

# Homework 4

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*10/28/2014*

## Perpare R envrioment

```
library(leaps)
library(knitr)
library(reshape2)
library(ggplot2)
library(grid)
library(plyr)
library(glmulti)
```

```
## Loading required package: rJava
```

```
opts_chunk$set(fig.width = 8, message = FALSE, warning = FALSE)
```

## Data preparation

```
data <- read.table("emap.build08.txt", header = TRUE)
vars_to_log <- c("LK.HA", "POPDENKM", "TOT.RD")
data[vars_to_log] <- lapply(data[vars_to_log], function(x) log(x + 1))
names(data) <- ifelse(names(data) %in% vars_to_log,
                      paste("LOG", names(data), sep = "."),
                      names(data))
explanatory <- data[, -3]
response <- data[, 3, drop = FALSE]
```

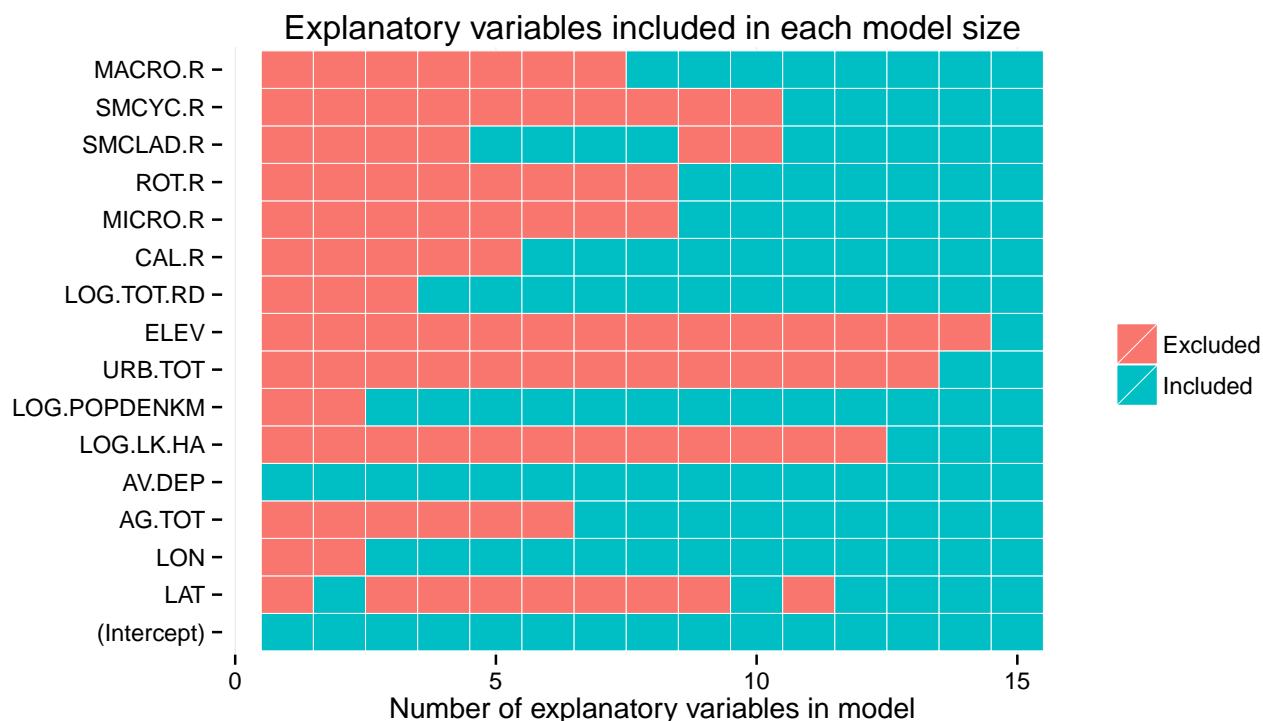
## Naive all subsets selction without interactions

