GradAnalysis.r

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Wed Apr 12 00:57:19 2017

```r
rm(list=ls())
setwd('~/19. UBC 2016 Winter Term 2/STAT 550/Case/Code')

library('ggplot2') # for plotting
```

```
## Warning: package 'ggplot2' was built under R version 3.2.4
```

```r
library('lme4') # for mixed-effects models
```

```
## Warning: package 'lme4' was built under R version 3.2.5
```

```
## Loading required package: Matrix
```

```r
library('reshape2') # for ...
library('dplyr') # for %>%
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library('MASS') # for ...
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```r
library('base') # for ...

# Import the MWD data.
soil <- read.table('MWD.csv', sep=',', header=T)
soil.unreleveled <- soil
soil$Treatment <- relevel(soil$Treatment, ref='con')
head(soil)
```

```
##   Sample  Date Block Treatment Transect  MWD
## 1      1 April    b1       bio        1 1.05
## 2      2 April    b1       bio        2 0.95
## 3      3 April    b1       bio        3 0.99
## 4      4 April    b3       bio        1 0.82
## 5      5 April    b3       bio        2 0.84
## 6      6 April    b3       bio        3 0.96
```

```
str(soil)
```

```
## 'data.frame':    96 obs. of  6 variables:
##  $ Sample   : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ Date     : Factor w/ 4 levels "April","Aug",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Block    : Factor w/ 4 levels "b1","b2","b3",..: 1 1 1 3 3 3 2 2 2 4 ...
##  $ Treatment: Factor w/ 2 levels "con","bio": 2 2 2 2 2 2 2 2 2 2 ...
##  $ Transect : int  1 2 3 1 2 3 1 2 3 1 ...
##  $ MWD      : num  1.05 0.95 0.99 0.82 0.84 0.96 1.11 1.25 1.11 1.23 ...
```

```
with(soil, table(Treatment,Date))
```

```
##          Date
## Treatment April Aug June Oct
##       con    12  12   12  12
##       bio    12  12   12  12
```

```
# Import the cover value data.
pc <- read.csv('plant_cover.csv', header=T)
pc$Block <- as.factor(pc$Block)
head(pc)
```

```
##                         Project         Date Block Treatment Transect Plot
## 1 OK Ranch Biosolids Resample June 21, 2016     1 Biosolids        1    2
## 2 OK Ranch Biosolids Resample June 21, 2016     1 Biosolids        1    2
## 3 OK Ranch Biosolids Resample June 21, 2016     1 Biosolids        1    2
## 4 OK Ranch Biosolids Resample June 21, 2016     1 Biosolids        1    2
## 5 OK Ranch Biosolids Resample June 21, 2016     1 Biosolids        1    2
## 6 OK Ranch Biosolids Resample June 21, 2016     1 Biosolids        1    2
##   Species Cover.class Cover.value
## 1    ACMI           1         2.5
## 2    ALCE           1         2.5
## 3    ASAG           1         2.5
## 4    BIOS           2        15.0
## 5    HECO           4        62.5
## 6    LITT           5        85.0
```

```
str(pc)
```

```
## 'data.frame':    2669 obs. of  9 variables:
##  $ Project    : Factor w/ 1 level "OK Ranch Biosolids Resample": 1 1 1 1 1 1 1 1 1 1 1 ...
##  $ Date       : Factor w/ 2 levels "June 21, 2016",..: 1 1 1 1 1 1 1 1 1 1 1 ...
##  $ Block      : Factor w/ 4 levels "1","2","3","4": 1 1 1 1 1 1 1 1 1 1 1 ...
```

```
##  $ Treatment  : Factor w/ 2 levels "Biosolids","Control": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Transect   : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ Plot       : int  2 2 2 2 2 2 2 2 2 3 ...
##  $ Species    : Factor w/ 50 levels "ACMI","ACRI",..: 1 3 9 11 29 33 39 47 48 3 ...
##  $ Cover.class: int  1 1 1 2 4 5 3 3 1 2 ...
##  $ Cover.value: num  2.5 2.5 2.5 15 62.5 85 37.5 37.5 2.5 15 ...
```

```r
with(pc, table(Treatment,Block))
```

```
##            Block
## Treatment     1   2   3   4
##   Biosolids 301 301 239 267
##   Control   420 406 353 382
```

```r
tapply(pc$Cover.value, pc$Treatment, table)
```

```
## $Biosolids
##
##  2.5   15 37.5 62.5   85 97.5
##  405  265  111   78   91  158
##
## $Control
##
##  2.5   15 37.5 62.5   85 97.5
##  676  510  243   94   35    3
```

```r
###############################
# Grad Analysis:
###############################

# Obtain the relevant species.
# Note: The client said they are interested in POPR, PSSP, POJU, HECO,
#       ALCE, ANDI, TAOF, SOIL and BRYO, as well as anything with a cover
#       greater than 5% across all the sites.
#     : None of the species occurred in all of the 400 sites (4 blocks x
#       2 treatments × 5 transects × 10 samples per transect), although HECO
#       and LITT were close. The rest occurred in below half of the sites.
#       So, we change our criterion to choose species whose averages over
#       the (occurring) transects and plots, for every block-treatment
#       combination, are all greater than 5%.
summary(pc$Species)
```

```
## ACMI ACRI ALCE ANDI ANMI ARCA ARFR ARHO ASAG ASMI BIOS BRTE BRYO CAFI CAMI
##   66    6  134   81  103    1   90   12  187   11   36    2  199    1    3
## CAOB CAPE CASP CEAR COUM DEPI ELTR ERCO FECE FEOC GAAR GABO GETR HECO JUBA
##    2    1    6    1    5   10    1   19   25    3    3    3    1  353   21
## KOMA LILE LITT LOMA ORLU OXSE PEPR POHI POJU POPR POSE PSSP ROAC SECA SIAL
##  183    9  398    2    1    3    3    1   62  120   84   48    5    1    3
## SOIL TAOF TRDU TRPR ZIVE
##  186  107   60    5    2
```

```
all.species <- levels(pc$Species)
interesting <- c('POPR', 'PSSP', 'POJU', 'HECO', 'ALCE', 'ANDI', 'TAOF',
                 'SOIL', 'BRYO')
with(pc, table(Species, Block))
```

```
##           Block
## Species    1    2    3    4
##     ACMI  17    6   15   28
##     ACRI   4    0    0    2
##     ALCE  83   46    4    1
##     ANDI  16   28   19   18
##     ANMI  27   37   28   11
##     ARCA   1    0    0    0
##     ARFR  12   27   18   33
##     ARHO   2    7    2    1
##     ASAG  50   30   51   56
##     ASMI  10    0    1    0
##     BIOS   6   17    2   11
##     BRTE   0    0    0    2
##     BRYO  50   52   47   50
##     CAFI   0    0    1    0
##     CAMI   0    0    0    3
##     CAOB   0    2    0    0
##     CAPE   1    0    0    0
##     CASP   0    0    5    1
##     CEAR   0    0    1    0
##     COUM   5    0    0    0
##     DEPI   0    0   10    0
##     ELTR   0    0    1    0
##     ERCO  16    0    0    3
##     FECE   0   23    0    2
##     FEOC   0    0    2    1
##     GAAR   2    0    0    1
##     GABO   2    0    1    0
##     GETR   0    0    1    0
##     HECO  89   95   91   78
##     JUBA   0    0    4   17
##     KOMA  37   61   37   48
##     LILE   9    0    0    0
##     LITT 100  100   99   99
##     LOMA   2    0    0    0
##     ORLU   1    0    0    0
##     OXSE   1    0    2    0
##     PEPR   3    0    0    0
##     POHI   0    0    0    1
##     POJU  12   41    4    5
##     POPR  34   14   30   42
##     POSE  15   28    7   34
##     PSSP  21   18    1    8
##     ROAC   0    0    0    5
##     SECA   0    0    0    1
##     SIAL   1    2    0    0
##     SOIL  50   65   34   37
```

```
##     TAOF  29   4  47  27
##     TRDU   9   2  26  23
##     TRPR   3   2   0   0
##     ZIVE   1   0   1   0
```

```r
with(pc, table(Species, Treatment))
```

```
##          Treatment
## Species Biosolids Control
##     ACMI        39      27
##     ACRI         2       4
##     ALCE        55      79
##     ANDI         0      81
##     ANMI         5      98
##     ARCA         0       1
##     ARFR        24      66
##     ARHO         1      11
##     ASAG        60     127
##     ASMI         1      10
##     BIOS        36       0
##     BRTE         2       0
##     BRYO         6     193
##     CAFI         1       0
##     CAMI         3       0
##     CAOB         0       2
##     CAPE         0       1
##     CASP         4       2
##     CEAR         0       1
##     COUM         0       5
##     DEPI        10       0
##     ELTR         1       0
##     ERCO         0      19
##     FECE        10      15
##     FEOC         0       3
##     GAAR         0       3
##     GABO         3       0
##     GETR         1       0
##     HECO       160     193
##     JUBA        19       2
##     KOMA        38     145
##     LILE         0       9
##     LITT       199     199
##     LOMA         1       1
##     ORLU         0       1
##     OXSE         1       2
##     PEPR         0       3
##     POHI         1       0
##     POJU        53       9
##     POPR       115       5
##     POSE        13      71
##     PSSP        38      10
##     ROAC         5       0
##     SECA         0       1
##     SIAL         3       0
```

```
##     SOIL         51         135
##     TAOF        101           6
##     TRDU         43          17
##     TRPR          3           2
##     ZIVE          0           2
```

```r
species.vec <- NULL
for (ii in 1:length(all.species))
