MV_Regression.R

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```r
# Lab 8
library(devtools)
```

```
## Loading required package: usethis
```

```r
library(mvpart)
devtools::install_github("cran/mvpart")
```

```
## Skipping install of 'mvpart' from a github remote, the SHA1 (acf0035f) has not changed since last ins
##   Use 'force = TRUE' to force installation
```
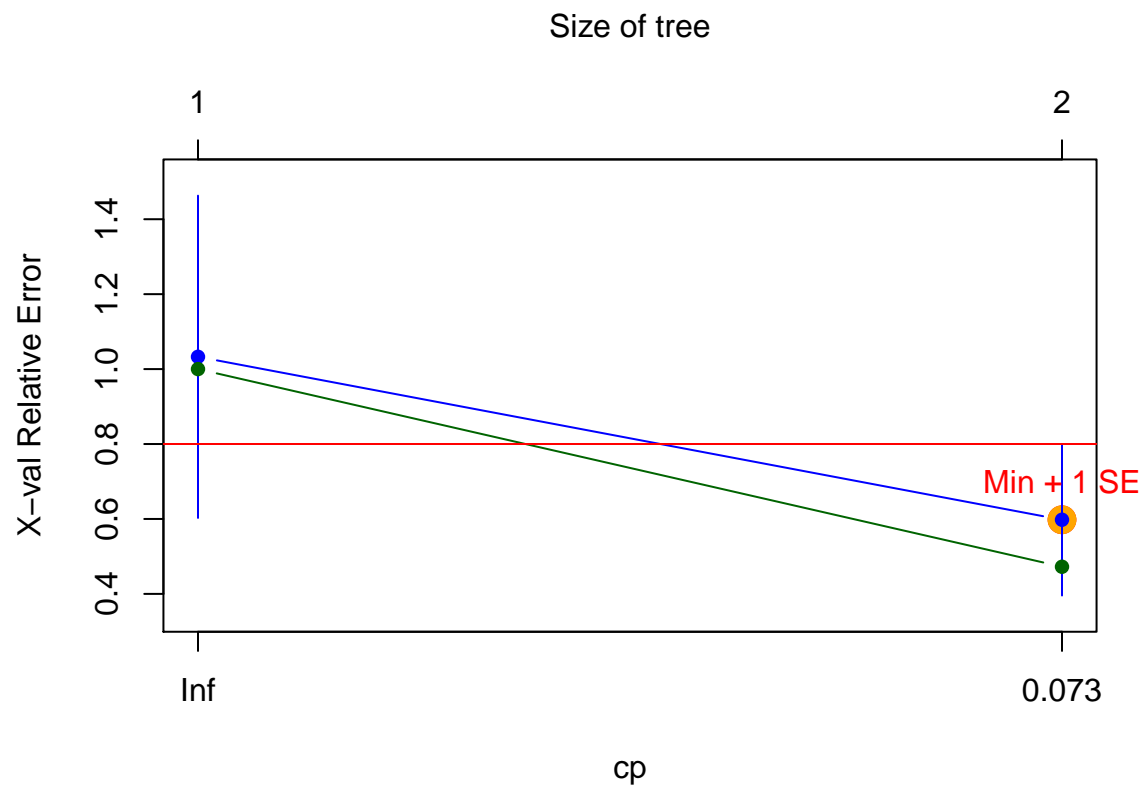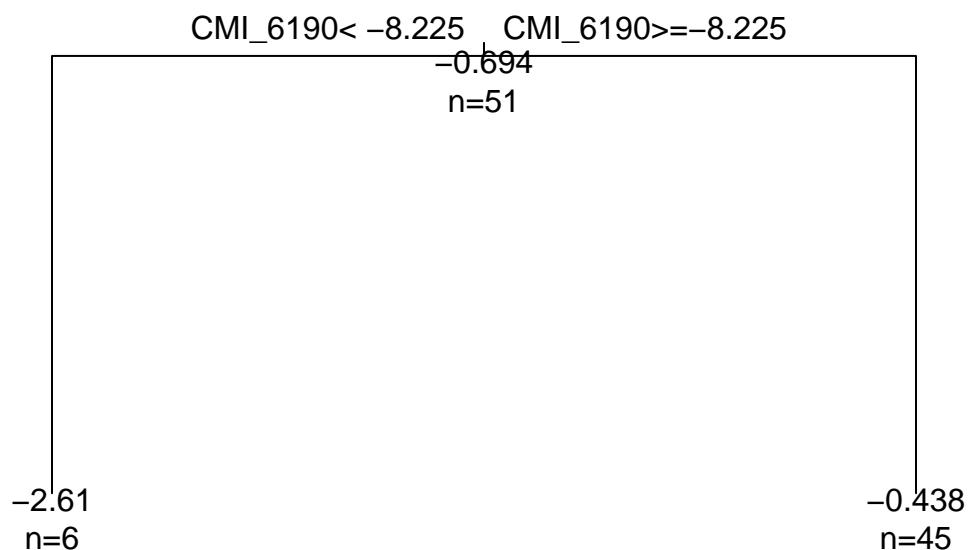
```r
library(mvpart)
dat_diversity=read.csv("Data_Diversity.csv")
dat_abundance=read.csv("Data_Abundance.csv")
dat_nitrogen=read.csv("Data_Nitrogen.csv")
dat_nutrients=read.csv("Data_Nutrients.csv")

out1=mvpart(Diversity~CMI_6190+CMI_avg_diff+CMI_ext, dat_diversity, xv="p", all.leaves = T)
```

Size of tree

CMI_6190< −8.225   CMI_6190>=−8.225
−0.694
n=51

−2.61
n=6

−0.438
n=45

Error : 0.472   CV Error : 0.598   SE : 0.202

```r
summary(out1)
```

```
## Call:
## mvpart(form = Diversity ~ CMI_6190 + CMI_avg_diff + CMI_ext,
##     data = dat_diversity, xv = "p", all.leaves = T)
##   n= 51
##
##          CP nsplit rel error    xerror      xstd
## 1 0.5275732      0 1.0000000 1.0328319 0.4300872
## 2 0.0100000      1 0.4724268 0.5978588 0.2022170
##
## Node number 1: 51 observations,    complexity param=0.5275732
##   mean=-0.6936906, MSE=0.9269981
##   left son=2 (6 obs) right son=3 (45 obs)
##   Primary splits:
##       CMI_6190     < -8.225    to the left,  improve=0.5275732, (0 missing)
##       CMI_ext      < -25.26    to the left,  improve=0.5275732, (0 missing)
##       CMI_avg_diff < 1.331333 to the left,  improve=0.1433272, (0 missing)
##
## Node number 2: 6 observations
##   mean=-2.608879, MSE=2.084264
##
## Node number 3: 45 observations
##   mean=-0.4383322, MSE=0.2184287
```

```r
plot(dat_diversity$Diversity,dat_diversity$CMI_ext)
```