Testing and Modeling Multiple Dependent Variables

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Suppose you measured two groups or conditions and have a lot of relatively weak measures of difference. You might find that each of the measures are correlated, and measure related constructs. Whether or not the individual measures show significant differences between groups, it might be nice to construct a composite of the DVs. But what is the right way to do that?

There are some problems to think about. Different measures might be negatively correlated with one another, so averaging them would wipe out any effect. Or they may be of different magnitudes (e.g., completion time in seconds for one task, and accuracy for another). If you averaged these, one would swamp the other. Even if you had the same scale (two likert-scale responses), differences in variance could make averaging together problematic.

Keeping them separate is also not always ideal. This produces multiple tests, and so you would have a greater chance of a false alarm. On the other hand, you may have several weak signals—each of which are noisy and none of which are significantly different, even if a composite score might be.

There have been a number of procedures and tests developed to solve this problem. These include:

- Hotellings T2: a generalization of the t-test for multiple DVs
- The MANOVA Procedure: a generalization of ANOVA for multiple DVs
- Canonical Correlation Analysis: correlating two sets of measures

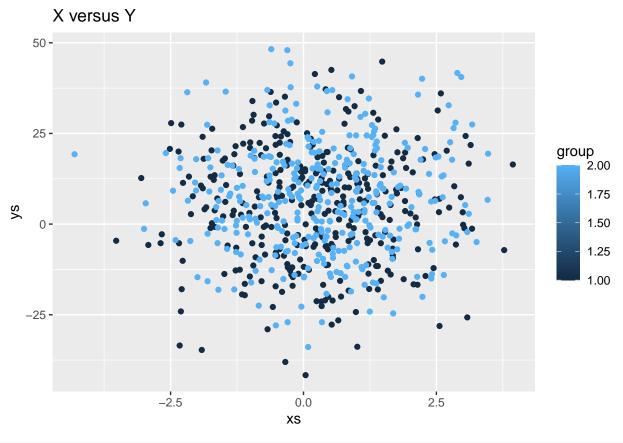
Hotelling T2

The MANOVA is an extension of the ANOVA that attempts to run an ANOVA on a number of dependent measures, combining them optimally. Hotellings T^2 is a simpler version for two groups or levels, but multiple DVs–much like the t-test.

We will start with an example data set in which three outcome variables are each weakly related to a group membership:

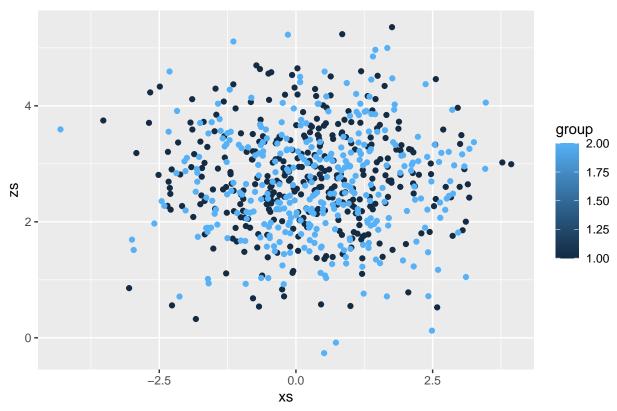
```
library(Hotelling)
library(ggplot2)
library(ICSNP)
library(reshape2)
set.seed(1000)
n <- 350
group <- rep(1:2, each = n)
xs <- rnorm(n * 2, mean = group * 0.2, sd = 1.4)
ys <- rnorm(n * 2, mean = 4 + group * 1.5, sd = 15)
zs <- rnorm(n * 2, mean = 3 - group * 0.2, sd = 0.9)

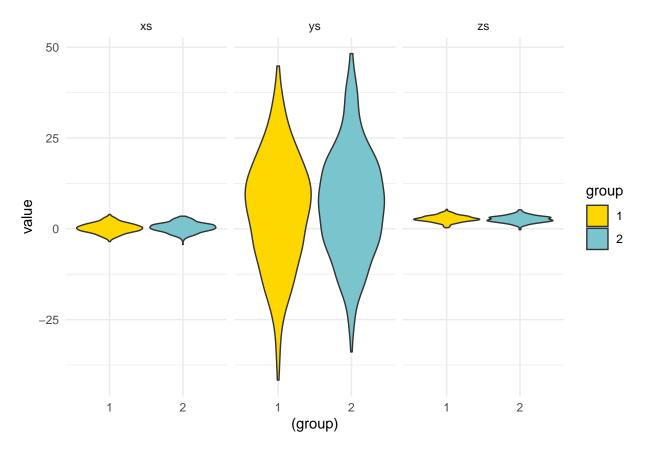
ggplot(data.frame(group, xs, ys), aes(x = xs, y = ys, color = group)) + geom_point() +
    labs(title = "X versus Y")</pre>
```



ggplot(data.frame(group, xs, zs), aes(x = xs, y = zs, color = group)) + geom_point() +
 labs(title = "X versus Z")

X versus Z





Notice that the three values we measured are on different scales, and they differ in different ways across groups.

```
t.test(xs ~ group)
```

Welch Two Sample t-test

```
data: xs by group
t = -1.3874, df = 697.9, p-value = 0.1658
```

alternative hypothesis: true difference in means between group 1 and group 2 is not equal to 0 95 percent confidence interval:

-0.33887615 0.05825459

sample estimates:

mean in group 1 mean in group 2 0.2250053 0.3653161

t.test(ys ~ group)

Welch Two Sample t-test

```
data: ys by group

t = -1.7294, df = 696.93, p-value = 0.08419

alternative hypothesis: true difference in r
```

alternative hypothesis: true difference in means between group 1 and group 2 is not equal to 0 95 percent confidence interval:

-4.2298935 0.2680513 sample estimates:

```
mean in group 1 mean in group 2
5.006313 6.987234

t.test(zs ~ group)

Welch Two Sample t-test

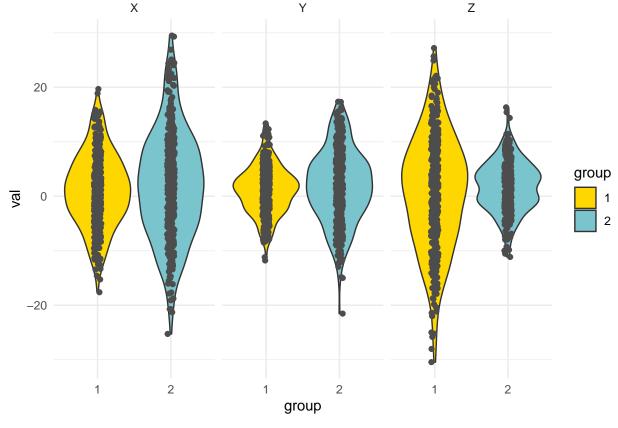
data: zs by group
t = 1.7669, df = 697.25, p-value = 0.07768
alternative hypothesis: true difference in means between group 1 and group 2 is not equal to 0
95 percent confidence interval:
-0.01332771 0.25302765
sample estimates:
mean in group 1 mean in group 2
2.75949 2.63964
```

None of these three measures differ significantly at a p<.05 level. Furthermore, the values are on different scales, and for some of them group 1 is higher, while for others group 1 is lower. If we had a high ICC, we might consider making a composite score-averaging these together, and trying to look at the measure that way. In this case, this would not be possible unless we either had some theory (expectations about positive/negative difference and scaling), or did some normalization to bring the measures all onto the same scale. So in an ideal world, maybe we would know something about the data and do this:

```
x2 <- xs/0.2
y2 <- (ys - 4)/1.5
z2 <- -(zs - 3)/(0.2)

tmp <- data.frame(group = as.factor(rep(group, 3)), val = c(x2, y2, z2), xyz = rep(c("X", "Y", "Z"), each = n))

ggplot(tmp, aes(x = group, y = val, col = group)) + geom_violin(aes(fill = group), colour = "grey20", scale = "width") + geom_jitter(color = "grey30", width = 0.05, height = 0) + facet_wrap(~xyz) + theme_minimal() + scale_fill_manual(values = c("gold", "cadetblue3"))</pre>
```



```
composite <- rowMeans(cbind(x2, y2, z2))
t.test(tmp$val ~ as.factor(tmp$group))</pre>
```

Welch Two Sample t-test

If we get lucky and have a good way of combining multiple values, we can still do a simple t-test. An alternative is the Hotelling T^2 test. This tests whether there is a difference between the groups on the three measures altogether. Hotelling's T^2 is available from several packages. But the way you call it differs across packages, so you need to be careful:

Hotelling test from ICSNP

```
HotellingsT2(cbind(xs, ys, zs) ~ group)
```

Hotelling's two sample T2-test

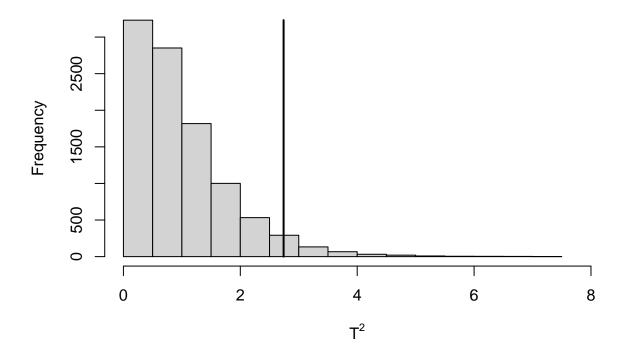
```
data: cbind(xs, ys, zs) by group T.2 = 2.7408, df1 = 3, df2 = 696, p-value = 0.04244 alternative hypothesis: true location difference is not equal to c(0,0,0)
```

hotelling.test from Hotelling package

Previously, the Hotelling package had a function called hotel.test that worked differently from HotellingsT2. Just be aware of this if you are looking for help online because they may provide a walkthrough of an older version. In recent versions this has been replaced by hotelling.test, that permits specifying the dependent measures either as a matrix or with + syntax on the left of the \sim sign:

```
measures either as a matrix or with + syntax on the left of the \sim sign:
## From Hotelling package
print(hotelling.test(cbind(xs, ys, zs) ~ group)) ##This won't work in earlier versions of hotel.test.
Test stat: 8.2459
Numerator df: 3
Denominator df: 696
P-value: 0.04244
print(hotelling.test(xs + ys + zs ~ group)) ##correct; value is the same as ICSNP
Test stat: 8.2459
Numerator df: 3
Denominator df: 696
P-value: 0.04244
Notice that the sign and scale of the components don't matter-z is negatively related to the others, but if we
reverse code it, the results are the same: ##Negatively code z
z2 <- 5 - zs
print(hotelling.test(xs + ys + z2 ~ group))
Test stat: 8.2459
Numerator df: 3
Denominator df: 696
P-value: 0.04244
print(HotellingsT2(cbind(xs, ys, z2) ~ group))
    Hotelling's two sample T2-test
data: cbind(xs, ys, z2) by group
T.2 = 2.7408, df1 = 3, df2 = 696, p-value = 0.04244
alternative hypothesis: true location difference is not equal to c(0,0,0)
plot(hotelling.test(xs + ys + z2 ~ group, perm = TRUE))
  1
```

Distribution of permuted test stats



Similarly, if we reduce scale of one of the components (y), everything stays the same:

```
y2 <- ys/10

print(hotelling.test(xs + y2 + z2 ~ group))
```

Test stat: 8.2459
Numerator df: 3
Denominator df: 696
P-value: 0.04244

```
print(HotellingsT2(cbind(xs, y2, z2) ~ group))
```

Hotelling's two sample T2-test

```
data: cbind(xs, y2, z2) by group T.2 = 2.7408, df1 = 3, df2 = 696, p-value = 0.04244 alternative hypothesis: true location difference is not equal to c(0,0,0)
```

So, Hotelling's T^2 provides a way of creating sort of a composite score, without worrying about the scale or coding direction of the components. Notice that each individual component did not differ significantly across groups, but the set of three did. This also protects against multiple testing—if we'd measured 10 things and expected them all to differ a little but none did, we'd still have a high chance of a type-II false alarm error. Here, we do just one test. However, notice that the T^2 was not as strong as our "theory-based" composite score above, so we could do better if we have a principled method for combining values (and we were right).