The regsubsets function from the leaps package provides a simple way of doing all subsets selection.

```
# Conduct all subsets model evaluation -----
naive_raw <- regsubsets(explanatory, response[[1]], nvmax = length(explanatory))
naive_results <- summary(naive_raw)

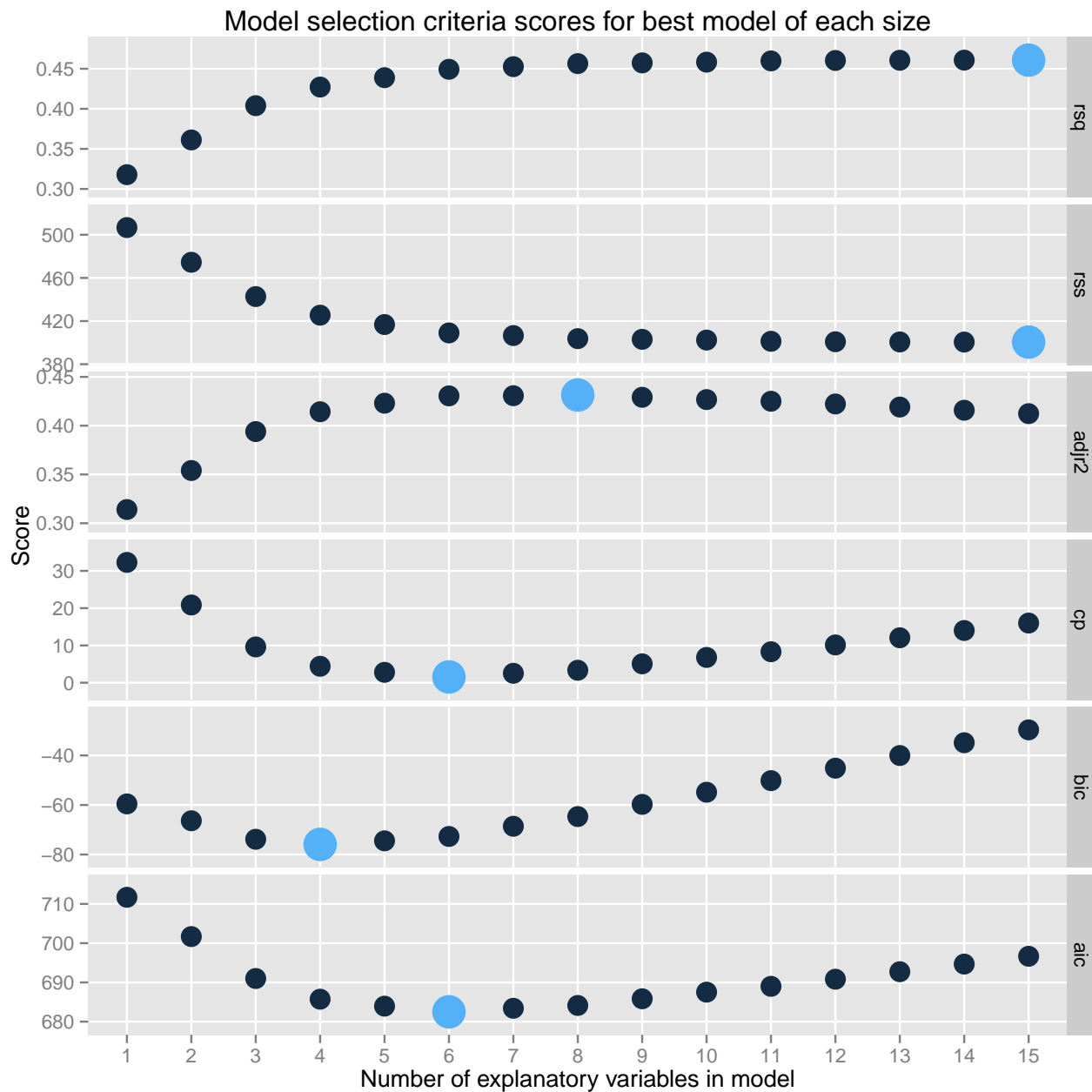
# Graph all subsets results -----
models <- melt(naive_results$which,
              varnames = c("size", "variables"),
              value.name = "included")
models$included = ifelse(models$included, "Included", "Excluded")
ggplot(models, aes(y = variables, x = size)) +
  geom_tile(aes(fill = included), color = "white") +
  labs(y = "",
       x = "Number of explanatory variables in model",
```

```
fill = "",
title = "Explanatory variables included in each model size" +
theme_minimal() + theme(panel.grid.major.y = element_blank())
```



```
# Graph information cirteria scores -----
scores <- data.frame(naive_results[c("rsq", "rss", "adjr2", "cp", "bic")])
scores$size <- 1:nrow(scores)
calculate_aic <- function(included) {
  vars <- explanatory[included]
  model <- as.formula(paste("response[[1]] ~", paste("explanatory", names(vars),
                                                    collapse = " + ", sep = "$")))
  AIC(lm(model))
}
scores$aic <- apply(naive_results$which[, -1], 1, calculate_aic)
scores <- melt(scores, variable.name = "method", id.vars = "size")
is_best <- function(x) {
  if (x$method %in% c("rsq", "adjr2"))
    x$value == max(x$value)
  else x$value == min(x$value)
}
scores$best <- as.numeric(unlist(dplyr(scores, "method", is_best)))
scores$size <- ordered(scores$size)
ggplot(scores, aes(x = size, y = value, color = best, size = best)) +
  geom_point(stat = "identity") +
  facet_grid(method ~ ., scales = "free_y") +
  scale_size(range = c(5, 8)) +
  scale_y_continuous(expand = c(.2, 0)) +
  labs(y = "Score",
       x = "Number of explanatory variables in model",
       title = "Model selection criteria scores for best model of each size") +
```

```
theme(legend.position = "none",
      panel.grid.minor = element_blank())
```



