Predicting Algae Blooms

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```
library(DMwR)
```

```
## Loading required package: lattice
```

```
## Loading required package: grid
```

```
data("algae")
head(algae)
```

```
##   season  size  speed mxPH  mnO2     Cl    NO3     NH4    oPO4     PO4 Chla
## 1 winter small medium 8.00   9.8 60.800  6.238 578.000 105.000 170.000 50.0
## 2 spring small medium 8.35   8.0 57.750  1.288 370.000 428.750 558.750  1.3
## 3 autumn small medium 8.10  11.4 40.020  5.330 346.667 125.667 187.057 15.6
## 4 spring small medium 8.07   4.8 77.364  2.302  98.182  61.182 138.700  1.4
## 5 autumn small medium 8.06   9.0 55.350 10.416 233.700  58.222  97.580 10.5
## 6 winter small   high 8.25  13.1 65.750  9.248 430.000  18.250  56.667 28.4
##     a1   a2   a3  a4   a5   a6  a7
## 1  0.0  0.0  0.0 0.0 34.2  8.3 0.0
## 2  1.4  7.6  4.8 1.9  6.7  0.0 2.1
## 3  3.3 53.6  1.9 0.0  0.0  0.0 9.7
## 4  3.1 41.0 18.9 0.0  1.4  0.0 1.4
## 5  9.2  2.9  7.5 0.0  7.5  4.1 1.0
## 6 15.1 14.6  1.4 0.0 22.5 12.6 2.9
```

```
dim(algae)
```

```
## [1] 200  18
```

```
#algae<-
read.csv("analysis.data",header=F,dec=".",col.names=c("season","size","
speed","mxPH","mnO2","Cl","NO3","NH4","oPO4","PO4","Chla","a1","a2","a3","a4"
,"a5","a6","a7"),na.strings=c("XXXXXXX"))
summary(algae)
```

```
##     season       size       speed        mxPH            mnO2
##  autumn:40   large :45   high  :84   Min.   :5.600   Min.   : 1.500
##  spring:53   medium:84   low    33   1st Qu.:7.700   1st Qu.: 7.725
##  summer:45   small :71   medium:83   Median :8.060   Median : 9.800
##  winter:62                           Mean   :8.012   Mean   : 9.118
```

```
##                                     3rd Qu.:8.400   3rd Qu.:10.800
##                                     Max.   :9.700   Max.   :13.400
##                                     NA's    1       NA's    2
```

```
##        Cl              NO3              NH4               oPO4        
##  Min.   :  0.222   Min.   : 0.050   Min.   :    5.00   Min.   :  1.00  
##  1st Qu.: 10.981   1st Qu.: 1.296   1st Qu.:   38.33   1st Qu.: 15.70  
##  Median : 32.730   Median : 2.675   Median :  103.17   Median : 40.15  
##  Mean   : 43.636   Mean   : 3.282   Mean   :  501.30   Mean   : 73.59  
##  3rd Qu.: 57.824   3rd Qu.: 4.446   3rd Qu.:  226.95   3rd Qu.: 99.33  
##  Max.   :391.500   Max.   :45.650   Max.   :24064.00   Max.   :564.60  
##  NA's    10        NA's    2        NA's    2          NA's    2       
##       PO4              Chla              a1               a2        
##  Min.   :  1.00   Min.   :  0.200   Min.   : 0.00   Min.   : 0.000  
##  1st Qu.: 41.38   1st Qu.:  2.000   1st Qu.: 1.50   1st Qu.: 0.000  
##  Median :103.29   Median :  5.475   Median : 6.95   Median : 3.000  
##  Mean   :137.88   Mean   : 13.971   Mean   :16.92   Mean   : 7.458  
##  3rd Qu.:213.75   3rd Qu.: 18.308   3rd Qu.:24.80   3rd Qu.:11.375  
##  Max.   :771.60   Max.   :110.456   Max.   :89.80   Max.   :72.600  
##  NA's    2        NA's    12                                        
##        a3               a4               a5               a6        
##  Min.   : 0.000   Min.   : 0.000   Min.   : 0.000   Min.   : 0.000  
##  1st Qu.: 0.000   1st Qu.: 0.000   1st Qu.: 0.000   1st Qu.: 0.000  
##  Median : 1.550   Median : 0.000   Median : 1.900   Median : 0.000  
##  Mean   : 4.309   Mean   : 1.992   Mean   : 5.064   Mean   : 5.964  
##  3rd Qu.: 4.925   3rd Qu.: 2.400   3rd Qu.: 7.500   3rd Qu.: 6.925  
##  Max.   :42.800   Max.   :44.600   Max.   :44.400   Max.   :77.600  
##                                                                     
##        a7        
##  Min.   : 0.000  
##  1st Qu.: 0.000  
##  Median : 1.000  
##  Mean   : 2.495  
##  3rd Qu.: 2.400  
##  Max.   :31.600  
##                  
```

```
algaeeval<-
read.csv("eval.data",header=F,dec=".",col.names=c("season","size","s
peed","mxPH","mnO2","Cl","NO3","NH4","oPO4","PO4","Chla"),na.strings=c("XXXXX
XX"))
```

```
## Warning in scan(file = file, what = what, sep = sep, quote = quote, dec =
## dec, : embedded nul(s) found in input
```

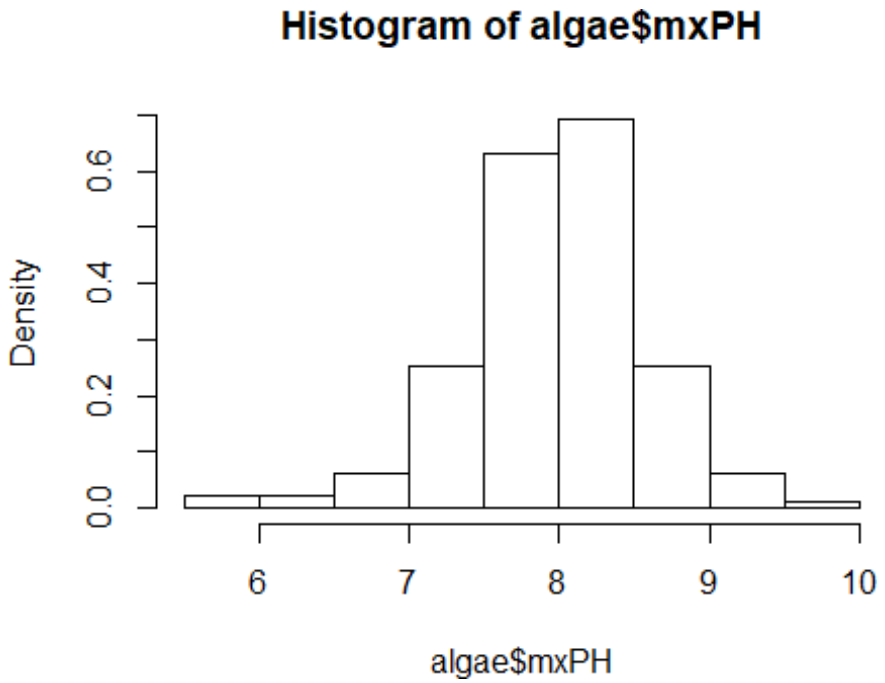
```
dim(algaeeval)
```

```
## [1] 140  11
```

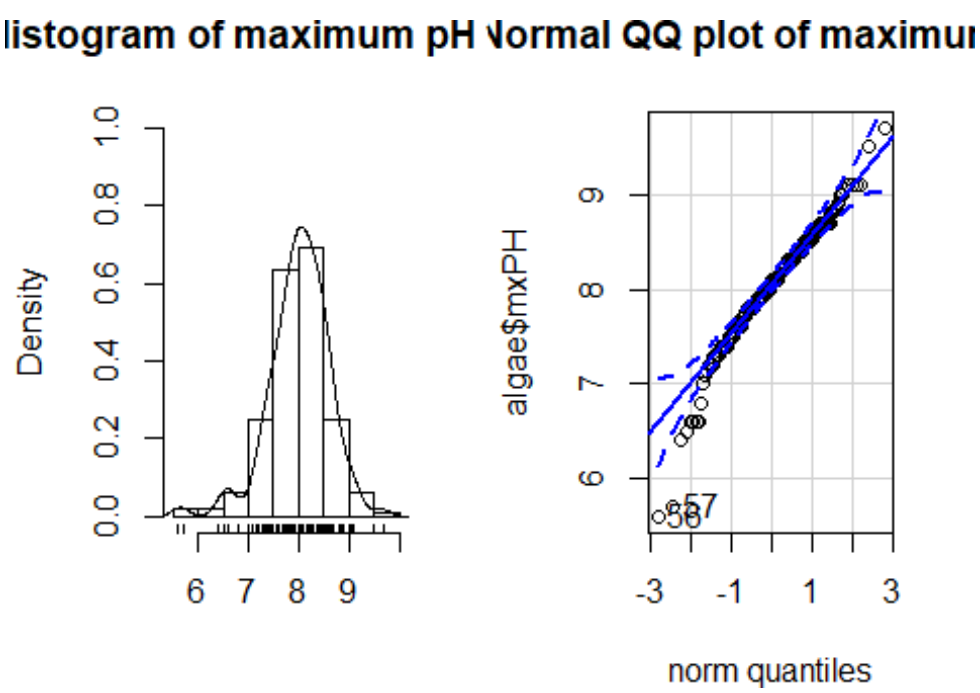
```
head(algaeeval)
```

