# Exersices and solutions — ANOVA tests for d-primes in sensR

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file: exerciseThursday2.Rnw

**Topics:**

ANOVA tests for $d'$ values from Triangle, Duo-Trio, Tetrad, 2-AFC and 3-AFC tests using the sensR functions

- dprime_compare
- dprime_test
- dprime_table and
- posthoc

## Preliminaries

Before we you get started with the exercises, you need to make sure that you have a reasonably new version of sensR. When you run sessionInfo() you should have at least the version of the sensR package shown here:

```
R> sessionInfo()

R version 3.0.1 (2013-05-16)
Platform: x86_64-apple-darwin10.8.0 (64-bit)

locale:
[1] C

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods
[7] base

other attached packages:
[1] sensR_1.2-22      numDeriv_2012.9-1 ordinal_2013.8-25
[4] Matrix_1.0-12     lattice_0.20-15   ucminf_1.1-3

loaded via a namespace (and not attached):
[1] MASS_7.3-28     grid_3.0.1      multcomp_1.2-19 tools_3.0.1
```

If you don't have the newest version, you are probably able to get a newer version with the following command:

```
R> install.packages("sensR", repos="http://R-Forge.R-project.org")
```

# Exercise 1

You have been trying to lower the saturated fat content in one of your products and so you have been experimenting with a number of different formulations. You have compared 5 alternate products to your current standard in discrimination tests and received the following data table.

```
  correct total protocol
1      46   100 triangle
2      70   200   tetrad
3      86   150   tetrad
4     139   200  duotrio
5      35    50 triangle
```

1. Test if the discriminability ($d'$) of the five alternate products differs from each other.
2. What is the concensus discriminability if all alternate products are considered together? Is it appropriate to talk about a common/concensus d-prime here?
3. Summarize any differences among the alternate products:
   (a) Do one or more products differ significantly from the concensus?
   (b) Can the alternate products be categorized in two or more significantly different groups?
4. Your boss favours the third alternate product in particular. Test which of the other products have $d'$-values that are significantly different from this one.

**Answer to the exercise:**

1. 
```
R> dpc <- dprime_compare(correct, total, protocol=protocol)
R> dpc
```

```
Test of multiple d-primes:

Estimation method: Maximum likelihood
0.95% two-sided confidence interval method: Wald

Estimate of common d-prime:
        Estimate Std. Error  Lower Upper
d-prime    1.048    0.08352 0.8842 1.212

Significance test:
  Null hypothesis:  All d-primes are equal
  Alternative:      At least 2 d-primes are different
  Chi-square statistic (Likelihood Ratio) = 48.02, df = 4
  p-value = 9.3334e-10
```

2. *R> coef(dpc)*

```
        Estimate Std. Error     Lower    Upper
d-prime 1.047858 0.08352089 0.8841601 1.211556
```

3. *R> posthoc(dpc, test="common")*

```
Post-hoc comparison of d-primes:

Group-wise d-primes:
       Estimate Std. Error  Lower  Upper   p-value
group1   1.2500     0.2796 0.5885 1.7622 0.4713873
group2   0.3031     0.3106 0.0000 0.7008  1.09e-08
group3   1.2735     0.1353 0.9987 1.5333 0.0920628
group4   1.6857     0.1926 1.2950 2.0585 0.0029253
group5   2.5037     0.3633 1.7996 3.2370 0.0002632
---
p-values are adjusted with holm's method

Alternative hypotheses:
  d-primes are different from common d-prime
```

Look at the compact letter display here

*R> posthoc(dpc)*

```
Post-hoc comparison of d-primes:

Pairwise d-prime differences:
                Estimate Std. Error   p-value
group2 - group1  -0.9469     0.4179 0.1108313
group3 - group1   0.0235     0.3106 0.9396501
group4 - group1   0.4357     0.3395 0.3763159
group5 - group1   1.2537     0.4585 0.0295309
group3 - group2   0.9704     0.3388 0.0002442
group4 - group2   1.3826     0.3654 1.370e-05
group5 - group2   2.2006     0.4780 6.227e-06
group4 - group3   0.4122     0.2353 0.2499921
group5 - group3   1.2302     0.3877 0.0101205
group5 - group4   0.8180     0.4112 0.1774114
---
p-values are adjusted with holm's method

Alternative hypotheses:
  pairwise differences are different from zero

Letter display based on pairwise comparisons:
  group1 group2 group3 group4 group5
  "bc"    "c"    "b"   "ab"    "a"
```

