01-readme

Using the source data (Animals), re-coded subject identifiers from 1 to 3 for each species (1 to 3 for coyote and 1-3 for fox) to 1-6 for all individuals.

This would influence how you would specify the random effects in the model (crossed versus nested). Check *lme4* or *lmerTest* report for correct number of groups, subjects, etc.

This is a built-in scripted example from JMP. JMP takes FOX first because it is first in the list of species, R takes COYOTE first as it is alphabetically first; outputs differ as a result but they give same info.