```
##   season   size  speed mxPH mnO2     Cl      NO3     NH4    oPO4     PO4
## 1 summer small_ medium 7.95  5.7 57.333 2.46000 273.333 295.667 380.000
## 2 winter small_ medium 7.98  8.8 59.333 7.39200 286.667  33.333 138.000
## 3 summer small_ medium 8.00  7.2 80.000 1.95700 174.286  47.857 113.714
```

```
## 4 spring small_ high___8.35  8.4 68.000 3.02600 458.000  45.200 111.800
## 5 spring small_ medium 8.10 13.2 19.000 0.00000 130.000   6.000  40.000
## 6 summer small_ medium 8.37 12.1 12.850 0.84000  15.000   5.000  10.507
##    Chla
## 1    NA
## 2   7.1
## 3   4.5
## 4   3.2
## 5   2.0
## 6  13.8

hist(algae$mxPH, prob = T)
```

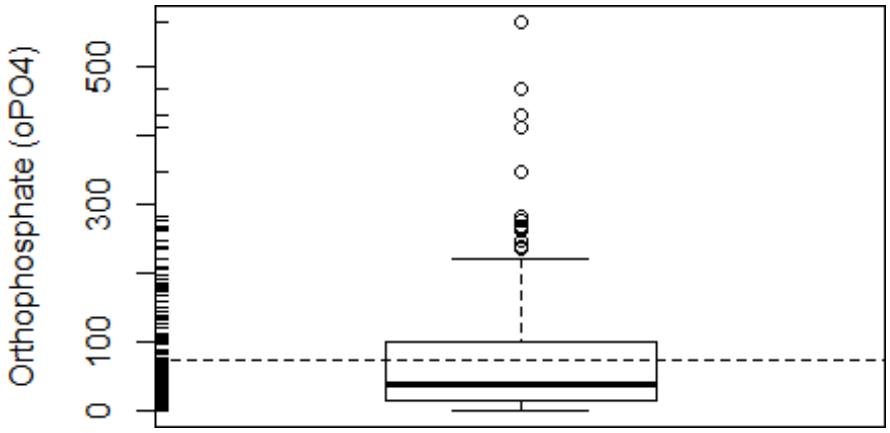



```
library(car)

## Loading required package: carData

par(mfrow=c(1,2))
hist(algae$mxPH, prob=T, xlab="",main="Histogram of maximum pH value",ylim=0:
1)
lines(density(algae$mxPH,na.rm=T))
rug(jitter(algae$mxPH))
qqPlot(algae$mxPH,main="Normal QQ plot of maximum pH")
```

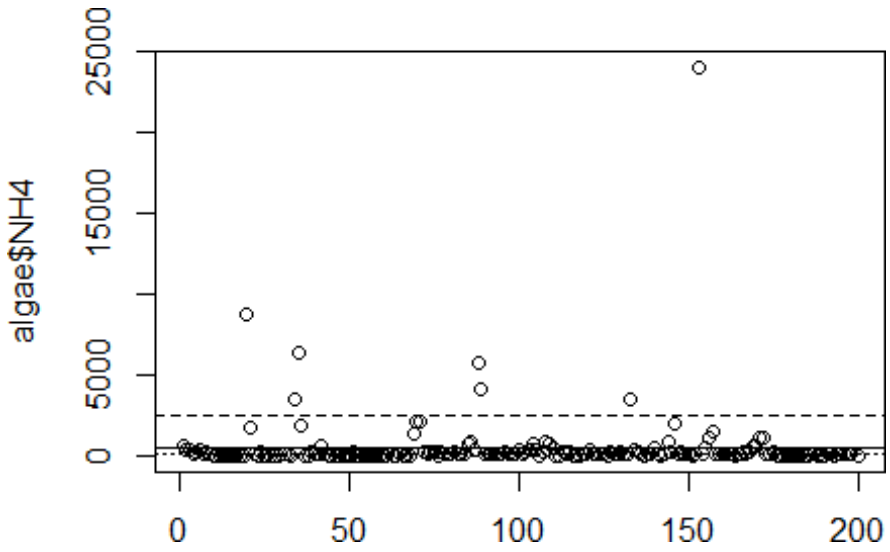



```
## [1] 56 57
```

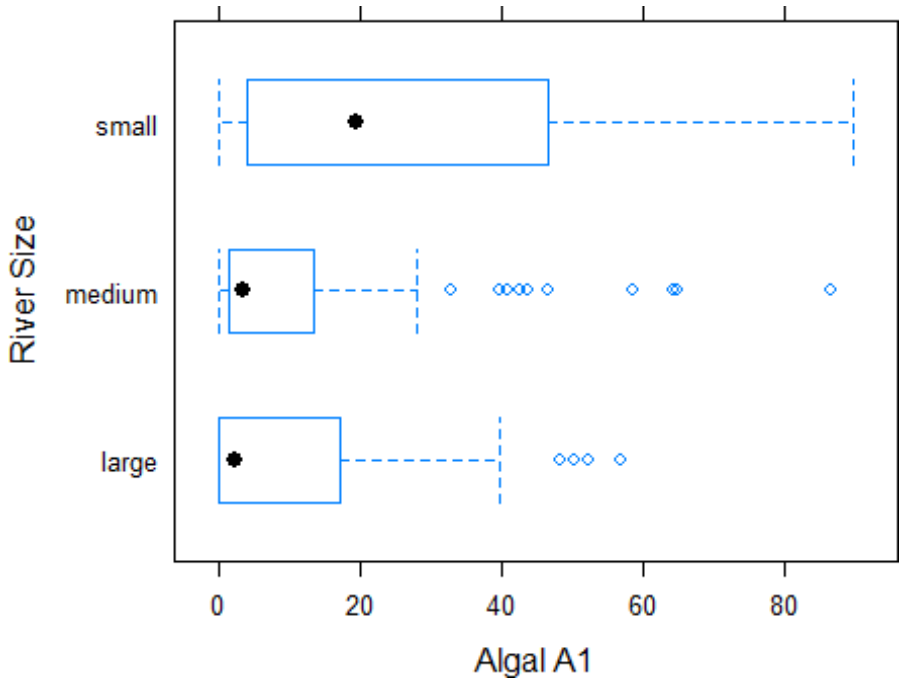
```
par(mfrow=c(1,1))

boxplot(algae$oPO4, ylab = "Orthophosphate (oPO4)")
rug(jitter(algae$oPO4), side = 2)
abline(h = mean(algae$oPO4, na.rm = T), lty = 2)
```




```
plot(algae$NH4, xlab = "")
abline(h = mean(algae$NH4, na.rm = T), lty = 1)
abline(h = mean(algae$NH4, na.rm = T) + sd(algae$NH4, na.rm = T),lty=2)
abline(h = median(algae$NH4, na.rm = T), lty = 3)
```




```
#identify(algae$NH4)

#plot(algae$NH4, xlab = "")
#clicked.lines <- identify(algae$NH4)
#algae[clicked.lines, ]


algae[algae$NH4 > 19000, ]

##       season   size speed mxPH mnO2      Cl   NO3   NH4 oPO4 PO4 Chla  a1 a2
## NA <NA> <NA> <NA> NA NA NA NA NA NA NA NA NA NA ## 153   autumn medium
high  7.3 11.8 44.205 45.65 24064   44   34 53.1 2.2   0 ## NA.1   <NA>   <NA>
<NA>   NA   NA      NA     NA     NA   NA   NA   NA  NA NA
##       a3  a4  a5   a6  a7
## NA  NA  NA  NA  NA  NA ##
153    0  1.2 5.9 77.6   0 ##
NA.1 NA   NA   NA   NA NA

algae[!is.na(algae$NH4)&algae$NH4 >19000,]

##      season   size speed mxPH mnO2      Cl   NO3   NH4 oPO4 PO4 Chla  a1 a2
## 153 autumn medium  high  7.3 11.8 44.205 45.65 24064   44   34 53.1 2.2  0
##      a3  a4  a5   a6 a7
## 153  0  1.2 5.9 77.6  0

library(lattice)
bwplot(size ~ a1, data=algae, ylab="River Size",xlab="Algal A1")
```




```
library(Hmisc)
```

```
## Loading required package: survival
```

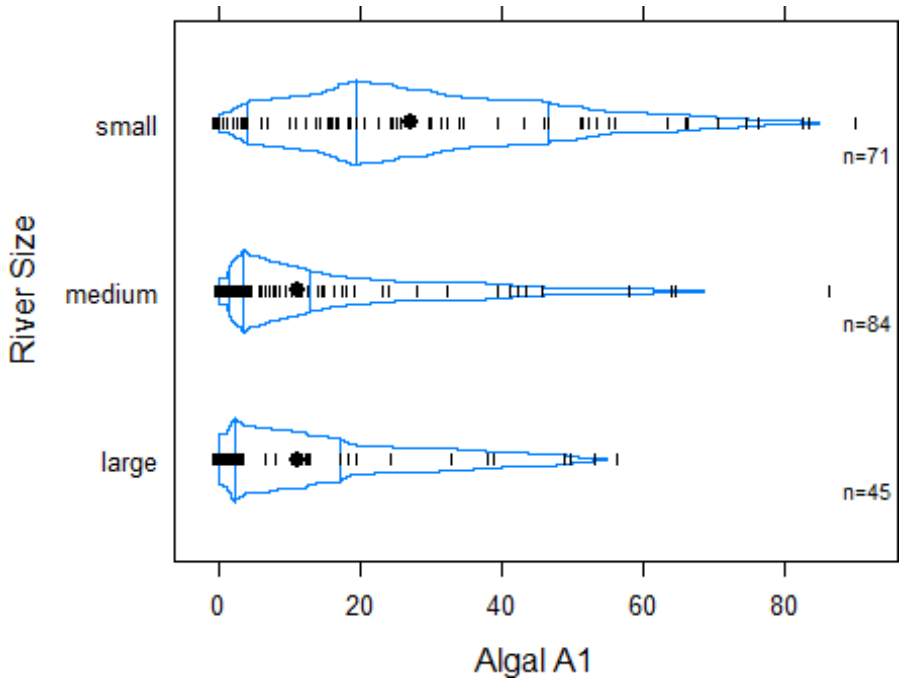
```
## Loading required package: Formula
```