*R> ## Alternatively:*
*R> posthoc(dpc, padj="none")*

```
Post-hoc comparison of d-primes:

Pairwise d-prime differences:
                Estimate Std. Error   p-value
```

```
group2 - group1  -0.9469     0.4179  0.022166
group3 - group1   0.0235     0.3106  0.939650
group4 - group1   0.4357     0.3395  0.188158
group5 - group1   1.2537     0.4585  0.004922
group3 - group2   0.9704     0.3388 3.053e-05
group4 - group2   1.3826     0.3654 1.522e-06
group5 - group2   2.2006     0.4780 6.227e-07
group4 - group3   0.4122     0.2353  0.083331
group5 - group3   1.2302     0.3877  0.001446
group5 - group4   0.8180     0.4112  0.044353
---
p-values are not adjusted for multiplicity

Alternative hypotheses:
  pairwise differences are different from zero

Letter display based on pairwise comparisons:
  group1 group2 group3 group4 group5
   "b"    "c"    "b"    "b"    "a"
```

4. *R> posthoc(dpc, test="base", base=3)*

```
Post-hoc comparison of d-primes:

Differences to group 3:
                Estimate Std. Error   p-value
group1 - group3  -0.0235     0.3106 0.9396501
group2 - group3  -0.9704     0.3388 0.0001221
group4 - group3   0.4122     0.2353 0.1666614
group5 - group3   1.2302     0.3877 0.0043374
---
p-values are adjusted with holm's method

Alternative hypotheses:
  d-primes differences are different from zero
```

*R> posthoc(dpc, test="base", base=3, padj="none")*

```
Post-hoc comparison of d-primes:

Differences to group 3:
                Estimate Std. Error   p-value
group1 - group3  -0.0235     0.3106  0.939650
group2 - group3  -0.9704     0.3388 3.053e-05
group4 - group3   0.4122     0.2353  0.083331
group5 - group3   1.2302     0.3877  0.001446
---
p-values are not adjusted for multiplicity

Alternative hypotheses:
  d-primes differences are different from zero
```

# Exercise 2

A company has launched a product that seems remarkably similar to one of your products. In order to test just how similar the competitors product is to your product, and ultimately to clarify if you should demand your competitors product of the market, you initiate consumer discrimination tests in a number of different locations to cover the custumer base. You receive the following results:

```
    location correct total protocol
1 location 1      19    50   tetrad
2 location 2      20    50 triangle
3 location 3      19    50 triangle
4 location 4      24    50  duotrio
5 location 5      32    50  duotrio
6 location 6      16    50 triangle
```

1. Use `dprime_table` to summarize the data. Now try to set the argument `restrict.above.guess` to `FALSE` in `dprime_table`. What happens to the `pHat` estimates? Which results make most sense to you?
2. Now test if there are any differences among d-primes between the different locations using `dprime_compare` - compare the results of using all four different `statistics` arguments and both of the `estim` arguments. Which gives similar results and which would you avoid?
3. The main goal with the analysis is to assess similarity — perform a similarity test by taking all the data into account on the 5% level. How similar can you say that the products are? Is there statistical significance if you adopt $d'_0 = 1$?
4. Now perform similarity tests for each location separately — how similar are you able to say the products are in this case? Is there statistical significance if you adopt $d'_0 = 1$?

