(in brackets: column names from the dataset that are referenced)

Research question: How leafminer abundance (abun) depends on fragmentation (fragmean)

Set-up: Plots with treatments (monoculture, two species of trees, three species of trees). From each plot three trees from each species were sampled for 50 leaves. On each leaf leafminer abundeces were estimated. This results in 3 trees and 150 total leaves in monoculture patches, 6 trees and 300 leaves in two-species plots and 9 trees and 450 leaves in three-species plots leaves

Problem: (We want to resample the leaves from each sampled tree in a way that 48 random leaves from each tree in monoculture is sampled, 24 leaves from each tree in two-species plots and 16 leaves from trees in three-species plots, resulting in 144 leaves per plot and equal distribution of leaves from different species per plot.

We want to repeat this resampling 1000 times and estimate the strength of three different statistical models on it using AIC-values

- abun ~ fragmean + total_all_ba
- abun ~ -1 + rel_qrob + rel_qrub + rel_fsyl + fragmean + total_all_ba
- abun ~ -1 + rel_qrob + rel_qrub + rel_fsyl + fragmean + total_all_ba + rel_qrob:rel_qrub + rel_qrob:rel_fsyl + rel_qrub:rel_fsyl

Try and find the best fitting model using this mode of resampling and using only base R (using loops, apply(),...)

To explain the dataset:

Each measured leaf (leaf_id) was sampled from a certain tree (tree_id), member of a certain tree species (tree_spec), that was found in a certain plot (id_plot). Each plot has a certain tree species richness (specrich) with certain relative abundances of tree species (rel_fsyl, rel_qrob, rel_qrub), a corrected tree diversity (truediv), a total base area of trunks (total_all_ba), an amount of fragmentation (fragmean)