{
  # Obtain the subset of the data corresponding to this species.
  species.try <- all.species[ii]
  pc.sub.try <- subset(pc, Species==species.try)
  pc.sub.try <- pc.sub.try[ ,c(3,4,5,6,9)]

  # Check if this species occurrs in every block-treatment combination.
  # Note: entries.try is the table of counts for each block, by treatment
  #       group, for this species.
  entries.try <- table(pc.sub.try$Block, pc.sub.try$Treatment)
  which.entries.miss.try <- which(entries.try==0, arr.ind=TRUE)
  is.in.all.combs <- ifelse(test=(nrow(which.entries.miss.try)==0), yes=1,
                            no=0)

  # Obtain averages over the (occurring) transects and plots, for every
  # (occurring) block-treatment combination.
  by_blockTrt.try <- group_by(pc.sub.try, Block, Treatment)
  #dat.avg.try <- summarise(by_blockTrt.try, y.avg=sum(Cover.value)/50)
  dat.avg.try2 <- summarise(by_blockTrt.try, y.avg=mean(Cover.value))
  print(species.try)
  print(dat.avg.try2)
  all.occurring.greater.than5 <- ifelse(test=(sum(dat.avg.try2$y.avg<5)==0),
                                        yes=1, no=0)
  all.greater.than5 <- is.in.all.combs * all.occurring.greater.than5

  # Determine whether the species should be included.
  if ((species.try%in%interesting) || (all.greater.than5))
  {
    species.vec <- c(species.vec, species.try)
  }
}
```

```
## [1] "ACMI"
## Source: local data frame [7 x 3]
## Groups: Block [?]
##
##     Block Treatment       y.avg
##    (fctr)    (fctr)       (dbl)
## 1       1  Biosolids   5.441176
## 2       2  Biosolids   2.500000
## 3       2    Control   2.500000
## 4       3  Biosolids   8.750000
## 5       3    Control  10.961538
## 6       4  Biosolids   5.666667
## 7       4    Control   2.500000
## [1] "ACRI"
```

```
## Source: local data frame [3 x 3]
## Groups: Block [?]
##
##    Block  Treatment  y.avg
##   (fctr)     (fctr)  (dbl)
## 1      1  Biosolids  26.25
## 2      1    Control  15.00
## 3      4    Control  20.00
## [1] "ALCE"
## Source: local data frame [7 x 3]
## Groups: Block [?]
##
##    Block  Treatment      y.avg
##   (fctr)     (fctr)      (dbl)
## 1      1  Biosolids  21.060606
## 2      1    Control  19.700000
## 3      2  Biosolids   6.875000
## 4      2    Control   4.903846
## 5      3  Biosolids   2.500000
## 6      3    Control   2.500000
## 7      4    Control   2.500000
## [1] "ANDI"
## Source: local data frame [4 x 3]
## Groups: Block [?]
##
##    Block  Treatment     y.avg
##   (fctr)     (fctr)     (dbl)
## 1      1    Control  2.500000
## 2      2    Control  6.071429
## 3      3    Control  3.157895
## 4      4    Control  3.194444
## [1] "ANMI"
## Source: local data frame [7 x 3]
## Groups: Block [?]
##
##    Block  Treatment     y.avg
##   (fctr)     (fctr)     (dbl)
## 1      1  Biosolids   2.50000
## 2      1    Control  15.00000
## 3      2  Biosolids  22.50000
## 4      2    Control  13.38235
## 5      3    Control  12.41071
## 6      4  Biosolids  15.00000
## 7      4    Control   8.75000
## [1] "ARCA"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block  Treatment  y.avg
##   (fctr)     (fctr)  (dbl)
## 1      1    Control     15
## [1] "ARFR"
## Source: local data frame [8 x 3]
## Groups: Block [?]
```

```
##
##     Block Treatment      y.avg
##    (fctr)    (fctr)       (dbl)
## 1      1 Biosolids 14.375000
## 2      1   Control 10.000000
## 3      2 Biosolids  8.750000
## 4      2   Control  4.705882
## 5      3 Biosolids  2.500000
## 6      3   Control 11.029412
## 7      4 Biosolids 11.666667
## 8      4   Control 10.729167
## [1] "ARHO"
## Source: local data frame [5 x 3]
## Groups: Block [?]
##
##     Block Treatment y.avg
##    (fctr)    (fctr) (dbl)
## 1      1 Biosolids   2.5
## 2      1   Control   2.5
## 3      2   Control   2.5
## 4      3   Control   2.5
## 5      4   Control   2.5
## [1] "ASAG"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##     Block Treatment      y.avg
##    (fctr)    (fctr)       (dbl)
## 1      1 Biosolids 11.300000
## 2      1   Control  6.500000
## 3      2 Biosolids  3.636364
## 4      2   Control  3.815789
## 5      3 Biosolids 11.250000
## 6      3   Control 10.000000
## 7      4 Biosolids  7.857143
## 8      4   Control  5.119048
## [1] "ASMI"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##     Block Treatment y.avg
##    (fctr)    (fctr) (dbl)
## 1      1   Control  8.75
## 2      3 Biosolids  2.50
## [1] "BIOS"
## Source: local data frame [4 x 3]
## Groups: Block [?]
##
##     Block Treatment      y.avg
##    (fctr)    (fctr)       (dbl)
## 1      1 Biosolids 6.666667
## 2      2 Biosolids 6.176471
## 3      3 Biosolids 2.500000
## 4      4 Biosolids 7.045455
```

```
## [1] "BRTE"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      4 Biosolids  8.75
## [1] "BRYO"
## Source: local data frame [6 x 3]
## Groups: Block [?]
##
##    Block Treatment    y.avg
##   (fctr)    (fctr)    (dbl)
## 1      1   Control 40.60000
## 2      2 Biosolids  8.75000
## 3      2   Control 24.73958
## 4      3   Control 33.13830
## 5      4 Biosolids 26.25000
## 6      4   Control 30.26042
## [1] "CAFI"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      3 Biosolids   2.5
## [1] "CAMI"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      4 Biosolids   2.5
## [1] "CAOB"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      2   Control   2.5
## [1] "CAPE"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1   Control    15
## [1] "CASP"
## Source: local data frame [3 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      3 Biosolids  15.0
```