**Answer to the exercise:**

1. *R> dprime_table(cor, tot, prot)*

```
       correct total protocol      pHat    se.pHat    dprime
group1      19    50   tetrad 0.3800000 0.06864401 0.5131564
group2      20    50 triangle 0.4000000 0.06928203 0.8791146
group3      19    50 triangle 0.3800000 0.06864401 0.7283931
group4      24    50  duotrio 0.5000000 0.07071068 0.0000000
group5      32    50  duotrio 0.6400000 0.06788225 1.3611210
group6      16    50 triangle 0.3333333 0.06666667 0.0000000
        se.dprime
group1 0.3915538
group2 0.4869836
group3 0.5597751
group4        NA
group5 0.4051837
group6        NA
```

*R> dprime_table(cor, tot, prot, restric=FALSE)*

```
       correct total protocol pHat    se.pHat    dprime se.dprime
group1      19    50   tetrad 0.38 0.06864401 0.5131564 0.3915538
group2      20    50 triangle 0.40 0.06928203 0.8791146 0.4869836
group3      19    50 triangle 0.38 0.06864401 0.7283931 0.5597751
group4      24    50  duotrio 0.48 0.07065409 0.0000000        NA
group5      32    50  duotrio 0.64 0.06788225 1.3611210 0.4051837
group6      16    50 triangle 0.32 0.06596969 0.0000000        NA
```

2. *R> dprime_compare(cor, tot, prot)*

```
Test of multiple d-primes:

Estimation method: Maximum likelihood
0.95% two-sided confidence interval method: Wald

Estimate of common d-prime:
        Estimate Std. Error  Lower Upper
d-prime   0.6284     0.2199 0.1975 1.059

Significance test:
  Null hypothesis:  All d-primes are equal
  Alternative:      At least 2 d-primes are different
  Chi-square statistic (Likelihood Ratio) = 3.723, df = 5
  p-value = 0.5899
```

```
R> stat <- c("likelihood", "Pearson", "Wald.p", "Wald.d")
R> est <- c("ML", "weighted.avg")
R> sapply(stat, function(S) {
+   sapply(est, function(E) {
+     pval <- try(dprime_compare(cor, tot, prot, statistic=S, estim=E)$p.value, silent=TRUE)
+     if(inherits(pval, "try-error")) NaN else pval
+   })
+ })
```

```
             likelihood   Pearson    Wald.p Wald.d
ML             0.589897 0.5967866 0.6596364    NaN
weighted.avg        NaN       NaN       NaN    NaN
```

3. *R> dpt <- dprime_test(cor, tot, prot, dprime0=1, alternative="simil", conf.level=0.90)*
   *R> dpt*

```
Test of common d-prime:

Estimation method: Maximum likelihood
0.9% two-sided confidence interval method: Wald

Estimate of common d-prime:
        Estimate Std. Error  Lower Upper
d-prime   0.6284     0.2199 0.2667  0.99

Significance test:
  Likelihood root statistic = -2.028, p-value: 0.02126
  Alternative hypothesis: d-prime is less than 1
```

4. *R> posthoc(dpt, test=1, alternative="less")*

```
Post-hoc comparison of d-primes:

Group-wise d-primes:
       Estimate Std. Error  Lower Upper p-value
group1   0.5132     0.3916 0.0000 1.086  0.3168
group2   0.8791     0.4870 0.0000 1.663  0.8755
group3   0.7284     0.5598 0.0000 1.560  0.8755
group4   0.0000         NA 0.0000 1.221  0.3817
group5   1.3611     0.4052 0.1607 2.107  0.8755
group6   0.0000         NA 0.0000 1.228  0.3817
---
p-values are adjusted with holm's method

Alternative hypotheses:
  d-primes are less than 1
```

```
R> posthoc(dpt, test=1, alternative="less", padj="none")
```

```
Post-hoc comparison of d-primes:

Group-wise d-primes:
       Estimate Std. Error  Lower Upper p-value
group1   0.5132     0.3916 0.0000 1.086 0.05280
group2   0.8791     0.4870 0.0000 1.663 0.39771
group3   0.7284     0.5598 0.0000 1.560 0.29182
group4   0.0000         NA 0.0000 1.221 0.07634
group5   1.3611     0.4052 0.1607 2.107 0.79708
group6   0.0000         NA 0.0000 1.228 0.07892
---
p-values are not adjusted for multiplicity

Alternative hypotheses:
  d-primes are less than 1
```