Also, it is looking for a combined difference across all the measures. Adding garbage does not help, and actually makes things worse in this case:

```
xx <- rnorm(700)
vv <- rnorm(700)
print(hotelling.test(xs + y2 + z2 + xx + yy ~ group))
```

Test stat: 8.4169 Numerator df: 5 Denominator df: 694 P-value: 0.1386

MANOVA: Extending to Multiple Groups

Just as we use one-way and multi-way ANOVA to generalize the t-test, we use the MANOVA ('multivariate analysis of variance') to generalize T^2 . Sometimes people refer to the Wilks's Lambda as the alternative to MANOVA corresponding to the one-way ANOVA, but this is mostly nomenclature. R will sometimes do this automatically if given the right inputs. The simplest version is of course the two-group version, and we can see that the car library Anova, when implementing a MANOVA, will produce the same F test as Hotelling. The Manova() function is basically a specialized name for the same analysis.

Doing just an 1m essentially creates three regression models

```
library(car)
lm(cbind(xs, ys, zs) ~ group)
Call:
lm(formula = cbind(xs, ys, zs) ~ group)
Coefficients:
                                  zs
                       ٧s
(Intercept)
              0.08469
                        3.02539
                                  2.87934
              0.14031
group
                        1.98092
                                 -0.11985
lm(cbind(xs, ys, zs) ~ group) |>
    summary()
Response xs :
Call:
lm(formula = xs ~ group)
Residuals:
   Min
             1Q Median
                             3Q
                                    Max
-4.6717 -0.8775 -0.0035 0.8957 3.7131
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.08469
                        0.15991
                                  0.530
                                            0.597
             0.14031
                        0.10114
                                  1.387
                                            0.166
group
Residual standard error: 1.338 on 698 degrees of freedom
Multiple R-squared: 0.00275,
                               Adjusted R-squared: 0.001321
F-statistic: 1.925 on 1 and 698 DF, p-value: 0.1658
Response ys :
```

```
Call:
lm(formula = ys ~ group)
Residuals:
   Min
                            3Q
            1Q Median
                                   Max
-46.662 -10.346 0.431
                         9.946 41.251
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)
              3.025
                         1.811
                                 1.670
                                         0.0953 .
                                 1.729
               1.981
                          1.145
                                         0.0842 .
group
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 15.15 on 698 degrees of freedom
Multiple R-squared: 0.004266, Adjusted R-squared: 0.00284
F-statistic: 2.991 on 1 and 698 DF, p-value: 0.08419
Response zs :
Call:
lm(formula = zs ~ group)
Residuals:
    Min
              1Q Median
                                3Q
                                        Max
-2.90443 -0.57216 -0.03638 0.60867 2.59755
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.87934
                       0.10725 26.847
                                         <2e-16 ***
           -0.11985
                       0.06783 -1.767
                                         0.0777 .
group
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.8973 on 698 degrees of freedom
Multiple R-squared: 0.004453, Adjusted R-squared: 0.003026
F-statistic: 3.122 on 1 and 698 DF, p-value: 0.07768
In Base R, we can use anova too but manova gives us a similar results in terms of the Pillai's trace
anova(lm(cbind(xs, ys, zs) ~ group))
Analysis of Variance Table
            Df Pillai approx F num Df den Df Pr(>F)
(Intercept)
             1 0.90204 2136.32
                                     3
                                          696 < 2e-16 ***
             1 0.01168
                           2.74
                                          696 0.04244 *
group
                                     3
Residuals
            698
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
manova(lm(cbind(xs, ys, zs) ~ group))
```

Call:

```
Terms:
                    group Residuals
xs
                     3.45
                             1249.39
                    686.71 160271.31
уs
                      2.51
                              562.02
zs
Deg. of Freedom
                         1
                                 698
Residual standard errors: 1.337891 15.15305 0.8973211
Estimated effects may be unbalanced
manova(lm(cbind(xs, ys, zs) ~ group)) |>
    summary()
                Pillai approx F num Df den Df Pr(>F)
group
            1 0.011676 2.7408
                                      3
                                           696 0.04244 *
Residuals 698
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Now, look at the car library functions—these are identical (but report Type-II tests).
Anova(lm(cbind(xs, ys, zs) ~ group))
Type II MANOVA Tests: Pillai test statistic
      Df test stat approx F num Df den Df Pr(>F)
                    2.7408
                                       696 0.04244 *
group 1 0.011676
                                  3
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Manova(lm(cbind(xs, y2, z2) ~ group))
Type II MANOVA Tests: Pillai test statistic
      Df test stat approx F num Df den Df Pr(>F)
group 1 0.011676
                    2.7408
                                  3
                                       696 0.04244 *
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
We can see that the Pillai statistic in MANOVA provides the same results (in each case) as the T^2: .04244.
Again, it doesn't matter the scale or direction of the individual DVs.
Now, let's see what happens when we have three groups? We can actually give a multiple-column dependent
measure to lm, but it does not really do what we might expect:
set.seed(1001)
val <- rnorm(500)</pre>
group <- as.factor(sample(c("A", "B", "C"), 500, replace = T))</pre>
out1 <- 30 + val * 0.3 - as.numeric(group) * 0.25 + rnorm(500) * 4
out2 <- 40 - val * 0.4 + as.numeric(group) * 0.3 + rnorm(500) * 4
```