```
## 2        3    Control    2.5
## 3        4    Control    2.5
## [1] "CEAR"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##      Block Treatment y.avg
##    (fctr)    (fctr) (dbl)
## 1       3    Control  37.5
## [1] "COUM"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##      Block Treatment y.avg
##    (fctr)    (fctr) (dbl)
## 1       1    Control     5
## [1] "DEPI"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##      Block Treatment y.avg
##    (fctr)    (fctr) (dbl)
## 1       3 Biosolids     5
## [1] "ELTR"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##      Block Treatment y.avg
##    (fctr)    (fctr) (dbl)
## 1       3 Biosolids    85
## [1] "ERCO"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##      Block Treatment    y.avg
##    (fctr)    (fctr)    (dbl)
## 1       1    Control 3.28125
## 2       4    Control 2.50000
## [1] "FECE"
## Source: local data frame [4 x 3]
## Groups: Block [?]
##
##      Block Treatment      y.avg
##    (fctr)    (fctr)      (dbl)
## 1       2 Biosolids  6.388889
## 2       2    Control  6.964286
## 3       4 Biosolids  2.500000
## 4       4    Control 37.500000
## [1] "FEOC"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##      Block Treatment y.avg
##    (fctr)    (fctr) (dbl)
```

```
## 1      3   Control  8.75
## 2      4   Control  2.50
## [1] "GAAR"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)   (fctr) (dbl)
## 1      1  Control   2.5
## 2      4  Control   2.5
## [1] "GABO"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)   (fctr) (dbl)
## 1      1 Biosolids  8.75
## 2      3 Biosolids 37.50
## [1] "GETR"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)   (fctr) (dbl)
## 1      3 Biosolids   2.5
## [1] "HECO"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##    Block Treatment     y.avg
##   (fctr)   (fctr)     (dbl)
## 1      1 Biosolids 35.37500
## 2      1   Control 24.13265
## 3      2 Biosolids 31.08696
## 4      2   Control 29.48980
## 5      3 Biosolids 58.39286
## 6      3   Control 44.23469
## 7      4 Biosolids 42.34375
## 8      4   Control 30.05435
## [1] "JUBA"
## Source: local data frame [3 x 3]
## Groups: Block [?]
##
##    Block Treatment     y.avg
##   (fctr)   (fctr)     (dbl)
## 1      3 Biosolids 11.875000
## 2      4 Biosolids  8.166667
## 3      4   Control  2.500000
## [1] "KOMA"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##    Block Treatment     y.avg
##   (fctr)   (fctr)     (dbl)
```

```
## 1      1 Biosolids  8.500000
## 2      1   Control  7.129630
## 3      2 Biosolids 12.125000
## 4      2   Control  9.451220
## 5      3 Biosolids  6.666667
## 6      3   Control  8.308824
## 7      4 Biosolids  7.500000
## 8      4   Control 12.093023
## [1] "LILE"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)   (fctr) (dbl)
## 1      1   Control   2.5
## [1] "LITT"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##    Block Treatment    y.avg
##   (fctr)   (fctr)     (dbl)
## 1      1 Biosolids 93.70000
## 2      1   Control 30.30000
## 3      2 Biosolids 82.85000
## 4      2   Control 28.35000
## 5      3 Biosolids 94.23469
## 6      3   Control 46.30000
## 7      4 Biosolids 86.15000
## 8      4   Control 33.36735
## [1] "LOMA"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)   (fctr) (dbl)
## 1      1 Biosolids   2.5
## 2      1   Control   2.5
## [1] "ORLU"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)   (fctr) (dbl)
## 1      1   Control   2.5
## [1] "OXSE"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)   (fctr) (dbl)
## 1      1 Biosolids 85.00
## 2      3   Control  8.75
## [1] "PEPR"
## Source: local data frame [1 x 3]
```

```
## Groups: Block [?]
##
##     Block Treatment    y.avg
##    (fctr)    (fctr)    (dbl)
## 1       1   Control 6.666667
## [1] "POHI"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##     Block Treatment y.avg
##    (fctr)    (fctr) (dbl)
## 1       4 Biosolids    15
## [1] "POJU"
## Source: local data frame [6 x 3]
## Groups: Block [?]
##
##     Block Treatment    y.avg
##    (fctr)    (fctr)    (dbl)
## 1       1 Biosolids 14.54545
## 2       1   Control 15.00000
## 3       2 Biosolids 33.71622
## 4       2   Control  8.75000
## 5       3   Control  2.50000
## 6       4 Biosolids 12.50000
## [1] "POPR"
## Source: local data frame [7 x 3]
## Groups: Block [?]
##
##     Block Treatment    y.avg
##    (fctr)    (fctr)    (dbl)
## 1       1 Biosolids 37.82258
## 2       1   Control  2.50000
## 3       2 Biosolids 34.82143
## 4       3 Biosolids 46.29310
## 5       3   Control  2.50000
## 6       4 Biosolids 52.92683
## 7       4   Control 15.00000
## [1] "POSE"
## Source: local data frame [6 x 3]
## Groups: Block [?]
##
##     Block Treatment     y.avg
##    (fctr)    (fctr)     (dbl)
## 1       1   Control  4.166667
## 2       2 Biosolids 14.545455
## 3       2   Control  9.705882
## 4       3   Control  6.071429
## 5       4 Biosolids  2.500000
## 6       4   Control  7.890625
## [1] "PSSP"
## Source: local data frame [7 x 3]
## Groups: Block [?]
##
##     Block Treatment      y.avg
```

```
##    (fctr)     (fctr)      (dbl)
## 1       1 Biosolids 44.264706
## 2       1   Control 11.875000
## 3       2 Biosolids 21.666667
## 4       2   Control  2.500000
## 5       3 Biosolids 37.500000
## 6       4 Biosolids 19.500000
## 7       4   Control  6.666667
## [1] "ROAC"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      4 Biosolids   9.5
## [1] "SECA"
## Source: local data frame [1 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      4   Control    15
## [1] "SIAL"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1 Biosolids   2.5
## 2      2 Biosolids   2.5
## [1] "SOIL"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##    Block Treatment      y.avg
##   (fctr)    (fctr)      (dbl)
## 1      1 Biosolids  3.888889
## 2      1   Control  6.341463
## 3      2 Biosolids  4.880952
## 4      2   Control 11.022727
## 5      3 Biosolids  3.636364
## 6      3   Control  4.673913
## 7      4 Biosolids  2.500000
## 8      4   Control 12.314815
## [1] "TAOF"
## Source: local data frame [7 x 3]
## Groups: Block [?]
##
##    Block Treatment      y.avg
##   (fctr)    (fctr)      (dbl)
## 1      1 Biosolids  5.648148
## 2      1   Control  2.500000
## 3      2 Biosolids  2.500000
## 4      3 Biosolids 12.555556
```

```
## 5       3   Control  2.500000
## 6       4 Biosolids  6.400000
## 7       4   Control  2.500000
## [1] "TRDU"
## Source: local data frame [6 x 3]
## Groups: Block [?]
##
##     Block Treatment     y.avg
##   (fctr)    (fctr)     (dbl)
## 1      1 Biosolids 2.500000
## 2      2 Biosolids 2.500000
## 3      3 Biosolids 8.815789
## 4      3   Control 4.285714
## 5      4 Biosolids 5.384615
## 6      4   Control 2.500000
## [1] "TRPR"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##     Block Treatment     y.avg
##   (fctr)    (fctr)     (dbl)
## 1      1 Biosolids 10.83333
## 2      2   Control  2.50000
## [1] "ZIVE"
## Source: local data frame [2 x 3]
## Groups: Block [?]
##
##     Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1   Control  15.0
## 2      3   Control   2.5
```

```r
print(species.vec)
```

```
##  [1] "ALCE" "ANDI" "BRYO" "HECO" "KOMA" "LITT" "POJU" "POPR" "PSSP" "SOIL"
## [11] "TAOF"
```

```r
# Obtain the MWD averages (to be used in calculating the correlations).
a <- group_by(soil.unreleveled, Block, Treatment) %>%
    summarise(mean(MWD))
b <- a$`mean(MWD)`
mean.MWD <- b

# Loop over all the relevant species.
model.avg.list <-list()
p.vals.vec <- rep(NA, times=length(species.vec))
coefs.vec <- rep(NA, times=length(species.vec))
nonparam.model.list <-list()
nonparam.p.vals.vec <- rep(NA, times=length(species.vec))
nonparam.coefs.vec <- rep(NA, times=length(species.vec))
cor.vec <- rep(NA, times=length(species.vec))
for (ii in 1:length(species.vec))
{
```

```r
# Obtain the subset of the data corresponding to this species.
this.species <- species.vec[ii]
pc.this.species <- subset(pc, Species==this.species)
pc.this.species <- pc.this.species[ ,c(3,4,9)]
print(this.species)

