

Test Exercise 2 (R)

1. Read the data in **Flies.txt**, which consist of counts of the number of adult fruit flies emerging from culture jars prepared with different medium formulations. Medium A contained DDT whereas medium B did not. Your job is to determine if fewer flies emerged from jars with medium A. **(a)** First determine if the data need transforming and, if so, find a suitable transformation (since there is one observation with zero flies, one needs to add something, e.g. 0.5, to each count before taking the logarithm or inverse, and this can be used also for the square root). Preferably the Fligner-Killen test, or the more traditionally used Bartlett test and/or a graphical approach are suitable methods to investigate variance homogeneity. For a graphical approach, the `plot.groups.sd` function might be useful (the command `source("PlotGroups.R")` will load it). **(b)** Did fewer flies emerge from jars with DDT medium? **(c)** Looking at the data, was it really necessary to perform a statistical test?

2. Read the data in **Spider2.txt**. The data are from staged fights between pairs of males of the bowl and doily spider (*Frontinella pyramitela*), in the presence of a female (you used similar data in an exercise in week 1). Each row corresponds to a fight between a different pair of males. The variable `Value` is the value of the female, measured in number of fertilizable eggs (either 3, 13, or 40). The variable `Grapple` is the number of seconds of grappling until the fight ends (because one male gives up or is killed). Your job is now to determine if female value influences contest duration. First make `Value` a factor

```
dat$Value <- factor(dat$Value)
```

Then check the distribution of `Grapple` in each group (treatment), how do the variances compare among the different groups? Try to find a transformation that gives homogeneous variances and a nice-looking distribution of residuals (for graphical display, you can use the `plot.groups.sd` function and, to examine the distribution of residuals, the `norm.fit` function, which you can load with a `source("NormFit.R")` command). **(a)** Which transformation do you choose and what is your conclusion about the effect of female value? **(b)** Which treatment pairs do you regard as showing a statistically significant difference? (You can look at exercise 3.6 and exercise 4.2 from last week to remind yourself about post-hoc testing in R.)

3. Read the data in **Skeleton.txt**. The file contains data on skeleton weights and body weights (in kg) for 25 bird species and 25 mammal species. For birds, the species range from emus to bee-eaters and for mammals the range is from elephants to the shrews, including humans, dogs and cats. Since most birds fly, one might expect the skeleton of a bird to be lighter than that of an earthbound mammal of the same body weight. Your job is to check if this expectation turns out to be correct (using analysis of covariance). **(a)** First, should you transform the weights and, if so, which transformation is likely to be useful? (Hint: yes, you should transform. Don't forget to try the transformation that typically works well for body size data. Also, check the assumption of parallel regression lines in the same way as you did in exercise 4.3 last week.) **(b)** Do birds have relatively lighter skeletons? (Use either the `Anova` function in the `car` package or the `summary` function to test the effect of `Class` from the fitted model.) To look at a graphical display, you can use the function `plot.ancova.com` from exercise 4.3 (load it with the `source("PlotAncova.R")` command).