have a function called select, and *they do different things*.
- How do you know which select is going to get called?
- With library: one loaded *last* visible, others not.
- Thus we can access the select in dplyr but not the one in MASS.
- Better: load conflicted package. Any time you load two packages containing functions with same name, get error, choose between them.

Example 1: seed yields and weights

```
my_url <- "http://ritsokiguess.site/datafiles/manova1.txt"
hilo <- read_delim(my_url, " ")
g <- ggplot(hilo, aes(x = yield, y = weight,
  colour = fertilizer)) + geom_point(size = 4)
```

Recall data from MANOVA:
needed a multivariate analysis
to find difference in seed yield
and weight based on whether
they were high or low
fertilizer.



Basic discriminant analysis

```
hilo.1 <- lda(fertilizer ~ yield + weight, data = hilo)
```

- Uses lda from package MASS.
- “Predicting” group membership from measured variables.

Output (in hilo.1)

Call:

```
lda(fertilizer ~ yield + weight, data = hilo)
```

Prior probabilities of groups:

high	low
0.5	0.5

Group means:

	yield	weight
high	35.0	13.25
low	32.5	12.00

Coefficients of linear discriminants:

	LD1
yield	-0.7666761
weight	-1.2513563

Things to take from output 1/2

- Group means: high-fertilizer plants have (slightly) higher mean yield and weight than low-fertilizer plants.
- “Coefficients of linear discriminants”: LD1, LD2, ...are scores constructed from observed variables that best separate the groups.
- For any plant, get LD1 score by taking -0.76 times yield plus -1.25 times weight, add up, standardize.

Things to take from output 1/2

- the LD1 coefficients are like slopes:
 - ▶ if yield higher, LD1 score for a plant lower
 - ▶ if weight higher, LD1 score for a plant lower
- High-fertilizer plants have higher yield and weight, thus low (negative) LD1 score. Low-fertilizer plants have low yield and weight, thus high (positive) LD1 score.
- One LD1 score for each observation. Plot with actual groups.

How many linear discriminants?

- Smaller of these:
 - ▶ Number of variables
 - ▶ Number of groups *minus 1*
- Seed yield and weight: 2 variables, 2 groups, $\min(2, 2 - 1) = 1$.

Getting LD scores

Feed output from LDA into predict:

```
p <- predict(hilo.1)
hilo.2 <- cbind(hilo, p)
```

the LD scores

```
hilo.2
```

	fertilizer	yield	weight	class	posterior.high	posterior.low	LD1
1	low	34	10	low	2.108619e-05	9.999789e-01	3.0931414
2	low	29	14	low	1.245320e-03	9.987547e-01	1.9210963
3	low	35	11	low	2.315016e-02	9.768498e-01	1.0751090
4	low	32	13	low	4.579036e-02	9.542096e-01	0.8724245
5	high	33	14	high	9.817958e-01	1.820422e-02	-1.1456079
6	high	38	12	high	9.998195e-01	1.804941e-04	-2.4762756
7	high	34	13	high	9.089278e-01	9.107216e-02	-0.6609276
8	high	35	14	high	9.999109e-01	8.914534e-05	-2.6789600

LD1 scores in order

```
hilo.2 %>% select(fertilizer, yield, weight, LD1) %>%  
  arrange(desc(LD1))
```

	fertilizer	yield	weight	LD1
1	low	34	10	3.0931414
2	low	29	14	1.9210963
3	low	35	11	1.0751090
4	low	32	13	0.8724245
7	high	34	13	-0.6609276
5	high	33	14	-1.1456079
6	high	38	12	-2.4762756
8	high	35	14	-2.6789600

LD1 scores and fertilizer

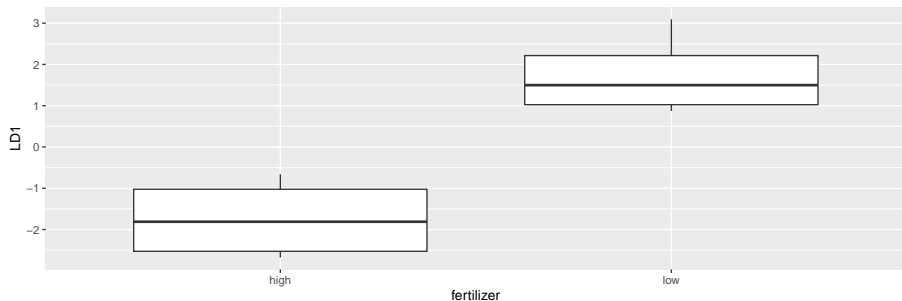
Most positive LD1 score is most obviously low fertilizer, most negative is most obviously high.

High fertilizer have yield and weight high, negative LD1 scores.

Plotting LD1 scores

With one LD score, plot against (true) groups, eg. boxplot:

```
ggplot(hilo.2, aes(x = fertilizer, y = LD1)) + geom_boxplot()
```



What else is in `hilo.2`?

- `class`: predicted fertilizer level (based on values of `yield` and `weight`).
- `posterior`: predicted probability of being low or high fertilizer given `yield` and `weight`.
- `LD1`: scores for (each) linear discriminant (here is only LD1) on each observation.