# Table of counts for each class of cover value, by treatment group, for
# this species.
#print(tapply(pc.this.species$Cover.value, pc.this.species$Treatment, table))

# Table of counts for each block, by treatment group, for this species.
entries <- table(pc.this.species$Block, pc.this.species$Treatment)
which.entries.miss <- which(t(entries)==0)
which.entries.miss.ind <- which(entries==0, arr.ind=TRUE)

# Obtain averages over the transects and plots.
by_blockTrt.this.species <- group_by(pc.this.species, Block, Treatment)
dat.avg.this.species <- summarise(by_blockTrt.this.species,
                                  y.avg=sum(Cover.value)/50)
if (length(which.entries.miss) > 0)
{
  for (jj in 1:length(which.entries.miss))
  {
    which.row <- which.entries.miss[jj]
    which.block <- toString(which.entries.miss.ind[jj,1])
    which.trt <- ifelse(test=(which.entries.miss.ind[jj,2]==1), yes='Biosolids',
                    no='Control')
    new.row <- c(which.block, which.trt, 0)
    dat.avg.this.species <- rbind(dat.avg.this.species[1:(which.row-1),],
                              new.row,
                              dat.avg.this.species[-(1:(which.row-1)),])
  }
}
dat.avg.this.species$y.avg <- as.numeric(dat.avg.this.species$y.avg)
print(dat.avg.this.species)

###########################
# Plots:
###########################

# Histogram of cover value for this species.
hist(pc.this.species$Cover.value,
     main=paste('Histogram of cover value for ',this.species,sep=''),
     xlab=paste(this.species,' Cover Value (%)',sep=''), col='mistyrose')

# Normal Q-Q plot of cover value for this species.
# Note: Strange behaviour due to discreteness.
#qqnorm(pc.this.species$Cover.value)

# Boxplots of cover value for this species, for the two treatments.
#print(ggplot(aes(y=Cover.value, x=Treatment, fill=Treatment, alpha=0.4),
#             data=pc.this.species) +
#      geom_boxplot() +
```

```r
#       geom_point())

# Boxplot of cover value for this species, for the two treatments,
# across the four blocks.
#print(ggplot(aes(y=Cover.value, x=Treatment, fill=Treatment, alpha=0.4),