```
## Loading required package: ggplot2
```

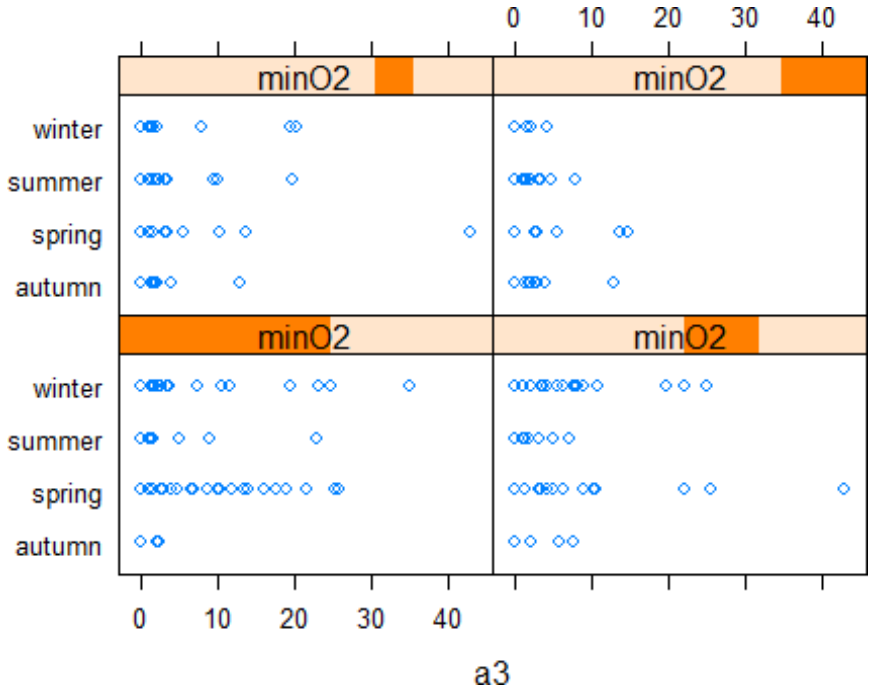
```
##
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
bwplot(size ~ a1, data=algae,panel=panel.bpplot,probs=seq(.01,.49,by=.01), da
tadensity=TRUE,ylab="River Size",xlab="Algal A1")
```




```
minO2 <- equal.count(na.omit(algae$mnO2),number=4,overlap=1/5)

stripplot(season ~ a3|minO2,data=algae[!is.na(algae$mnO2),])
```



```r
#remove NA values
algae[!complete.cases(algae),]
```

```
##     season   size  speed mxPH mnO2     Cl    NO3 NH4     oPO4      PO4  Chla
## 28  autumn  small   high 6.80 11.1  9.000 0.630  20    4.000       NA  2.70
## 38  spring  small   high 8.00   NA  1.450 0.810  10    2.500    3.000  0.30
## 48  winter  small    low   NA 12.6  9.000 0.230  10    5.000    6.000  1.10
## 55  winter  small   high 6.60 10.8     NA 3.245  10    1.000    6.500    NA
## 56  spring  small medium 5.60 11.8     NA 2.220   5    1.000    1.000    NA
## 57  autumn  small medium 5.70 10.8     NA 2.550  10    1.000    4.000    NA
## 58  spring  small   high 6.60  9.5     NA 1.320  20    1.000    6.000    NA
## 59  summer  small   high 6.60 10.8     NA 2.640  10    2.000   11.000    NA
## 60  autumn  small medium 6.60 11.3     NA 4.170  10    1.000    6.000    NA
## 61  spring  small medium 6.50 10.4     NA 5.970  10    2.000   14.000    NA
## 62  summer  small medium 6.40   NA     NA    NA  NA       NA   14.000    NA
## 63  autumn  small   high 7.83 11.7  4.083 1.328  18    3.333    6.667    NA
## 116 winter medium   high 9.70 10.8  0.222 0.406  10   22.444   10.111    NA
## 161 spring  large    low 9.00  5.8     NA 0.900 142 102.000  186.000 68.05
## 184 winter  large   high 8.00 10.9  9.055 0.825  40   21.083   56.091    NA
## 199 winter  large medium 8.00  7.6     NA    NA  NA       NA       NA    NA
##       a1   a2  a3   a4  a5  a6  a7
## 28  30.3  1.9 0.0  0.0 2.1 1.4 2.1
## 38  75.8  0.0 0.0  0.0 0.0 0.0 0.0
## 48  35.5  0.0 0.0  0.0 0.0 0.0 0.0
## 55  24.3  0.0 0.0  0.0 0.0 0.0 0.0
## 56  82.7  0.0 0.0  0.0 0.0 0.0 0.0
## 57  16.8  4.6 3.9 11.5 0.0 0.0 0.0
## 58  46.8  0.0 0.0 28.8 0.0 0.0 0.0
## 59  46.9  0.0 0.0 13.4 0.0 0.0 0.0
## 60  47.1  0.0 0.0  0.0 0.0 1.2 0.0
## 61  66.9  0.0 0.0  0.0 0.0 0.0 0.0
## 62  19.4  0.0 0.0  2.0 0.0 3.9 1.7
## 63  14.4  0.0 0.0  0.0 0.0 0.0 0.0
## 116 41.0  1.5 0.0  0.0 0.0 0.0 0.0
## 161  1.7 20.6 1.5  2.2 0.0 0.0 0.0
## 184 16.8 19.6 4.0  0.0 0.0 0.0 0.0
## 199  0.0 12.5 3.7  1.0 0.0 0.0 4.9
```

```r
nrow(algae[!complete.cases(algae),])
```

```
## [1] 16
```

```r
algae <- na.omit(algae)

algae <- algae[-c(62, 199), ]
apply(algae, 1, function(x) sum(is.na(x)))
```

```
##   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
##  19  20  21  22  23  24  25  26  27  29  30  31  32  33  34  35  36  37
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
```

```
##  39  40  41  42  43  44  45  46  47  49  50  51  52  53  54  64  65  66
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
##  67  68  69  70  71  72  73  75  76  77  78  79  80  81  82  83  84  85
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
##  86  87  88  89  90  91  92  93  94  95  96  97  98  99 100 101 102 103
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
## 104 105 106 107 108 109 110 111 112 113 114 115 117 118 119 120 121 122
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
## 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
## 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
## 159 160 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
## 178 179 180 181 182 183 185 186 187 188 189 190 191 192 193 194 195 196
##   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
## 197 198 200
##   0   0   0
```

```
data(algae)
manyNAs(algae, 0.2)
```

```
## [1]  62 199
```

```
algae <- algae[-manyNAs(algae), ]

algae[48, "mxPH"] <- mean(algae$mxPH, na.rm = T)
algae[is.na(algae$Chla), "Chla"] <- median(algae$Chla, na.rm = T)

data(algae)
algae <- algae[-manyNAs(algae), ]
algae <- centralImputation(algae)

cor(algae[, 4:18], use = "complete.obs")
```

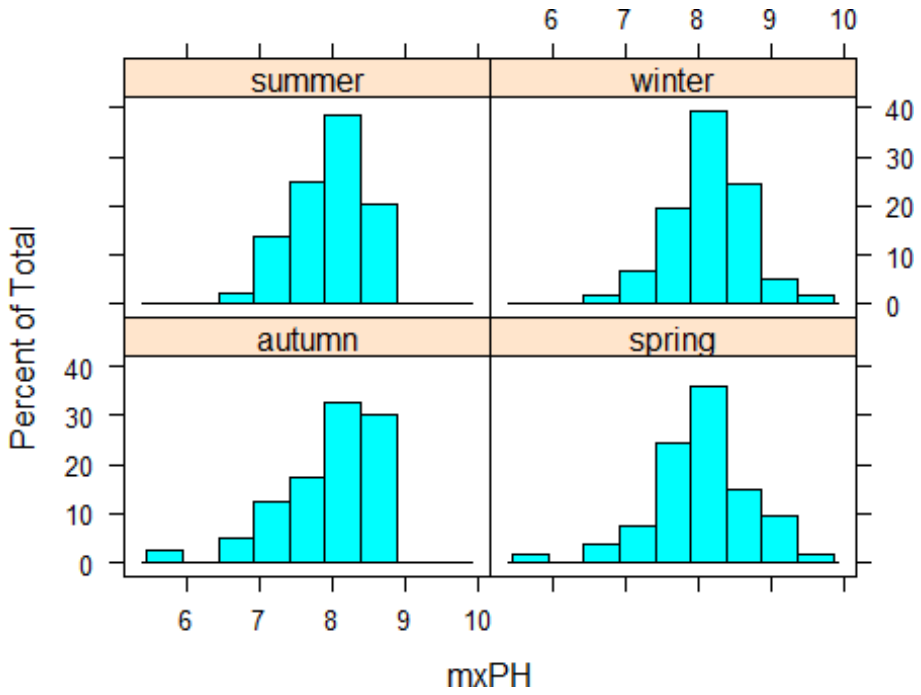
```
##                mxPH         mnO2           Cl          NO3          NH4
## mxPH   1.00000000 -0.16749178  0.13285681 -0.13103951 -0.09360612
## mnO2  -0.16749178  1.00000000 -0.27873229  0.09837676 -0.08780541
## Cl     0.13285681 -0.27873229  1.00000000  0.22504071  0.07407466
## NO3   -0.13103951  0.09837676  0.22504071  1.00000000  0.72144352
## NH4   -0.09360612 -0.08780541  0.07407466  0.72144352  1.00000000
## oPO4   0.15850785 -0.41655069  0.39230733  0.14458782  0.22723723
## PO4    0.18033494 -0.48772564  0.45652107  0.16931401  0.20844445
## Chla   0.39121495 -0.16678069  0.15082753  0.14290962  0.09375115
## a1    -0.26823725  0.28389830 -0.36078101 -0.24121109 -0.13265601
## a2     0.32584814 -0.09935631  0.08949837  0.02368832 -0.02968344
## a3     0.03077250 -0.25155437  0.09429722 -0.07621407 -0.10143974
## a4    -0.24876290 -0.31513753  0.12045912 -0.02578257  0.22822914
## a5    -0.01697947  0.17008979  0.16514900  0.22359794  0.02745909
## a6    -0.08388657  0.15864906  0.18369968  0.54640569  0.40571045
```