Predictions and predicted groups

...based on yield and weight:

```
hilo.2 %>% select(yield, weight, fertilizer, class)
```

	yield	weight	fertilizer	class
1	34	10	low	low
2	29	14	low	low
3	35	11	low	low
4	32	13	low	low
5	33	14	high	high
6	38	12	high	high
7	34	13	high	high
8	35	14	high	high

Count up correct and incorrect classification

```
with(hilo.2, table(obs = fertilizer, pred = class))
```

	pred	
obs	high	low
high	4	0
low	0	4

- Each predicted fertilizer level is exactly same as observed one (perfect prediction).
- Table shows no errors: all values on top-left to bottom-right diagonal.

Posterior probabilities

show how clear-cut the classification decisions were:

```
hilo.2 %>%  
  mutate(across(starts_with("posterior"), \(p) round(p, 4))) %>%  
  select(-LD1)
```

	fertilizer	yield	weight	class	posterior.high	posterior.low
1	low	34	10	low	0.0000	1.0000
2	low	29	14	low	0.0012	0.9988
3	low	35	11	low	0.0232	0.9768
4	low	32	13	low	0.0458	0.9542
5	high	33	14	high	0.9818	0.0182
6	high	38	12	high	0.9998	0.0002
7	high	34	13	high	0.9089	0.0911
8	high	35	14	high	0.9999	0.0001

Comments

Only obs. 7 has any doubt: yield low for a high-fertilizer, but high weight makes up for it.

Example 2: the peanuts

```
my_url <- "http://ritsokiguess.site/datafiles/peanuts.txt"
peanuts <- read_delim(my_url, " ")
peanuts
```

A tibble: 12 x 6

	obs	location	variety	y	smk	w
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	1	1	5	195.	153.	51.4
2	2	1	5	194.	168.	53.7
3	3	2	5	190.	140.	55.5
4	4	2	5	180.	121.	44.4
5	5	1	6	203	157.	49.8
6	6	1	6	196.	166	45.8
7	7	2	6	203.	166.	60.4
8	8	2	6	198.	162.	54.1
9	9	1	8	194.	164.	57.8
10	10	1	8	187	165.	58.6
11	11	2	8	202.	167.	65
12	12	2	8	200	174.	67.2

Comment

- Recall: location and variety both significant in MANOVA.
- Make combo of them:

```
peanuts %>%  
  unite(combo, c(variety, location)) -> peanuts.combo  
peanuts.combo
```

```
# A tibble: 12 x 5
```

	obs	combo	y	smk	w
	<dbl>	<chr>	<dbl>	<dbl>	<dbl>
1	1	5_1	195.	153.	51.4
2	2	5_1	194.	168.	53.7
3	3	5_2	190.	140.	55.5
4	4	5_2	180.	121.	44.4
5	5	6_1	203.	157.	49.8
6	6	6_1	196.	166.	45.8
7	7	6_2	203.	166.	60.4
8	8	6_2	198.	162.	54.1
9	9	8_1	194.	164.	57.8
10	10	8_1	187.	165.	58.6

Discriminant analysis

```
# peanuts.1 <- lda(str_c(location, variety, sep = "_") ~ y + smk + w, data = peanuts)
peanuts.1 <- lda(combo ~ y + smk + w, data = peanuts.combo)
peanuts.1
```

Call:

```
lda(combo ~ y + smk + w, data = peanuts.combo)
```

Prior probabilities of groups:

	5_1	5_2	6_1	6_2	8_1	8_2
	0.1666667	0.1666667	0.1666667	0.1666667	0.1666667	0.1666667

Group means:

	y	smk	w
5_1	194.80	160.40	52.55
5_2	185.05	130.30	49.95
6_1	199.45	161.40	47.80
6_2	200.15	163.95	57.25
8_1	190.25	164.80	58.20
8_2	200.75	170.30	66.10

Coefficients of linear discriminants:

	LD1	LD2	LD3
y	0.4027356	0.02967881	0.18839237
smk	0.1727459	-0.06794271	-0.09386294
w	-0.5792456	-0.16300221	0.07341123

Proportion of trace:

	LD1	LD2	LD3
	0.8424	0.1317	0.0258

Comments

- Now 3 LDs (3 variables, 6 groups, $\min(3, 6 - 1) = 3$).
- Relationship of LDs to original variables. Look for coeffs far from zero:

```
peanuts.1$scaling
```

	LD1	LD2	LD3
y	0.4027356	0.02967881	0.18839237
smk	0.1727459	-0.06794271	-0.09386294
w	-0.5792456	-0.16300221	0.07341123

- high LD1 mainly high y or low w.
- high LD2 mainly low w.
- Proportion of trace values show relative importance of LDs: LD1 much more important than LD2; LD3 worthless.