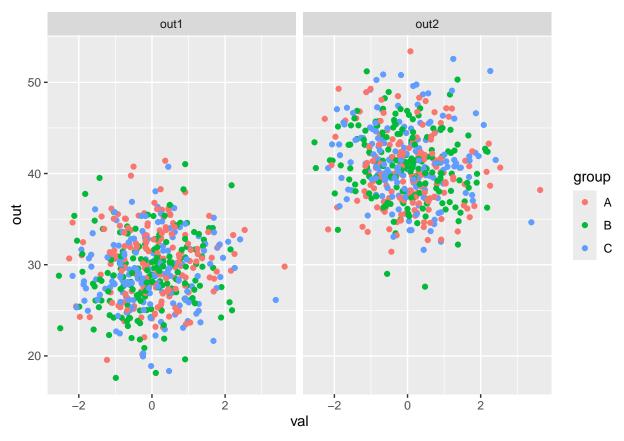
manova(lm(cbind(xs, ys, zs) ~ group))

dat1 <- data.frame(val, group, out1, out2)</pre>

each = 500)

dat2 <- data.frame(val, group, out = c(out1, out2), measure = rep(c("out1", "out2"),</pre>

ggplot(dat2, aes(x = val, y = out, color = group)) + geom_point() + facet_wrap(~measure)



```
## this just does things 'in parallel'
lm1 <- lm(cbind(out1, out2) ~ val + group)
summary(lm1)</pre>
```

Response out1 :

Call:

lm(formula = out1 ~ val + group)

Residuals:

Min 1Q Median 3Q Max -11.1879 -2.5912 -0.0488 2.5191 11.6169

Coefficients:

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

Residual standard error: 3.941 on 496 degrees of freedom Multiple R-squared: 0.02762, Adjusted R-squared: 0.02173

```
F-statistic: 4.695 on 3 and 496 DF, p-value: 0.003039
Response out2 :
Call:
lm(formula = out2 ~ val + group)
Residuals:
     Min
               1Q
                   Median
                                 3Q
                                         Max
-13.0958 -2.7026 -0.2365
                             2.5003 13.2246
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 40.2092
                         0.3084 130.392 < 2e-16 ***
val
             -0.4676
                         0.1782 -2.623 0.00897 **
              0.7005
                                  1.623 0.10523
                         0.4316
groupB
              1.1582
                         0.4335
                                  2.672 0.00779 **
groupC
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Residual standard error: 3.935 on 496 degrees of freedom
Multiple R-squared: 0.02858, Adjusted R-squared: 0.0227
F-statistic: 4.864 on 3 and 496 DF, p-value: 0.002414
Here, it really just runs a regression twice, once on each outcome variable. But if we give this lm to anova, it
will do a MANOVA
library(car)
anova(lm1)
Analysis of Variance Table
             Df Pillai approx F num Df den Df
                                                  Pr(>F)
                           38603
                                      2
                                           495 < 2.2e-16 ***
(Intercept)
              1 0.99363
val
              1 0.02359
                               6
                                      2
                                           495 0.002715 **
group
              2 0.03591
                               5
                                      4
                                           992 0.001239 **
Residuals
            496
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
However, this uses a "Type-I" MANOVA. Because we have multiple predictors, maybe we want a type-II
MANOVA, which car::Anova and car::Manova do.
## these two produce the same results:
Anova(lm1)
Type II MANOVA Tests: Pillai test statistic
     Df test stat approx F num Df den Df
                                           Pr(>F)
      1 0.021684
                     5.4857
                                 2
                                      495 0.004402 **
group 2 0.035909
                     4.5342
                                 4
                                      992 0.001239 **
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Manova(lm1)
```

```
Type II MANOVA Tests: Pillai test statistic

Df test stat approx F num Df den Df Pr(>F)

val 1 0.021684 5.4857 2 495 0.004402 **

group 2 0.035909 4.5342 4 992 0.001239 **

---

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

Overall, we get much of the same capabilities from the MANOVA as we did from simple anova models, but with multiple DVs. At the end of the day, the challenge with a MANOVA is interpreting what it means, because your multiple DVs typically have different interpretations. There is another more technical issue—what does a significant MANOVA really mean, and what does it do? We can think of it as doing a regression or ANOVA on a PCA, but even then it is tricky because we have multiple dimensions of the PCA to deal with.

Interpreting the MANOVA Statistics

When computing a standard ANOVA, we are dividing up our variance into pools accounted for by different predictors and combinations of predictors. In MANOVA, instead of variance, we have a covariance matrix that we are trying to do the same thing with. For N outcomes, this involves N variance terms, plus N*(N-1)/2 covariance (correlation) terms. The test statistics work by computing eigenvalues (i.e., a PCA) of this covariance matrix, and denote λ_i as the ith eigenvalue. Most test statistics are function of these λ values, and there are a number of ways to combine these, and each has its own null-hypothesis distribution that is generally related to the F test.

The following is from: https://en.wikiversity.org/wiki/Advanced ANOVA/MANOVA

Choose from among these multivariate test statistics to assess whether there are statistically significant differences across the levels of the IV(s) for a linear combination of DVs. In general Wilks' λ is recommended unless there are problems with small N, unequal ns, violations of assumptions, etc. in which case Pillai's trace is more robust:

Roy's greatest characteristic root

- Tests for differences on only the first discriminant function
- Most appropriate when DVs are strongly interrelated on a single dimension
- Highly sensitive to violation of assumptions most powerful when all assumptions are met

Wilks' lambda (Λ)

- Most commonly used statistic for overall significance
- Considers differences over all the characteristic roots (principal components)
- The smaller the value of Wilks' lambda, the larger the between-groups dispersion

Hotelling's trace

• Considers differences over all the characteristic roots

Pillai's criterion/Trace

- Considers differences over all the characteristic roots
- More robust than Wilks'; should be used when sample size decreases, unequal cell sizes or homogeneity
 of covariances is violated

Typically, packages will report Pillai's criterion or Pillai's trace. It is the sum of $(\lambda)/(1-\lambda)$, which should remind you of the effect size f^2 used in calculating power, since the eigenvalue is a measure of the proportion of variance. Hotelling's Trace (or Hotelling-Lawley's Trace) is the sum of the eigenvalues; Wilks λ is the sum of $1/(1+\lambda_i)$. Roy's greatest root is the largest λ ; essentially considering just the first principle component.

Each of these tests are available for specifying in Anova, but "Pillai" is the default:

```
Manova(lm1, test.statistic = "Wilks")
Type II MANOVA Tests: Wilks test statistic
      Df test stat approx F num Df den Df
                                            Pr(>F)
val
       1
          0.97832
                    5.4857
                                 2
                                      495 0.004402 **
group 2
          0.96413
                    4.5619
                                 4
                                      990 0.001180 **
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Manova(lm1, test.statistic = "Hotelling-Lawley")
Type II MANOVA Tests: Hotelling-Lawley test statistic
      Df test stat approx F num Df den Df
                                           Pr(>F)
       1 0.022164
                    5.4857
                                 2
                                      495 0.004402 **
val
      2 0.037162
                                 4
                                      988 0.001124 **
                     4.5895
group
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Manova(lm1, test.statistic = "Roy")
Type II MANOVA Tests: Roy test statistic
      Df test stat approx F num Df den Df
                                            Pr(>F)
         0.022164
                    5.4857
                                 2
                                      495 0.0044017 **
val
                     8.9300
                                 2
                                      496 0.0001549 ***
      2
         0.036008
group
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

The different statistics give different interpretations. Roy's greatest root essentially asks whether there is a difference on the primary dimension of shared variance of the dependent variables. The others consider all the dimensions of shared variance, but combine these differently.

Ultimately, the MANOVA often hides more than it reveals. Many statisticians have recommended you avoid using it unless you really need to, but it can come in handy, and understanding is important for evaluating other research.

Conceptual relationship to PCA

Conceptually, MANOVA is sort of like doing something like the following, which performs a regression on dimensions of a principal components analysis. The real action in the MANOVA is choosing the test statistic, which determines how to combine or consider different components. If you are trying to do something like this, it would usually be better to use the MANOVA directly rather than trying to figure out something ad hoc like predicting eigen vectors 'by hand'. However, this is also a way of handling multi-colinearity in a regression model, and may give you a better understanding of what is going on because you can trace back each component to the original variables.

```
E <- eigen(cor((dat1[, 3:4])))
print(E)

eigen() decomposition
$values
[1] 1.0331709 0.9668291</pre>
$vectors
```

```
[,1]
                  [,2]
[1,] 0.7071068 -0.7071068
[2,] 0.7071068 0.7071068
p1 <- as.matrix(dat1[, 3:4]) %*% as.matrix(E$vectors[, 1])
p2 <- as.matrix(dat1[, 3:4]) %*% as.matrix(E$vectors[, 2])
m1 \leftarrow (lm(p1 \sim val + group))
summary(m1)
Call:
lm(formula = p1 ~ val + group)
Residuals:
    Min
             1Q Median
                             3Q
-13.5333 -2.4216 -0.1097
                         2.7163 11.3580
Coefficients:
          Estimate Std. Error t value Pr(>|t|)
-0.09538 0.18372 -0.519
                                    0.604
val
                   0.44495 -0.763
groupB
          -0.33967
                                     0.446
         -0.04186 0.44686 -0.094 0.925
groupC
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Residual standard error: 4.057 on 496 degrees of freedom
Multiple R-squared: 0.001911, Adjusted R-squared: -0.004126
F-statistic: 0.3165 on 3 and 496 DF, p-value: 0.8134
Anova(m1)
Anova Table (Type II tests)
Response: p1
         Sum Sq Df F value Pr(>F)
val
          4.4 1 0.2695 0.6039
               2 0.3500 0.7049
          11.5
group
Residuals 8162.5 496
m2 \leftarrow lm(p2 \sim val + group)
summary(m2)
lm(formula = p2 ~ val + group)
Residuals:
    Min
            1Q Median
                             3Q
                                    Max
-10.4104 -2.4849 -0.2255
                          2.5036 13.4315
Coefficients:
          Estimate Std. Error t value Pr(>|t|)
(Intercept) 7.0150 0.2990 23.458 < 2e-16 ***
val
```

```
groupB
             1.3304
                        0.4186
                                 3.178 0.00157 **
             1.6798
                        0.4204
                                 3.996 7.42e-05 ***
groupC
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Residual standard error: 3.816 on 496 degrees of freedom
Multiple R-squared: 0.05608,
                               Adjusted R-squared: 0.05037
F-statistic: 9.822 on 3 and 496 DF, p-value: 2.649e-06
Anova(m2)
Anova Table (Type II tests)
Response: p2
         Sum Sq Df F value
                               Pr(>F)
          156.1
                  1 10.7188 0.0011346 **
val
                  2 8.8685 0.0001643 ***
          258.3
group
Residuals 7223.8 496
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Notice that for two groups, the eigenvectors are essentially the mean and the difference between the observations. As the number of outcomes increases, these would be less constrained. If you look at the F tests for each predictor, you will see that the values are very similar to those produced in the PCA version (either on average, or max values, etc.). But this means that, depending on the test statistic, a MANOVA might also be considering strange and non-intuitive combinations of variables. Importantly, the group of dependent measures do not need to be correlated. Consider the following dependent variables. Here, out1 and out2 are independent, but group is related to the difference between them. Group is thus also indirectly related to each one, because the difference is larger when one is large or when the other is small (or both). Group2 and out3 are unrelated to the others.

Some statisticians have explored procedures like this for doing ANOVA on PCA (e.g., https://iopscience.i op.org/article/10.1088/1742-6596/1899/1/012103/pdf). According to Abapihi et al. (2021), practitioners sometimes have found the MANOVA difficult to apply because of its strict assumptions, and propose ANOVA on the first principal component as an alternative. It seems like this would be successful if your first dimension is highly interpretable, but I wouldn't recommend it unless you take the PCA seriously first. For example, if your first component is highly interpretable and accounts for a substantial amount of variance, this might be easily justified, but it is mostly a similar procedure as Roy's GCR statistic. Other MANOVA statistics will incorporate all dimensions.

