# Example 2: Community-level Hypothesis Test using BlockBootID with myabund

## Setting Up

First load the data and R packages you need into the R workspace.

```
load("PlayData_for_Examples.RData") ### load the data for the examples
source("LoadFunctions.R") #### Source the functions required to run the block bootstrap

#Install packages if required
if(!require(mvabund)) { install.packages("mvabund", repos = "http://cran.us.r-project.org");
require(mvabund) }
library(mvabund)
```

#### Motivation

We want to test an assemblage/ community of species for the significance of a bunch of variables, using "mvabund::summary".

This example assumes a block size is selected by the user already, from either pilot study or as in Example 3. They can then use **BlockBootID** to generate an ID matrix for input into myabund.

```
## [1] "file exists"
```

## [1] "creating lookup table LookupTables/ lookup\_table \_L 0.1 \_grid\_space\_ 0.01 \_sampling\_type\_ sites

#### Run hypothesis test/ summary in mvabund

### running time <2 minutes

```
responseMultiSpecies=mvabund(multispecies_dat[,1:20]) #20 species multivariate reponse
mod.1 = manyglm(responseMultiSpecies~temperature, data = multispecies_dat,family="binomial")
mod.2 = manyglm(responseMultiSpecies~temperature*treatment, data = multispecies_dat,family="binomial")
anova.results = anova(mod.1, mod.2, bootID=BootID.example2, resamp="case")
## Warning in anova.manyglm(mod.1, mod.2, bootID = BootID.example2, resamp =
## "case"): 'montecarlo' or 'pit.trap' should be used for binomial regression.
```

```
## Warning in anova.manyglm(mod.1, mod.2, bootID = BootID.example2, resamp =
## "case"): case resampling with score and LR tests is under development. try
## case resampling with wald test.
## Using <int> bootID matrix from input.
## Time elapsed: 0 hr 0 min 34 sec
```

The treatment is not significant.