The predictions, badly

```
p <- predict(peanuts.1)
peanuts.2 <- cbind(peanuts.combo, p)
peanuts.2
```

	obs	combo	y	smk	w	class	posterior.5_1	posterior.5_2	posterior.6
1 06	1	5_1	195.3	153.1	51.4	5_1	6.862288e-01	1.825787e-12	1.626712e-
2 05	2	5_1	194.3	167.7	53.7	5_1	7.269338e-01	7.555850e-17	1.265614e-
3 32	3	5_2	189.7	139.5	55.5	5_2	1.624097e-12	9.996353e-01	1.501005e-
4 36	4	5_2	180.4	121.1	44.4	5_2	1.702156e-16	1.000000e+00	1.070250e-
5 01	5	6_1	203.0	156.8	49.8	6_1	4.262552e-05	1.500083e-31	9.999036e-
6 01	6	6_1	195.9	166.0	45.8	6_1	9.681355e-07	1.071193e-37	9.999989e-
7 08	7	6_2	202.7	166.1	60.4	6_2	1.324922e-01	5.989065e-15	7.932019e-
8 05	8	6_2	197.6	161.8	54.1	5_1	5.286987e-01	2.037992e-16	3.255237e-

Comments

- Hard to read:
 - ▶ The posterior probabilities are in scientific notation
 - ▶ The *names* of the posterior columns are rather long; names like `p.5_1` would be better.

```
peanuts.2 %>%  
  mutate(across(starts_with("posterior"),  
                 \ (p) round(p, 3))) %>%  
  rename_with(\ (p) str_remove(p, "osterior"),  
              starts_with("posterior")) -> peanuts.2a
```

Result (slightly better)

peanuts.2a

	obs	combo	y	smk	w	class	p.5_1	p.5_2	p.6_1	p.6_2	p.8_1	p.8_2
1	1	5_1	195.3	153.1	51.4	5_1	0.686	0	0	0.314	0.000	0.000
2	2	5_1	194.3	167.7	53.7	5_1	0.727	0	0	0.273	0.000	0.000
3	3	5_2	189.7	139.5	55.5	5_2	0.000	1	0	0.000	0.000	0.000
4	4	5_2	180.4	121.1	44.4	5_2	0.000	1	0	0.000	0.000	0.000
5	5	6_1	203.0	156.8	49.8	6_1	0.000	0	1	0.000	0.000	0.000
6	6	6_1	195.9	166.0	45.8	6_1	0.000	0	1	0.000	0.000	0.000
7	7	6_2	202.7	166.1	60.4	6_2	0.132	0	0	0.866	0.000	0.002
8	8	6_2	197.6	161.8	54.1	5_1	0.529	0	0	0.471	0.000	0.000
9	9	8_1	193.5	164.5	57.8	8_1	0.023	0	0	0.018	0.750	0.209
10	10	8_1	187.0	165.1	58.6	8_1	0.000	0	0	0.000	0.994	0.006
11	11	8_2	201.5	166.8	65.0	8_2	0.000	0	0	0.001	0.027	0.972
12	12	8_2	200.0	173.8	67.2	8_2	0.000	0	0	0.000	0.059	0.941

	x.LD1	x.LD2	x.LD3
1	1.417354	1.01233393	0.26467918
2	2.204444	-0.38421359	-1.12526629
3	-5.562217	1.10184441	0.78720394
4	-6.056558	3.88530191	-0.05263163
5	6.084370	1.25027629	1.25054957
6	7.131192	1.06649258	-1.24422021
7	1.430084	-1.11831802	1.09926555
8	2.282572	0.04938762	0.07958437
9	-1.045438	-0.85884902	-0.67463274

Misclassification

```
with(peanuts.2, table(obs = combo, pred = class))
```

	pred					
obs	5_1	5_2	6_1	6_2	8_1	8_2
5_1	2	0	0	0	0	0
5_2	0	2	0	0	0	0
6_1	0	0	2	0	0	0
6_2	1	0	0	1	0	0
8_1	0	0	0	0	2	0
8_2	0	0	0	0	0	2

Actually classified very well. Only one 6_2 classified as a 5_1, rest all correct.

Posterior probabilities

```
peanuts.2a %>%  
  select(combo, class, starts_with("p"))
```

	combo	class	p.5_1	p.5_2	p.6_1	p.6_2	p.8_1	p.8_2
1	5_1	5_1	0.686	0	0	0.314	0.000	0.000
2	5_1	5_1	0.727	0	0	0.273	0.000	0.000
3	5_2	5_2	0.000	1	0	0.000	0.000	0.000
4	5_2	5_2	0.000	1	0	0.000	0.000	0.000
5	6_1	6_1	0.000	0	1	0.000	0.000	0.000
6	6_1	6_1	0.000	0	1	0.000	0.000	0.000
7	6_2	6_2	0.132	0	0	0.866	0.000	0.002
8	6_2	5_1	0.529	0	0	0.471	0.000	0.000
9	8_1	8_1	0.023	0	0	0.018	0.750	0.209
10	8_1	8_1	0.000	0	0	0.000	0.994	0.006
11	8_2	8_2	0.000	0	0	0.001	0.027	0.972
12	8_2	8_2	0.000	0	0	0.000	0.059	0.941

Comments

- *Some* doubt about which combo each plant belongs in, but not too much.
- The one misclassified plant (row 8) was a close call.

Discriminant scores, again

- How are discriminant scores related to original variables?

```
peanuts.1$scaling
```

	LD1	LD2	LD3
y	0.4027356	0.02967881	0.18839237
smk	0.1727459	-0.06794271	-0.09386294
w	-0.5792456	-0.16300221	0.07341123

- LD1 positive if y large and/or w small.
- LD2 positive if w small.