```
set.seed(150)
yout1 <- rnorm(150)
yout2 <- rnorm(150)
yout3 <- rnorm(150)
delta <- ((yout1 - mean(yout1)) - (yout2 - mean(yout2))) + rnorm(150) * 5
group1 <- floor(rank(delta)/50) + 1
group2 <- sample(1:5, replace = T, size = 150)
out <- cbind(yout1, yout2, yout3)
summary(lm(out ~ group1))</pre>
```

Response yout1 :

Call

lm(formula = yout1 ~ group1)

Residuals:

```
1Q
                 Median
                                3Q
-2.41516 -0.71119 0.00642 0.75209 2.45372
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
                               -0.99
(Intercept) -0.21468
                       0.21687
                                         0.324
group1
            0.14901
                       0.09933
                                 1.50
                                         0.136
Residual standard error: 1.008 on 148 degrees of freedom
Multiple R-squared: 0.01498,
                               Adjusted R-squared: 0.008322
F-statistic: 2.25 on 1 and 148 DF, p-value: 0.1357
Response yout2:
Call:
lm(formula = yout2 ~ group1)
Residuals:
    Min
              1Q
                 Median
                               3Q
-2.80585 -0.52989 -0.04297 0.60846 2.24696
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.40930
                       0.20202 2.026 0.0446 *
group1
           -0.23560
                       0.09253 -2.546
                                        0.0119 *
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.9388 on 148 degrees of freedom
Multiple R-squared: 0.04197,
                              Adjusted R-squared: 0.0355
F-statistic: 6.484 on 1 and 148 DF, p-value: 0.01191
Response yout3:
Call:
lm(formula = yout3 ~ group1)
Residuals:
              1Q Median
                               3Q
-2.99510 -0.70386 -0.03446 0.70520 2.32555
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
                       0.21535
                               0.263 0.793
(Intercept) 0.05673
           -0.03119
                       0.09864 -0.316
                                         0.752
group1
Residual standard error: 1.001 on 148 degrees of freedom
Multiple R-squared: 0.0006752, Adjusted R-squared: -0.006077
```

F-statistic: 0.09999 on 1 and 148 DF, p-value: 0.7523
Manova(lm(out ~ group1 + group2), test.statistic = "Roy")

```
Type II MANOVA Tests: Roy test statistic
      Df test stat approx F num Df den Df Pr(>F)
group1 1 0.053897 2.60501
                                  3
                                       145 0.05412 .
group2 1 0.016187 0.78238
                                       145 0.50559
                                  3
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Manova(lm(out ~ group1 + group2), test.statistic = "Pillai")
Type II MANOVA Tests: Pillai test statistic
      Df test stat approx F num Df den Df Pr(>F)
group1 1 0.051140 2.60501
                                  3
                                       145 0.05412 .
group2 1 0.015929 0.78238
                                  3
                                       145 0.50559
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Manova(lm(out ~ group1 + group2), test.statistic = "Wilks")
Type II MANOVA Tests: Wilks test statistic
      Df test stat approx F num Df den Df Pr(>F)
           0.94886 2.60501
                                  3
                                       145 0.05412 .
           0.98407 0.78238
                                       145 0.50559
group2 1
                                  3
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Relation to Repeated Measures ANOVA
This all seems like it is a bit like a repeated-measures ANOVA. By putting the data in 'long' format, we
can just combine out 1 and out 2 into a single DV, then predict the mean difference between the two with a
categorical value:
dat2 <- data.frame(val, group, out = c(out1, out2), measure = rep(c("out1", "out2"),</pre>
    500))
model.rm <- lm(out ~ val + group + measure, data = dat2)</pre>
summary(model.rm)
Call:
lm(formula = out ~ val + group + measure, data = dat2)
Residuals:
    Min
              1Q
                    Median
                                 3Q
                                         Max
                    0.1021
-17.3432 -5.8142
                            5.6072 18.0186
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
                       0.44659 79.231
(Intercept) 35.38334
                                          <2e-16 ***
           -0.06344
val
                       0.22260 -0.285
                                           0.776
                                           0.643
groupB
            -0.25003
                       0.53912 -0.464
```

0.954

0.552

-0.03096

measureout2 -0.26154

groupC

0.54119 -0.057

0.43988 -0.595

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

Residual standard error: 6.948 on 995 degrees of freedom

Multiple R-squared: 0.0006802, Adjusted R-squared: -0.003337

F-statistic: 0.1693 on 4 and 995 DF, p-value: 0.9541
```

This might be OK is some situations. But this is assuming that the two measures differ just by a constant. What if they have different scales, different variances, different directional relationships? Just like the t-test above, if we had a theory that could be used to combine these, it might be a better approach, but in this case, we are restricted in the inferences we can make. Notice that for each sub-model, the effects are in different directions, and so cancel out one another if we do it this way. We could sort of do this by predicting all the interactions too, but this begins to get very complicated such that a MANOVA might be preferred.

Relationship to Logistic Regression, PCA, LDA, and Classification

As we can see, although MANOVA seems like it is just a simple extension of ANOVA, it relates to many multi-variate concepts. For Hotelling's T^2 version, we are attempting to find whether there is a difference between two groups on multiple measures. We could easily turn this around; predicting group membership based on those multiple 'predictors'. This is what methods such as logistic regression and linear discriminant analysis do. As we extend to multiple categories in MANOVA, this becomes similar to what some machine classification schemes permit—classifying categories based on multiple observed 'features'. Finally, we can understand MANOVA as sort of doing regressions on each principle component, and determining a reasonable means of combining those regressions at the end of the day.

Exercise:

The bfi data set in psych has data from a big-five inventory, and includes gender and age. Look at conscientiousness as a subscale, and examine whether it appears to be a coherent factor. Then, use MANOVA to predict the set of conscientiousness questions using gender and age. Does the personality depend on these? Recode age to a categorical 2- or 3-group factor, and test the interaction between gender and age.

```
library(psych)
library(car)
data(bfi)
dplyr::select(bfi, A1:05)
      A1 A2 A3 A4 A5 C1 C2 C3 C4 C5 E1 E2 E3 E4 E5 N1 N2 N3 N4 N5 O1 O2 O3 O4
61617
                 4
                    4
                       2
                          3
                             3
                                 4
                                    4
                                          3
                                             3
                                                 4
                                                       3
                                                          4
                                                              2
                                                                 2
                                                                    3
                                                                       3
                                       3
                                                    4
       2
                 2
                    5
                       5
                          4
                             4
                                 3
                                             6
                                                    3
                                                          3
                                                             3
                                                                 5
                                                                    5
61618
                                    4
                                       1
                                          1
                                                       3
61620
       5
                       4
                          5
                             4
                                 2
                                    5
                                       2
      05
61617
       3
61618
       3
61620
 [ reached 'max' / getOption("max.print") -- omitted 2797 rows ]
lm1 <- lm(as.matrix(dplyr::select(bfi, A1:05)) ~ bfi$gender)</pre>
Manova(lm1)
Type II MANOVA Tests: Pillai test statistic
           Df test stat approx F num Df den Df
                                                     Pr(>F)
                                             2410 < 2.2e-16 ***
bfi$gender 1
                 0.14813
                           16.763
                                       25
```