#               data=pc.this.species) +
#       geom_boxplot() +
#       geom_point() +
#       facet_wrap(~Block))

# Boxplot of average cover value for this species, for the two treatments.
print(ggplot(aes(y=y.avg, x=Treatment, fill=Treatment, alpha=0.4),
                  data=dat.avg.this.species) +
       geom_boxplot() +
       geom_point() +
       labs(y=paste(this.species,' Cover Value (%)',sep=''),
             title=paste('Boxplot of ',this.species,' Cover Value',sep='')))

# Interaction plot for block and treatment, with cover value for this
# species as the response.
#print(ggplot(aes(x=Block, y=Cover.value, group=Treatment,
#                 colour=Treatment),
#               data=pc.this.species) +
#       stat_summary(fun.y='mean', geom='line') +
#       labs(x='Block', y=paste(this.species,' Cover Value',sep=''),
#             title=paste('Change in ',this.species,'
#                         Cover Value over Different Blocks'),sep=''))

# Interaction plot for block and treatment, with average cover value for
# this species as the response.
#print(ggplot(aes(x=Block, y=y.avg, group=Treatment, colour=Treatment),
#               data=dat.avg.this.species) +
#       geom_point() +
#       geom_line() +
#       labs(x='Block', y=paste(this.species,' Cover Value (%)',sep=''),
#             title=paste('Comparison of ',this.species,
#                         ' Cover Values between Biosolids and Control',
#                         sep='')))

#########################
# Modelling cover value:
#########################

# Linear regression of average cover value for this species, with treatment
# effect.
dat.avg.this.species$Treatment <- relevel(dat.avg.this.species$Treatment,
                                          ref='Control')
model_avg.this.species <- lm(as.numeric(y.avg)~Treatment,
                              data=dat.avg.this.species)
print(summary(model_avg.this.species))
model.avg.list[[ii]] <- model_avg.this.species
p.vals.vec[ii] <- summary(model_avg.this.species)$coefficients[2,4]