Discriminant scores for data

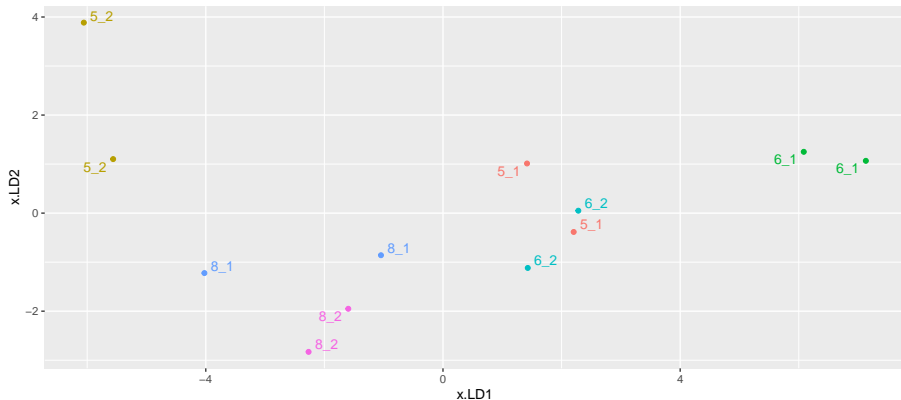
```
peanuts.2 %>% select(y, w, starts_with("x"))
```

	y	w	x.LD1	x.LD2	x.LD3
1	195.3	51.4	1.417354	1.01233393	0.26467918
2	194.3	53.7	2.204444	-0.38421359	-1.12526629
3	189.7	55.5	-5.562217	1.10184441	0.78720394
4	180.4	44.4	-6.056558	3.88530191	-0.05263163
5	203.0	49.8	6.084370	1.25027629	1.25054957
6	195.9	45.8	7.131192	1.06649258	-1.24422021
7	202.7	60.4	1.430084	-1.11831802	1.09926555
8	197.6	54.1	2.282572	0.04938762	0.07958437
9	193.5	57.8	-1.045438	-0.85884902	-0.67463274
10	187.0	58.6	-4.022969	-1.22292871	-1.89677191
11	201.5	65.0	-1.596806	-1.95130266	1.14518230
12	200.0	67.2	-2.266028	-2.83002474	0.36705787

- Obs. 5 and 6 have most positive LD1: large y, small w.
- Obs. 4 has most positive LD2: small w.

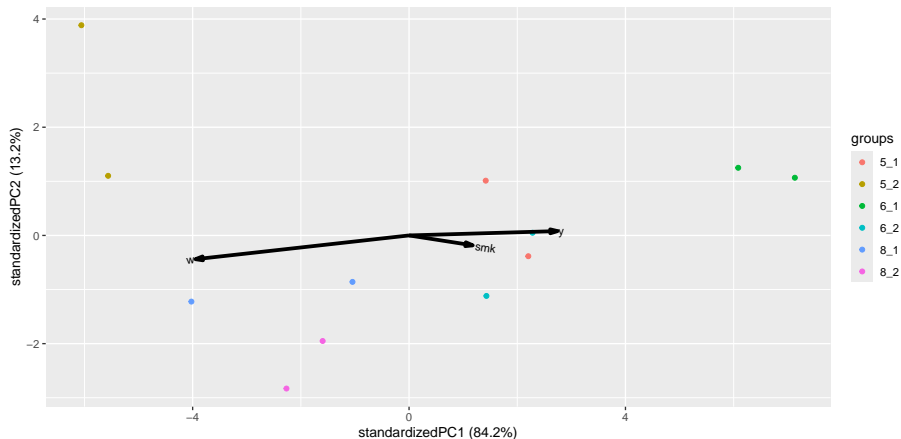
Plot LD1 vs. LD2, labelling by combo

```
g <- ggplot(peanuts.2, aes(x = x.LD1, y = x.LD2, colour = combo,  
                           label = combo)) + geom_point() +  
  geom_text_repel() + guides(colour = "none")  
g
```



“Bi-plot” from ggbiplot

```
ggbiplot(peanuts.1, groups = factor(peanuts.combo$combo))
```



Installing ggbiplot

- ggbiplot not on CRAN, so usual `install.packages` will not work.
- Install package `devtools` first (once):

```
install.packages("devtools")
```

- Then install `ggbiplot` (once):

```
library(devtools)  
install_github("vqv/ggbiplot")
```

Cross-validation

- So far, have predicted group membership from same data used to form the groups — dishonest!
- Better: *cross-validation*: form groups from all observations *except one*, then predict group membership for that left-out observation.
- No longer cheating!
- Illustrate with peanuts data again.