```
## a7   -0.08726106 -0.12117098 -0.02793640  0.08509789 -0.01672691
##              oPO4         PO4        Chla          a1          a2
## mxPH  0.15850785  0.18033494  0.39121495 -0.26823725  0.32584814
## mnO2 -0.41655069 -0.48772564 -0.16678069  0.28389830 -0.09935631
## Cl    0.39230733  0.45652107  0.15082753 -0.36078101  0.08949837
## NO3   0.14458782  0.16931401  0.14290962 -0.24121109  0.02368832
## NH4   0.22723723  0.20844445  0.09375115 -0.13265601 -0.02968344
## oPO4  1.00000000  0.91387767  0.12941615 -0.41735761  0.14768993
## PO4   0.91387767  1.00000000  0.26758873 -0.48730097  0.16246963
## Chla  0.12941615  0.26758873  1.00000000 -0.28380049  0.38192280
## a1   -0.41735761 -0.48730097 -0.28380049  1.00000000 -0.29251967
## a2    0.14768993  0.16246963  0.38192280 -0.29251967  1.00000000
## a3    0.03362906  0.06587312 -0.04975884 -0.14695028  0.03031095
## a4    0.29574585  0.30462623 -0.08364618 -0.03892441 -0.17168171
## a5    0.15147500  0.19111521 -0.05945318 -0.29503346 -0.16186215
## a6    0.02876159  0.08316987  0.01815732 -0.27602608 -0.11613061
## a7    0.04849832  0.10671057  0.02405581 -0.21142489  0.04749242
##               a3          a4          a5          a6          a7
## mxPH  0.03077250 -0.24876290 -0.01697947 -0.08388657 -0.08726106
## mnO2 -0.25155437 -0.31513753  0.17008979  0.15864906 -0.12117098
## Cl    0.09429722  0.12045912  0.16514900  0.18369968 -0.02793640
## NO3  -0.07621407 -0.02578257  0.22359794  0.54640569  0.08509789
## NH4  -0.10143974  0.22822914  0.02745909  0.40571045 -0.01672691
## oPO4  0.03362906  0.29574585  0.15147500  0.02876159  0.04849832
## PO4   0.06587312  0.30462623  0.19111521  0.08316987  0.10671057
## Chla -0.04975884 -0.08364618 -0.05945318  0.01815732  0.02405581
## a1   -0.14695028 -0.03892441 -0.29503346 -0.27602608 -0.21142489
## a2    0.03031095 -0.17168171 -0.16186215 -0.11613061  0.04749242
## a3    1.00000000  0.01218370 -0.11111997 -0.17283566  0.05618729
## a4    0.01218370  1.00000000 -0.11006558 -0.09074936  0.04362334
## a5   -0.11111997 -0.11006558  1.00000000  0.40360881 -0.02686306
## a6   -0.17283566 -0.09074936  0.40360881  1.00000000 -0.01244488
## a7    0.05618729  0.04362334 -0.02686306 -0.01244488  1.00000000
```

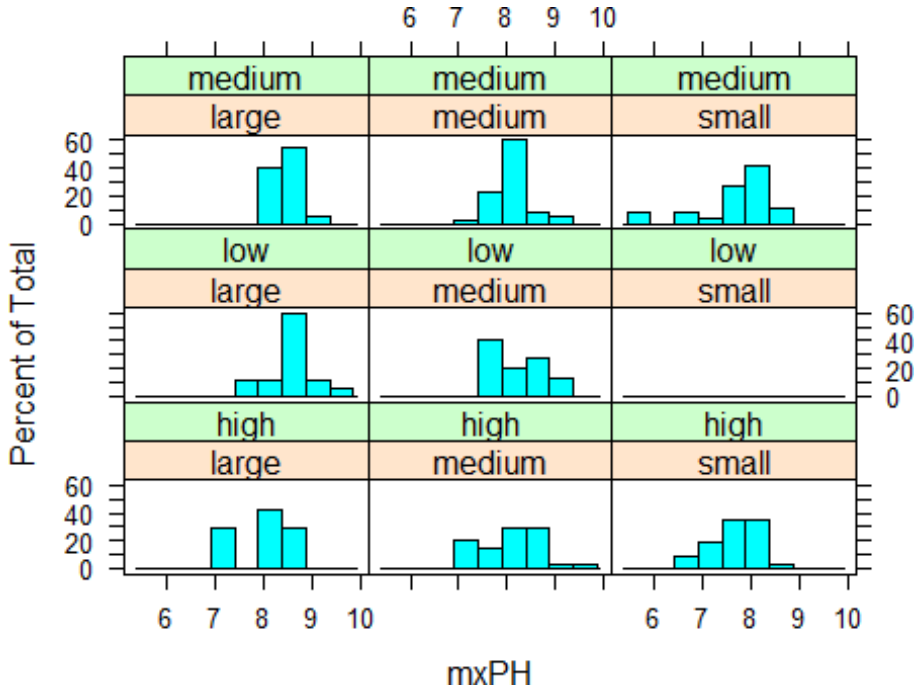
```
symnum(cor(algae[,4:18],use="complete.obs"))
```

```
##      mP mO Cl NO NH o P Ch a1 a2 a3 a4 a5 a6 a7
## mxPH 1
## mnO2   1
## Cl        1
## NO3          1
## NH4          ,  1
## oPO4    .  .        1
## PO4     .  .        * 1
## Chla .                   1
## a1         .        . .    1
## a2   .                    .     1
## a3                           1
## a4      .             .            1
## a5                                   1
```

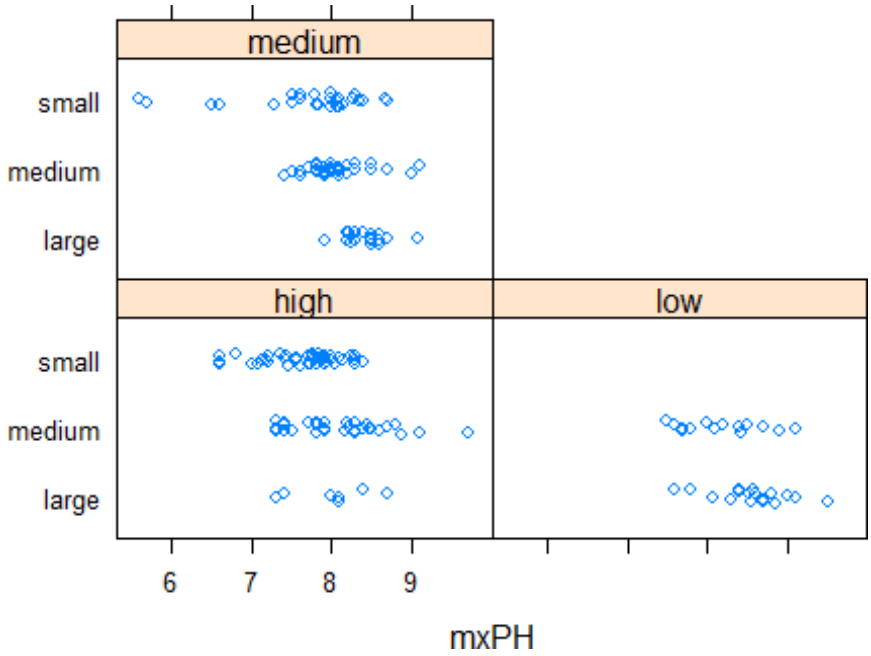
```
## a6            .  .                     .  1
## a7                                        1
## attr(,"legend")
## [1] 0 ' ' 0.3 '.' 0.6 ',' 0.8 '+' 0.9 '*' 0.95 'B' 1

data(algae)
algae <- algae[-manyNAs(algae), ]
lm(PO4 ~ oPO4, data = algae)

##
## Call:
## lm(formula = PO4 ~ oPO4, data = algae)
##
## Coefficients:
## (Intercept)         oPO4
##      42.897        1.293

algae[28, "PO4"] <- 42.897 + 1.293 * algae[28, "oPO4"]

data(algae)
algae <- algae[-manyNAs(algae), ]
fillPO4 <- function(oP)
  {
  if(is.na(oP))
    return(NA)
  else return(42.897+1.293*oP)
  }
algae[is.na(algae$PO4), "PO4"] <- sapply(algae[is.na(algae$PO4),"oPO4"],fillP
O4)
histogram(~mxPH | season, data = algae)
```