coefs.vec[ii] <- summary(model_avg.this.species)$coefficients[2,1]
```

```
##########################
# Non-parametric test:
##########################

# Parametric tests:
#t.test(x=dat.avg.this.species$y.avg[dat.avg.this.species$Treatment=='Biosolids'],
#       y=dat.avg.this.species$y.avg[dat.avg.this.species$Treatment=='Control'],
#       alternative='two.sided', mu=0, paired=FALSE, var.equal=TRUE,
#       conf.level=0.95)
#t.test(x=dat.avg.this.species$y.avg[dat.avg.this.species$Treatment=='Biosolids'],
#       y=dat.avg.this.species$y.avg[dat.avg.this.species$Treatment=='Control'],
#       alternative='two.sided', mu=0, paired=TRUE, var.equal=TRUE,
#       conf.level=0.95)

# Non-parametric test:
wilcox.this.species <- wilcox.test(x=dat.avg.this.species$y.avg[dat.avg.this.species$Treatment=='Bioso
                                   y=dat.avg.this.species$y.avg[dat.avg.this.species$Treatment=='Contr
                                   alternative='two.sided', mu=0, paired=TRUE,
                                   conf.int=TRUE, conf.level=0.95)
nonparam.model.list[[ii]] <- wilcox.this.species
nonparam.p.vals.vec[ii] <- wilcox.this.species$p.value
nonparam.coefs.vec[ii] <- wilcox.this.species$estimate


##########################
# Correlations:
##########################

# Find the correlation between MWD and the average cover value for this
# species.
mean.cv.this.species <- as.numeric(as.character(dat.avg.this.species$y.avg))
cor.vec[ii] <- cor(mean.MWD, mean.cv.this.species)
}
```
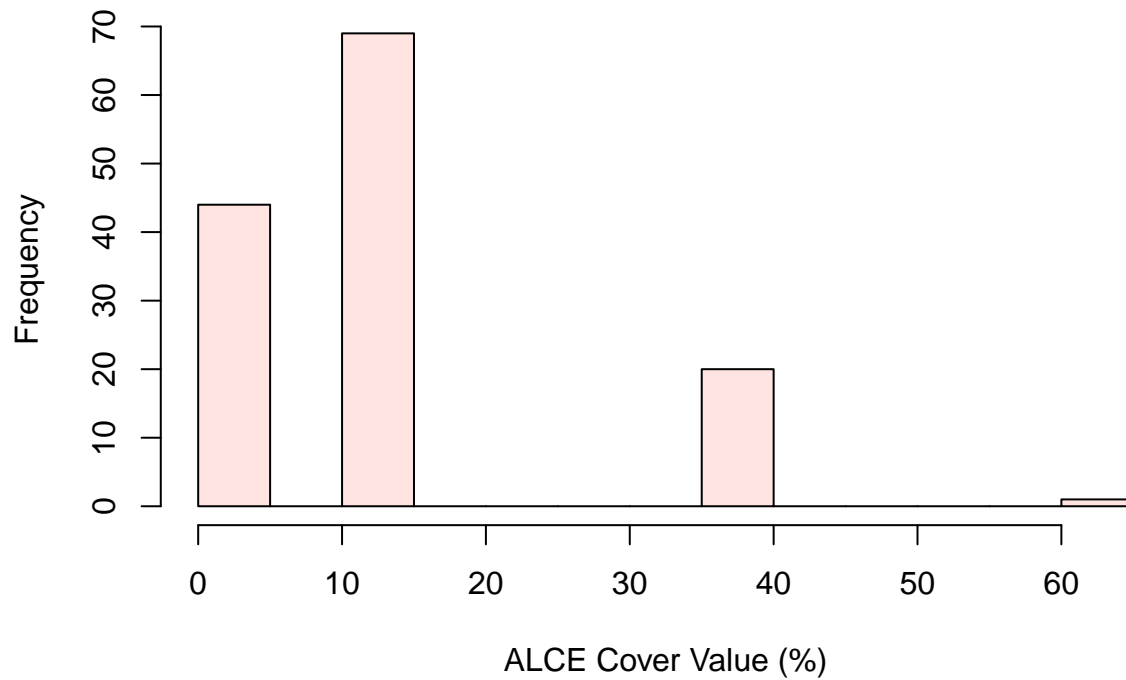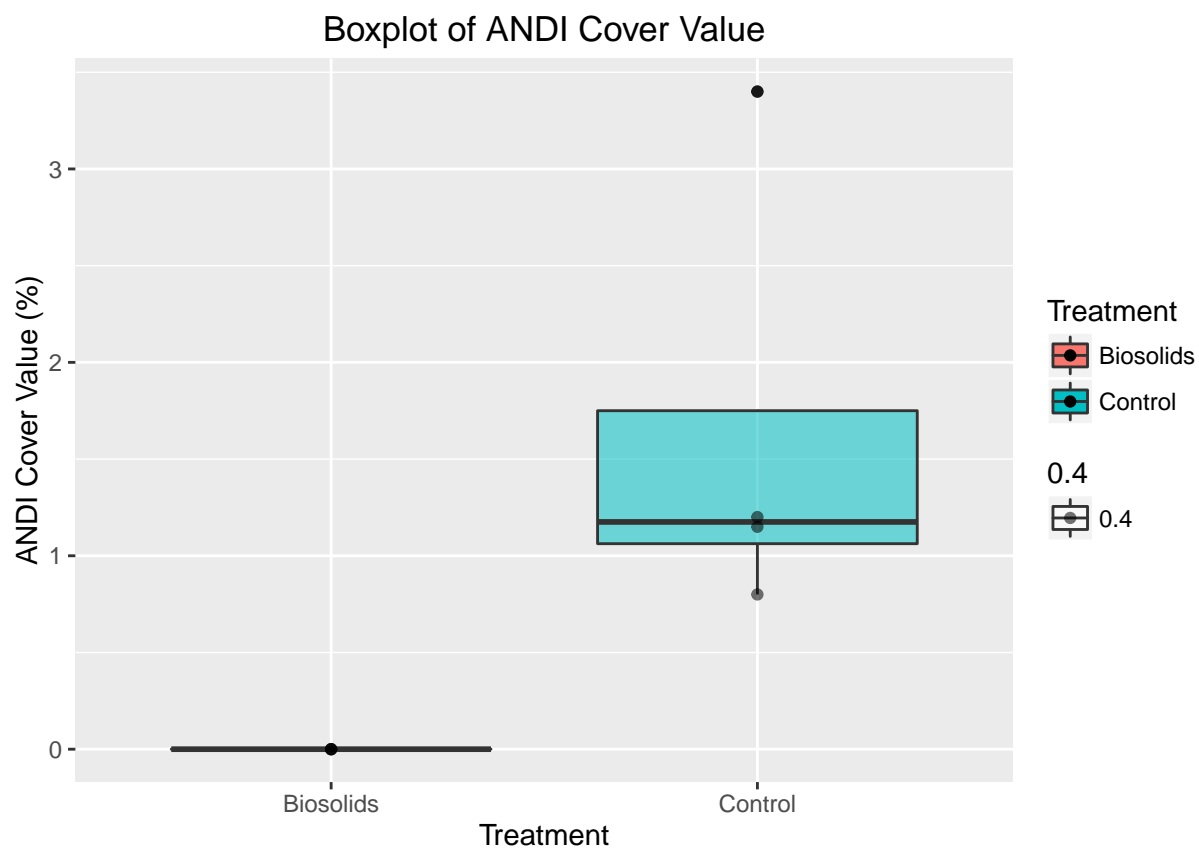
```
## [1] "ALCE"
## Source: local data frame [8 x 3]
## Groups: Block [3]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1 Biosolids 13.90
## 2      1   Control 19.70
## 3      2 Biosolids  2.75
## 4      2   Control  2.55
## 5      3 Biosolids  0.10
## 6      3   Control  0.10
## 7      4 Biosolids  0.00
## 8      4   Control  0.05
```
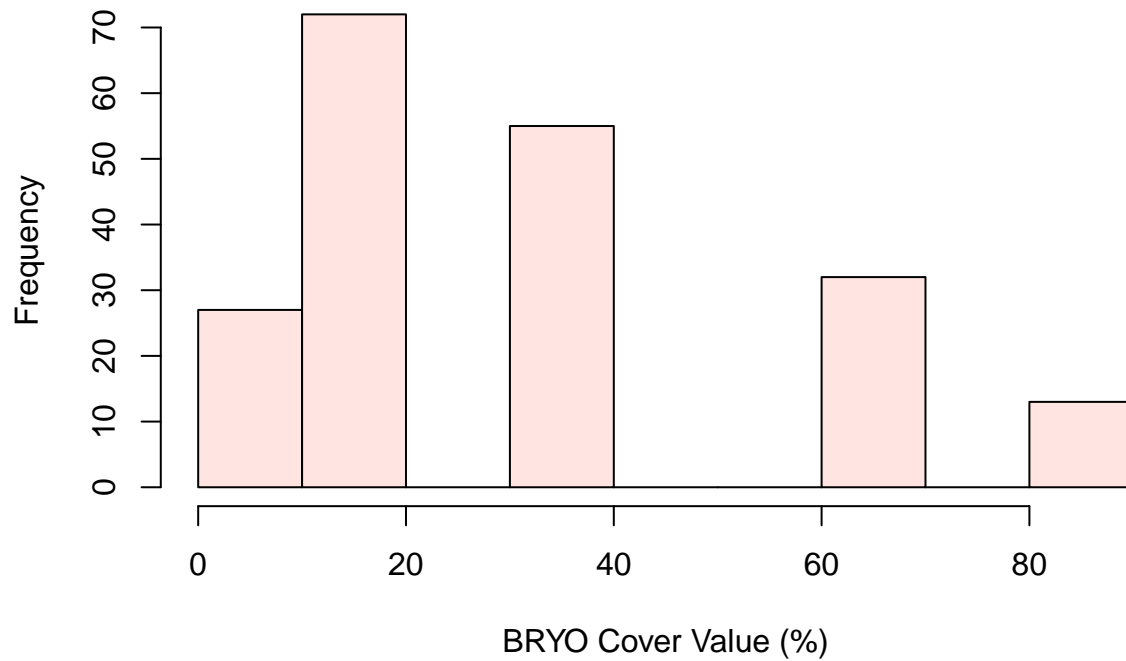
Histogram of cover value for ALCE


```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