Misclassifications

- Fitting and prediction all in one go:

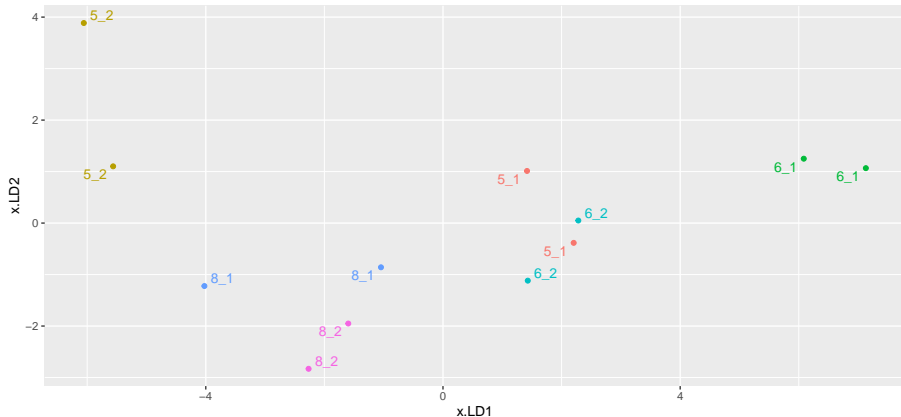
```
p <- lda(combo ~ y + smk + w,  
  data = peanuts.combo, CV = TRUE)  
peanuts.3 <- cbind(peanuts.combo, class = p$class,  
  posterior = p$posterior)  
with(peanuts.3, table(obs = combo, pred = class))
```

	pred					
obs	5_1	5_2	6_1	6_2	8_1	8_2
5_1	0	0	0	2	0	0
5_2	0	1	0	0	1	0
6_1	0	0	2	0	0	0
6_2	1	0	0	1	0	0
8_1	0	1	0	0	0	1
8_2	0	0	0	0	0	2

- Some more misclassification this time.

Repeat of LD plot

g



Posterior probabilities

```
peanuts.3 %>%  
  mutate(across(starts_with("posterior"), \(p) round(p, 3))) %>%  
  rename_with(\(p) str_remove(p, "osterior"),  
             starts_with("posterior")) %>%  
  select(combo, class, starts_with("p."))
```

	combo	class	p.5_1	p.5_2	p.6_1	p.6_2	p.8_1	p.8_2
1	5_1	6_2	0.162	0.00	0.000	0.838	0.000	0.000
2	5_1	6_2	0.200	0.00	0.000	0.799	0.000	0.000
3	5_2	8_1	0.000	0.18	0.000	0.000	0.820	0.000
4	5_2	5_2	0.000	1.00	0.000	0.000	0.000	0.000
5	6_1	6_1	0.194	0.00	0.669	0.137	0.000	0.000
6	6_1	6_1	0.000	0.00	1.000	0.000	0.000	0.000
7	6_2	6_2	0.325	0.00	0.000	0.667	0.001	0.008
8	6_2	5_1	0.821	0.00	0.000	0.179	0.000	0.000
9	8_1	8_2	0.000	0.00	0.000	0.000	0.000	1.000
10	8_1	5_2	0.000	1.00	0.000	0.000	0.000	0.000
11	8_2	8_2	0.001	0.00	0.000	0.004	0.083	0.913
12	8_2	8_2	0.000	0.00	0.000	0.000	0.167	0.833

Why more misclassification?

- When predicting group membership for one observation, only uses the *other one* in that group.
- So if two in a pair are far apart, or if two groups overlap, great potential for misclassification.
- Groups 5_1 and 6_2 overlap.
- 5_2 closest to 8_1s looks more like an 8_1 than a 5_2 (other one far away).
- 8_1s relatively far apart and close to other things, so one appears to be a 5_2 and the other an 8_2.

Example 3: professions and leisure activities

- 15 individuals from three different professions (politicians, administrators and belly dancers) each participate in four different leisure activities: reading, dancing, TV watching and skiing. After each activity they rate it on a 0–10 scale.
- How can we best use the scores on the activities to predict a person's profession?
- Or, what combination(s) of scores best separate data into profession groups?

The data

```
my_url <- "http://ritsokiguess.site/datafiles/profile.txt"
active <- read_delim(my_url, " ")
active
```

A tibble: 15 x 5

	job	reading	dance	tv	ski
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
1	bellydancer	7	10	6	5
2	bellydancer	8	9	5	7
3	bellydancer	5	10	5	8
4	bellydancer	6	10	6	8
5	bellydancer	7	8	7	9
6	politician	4	4	4	4
7	politician	6	4	5	3
8	politician	5	5	5	6
9	politician	6	6	6	7
10	politician	4	5	6	5
11	admin	3	1	1	2
12	admin	5	3	1	5
13	admin	4	2	2	5
14	admin	7	1	2	4
15	admin	6	3	3	3

Discriminant analysis

```
active.1 <- lda(job ~ reading + dance + tv + ski, data = active)
active.1
```

Call:

```
lda(job ~ reading + dance + tv + ski, data = active)
```

Prior probabilities of groups:

	admin	bellydancer	politician
	0.3333333	0.3333333	0.3333333

Group means:

	reading	dance	tv	ski
admin	5.0	2.0	1.8	3.8
bellydancer	6.6	9.4	5.8	7.4
politician	5.0	4.8	5.2	5.0

Coefficients of linear discriminants:

	LD1	LD2
reading	-0.01297465	-0.4748081
dance	-0.95212396	-0.4614976
tv	-0.47417264	1.2446327
ski	0.04153684	-0.2033122

Proportion of trace:

	LD1	LD2
	0.8917	0.1083

Comments

- Two discriminants, first fair bit more important than second.
- LD1 depends (negatively) most on dance, a bit on tv.
- LD2 depends mostly (positively) on tv.