```
algae$season <- factor(algae$season, levels = c("spring","summer","autumn","w
inter"))

histogram(~mxPH | size * speed, data = algae)
```




```
stripplot(size ~ mxPH | speed, data = algae, jitter = T)
```



```r
data("algae")
algae <- algae[-manyNAs(algae), ]

algae <- knnImputation(algae, k = 10)

algae <- knnImputation(algae, k = 10, meth = "median")

## Warning in knnImputation(algae, k = 10, meth = "median"): No case has
## missing values. Stopping as there is nothing to do.

data("algae")
algae <- algae[-manyNAs(algae), ]
clean.algae <- knnImputation(algae, k = 10)

lm.a1 <- lm(a1 ~ ., data = clean.algae[, 1:12])

summary(lm.a1)

##
## Call:
## lm(formula = a1 ~ ., data = clean.algae[, 1:12])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -37.679 -11.893  -2.567   7.410  62.190
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  42.942055  24.010879   1.788  0.07537 .
## seasonspring  3.726978   4.137741   0.901  0.36892
## seasonsummer  0.747597   4.020711   0.186  0.85270
## seasonwinter  3.692955   3.865391   0.955  0.34065
## sizemedium    3.263728   3.802051   0.858  0.39179
## sizesmall     9.682140   4.179971   2.316  0.02166 *
## speedlow      3.922084   4.706315   0.833  0.40573
## speedmedium   0.246764   3.241874   0.076  0.93941
## mxPH         -3.589118   2.703528  -1.328  0.18598
## mnO2          1.052636   0.705018   1.493  0.13715
## Cl           -0.040172   0.033661  -1.193  0.23426
## NO3          -1.511235   0.551339  -2.741  0.00674 **
## NH4           0.001634   0.001003   1.628  0.10516
## oPO4         -0.005435   0.039884  -0.136  0.89177
## PO4          -0.052241   0.030755  -1.699  0.09109 .
## Chla         -0.088022   0.079998  -1.100  0.27265
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.65 on 182 degrees of freedom
## Multiple R-squared:  0.3731, Adjusted R-squared:  0.3215
## F-statistic: 7.223 on 15 and 182 DF,  p-value: 2.444e-12
```

```r
anova(lm.a1)
```

```
## Analysis of Variance Table
##
## Response: a1
##            Df  Sum Sq Mean Sq F value    Pr(>F)
## season      3      85    28.2  0.0905 0.9651944
## size        2   11401  5700.7 18.3088  5.69e-08 ***
## speed       2    3934  1967.2  6.3179 0.0022244 **
## mxPH        1    1329  1328.8  4.2677 0.0402613 *
## mnO2        1    2287  2286.8  7.3444 0.0073705 **
## Cl          1    4304  4304.3 13.8239 0.0002671 ***
## NO3         1    3418  3418.5 10.9789 0.0011118 **
## NH4         1     404   403.6  1.2963 0.2563847
## oPO4        1    4788  4788.0 15.3774 0.0001246 ***
## PO4         1    1406  1405.6  4.5142 0.0349635 *
## Chla        1     377   377.0  1.2107 0.2726544
## Residuals 182   56668   311.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
lm2.a1 <- update(lm.a1, . ~ . - season)
summary(lm2.a1)
```

```
##
## Call:
## lm(formula = a1 ~ size + speed + mxPH + mnO2 + Cl + NO3 + NH4 +
##     oPO4 + PO4 + Chla, data = clean.algae[, 1:12])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -36.460 -11.953  -3.044   7.444  63.730
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 44.9532874 23.2378377   1.934  0.05458 .
## sizemedium   3.3092102  3.7825221   0.875  0.38278
## sizesmall   10.2730961  4.1223163   2.492  0.01358 *
## speedlow     3.0546270  4.6108069   0.662  0.50848
## speedmedium -0.2976867  3.1818585  -0.094  0.92556
## mxPH        -3.2684281  2.6576592  -1.230  0.22033
## mnO2         0.8011759  0.6589644   1.216  0.22561
## Cl          -0.0381881  0.0333791  -1.144  0.25407
## NO3         -1.5334300  0.5476550  -2.800  0.00565 **
## NH4          0.0015777  0.0009951   1.586  0.11456
## oPO4        -0.0062392  0.0395086  -0.158  0.87469
## PO4         -0.0509543  0.0305189  -1.670  0.09669 .
## Chla        -0.0841371  0.0794459  -1.059  0.29096
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' ).1 ' ' 1
```

```
##
## Residual standard error: 17.57 on 185 degrees of freedom
## Multiple R-squared:  0.3682, Adjusted R-squared:  0.3272
## F-statistic: 8.984 on 12 and 185 DF,  p-value: 1.762e-13
```

```
anova(lm.a1,lm2.a1)
```

```
## Analysis of Variance Table
##
## Model 1: a1 ~ season + size + speed + mxPH + mnO2 + Cl + NO3 + NH4 + oPO4
+
##     PO4 + Chla
## Model 2: a1 ~ size + speed + mxPH + mnO2 + Cl + NO3 + NH4 + oPO4 + PO4 +
##     Chla
##   Res.Df   RSS Df Sum of Sq      F Pr(>F)
## 1    182 56668
## 2    185 57116 -3   -447.62 0.4792 0.6971
```

```
final.lm <- step(lm.a1)
```

```
## Start:  AIC=1152.03
## a1 ~ season + size + speed + mxPH + mnO2 + Cl + NO3 + NH4 + oPO4 +
##     PO4 + Chla
##
##          Df Sum of Sq   RSS    AIC
## - season  3    447.62 57116 1147.6
## - speed   2    269.60 56938 1149.0
## - oPO4    1      5.78 56674 1150.0
## - Chla    1    376.96 57045 1151.3
## - Cl      1    443.46 57112 1151.6
## - mxPH    1    548.76 57217 1151.9
## <none>                56668 1152.0
## - mnO2    1    694.11 57363 1152.4
## - NH4     1    825.67 57494 1152.9
## - PO4     1    898.42 57567 1153.1
## - size    2   1857.16 58526 1154.4
## - NO3     1   2339.36 59008 1158.0
##
## Step:  AIC=1147.59
## a1 ~ size + speed + mxPH + mnO2 + Cl + NO3 + NH4 + oPO4 +  PO4 +
##     Chla
##
##         Df Sum of Sq   RSS    AIC
## - speed  2    210.64 57327 1144.3
## - oPO4   1      7.70 57124 1145.6
## - Chla   1    346.27 57462 1146.8
## - Cl     1    404.10 57520 1147.0
## - mnO2   1    456.37 57572 1147.2
## - mxPH   1    466.95 57583 1147.2
## <none>               57116 1147.6
## - NH4    1    776.11 57892 1148.3
```

```
## - PO4    1    860.62 57977 1148.5
## - size   2   2175.59 59292 1151.0
## - NO3    1   2420.47 59537 1153.8
##
## Step:  AIC=1144.31
## a1 ~ size + mxPH + mnO2 + Cl + NO3 + NH4 + oPO4 + PO4 + Chla
##
##        Df Sum of Sq   RSS    AIC
## - oPO4  1     16.29 57343 1142.4
## - Chla  1    223.29 57550 1143.1
## - mnO2  1    413.77 57740 1143.7
## - Cl    1    472.70 57799 1143.9
## - mxPH  1    483.56 57810 1144.0
## <none>              57327 1144.3
## - NH4   1    720.19 58047 1144.8
## - PO4   1    809.30 58136 1145.1
## - size  2   2060.95 59388 1147.3
## - NO3   1   2379.75 59706 1150.4
##
## Step:  AIC=1142.37
## a1 ~ size + mxPH + mnO2 + Cl + NO3 + NH4 + PO4 + Chla
##
##        Df Sum of Sq   RSS    AIC
## - Chla  1     207.7 57551 1141.1
## - mnO2  1     402.6 57746 1141.8
## - Cl    1     470.7 57814 1142.0
## - mxPH  1     519.7 57863 1142.2
## <none>              57343 1142.4
## - NH4   1     704.4 58047 1142.8
## - size  2    2050.3 59393 1145.3
## - NO3   1    2370.4 59713 1148.4
## - PO4   1    5818.4 63161 1159.5
##
## Step:  AIC=1141.09
## a1 ~ size + mxPH + mnO2 + Cl + NO3 + NH4 + PO4
##
##        Df Sum of Sq   RSS    AIC
## - mnO2  1     435.3 57986 1140.6
## - Cl    1     438.1 57989 1140.6
## <none>              57551 1141.1
## - NH4   1     746.9 58298 1141.6
## - mxPH  1     833.1 58384 1141.9
## - size  2    2217.5 59768 1144.6
## - NO3   1    2667.1 60218 1148.1
## - PO4   1    6309.7 63860 1159.7
##
## Step:  AIC=1140.58
## a1 ~ size + mxPH + Cl + NO3 + NH4 + PO4
##
##        Df Sum of Sq   RSS    AIC
```

```
## - NH4   1     531.0 58517 1140.4
## - Cl    1     584.9 58571 1140.6
## <none>              57986 1140.6
## - mxPH  1     819.1 58805 1141.4
## - size  2    2478.2 60464 1144.9
## - NO3   1    2251.4 60237 1146.1
## - PO4   1    9097.9 67084 1167.4
##
## Step:  AIC=1140.38
## a1 ~ size + mxPH + Cl + NO3 + PO4
##
##        Df Sum of Sq   RSS    AIC
## <none>              58517 1140.4
## - mxPH  1     784.1 59301 1141.0
## - Cl    1     835.6 59353 1141.2
## - NO3   1    1987.9 60505 1145.0
## - size  2    2664.3 61181 1145.2
## - PO4   1    8575.8 67093 1165.5
```