##
## Residuals:
##    Min    1Q Median    3Q    Max
## -5.550 -4.516 -3.569  1.350 14.100
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          5.600      4.081   1.372    0.219
## TreatmentBiosolids  -1.413      5.772  -0.245    0.815
##
## Residual standard error: 8.163 on 6 degrees of freedom
## Multiple R-squared:  0.009882,   Adjusted R-squared:  -0.1551
## F-statistic: 0.05988 on 1 and 6 DF,  p-value: 0.8148


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : cannot compute exact p-value
## with zeroes


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : cannot compute exact confidence
## interval with zeroes
```
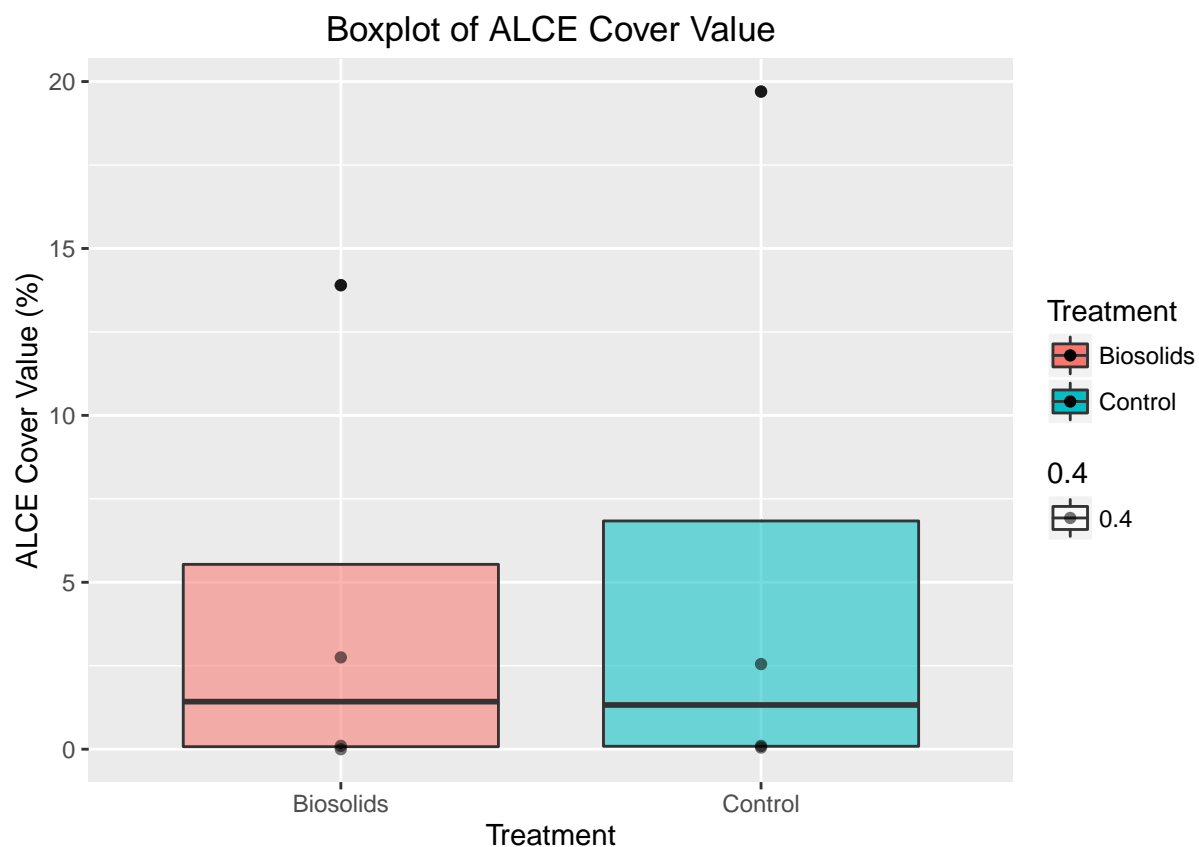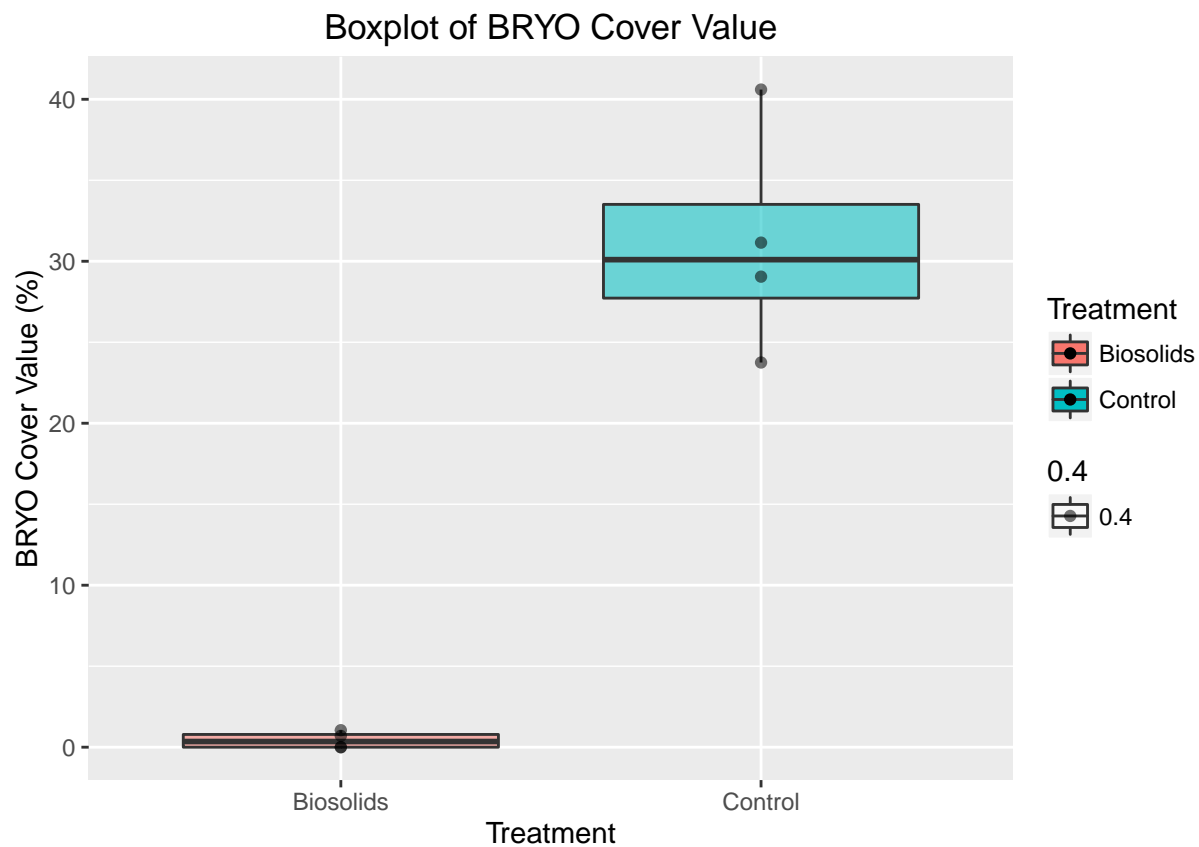
Boxplot of ALCE Cover Value


```
## [1] "ANDI"
## Source: local data frame [8 x 3]
## Groups: Block [3]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1   Control  0.80
## 2      1 Biosolids  0.00
## 3      2 Biosolids  0.00
## 4      2   Control  3.40
## 5      3 Biosolids  0.00
## 6      3   Control  1.20
## 7      4 Biosolids  0.00
## 8      4   Control  1.15
```

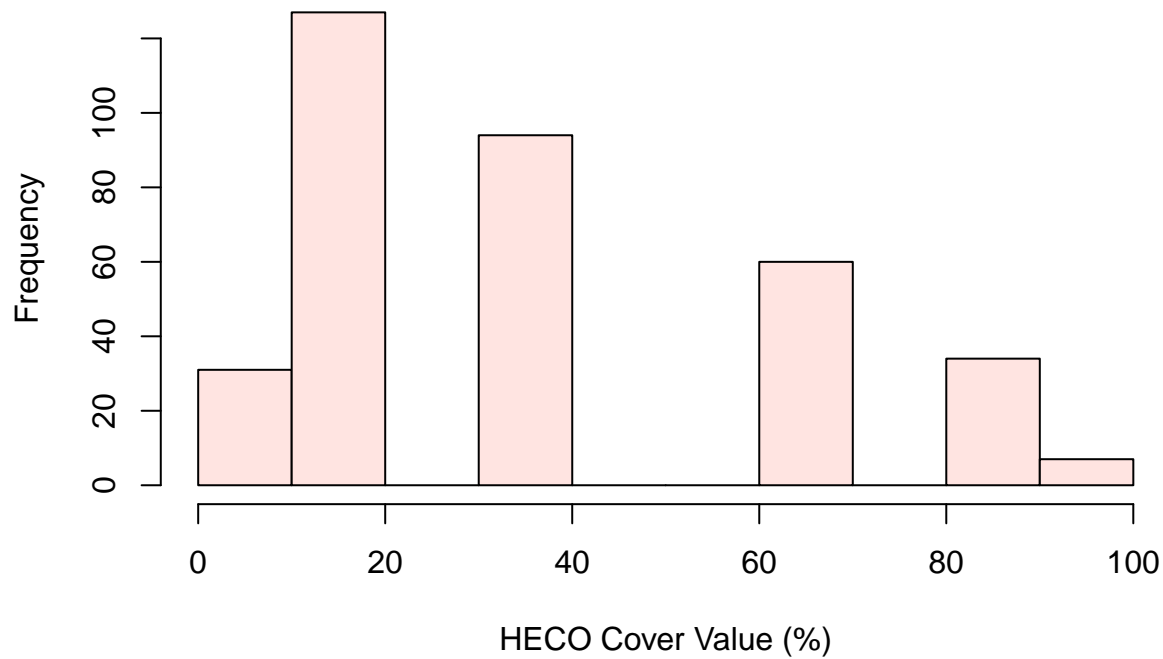## Histogram of cover value for ANDI
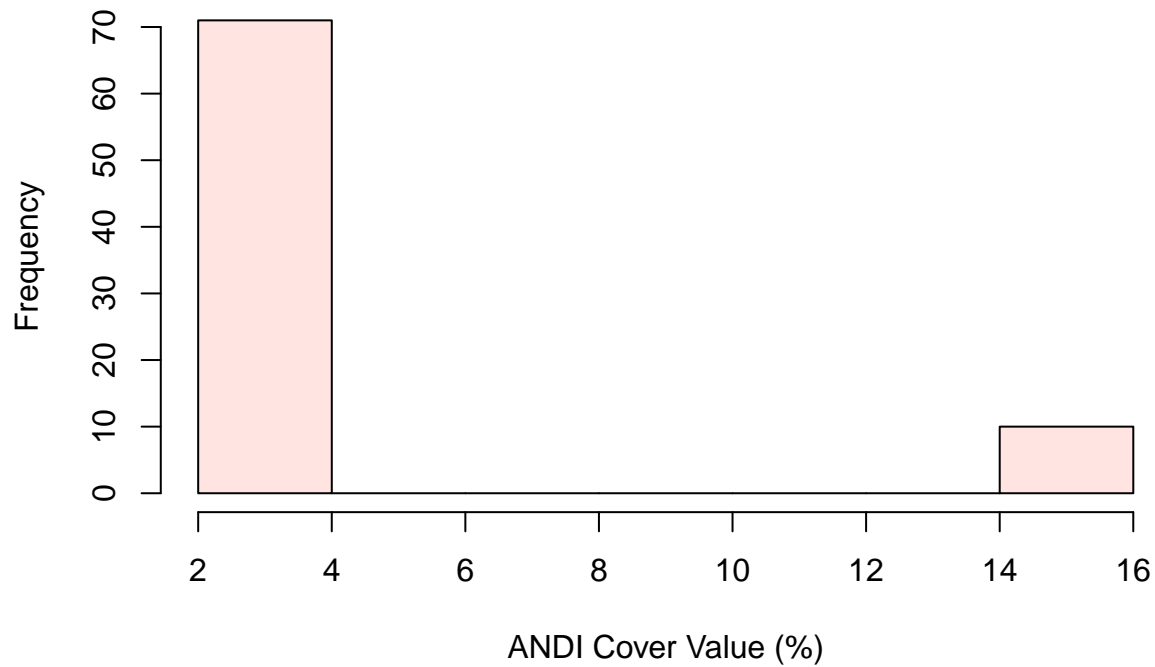

```
## 
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -0.8375 -0.4500  0.0000  0.0000  1.7625 
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         1.6375     0.4202   3.897  0.00801 **
## TreatmentBiosolids  -1.6375     0.5942  -2.756  0.03304 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.8403 on 6 degrees of freedom
## Multiple R-squared:  0.5586, Adjusted R-squared:  0.4851 
## F-statistic: 7.594 on 1 and 6 DF,  p-value: 0.03304


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```
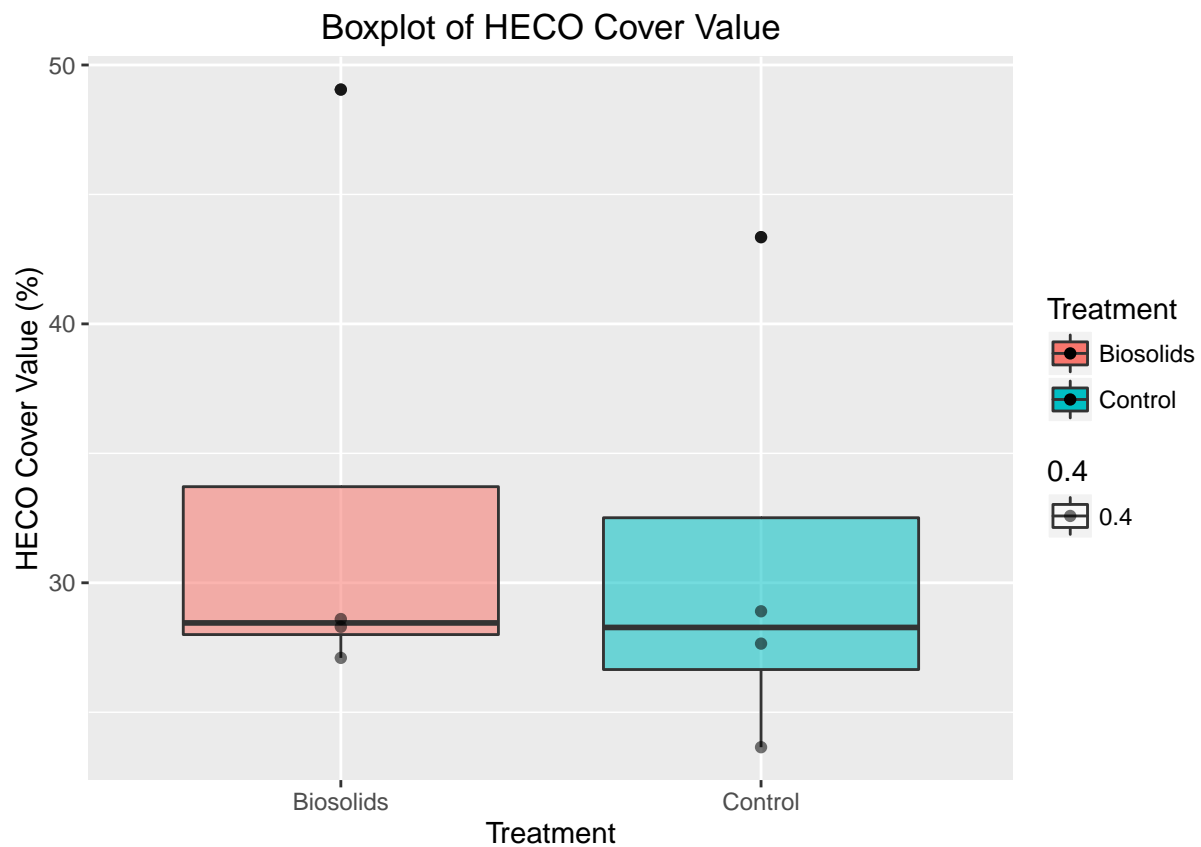
Boxplot of ANDI Cover Value


```
## [1] "BRYO"
## Source: local data frame [8 x 3]
## Groups: Block [2]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1   Control 40.60
## 2      1 Biosolids  0.00
## 3      2 Biosolids  0.70
## 4      2   Control 23.75
## 5      3 Biosolids  0.00
## 6      3   Control 31.15
## 7      4 Biosolids  1.05
## 8      4   Control 29.05
```