Misclassification

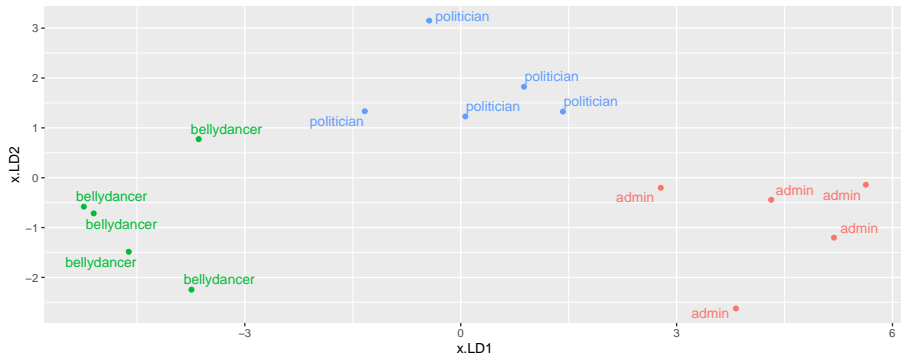
```
p <- predict(active.1)
active.2 <- cbind(active, p)
with(active.2, table(obs = job, pred = class))
```

	pred		
obs	admin	bellydancer	politician
admin	5	0	0
bellydancer	0	5	0
politician	0	0	5

Everyone correctly classified.

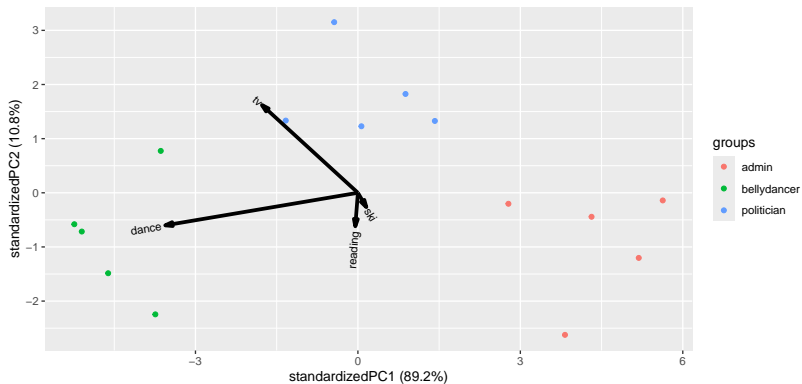
Plotting LDs

```
g <- ggplot(active.2, aes(x = x.LD1, y = x.LD2, colour = job, label =  
  geom_point() + geom_text_repel() + guides(colour = "none")  
g
```



Biplot

```
ggbiplot(active.1, groups = active$job)
```



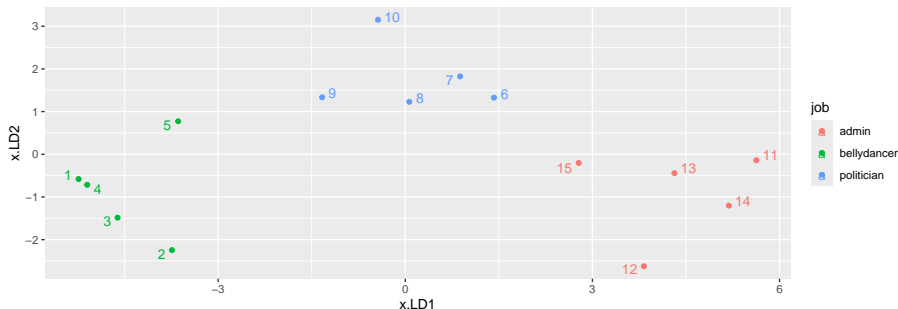
Comments on plot

- Groups well separated: bellydancers top left, administrators top right, politicians lower middle.
- Bellydancers most negative on LD1: like dancing most.
- Administrators most positive on LD1: like dancing least.
- Politicians most negative on LD2: like TV-watching most.

Plotting individual persons

Make label be identifier of person. Now need legend:

```
active.2 %>% mutate(person = row_number()) %>%  
  ggplot(aes(x = x.LD1, y = x.LD2, colour = job,  
             label = person)) +  
  geom_point() + geom_text_repel()
```



Posterior probabilities

```
active.2 %>% mutate(across(starts_with("posterior"), \ (p) round(p, 3))) %>%  
  rename_with(\ (p) str_remove(p, "osterior"),  
              starts_with("posterior")) %>%  
  select(job, class, starts_with("p."))
```

	job	class	p.admin	p.bellydancer	p.politician
1	bellydancer	bellydancer	0.000	1.000	0.000
2	bellydancer	bellydancer	0.000	1.000	0.000
3	bellydancer	bellydancer	0.000	1.000	0.000
4	bellydancer	bellydancer	0.000	1.000	0.000
5	bellydancer	bellydancer	0.000	0.997	0.003
6	politician	politician	0.003	0.000	0.997
7	politician	politician	0.000	0.000	1.000
8	politician	politician	0.000	0.000	1.000
9	politician	politician	0.000	0.002	0.998
10	politician	politician	0.000	0.000	1.000
11	admin	admin	1.000	0.000	0.000
12	admin	admin	1.000	0.000	0.000
13	admin	admin	1.000	0.000	0.000
14	admin	admin	1.000	0.000	0.000
15	admin	admin	0.982	0.000	0.018

Not much doubt.