```
summary(final.lm)
```

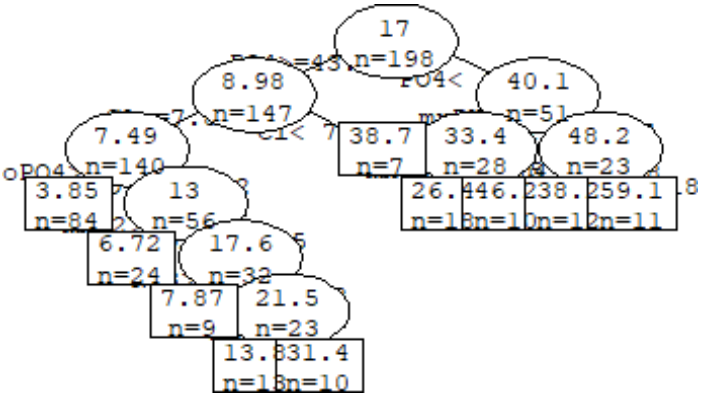
```
##
## Call:
## lm(formula = a1 ~ size + mxPH + Cl + NO3 + PO4, data = clean.algae[,
##     1:12])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -28.874 -12.732  -3.741   8.424  62.926
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 57.28555   20.96132   2.733  0.00687 **
## sizemedium   2.80050    3.40190   0.823  0.41141
## sizesmall   10.40636    3.82243   2.722  0.00708 **
## mxPH        -3.97076    2.48204  -1.600  0.11130
## Cl          -0.05227    0.03165  -1.651  0.10028
## NO3         -0.89529    0.35148  -2.547  0.01165 *
## PO4         -0.05911    0.01117  -5.291 3.32e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.5 on 191 degrees of freedom
## Multiple R-squared:  0.3527, Adjusted R-squared:  0.3324
## F-statistic: 17.35 on 6 and 191 DF,  p-value: 5.554e-16
```

```
library(rpart)
data(algae)
head(algae)
```

```
##   season  size  speed mxPH mnO2     Cl    NO3     NH4    oPO4     PO4 Chla
## 1 winter small medium 8.00  9.8 60.800  6.238 578.000 105.000 170.000 50.0
## 2 spring small medium 8.35  8.0 57.750  1.288 370.000 428.750 558.750  1.3
## 3 autumn small medium 8.10 11.4 40.020  5.330 346.667 125.667 187.057 15.6
## 4 spring small medium 8.07  4.8 77.364  2.302  98.182  61.182 138.700  1.4
## 5 autumn small medium 8.06  9.0 55.350 10.416 233.700  58.222  97.580 10.5
## 6 winter small   high 8.25 13.1 65.750  9.248 430.000  18.250  56.667 28.4
##     a1   a2   a3  a4   a5   a6  a7
## 1  0.0  0.0  0.0 0.0 34.2  8.3 0.0
## 2  1.4  7.6  4.8 1.9  6.7  0.0 2.1
## 3  3.3 53.6  1.9 0.0  0.0  0.0 9.7
## 4  3.1 41.0 18.9 0.0  1.4  0.0 1.4
## 5  9.2  2.9  7.5 0.0  7.5  4.1 1.0
## 6 15.1 14.6  1.4 0.0 22.5 12.6 2.9

algae <- algae[-manyNAs(algae), ]
rt.a1 <- rpart(a1 ~ ., data = algae[, 1:12])
rt.a1

## n= 198
##
## node), split, n, deviance, yval
##       * denotes terminal node
##
##  1) root 198 90401.290 16.996460
##    2) PO4>=43.818 147 31279.120  8.979592
##      4) Cl>=7.8065 140 21622.830  7.492857
##        8) oPO4>=51.118 84  3441.149  3.846429 *
##        9) oPO4< 51.118 56 15389.430 12.962500
##         18) mnO2>=10.05 24  1248.673  6.716667 *
##         19) mnO2< 10.05 32 12502.320 17.646870
##           38) NO3>=3.1875 9   257.080  7.866667 *
##           39) NO3< 3.1875 23 11047.500 21.473910
##             78) mnO2< 8 13  2919.549 13.807690 *
##             79) mnO2>=8 10  6370.704 31.440000 *
##      5) Cl< 7.8065 7  3157.769 38.714290 *
##    3) PO4< 43.818 51 22442.760 40.103920
##      6) mxPH< 7.87 28 11452.770 33.450000
##       12) mxPH>=7.045 18  5146.169 26.394440 *
##       13) mxPH< 7.045 10  3797.645 46.150000 *
##      7) mxPH>=7.87 23  8241.110 48.204350
##       14) PO4>=15.177 12  3047.517 38.183330 *
##       15) PO4< 15.177 11  2673.945 59.136360 *

prettyTree(rt.a1)

printcp(rt.a1)

##
## Regression tree:
## rpart(formula = a1 ~ ., data = algae[, 1:12])
```

```
##
## Variables actually used in tree construction:
## [1] Cl   mnO2 mxPH NO3  oPO4 PO4
##
## Root node error: 90401/198 = 456.57
##
## n= 198
##
##         CP nsplit rel error  xerror    xstd
## 1 0.405740      0   1.00000 1.01487 0.13114
## 2 0.071885      1   0.59426 0.71318 0.11965
## 3 0.030887      2   0.52237 0.68838 0.11982
## 4 0.030408      3   0.49149 0.66776 0.11637
## 5 0.027872      4   0.46108 0.66300 0.11640
## 6 0.027754      5   0.43321 0.66300 0.11640
## 7 0.018124      6   0.40545 0.65115 0.11495
## 8 0.016344      7   0.38733 0.66568 0.11377
## 9 0.010000      9   0.35464 0.64584 0.10491

rt2.a1 <- prune(rt.a1, cp = 0.08)
rt2.a1

## n= 198
##
## node), split, n, deviance, yval
##       * denotes terminal node
##
## 1) root 198 90401.29 16.996460
##   2) PO4>=43.818 147 31279.12  8.979592 *
##   3) PO4< 43.818 51 22442.76 40.103920 *

(rt.a1 <- rpartXse(a1 ~ ., data = algae[, 1:12]))

## n= 198
##
## node), split, n, deviance, yval
##       * denotes terminal node
##
## 1) root 198 90401.29 16.996460
##   2) PO4>=43.818 147 31279.12  8.979592 *
##   3) PO4< 43.818 51 22442.76 40.103920 *

first.tree <- rpart(a1 ~ ., data = algae[, 1:12])
snip.rpart(first.tree, c(4, 7))

## n= 198
##
## node), split, n, deviance, yval
##       * denotes terminal node
##
##  1) root 198 90401.290 16.996460
```

```
##     2) PO4>=43.818 147 31279.120  8.979592
##       4) Cl>=7.8065 140 21622.830  7.492857 *
##       5) Cl< 7.8065 7  3157.769 38.714290 *
##     3) PO4< 43.818 51 22442.760 40.103920
##       6) mxPH< 7.87 28 11452.770 33.450000
##        12) mxPH>=7.045 18  5146.169 26.394440 *
##        13) mxPH< 7.045 10  3797.645 46.150000 *
##       7) mxPH>=7.87 23  8241.110 48.204350 *

prettyTree(first.tree)
snip.rpart(first.tree)
```




```
## n= 198
##
## node), split, n, deviance, yval
##       * denotes terminal node
##
##  1) root 198 90401.290 16.996460
##    2) PO4>=43.818 147 31279.120  8.979592
##      4) Cl>=7.8065 140 21622.830  7.492857
##        8) oPO4>=51.118 84  3441.149  3.846429 *
##        9) oPO4< 51.118 56 15389.430 12.962500
##         18) mnO2>=10.05 24  1248.673  6.716667 *
##         19) mnO2< 10.05 32 12502.320 17.646870
##           38) NO3>=3.1875 9   257.080  7.866667 *
##           39) NO3< 3.1875 23 11047.500 21.473910
##             78) mnO2< 8 13   2919.549 13.807690 *
```

```
##             79) mnO2>=8 10  6370.704 31.440000 *
##       5) Cl< 7.8065 7  3157.769 38.714290 *
##     3) PO4< 43.818 51 22442.760 40.103920
##       6) mxPH< 7.87 28 11452.770 33.450000
##        12) mxPH>=7.045 18  5146.169 26.394440 *
##        13) mxPH< 7.045 10  3797.645 46.150000 *
##       7) mxPH>=7.87 23  8241.110 48.204350
##        14) PO4>=15.177 12  3047.517 38.183330 *
##        15) PO4< 15.177 11  2673.945 59.136360 *
```

```
#Model Evaluation

lm.predictions.a1 <- predict(final.lm, clean.algae)
rt.predictions.a1 <- predict(rt.a1, algae)

(mae.a1.lm <- mean(abs(lm.predictions.a1 - algae[, "a1"])))
```

```
## [1] 13.10681
```

```
(mae.a1.rt <- mean(abs(rt.predictions.a1 - algae[, "a1"])))
```

```
## [1] 11.61717
```

```
(mse.a1.lm <- mean((lm.predictions.a1 - algae[, "a1"])^2))
```

```
## [1] 295.5407
```

```
(mse.a1.rt <- mean((rt.predictions.a1 - algae[, "a1"])^2))
```

```
## [1] 271.3226
```

```
(nmse.a1.lm <- mean((lm.predictions.a1-algae[,"a1"])^2)/mean((mean(algae[,"a1
"])-algae[,"a1"])^2))
```