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

Canonical Correlation Analysis

MANOVA extends ANOVA/regression and allows multiple predictors and multiple outcome variables. A lesser-known alternative is Canonical Correlation Analysis (CCA), which tries to establish the cross-correlation between two sets of variables, and does so by establishing a dimensionality of the relationship.

This is akin to a PCA, but rather than just finding the dimension of variability that is greatest, it finds the dimension of the covariance between the two variables that is the greatest. So, each set of measures A and B have a mapping onto latent variables (like PCA), which we call X and Y. This mapping is done so that the first dimension of X and the first dimension of Y are as highly correlated as we can get. Then, we find another two orthogonal dimensions, which compose the second set of canonical correlations. This can go on until we have N canonical correlations, where N is the smaller of the two numbers of variables. That is, if one set has 4 variables and another set has 2, you can only calculate 2 canonical correlations.

Packages and resources

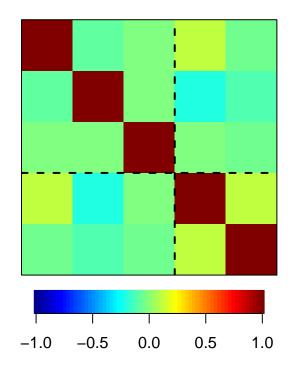
- https://stats.idre.ucla.edu/r/dae/canonical-correlation-analysis/
- cancor function in stats package
- CCA package
- candisc package

Example

Here, we start with calculating 'matcor', and visualizing them in an image plot. These aren't the canonical correlations, but rather a precursor:

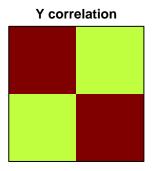
```
library(CCA)
matcor(out, cbind(group1, group2))
$Xcor
            yout1
                        yout2
                                    yout3
yout1 1.00000000 -0.06856134 -0.02984807
yout2 -0.06856134 1.00000000 -0.03009671
yout3 -0.02984807 -0.03009671 1.00000000
$Ycor
          group1
                    group2
group1 1.0000000 0.1070147
group2 0.1070147 1.0000000
$XYcor
                                                group1
                                                            group2
             yout1
                         yout2
                                     yout3
                                            0.12238444 -0.03493933
        1.00000000 -0.06856134 -0.02984807
yout1
      -0.06856134 1.00000000 -0.03009671 -0.20486423 -0.12148177
      -0.02984807 -0.03009671 1.00000000 -0.02598397 -0.04842062
group1 0.12238444 -0.20486423 -0.02598397
                                            1.00000000
                                                        0.10701468
group2 -0.03493933 -0.12148177 -0.04842062
                                           0.10701468 1.00000000
img.matcor(matcor(out, cbind(group1, group2)))
```

XY correlation

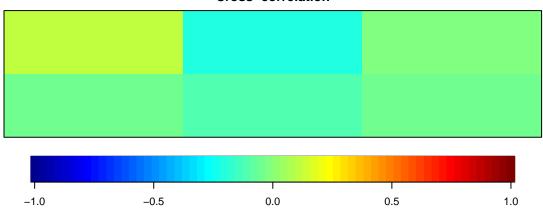


img.matcor(matcor(out, cbind(group1, group2)), type = 2)

X correlation



Cross-correlation



x <- cc(out, cbind(group1, group2))
print(x)</pre>

\$cor

[1] 0.24555116 0.09975194

\$names

\$names\$Xnames

[1] "yout1" "yout2" "yout3"

\$names\$Ynames

[1] "group1" "group2"

\$names\$ind.names

NULL

\$xcoef

[,1] [,2] yout1 -0.3316122 -0.8923137 yout2 0.9470580 -0.3420840 yout3 0.1802280 -0.3832381

\$ycoef

[,1] [,2] group1 -1.0892190 -0.5270819

group2 -0.2316294 0.6476470

\$scores

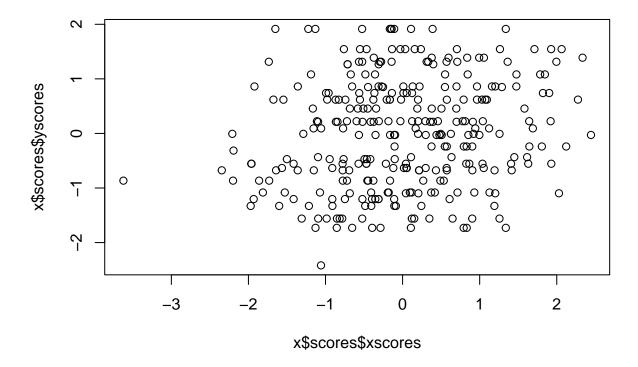
```
$scores$xscores
```

```
[,1]
                         [,2]
[1,] 1.36305021 0.995883466
[2,] -0.56565672 0.507227219
[3,] -0.91210575 1.338943099
 [4,] 0.04287964 0.109404897
[5,] -0.40624108 0.911386088
[6,] -0.94537667 0.595946887
[7,] 0.05491903 -0.853656228
[8,] 1.80673300 -0.959494532
[9,] 0.01749876 -0.286410996
[10,] -0.35742517 0.791743077
[11,] 0.50436696 -0.109395258
[12,] 0.45791621 1.929404728
[13,] 1.84623811 -0.978375490
[14,] -0.13690027 1.415658235
[15,] -0.48291423 0.965121629
[16,] -1.56541826 -0.654126001
[17,] 0.12005283 0.220043991
[18,] -0.81618654 -1.359155663
[19,] -1.60095541 0.393913477
[20,] 0.83146701 1.820576387
[21,] 0.92091739 -1.155230595
[22,] -0.68469957 -1.096972683
[23,] -0.25309080 -0.714380944
[24,] 0.57425159 -0.109118293
[25,] -1.05845240 -2.193440426
[26,] 0.19111584 -0.911822474
[27,] 0.03437887 -1.641895806
[28,] 0.20492095 1.615580213
[29,] -0.30816833 -1.963921730
[30,] -0.45679786 0.930771364
[31,] -1.73536337 -0.351629856
[32,] 0.55155071 2.275276390
[33,] -0.41845943 -0.373586254
[34,] -0.10720517 -1.095527309
[35,] -0.55227934 0.573454033
[36,] 1.25759802 -1.056976195
[37,] 0.62647125 -0.771836960
[ reached getOption("max.print") -- omitted 113 rows ]
```