### All subsets with interactions

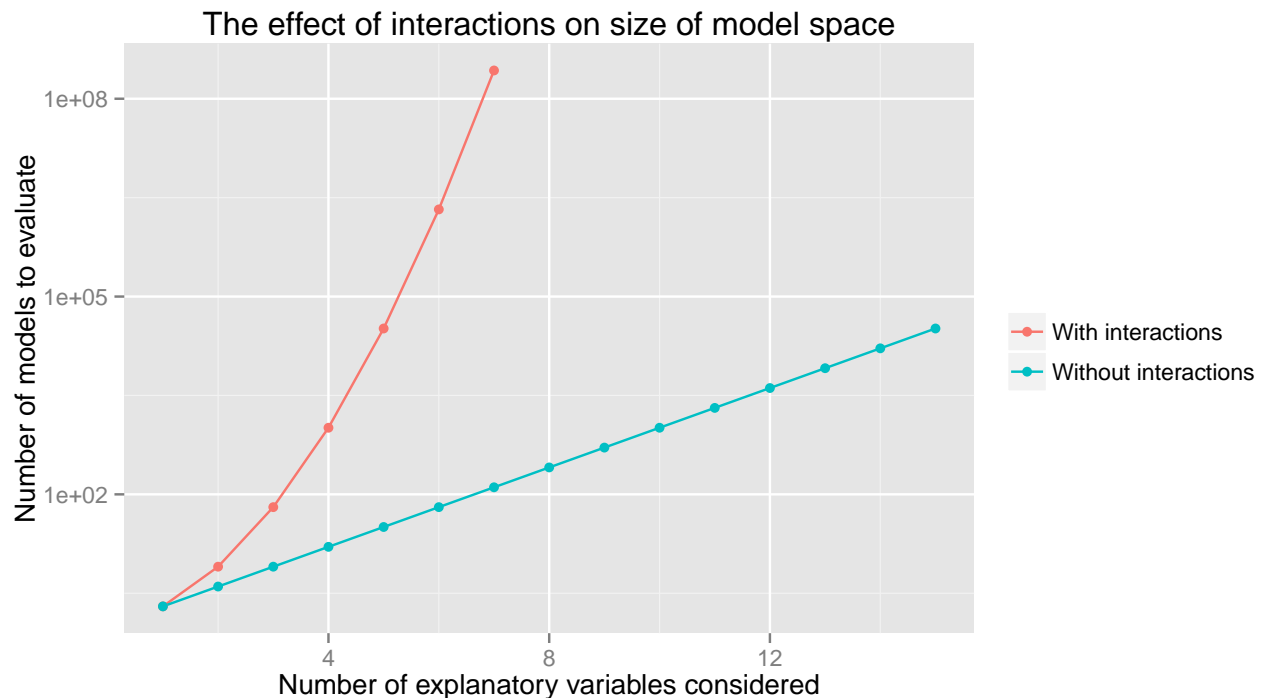
The R package `glmulti` allows for all subsets model selection with testing of all two way interactions. When interactions are included the number of potential models quickly increases with number of explanatory variables used.

```
# Calculate the number of potential models to evaluate -----
dont_print <- capture.output(
  count_with_iter <- sapply(1:7, function(x)
```

```

glmulti(y = names(response), xr = names(explanatory[1:x]), data = data,
        level = 2, crit = "bic", method = "d"))
dont_print <- capture.output(
  count_without_iter <- sapply(1:length(explanatory), function(x)
    glmulti(y = names(response), xr = names(explanatory[1:x]), data = data,
            level = 1, crit = "bic", method = "d")))
# Graph results -----
counts <- data.frame(size = 1:length(explanatory),
                     with = c(count_with_iter, rep(NA, 8)),
                     without = count_without_iter)
counts <- melt(counts, id.vars = "size")
levels(counts$variable) <- c('With interactions', 'Without interactions')
ggplot(counts, aes(x = size, y = value, group = variable, color = variable)) +
  geom_line() +
  geom_point() +
  scale_y_log10() +
  labs(x = "Number of explanatory variables considered",
       y = "Number of models to evaluate",
       title = "The effect of interactions on size of model space",
       color = "")

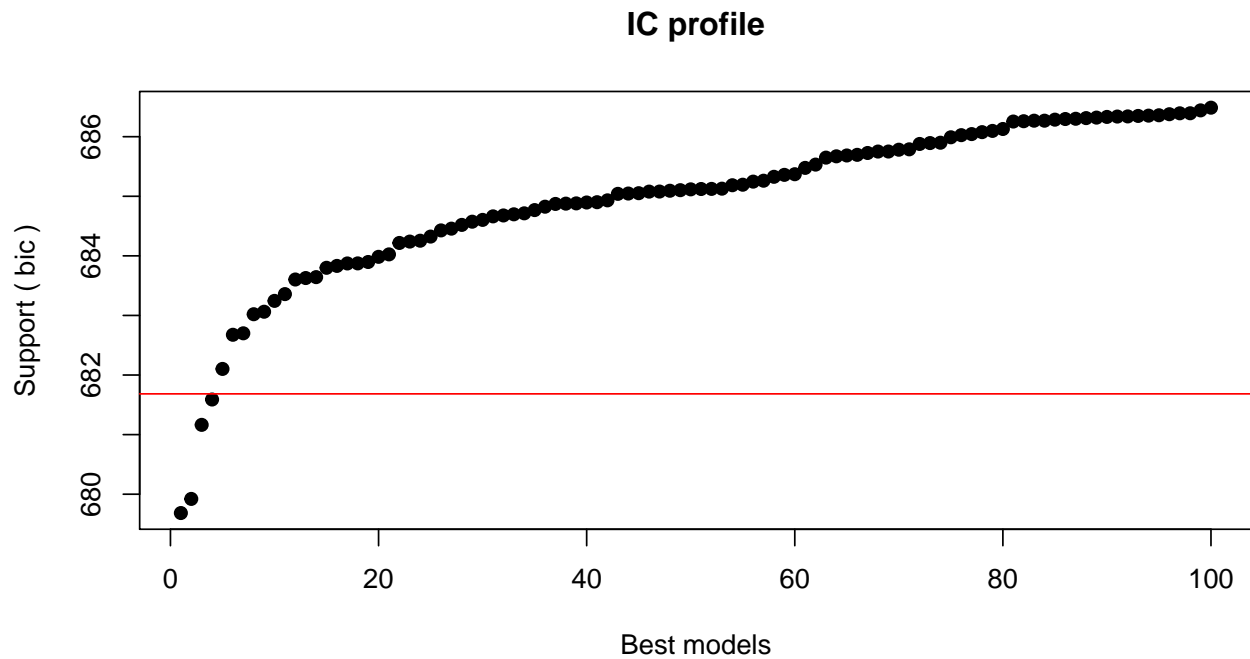
```