Cross-validating the jobs-activities data

Recall: no need for predict:

```
p <- lda(job ~ reading + dance + tv + ski, data = active, CV = TRUE)
active.3 <- cbind(active, class = p$class, posterior = p$posterior)
with(active.3, table(obs = job, pred = class))
```

	pred		
obs	admin	bellydancer	politician
admin	5	0	0
bellydancer	0	4	1
politician	0	0	5

This time one of the bellydancers was classified as a politician.

and look at the posterior probabilities

```
active.3 %>%  
  mutate(across(starts_with("posterior"), \ (p) round(p, 3))) %>%  
  rename_with(\ (p) str_remove(p, "osterior"),  
             starts_with("posterior")) %>%  
  select(job, class, starts_with("p."))
```

	job	class	p.admin	p.bellydancer	p.politician
1	bellydancer	bellydancer	0.000	1.000	0.000
2	bellydancer	bellydancer	0.000	1.000	0.000
3	bellydancer	bellydancer	0.000	1.000	0.000
4	bellydancer	bellydancer	0.000	1.000	0.000
5	bellydancer	politician	0.000	0.001	0.999
6	politician	politician	0.006	0.000	0.994
7	politician	politician	0.001	0.000	0.999
8	politician	politician	0.000	0.000	1.000
9	politician	politician	0.000	0.009	0.991
10	politician	politician	0.000	0.000	1.000
11	admin	admin	1.000	0.000	0.000
12	admin	admin	1.000	0.000	0.000
13	admin	admin	1.000	0.000	0.000
14	admin	admin	1.000	0.000	0.000
15	admin	admin	0.819	0.000	0.181

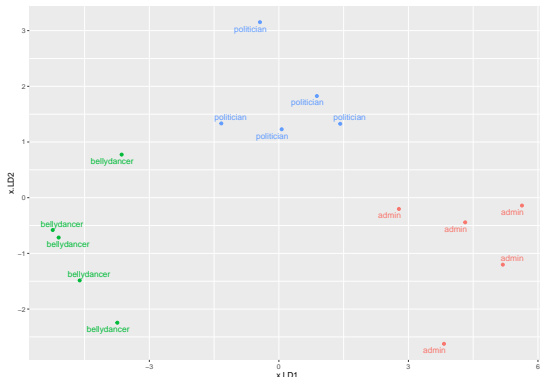
Comments

- Bellydancer was “definitely” a politician!
- One of the administrators might have been a politician too.

Why did things get misclassified?

Go back to plot of discriminant scores:

- one bellydancer much closer to the politicians,
- one administrator a bit closer to the politicians.



Example 4: remote-sensing data

- View 25 crops from air, measure 4 variables x_1 – x_4 .
- Go back and record what each crop was.
- Can we use the 4 variables to distinguish crops?

The data

```
my_url <- "http://ritsokiguess.site/datafiles/remote-sensing.txt"
crops <- read_table(my_url)
crops
```

```
# A tibble: 25 x 6
```

	crop	x1	x2	x3	x4	cr
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>
1	Corn	16	27	31	33	r
2	Corn	15	23	30	30	r
3	Corn	16	27	27	26	r
4	Corn	18	20	25	23	r
5	Corn	15	15	31	32	r
6	Corn	15	32	32	15	r
7	Corn	12	15	16	73	r
8	Soybeans	20	23	23	25	y
9	Soybeans	24	24	25	32	y
10	Soybeans	21	25	23	24	y

```
# i 15 more rows
```

Discriminant analysis

```
crops.1 <- lda(crop ~ x1 + x2 + x3 + x4, data = crops)
crops.1
```

Call:

```
lda(crop ~ x1 + x2 + x3 + x4, data = crops)
```

Prior probabilities of groups:

Corn	Cotton	Soybeans	Sugarbeets
0.28	0.24	0.24	0.24

Group means:

	x1	x2	x3	x4
Corn	15.28571	22.71429	27.42857	33.14286
Cotton	34.50000	32.66667	35.00000	39.16667
Soybeans	21.00000	27.00000	23.50000	29.66667
Sugarbeets	31.00000	32.16667	20.00000	40.50000

Coefficients of linear discriminants:

	LD1	LD2	LD3
x1	0.14077479	0.007780184	-0.0312610362
x2	0.03006972	0.007318386	0.0085401510
x3	-0.06363974	-0.099520895	-0.0005309869
x4	-0.00677414	-0.035612707	0.0577718649

Proportion of trace:

LD1	LD2	LD3
0.8044	0.1832	0.0124

Assessing

- 3 LDs (four variables, four groups).
- 1st two important.
- LD1 mostly x_1 (plus)
- LD2 x_3 (minus)

Predictions

- Thus:

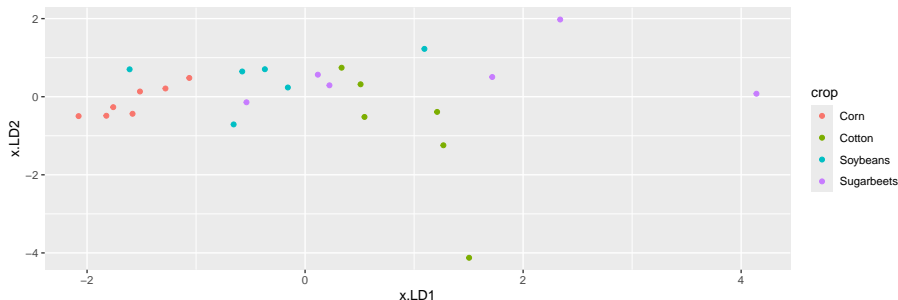
```
p <- predict(crops.1)
crops.2 <- cbind(crops, p)
with(crops.2, table(obs = crop, pred = class))
```

obs	pred			
	Corn	Cotton	Soybeans	Sugarbeets
Corn	6	0	1	0
Cotton	0	4	2	0
Soybeans	2	0	3	1
Sugarbeets	0	0	3	3

- Not very good, eg. only half the Soybeans and Sugarbeets classified correctly.

Plotting the LDs

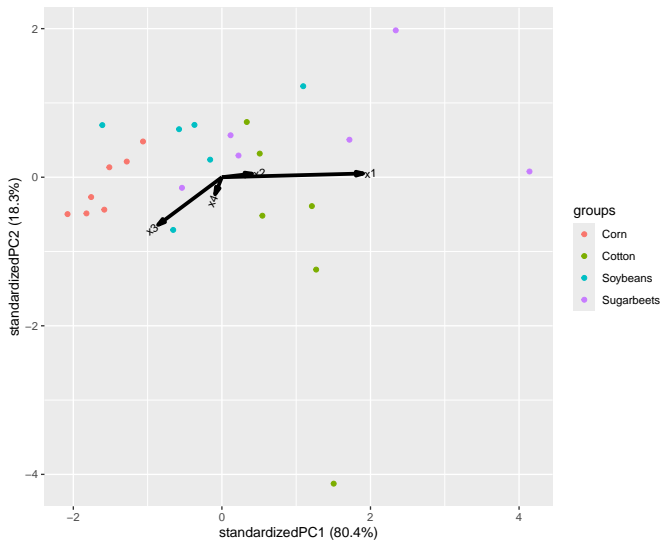
```
ggplot(crops.2, aes(x = x.LD1, y = x.LD2, colour = crop)) +  
  geom_point()
```



Corn (red) mostly left, cotton (green) sort of right, soybeans and sugarbeets (blue and purple) mixed up.

Biplot

```
ggbiplot(crops.1, groups = crops$crop)
```



Comments

- Corn low on LD1 (left), hence low on x_1
- Cotton tends to be high on LD1 (high x_1)
- one cotton very low on LD2 (high x_3 ?)
- Rather mixed up.

Posterior probs (some)

```
cropls.2 %>% mutate(across(starts_with("posterior"), \(p) round(p, 3))) %>%  
  rename_with(\(p) str_remove(p, "osterior"),  
              starts_with("posterior")) %>%  
  filter(crop != class) %>%  
  select(crop, class, starts_with("p."))
```

	crop	class	p.Corn	p.Cotton	p.Soybeans	p.Sugarbeets
4	Corn	Soybeans	0.443	0.034	0.494	0.029
11	Soybeans	Sugarbeets	0.010	0.107	0.299	0.584
12	Soybeans	Corn	0.684	0.009	0.296	0.011
13	Soybeans	Corn	0.467	0.199	0.287	0.047
15	Cotton	Soybeans	0.056	0.241	0.379	0.324
17	Cotton	Soybeans	0.066	0.138	0.489	0.306
20	Sugarbeets	Soybeans	0.381	0.146	0.395	0.078
21	Sugarbeets	Soybeans	0.106	0.144	0.518	0.232
24	Sugarbeets	Soybeans	0.088	0.207	0.489	0.216

Comments

- These were the misclassified ones, but the posterior probability of being correct was not usually too low.
- The correctly-classified ones are not very clear-cut either.

MANOVA

Began discriminant analysis as a followup to MANOVA. Do our variables significantly separate the crops?

```
response <- with(crops, cbind(x1, x2, x3, x4))
crops.manova <- manova(response ~ crop, data = crops)
summary(crops.manova)
```

	Df	Pillai	approx F	num Df	den Df	Pr(>F)
crop	3	0.9113	2.1815	12	60	0.02416 *
Residuals	21					

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

Box's M test

We should also run Box's M test to check for equal variance of each variable across crops:

```
summary(BoxM(response, crops$crop))
```

Box's M Test

Chi-Squared Value = 69.42634 , df = 30 and p-value: 5.79e-05

- The P-value for the M test is smaller even than our guideline of 0.001. So we should not take the MANOVA seriously.
- *Apparently* at least one of the crops differs (in means) from the others. So it is worth doing this analysis.
- We did this the wrong way around, though!

The right way around

- *First*, do a MANOVA to see whether any of the groups differ significantly on any of the variables.
- Check that the MANOVA is believable by using Box's M test.
- *If the MANOVA is significant*, do a discriminant analysis in the hopes of understanding how the groups are different.
- For remote-sensing data (without Clover):
 - ▶ LD1 a fair bit more important than LD2 (definitely ignore LD3).
 - ▶ LD1 depends mostly on x_1 , on which Cotton was high and Corn was low.
- Discriminant analysis in MANOVA plays the same kind of role that Tukey does in ANOVA.