\$scores\$yscores

[,1] [,2]
[1,] 1.313293056 -0.02798816
[2,] 1.313293056 -0.02798816
[3,] -0.633515672 -1.72979909
[4,] -1.096774378 -0.43450501
[5,] -1.328403731 0.21314202
[6,] -0.470814043 1.38787100
[7,] -0.633515672 -1.72979909
[8,] -0.239184690 0.74022397

```
[9,] -0.633515672 -1.72979909
 [10,] 1.081663703 0.61965887
 [11,] 0.455703369 -1.20271714
 [12,] 0.224074016 -0.55507011
 [13,] 1.081663703 0.61965887
 [14,] 1.544922409 -0.67563520
 [15,] 1.081663703 0.61965887
 [16,] -0.633515672 -1.72979909
 [17,] -1.560033084 0.86078906
 [18,] -1.560033084 0.86078906
 [19,] -1.328403731 0.21314202
 [20,] -0.239184690 0.74022397
 [21,] -0.007555337 0.09257693
 [22,] -1.096774378 -0.43450501
 [23,] 0.850034350 1.26730591
 [24,] 0.618404997 1.91495295
 [25,] -2.417622771 -0.31393992
 [26,] 0.455703369 -1.20271714
 [27,] 1.544922409 -0.67563520
 [28,] -1.096774378 -0.43450501
 [29,] 0.224074016 -0.55507011
 [30,] -0.865145025 -1.08215205
 [31,] 1.313293056 -0.02798816
 [32,] 1.081663703 0.61965887
 [33,] -0.470814043 1.38787100
 [34,] -1.328403731 0.21314202
 [35,] 1.544922409 -0.67563520
 [36,] -0.007555337 0.09257693
 [37,] -0.007555337 0.09257693
 [ reached getOption("max.print") -- omitted 113 rows ]
$scores$corr.X.xscores
                       [,2]
            [,1]
yout1 -0.4030366 -0.8692130
yout2 0.9228995 -0.2535793
yout3 0.1625920 -0.3455781
$scores$corr.Y.xscores
             [,1]
                         [,2]
group1 -0.2312088 -0.03359224
group2 -0.1069591 0.08979132
$scores$corr.X.yscores
             [,1]
                         [,2]
yout1 -0.09896611 -0.08670568
yout2 0.22661905 -0.02529503
yout3 0.03992466 -0.03447209
$scores$corr.Y.yscores
             [,1]
group1 -0.9415913 -0.3367578
group2 -0.4355880 0.9001461
```



Here, we see the canonical correlation uses two dimensions, because group only has two variables. The first dimension finds a correlation between groups of .24, and the second .09.

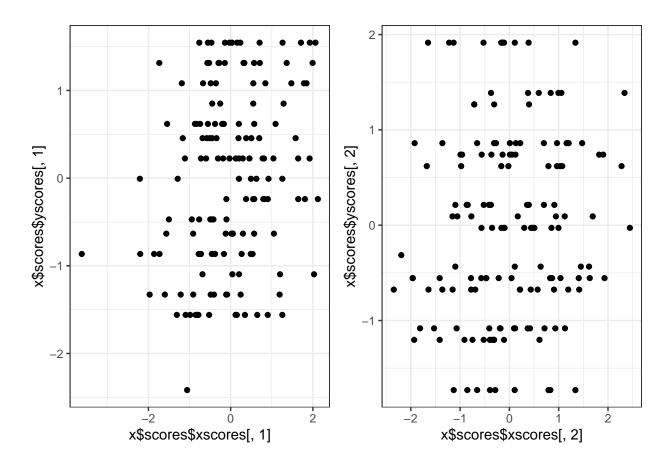
The first dimension correlates negatively with out1, positively with out2, and not with out3. The second dimension correlates with out3 only. On the other side, group 1 and group 2 correlate (negatively) with dimension 1, and group1 is positively related to dimension 2 but group2 is negatively related to dimension 2.

We can sort of look at what is going on by plotting the first dimension xscores and yscores for each person—this is how each person maps into each of the first canonical correlation dimensions. We can see the correlation is .24, which is a small but probably significant relationship. The second is even smaller.

```
library(gridExtra)
cor(x$scores$xscores[, 1], x$scores$yscores[, 1])
```

[1] 0.2455512

```
grid.arrange(ggplot(data.frame(x$scores$xscores, x$scores$yscores), aes(x = x$scores$xscores[,
    1], y = x$scores$yscores[, 1])) + geom_point() + theme_bw(), ggplot(data.frame(x$scores$xscores,
    x$scores$yscores), aes(x = x$scores$xscores[, 2], y = x$scores$yscores[, 2])) +
    geom_point() + theme_bw(), ncol = 2)
```



Exercise

Using the psych::bfi data set, use canonical correlation to determine a relationship between agreeableness and conscientiousness. Plot each individual's scores on the first pair of canonical correlation dimensions against one another.

```
## start with this:
img.matcor(matcor(dplyr::select(bfi, starts_with("c")), dplyr::select(bfi, starts_with("a"))))
```

XY correlation