```
## [1] 0.6473034
```

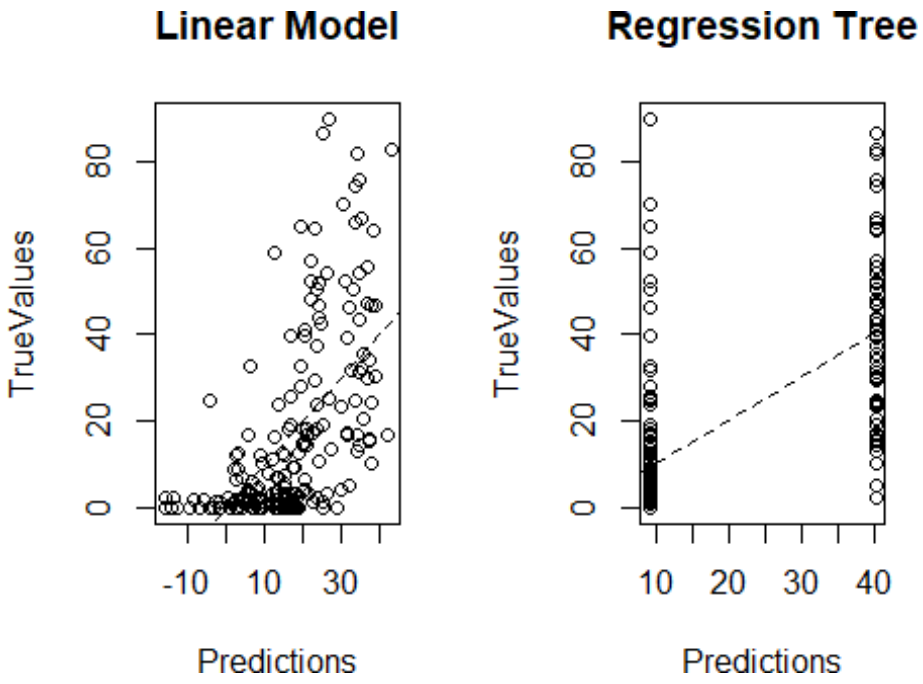
```
(nmse.a1.rt <- mean((rt.predictions.a1-algae[,"a1"])^2)/mean((mean(algae[,"a1
"])-algae[,"a1"])^2))
```

```
## [1] 0.5942601
```

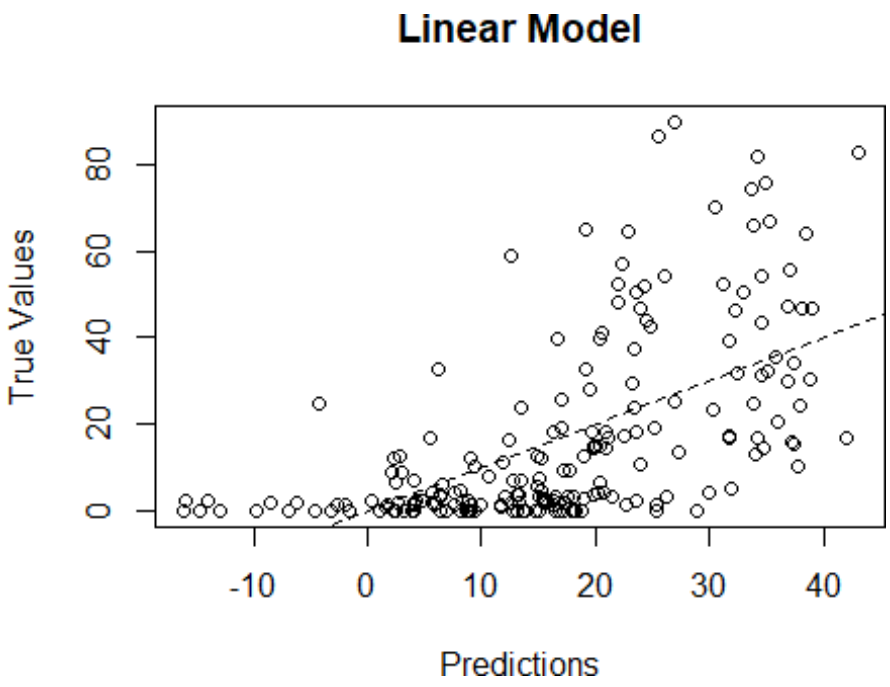
```
regr.eval(algae[, "a1"], rt.predictions.a1, train.y = algae[,"a1"])
```

```
##         mae         mse        rmse        mape        nmse        nmae
##  11.6171709 271.3226161  16.4718735         Inf   0.5942601   0.6953711
```

```
old.par <- par(mfrow = c(1, 2))
plot(lm.predictions.a1, algae[, "a1"], main = "Linear Model",xlab="Prediction
s",ylab="TrueValues")
abline(0, 1, lty = 2)
plot(rt.predictions.a1, algae[, "a1"], main = "Regression Tree",xlab="Predict
ions",ylab="TrueValues")
abline(0, 1, lty = 2)
```




```
par(old.par)

plot(lm.predictions.a1,algae[,'a1'],main="Linear Model",xlab="Predictions",yl
ab="True Values")
abline(0,1,lty=2)
```




```
#algae[identify(lm.predictions.a1,algae[,"a1"]),]


sensible.lm.predictions.a1 <- ifelse(lm.predictions.a1 <0,0,lm.predictions.a1
)
regr.eval(algae[, "a1"], lm.predictions.a1, stats = c("mae","mse"))

##       mae       mse
##  13.10681 295.54069

regr.eval(algae[, "a1"], sensible.lm.predictions.a1, stats = c("mae","mse"))

##       mae       mse
##  12.48276 286.28541

cv.rpart <- function(form,train,test,...)
  {
  m<-rpartXse(form,train,...)
  p<-predict(m,test)
  mse<-mean((p-resp(form,test))^2)
  c(nmse=mse/mean((mean(resp(form,train))-resp(form,test))^2))
  }
cv.lm <- function(form,train,test,...)
  {
  m<-lm(form,train,...)
  p<-predict(m,test)
  p<-ifelse(p<0,0,p)
```

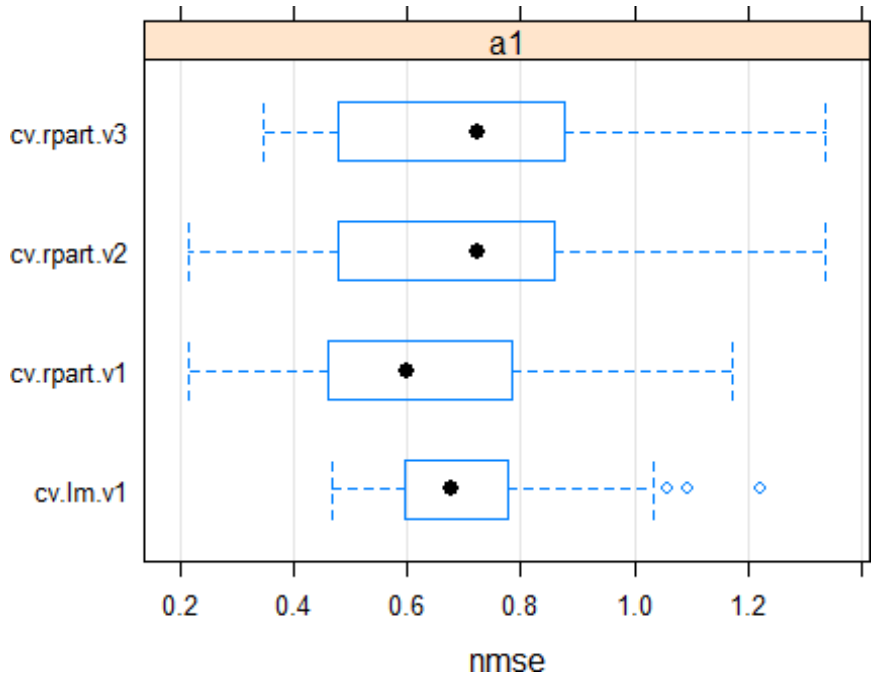
```
  mse<-mean((p-resp(form,test))^2)
  c(nmse=mse/mean((mean(resp(form,train))-resp(form,test))^2))
}

res <- experimentalComparison(c(dataset(a1 ~ .,clean.algae[,1:12],"a1")),c(va
riants("cv.lm"),variants("cv.rpart",se=c(0,0.5,1))),cvSettings(3,10,1234))

##
##
## #####  CROSS VALIDATION  EXPERIMENTAL COMPARISON #####
##
## ** DATASET :: a1
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  3 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  3 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  3 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  3 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
```

```
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
summary(res)
```

```
##
## == Summary of a  Cross Validation  Experiment ==
##
##  3 x 10 - Fold Cross Validation run with seed =  1234
##
## * Data sets ::  a1
## * Learners  ::  cv.lm.v1, cv.rpart.v1, cv.rpart.v2, cv.rpart.v3
##
## * Summary of Experiment Results:
##
##
## -> Dataset:  a1
##
##  *Learner: cv.lm.v1
##             nmse
## avg     0.7196105
## std     0.1833064
## min     0.4678248
## max     1.2218455
## invalid 0.0000000
##
##  *Learner: cv.rpart.v1
##             nmse
## avg     0.6440843
## std     0.2521952
## min     0.2146359
## max     1.1712674
## invalid 0.0000000
##
##  *Learner: cv.rpart.v2
##             nmse
## avg     0.6873747
## std     0.2669942
## min     0.2146359
## max     1.3356744
## invalid 0.0000000
##
##  *Learner: cv.rpart.v3
##             nmse
## avg     0.7167122
## std     0.2579089
## min     0.3476446
```

```
## max       1.3356744
## invalid 0.0000000

plot(res)
```




```
getVariant("cv.rpart.v1", res)