For this reason, it is not pheasable to test all 15 aviable explanatory variables with interactions. Preliminary testing indicated that only 6 explanatory variables can be evaluated. We decided to exclude LAT, LON, and ELEV since their effects, if any, are likely due to climatic effects on other explanatory variables. LK\_HA was excluded because it is probably correlated with AV.DEP, which is a much stronger predictor, as determined by the naive all-subsets analysis. Using similar logic, URB.TOT was excluded, since POPDENKM likly measures the same effect and was a strong predictor in the first analysis. Of the planktonic variables, all but MACRO.R and MICRO.R were exculded. The other planktonic variables measure the abundance of differnet taxa. Since none of the taxa are photosynthetic and likly lack pigment, the size of the organism is probably more important than taxonomic group. This leaves AG.TOT, AV.DEP, LOG.POPDENKM, LOG.TOT.RD, MACRO.R, and MICRO.R as the predictors that will be evaluated when considering interactions.

```
relevant_exp <- c("AG.TOT", "AV.DEP", "LOG.POPDENKM", "LOG.TOT.RD", "MACRO.R", "MICRO.R")
glmulti_model <- glmulti(y = names(response), xr = relevant_exp, data = data, level = 2, crit = "bic")
save.image()
```

```
load(file = ".RData")
plot(glmulti_model)
```



```
glmulti_model@objects[[1]]
```

```
##
## Call: fitfunc(formula = as.formula(x), data = data)
##
## Coefficients:
##      (Intercept)          AV.DEP      LOG.TOT.RD
##          1.41736          0.93104         -0.14314
## AV.DEP:LOG.TOT.RD  MACRO.R:AG.TOT  AV.DEP:MACRO.R
##          -0.03342          -0.00337         -0.04335
## LOG.TOT.RD:MACRO.R
##           0.03139
##
## Degrees of Freedom: 182 Total (i.e. Null);  176 Residual
## Null Deviance:      743
## Residual Deviance: 350  AIC: 654
```

```
glmulti_model@objects[[1]]$formula
```

```
## SECMEAN ~ 1 + AV.DEP + LOG.TOT.RD + LOG.TOT.RD:AV.DEP + MACRO.R:AG.TOT +
##      MACRO.R:AV.DEP + MACRO.R:LOG.TOT.RD
## <environment: 0x8c83818>
```

```
BIC(glmulti_model@objects[[1]])
```

```
## [1] 679.7
```