##
## Learner::  "cv.rpart"
##
## Parameter values
##   se  =  0

DSs <- sapply(names(clean.algae)[12:18],function(x,names.attrs)
  {
  f<- as.formula(paste(x,"~ ."))
  dataset(f,clean.algae[,c(names.attrs,x)],x)
  },
  names(clean.algae)[1:11])
res.all <- experimentalComparison(DSs,c(variants("cv.lm"),variants("cv.rpart"
,se=c(0,0.5,1))),cvSettings(5,10,1234))

##
##
## #####   CROSS VALIDATION  EXPERIMENTAL COMPARISON #####
##
## ** DATASET :: a1
##
```

```
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a2
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
```

```
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a3
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a4
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
```

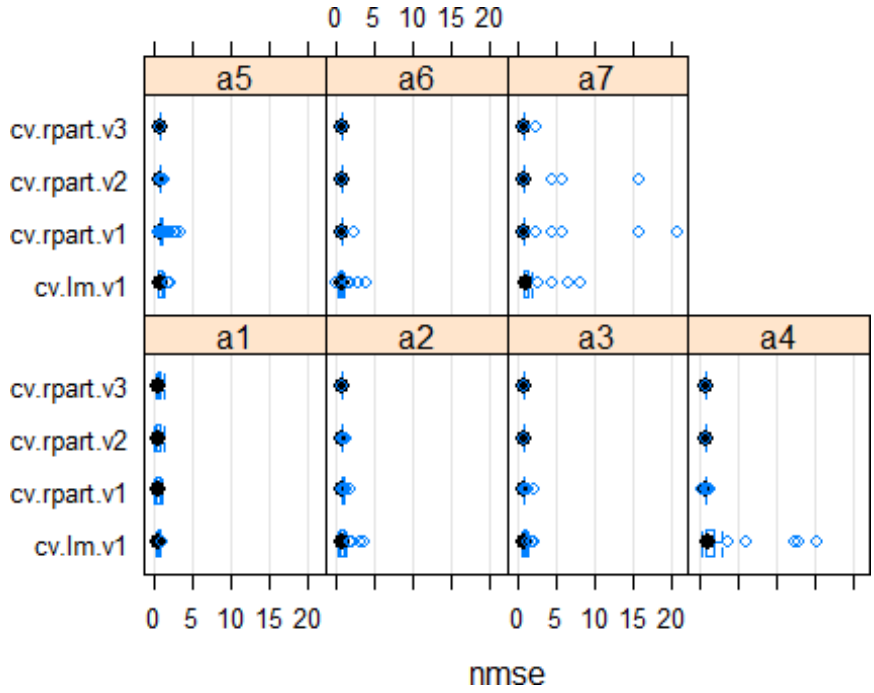
```
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a5
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
```

```
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a6
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
```

```
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a7
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run  with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run  with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10

plot(res.all)
```




```
bestScores(res.all)
```

```
## $a1
##           system   score
## nmse cv.rpart.v1 0.64231
##
## $a2
##           system score
## nmse cv.rpart.v3     1
##
## $a3
##           system score
## nmse cv.rpart.v2     1
##
## $a4
##           system score
## nmse cv.rpart.v2     1
##
## $a5
##         system     score
## nmse cv.lm.v1 0.9316803
##
## $a6
##         system     score
## nmse cv.lm.v1 0.9359697
##
## $a7
```

```
##           system    score
## nmse cv.rpart.v3 1.029505

library(randomForest)

## randomForest 4.6-14

## Type rfNews() to see new features/changes/bug fixes.

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:ggplot2':
##
##     margin

cv.rf <- function(form,train,test,...)
  {
  m<-randomForest(form,train,...)
  p<-predict(m,test)
  mse<-mean((p-resp(form,test))^2)
  c(nmse=mse/mean((mean(resp(form,train))-resp(form,test))^2))
  }
res.all <- experimentalComparison(DSs,c(variants('cv.lm'),variants('cv.rpart'
,se=c(0,0.5,1)),variants('cv.rf',ntree=c(200,500,700))),cvSettings(5,10,1234)
)

##
##
## #####  CROSS VALIDATION  EXPERIMENTAL COMPARISON #####
##
## ** DATASET :: a1
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
```

```
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
```

```
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a2
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++LEARNER :: cv.rf  variant ->  cv.rf.v1
```

```
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a3
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
```

```
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
```

```
##
## ** DATASET :: a4
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
```

```
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a5
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
```

```
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
```

```
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a6
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
```

```
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
```

```
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ** DATASET :: a7
##
## ++ LEARNER :: cv.lm  variant ->  cv.lm.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v2
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rpart  variant ->  cv.rpart.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v1
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v2
```

```
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
##
##
## ++ LEARNER :: cv.rf  variant ->  cv.rf.v3
##
##  5 x 10 - Fold Cross Validation run with seed =  1234
## Repetition  1
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  2
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  3
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  4
## Fold:  1  2  3  4  5  6  7  8  9  10
## Repetition  5
## Fold:  1  2  3  4  5  6  7  8  9  10
```

```
bestScores(res.all)
```

```
## $a1
##        system     score
## nmse cv.rf.v3 0.5467636
##
## $a2
##        system     score
## nmse cv.rf.v3 0.7695782
##
## $a3
##           system score
## nmse cv.rpart.v2     1
##
## $a4
##        system     score
## nmse cv.rf.v1 0.9728596
##
## $a5
##        system     score
## nmse cv.rf.v2 0.7916332
##
```

```
## $a6
##        system    score
## nmse cv.rf.v2 0.911758
##
## $a7
##           system    score
## nmse cv.rpart.v3 1.029505
```

```
compAnalysis(res.all,against="cv.rf.v3",datasets=c("a1","a2","a4","a6"))
```

```
##
## == Statistical Significance Analysis of Comparison Results ==
##
## Baseline Learner::    cv.rf.v3  (Learn.1)
##
## ** Evaluation Metric::    nmse
##
## - Dataset: a1
##       Learn.1   Learn.2 sig.2   Learn.3 sig.3   Learn.4 sig.4   Learn.5
## AVG 0.5467636 0.7077282    ++ 0.6423100    +  0.6569726    ++ 0.6875212
## STD 0.1727235 0.1639373       0.2399321       0.2397636       0.2348946
##     sig.5   Learn.6 sig.6   Learn.7 sig.7
## AVG    ++ 0.5505008       0.5473338
## STD       0.1783960       0.1724374
##
## - Dataset: a2
##       Learn.1   Learn.2 sig.2   Learn.3 sig.3    Learn.4 sig.4
## AVG 0.7695782 1.0449317    ++ 1.0426327    ++ 1.01626123    ++
## STD 0.1431761 0.6276144       0.2005522       0.07435826
##          Learn.5 sig.5   Learn.6 sig.6   Learn.7 sig.7
## AVG 1.000000e+00    ++ 0.7775628       0.7744307
## STD 2.389599e-16       0.1473327       0.1462083
##
## - Dataset: a4
##       Learn.1  Learn.2 sig.2   Learn.3 sig.3      Learn.4 sig.4
## AVG 0.9746980 2.111976       1.0073953    +  1.000000e+00    +
## STD 0.3823094 3.118196       0.1065607       2.774424e-16
##          Learn.5 sig.5   Learn.6 sig.6   Learn.7 sig.7
## AVG 1.000000e+00    +  0.9728596       0.9833417
## STD 2.774424e-16       0.3515190       0.3829643
##
## - Dataset: a6
##       Learn.1   Learn.2 sig.2   Learn.3 sig.3      Learn.4 sig.4
## AVG 0.9133912 0.9359697    ++ 1.0191041       1.000000e+00
## STD 0.3573499 0.6045963       0.1991436       2.451947e-16
##          Learn.5 sig.5   Learn.6 sig.6   Learn.7 sig.7
## AVG 1.000000e+00       0.9275673       0.9117580
## STD 2.451947e-16       0.3793325       0.3757454
##
## Legends:
```

```
## Learners -> Learn.1 = cv.rf.v3 ; Learn.2 = cv.lm.v1 ; Learn.3 = cv.rpart.v
1 ; Learn.4 = cv.rpart.v2 ; Learn.5 = cv.rpart.v3 ; Learn.6 = cv.rf.v1 ; Lear
n.7 = cv.rf.v2 ;
## Signif. Codes -> 0 '++' or '--' 0.001 '+' or '-' 0.05 ' ' 1

#Prediction to 7 algae

bestModelsNames <- sapply(bestScores(res.all),function(x) x['nmse','system'])
learners <- c(rf='randomForest',rpart='rpartXse')
funcs <- learners[sapply(strsplit(bestModelsNames,'\\.'),function(x) x[2])]
parSetts <- lapply(bestModelsNames,function(x) getVariant(x,res.all)@pars)
bestModels <- list()


for(a in 1:7)
  {
  form<-as.formula(paste(names(clean.algae)[11+a],'~ .'))
  bestModels[[a]]<-do.call(funcs[a],c(list(form,clean.algae[,c(1:11,11+a)]),p
arSetts[[a]]))
}

clean.test.algae <- knnImputation(test.algae, k = 10, distData = algae[,1:11]
)

preds <- matrix(ncol=7,nrow=140)
for(i in 1:nrow(clean.test.algae))preds[i,]<-sapply(1:7,function(x)predict(be
stModels[[x]],clean.test.algae[i,]))


avg.preds <- apply(algae[,12:18],2,mean)

apply( ((algae.sols-preds)^2), 2,mean) /apply( (scale(algae.sols,avg.preds,F)
^2),2,mean)

##        a1        a2        a3        a4        a5        a6        a7
## 0.4681785 0.8622797 1.0000000 0.7138057 0.7180793 0.8205594 1.0000000
```