Histogram of cover value for BRYO


```
## 
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7.3875 -0.8500 -0.2125  0.3500  9.4625
## 
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          31.137      2.494  12.484 1.61e-05 ***
## TreatmentBiosolids  -30.700      3.527  -8.704 0.000127 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 4.988 on 6 degrees of freedom
## Multiple R-squared:  0.9266, Adjusted R-squared:  0.9144
## F-statistic: 75.75 on 1 and 6 DF,  p-value: 0.0001271


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```

Boxplot of BRYO Cover Value


```
## [1] "HECO"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##   Block Treatment y.avg
##  (fctr)   (fctr) (dbl)
## 1     1 Biosolids 28.30
## 2     1   Control 23.65
## 3     2 Biosolids 28.60
## 4     2   Control 28.90
## 5     3 Biosolids 49.05
## 6     3   Control 43.35
## 7     4 Biosolids 27.10
## 8     4   Control 27.65
```
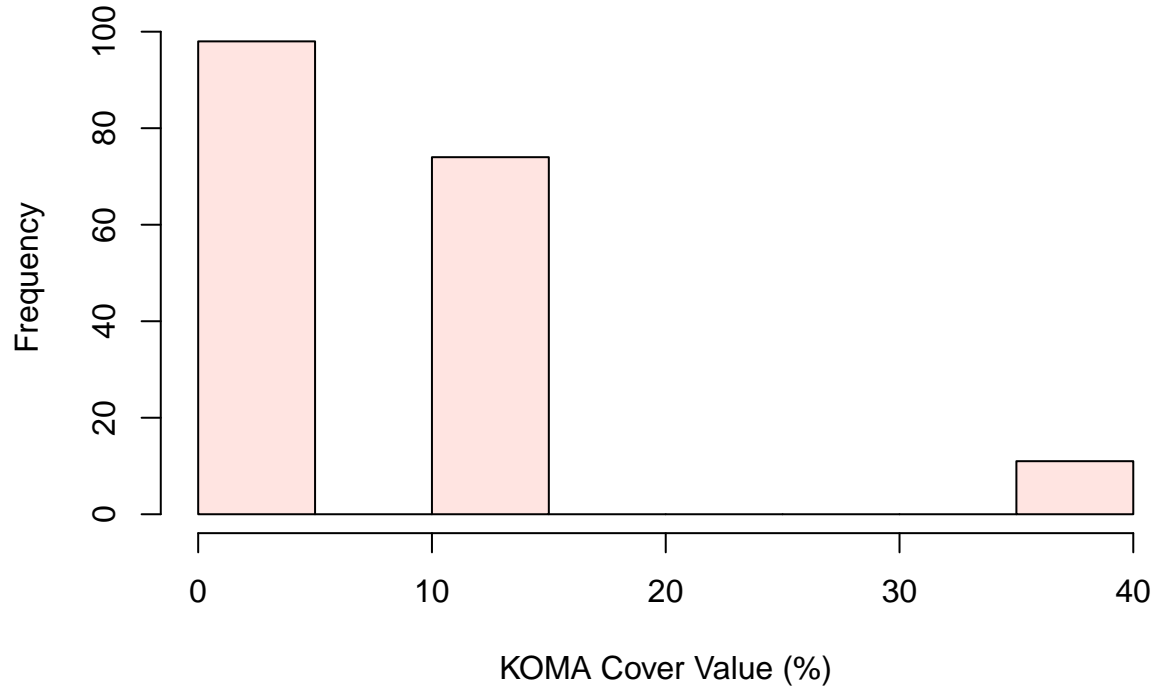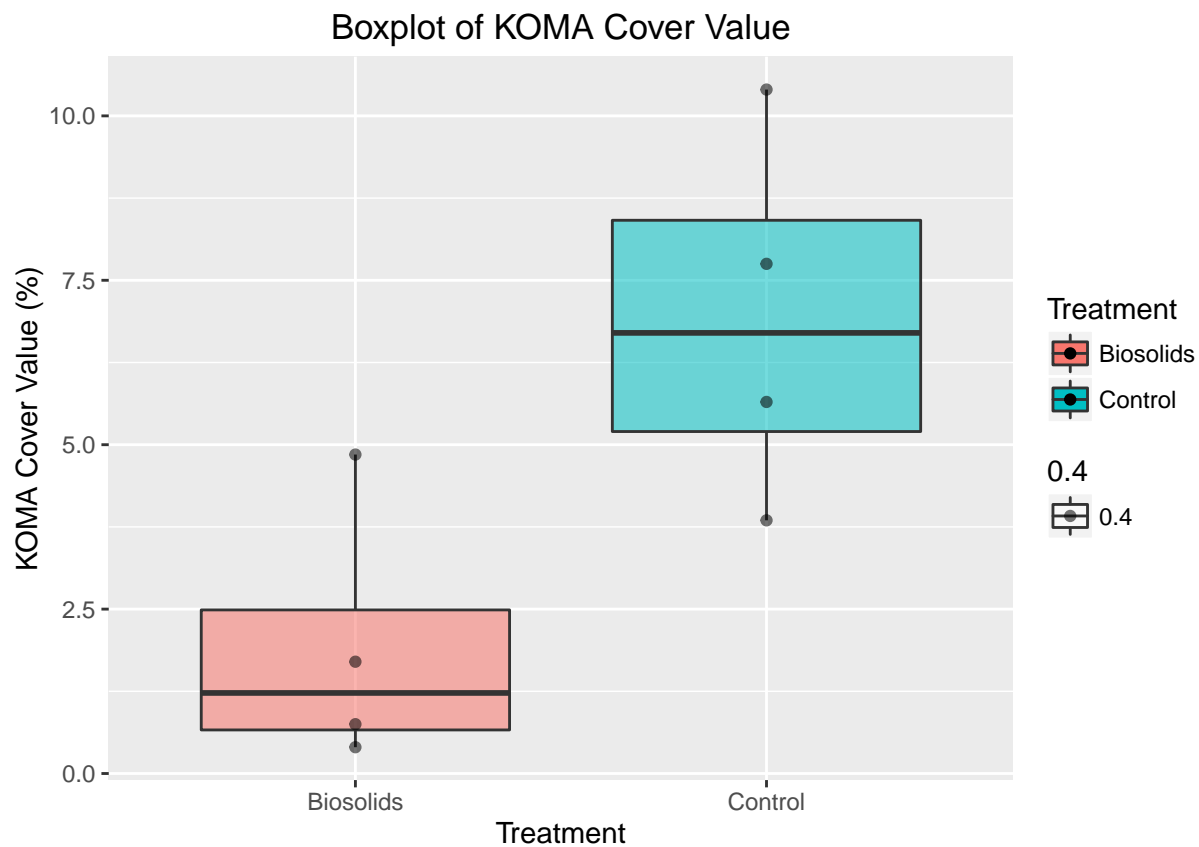
Histogram of cover value for HECO


```
## 
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
## 
## Residuals:
##    Min     1Q Median     3Q    Max 
## -7.237 -5.263 -3.950  1.625 15.787 
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         30.887      4.812   6.419 0.000675 ***
## TreatmentBiosolids   2.375      6.805   0.349 0.739009
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 9.624 on 6 degrees of freedom
## Multiple R-squared:  0.0199, Adjusted R-squared:  -0.1435 
## F-statistic: 0.1218 on 1 and 6 DF,  p-value: 0.739


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```

Boxplot of HECO Cover Value

```
## [1] "KOMA"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##     Block Treatment y.avg
##    (fctr)    (fctr) (dbl)
## 1       1 Biosolids  1.70
## 2       1   Control  3.85
## 3       2 Biosolids  4.85
## 4       2   Control  7.75
## 5       3 Biosolids  0.40
## 6       3   Control  5.65
## 7       4 Biosolids  0.75
## 8       4   Control 10.40
```
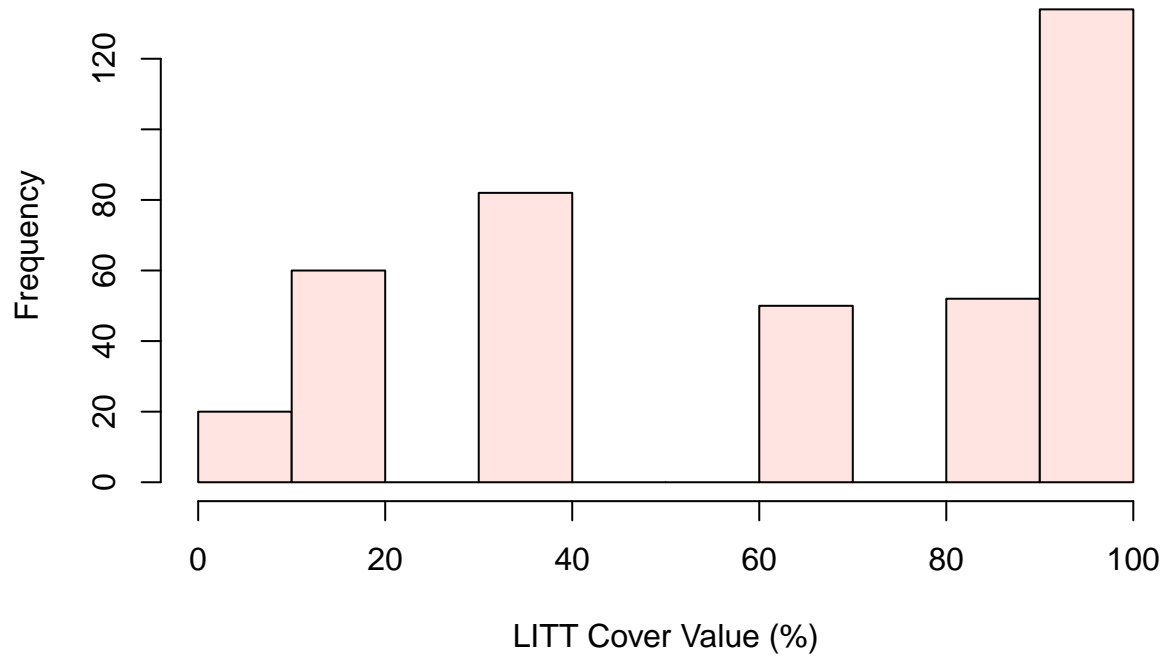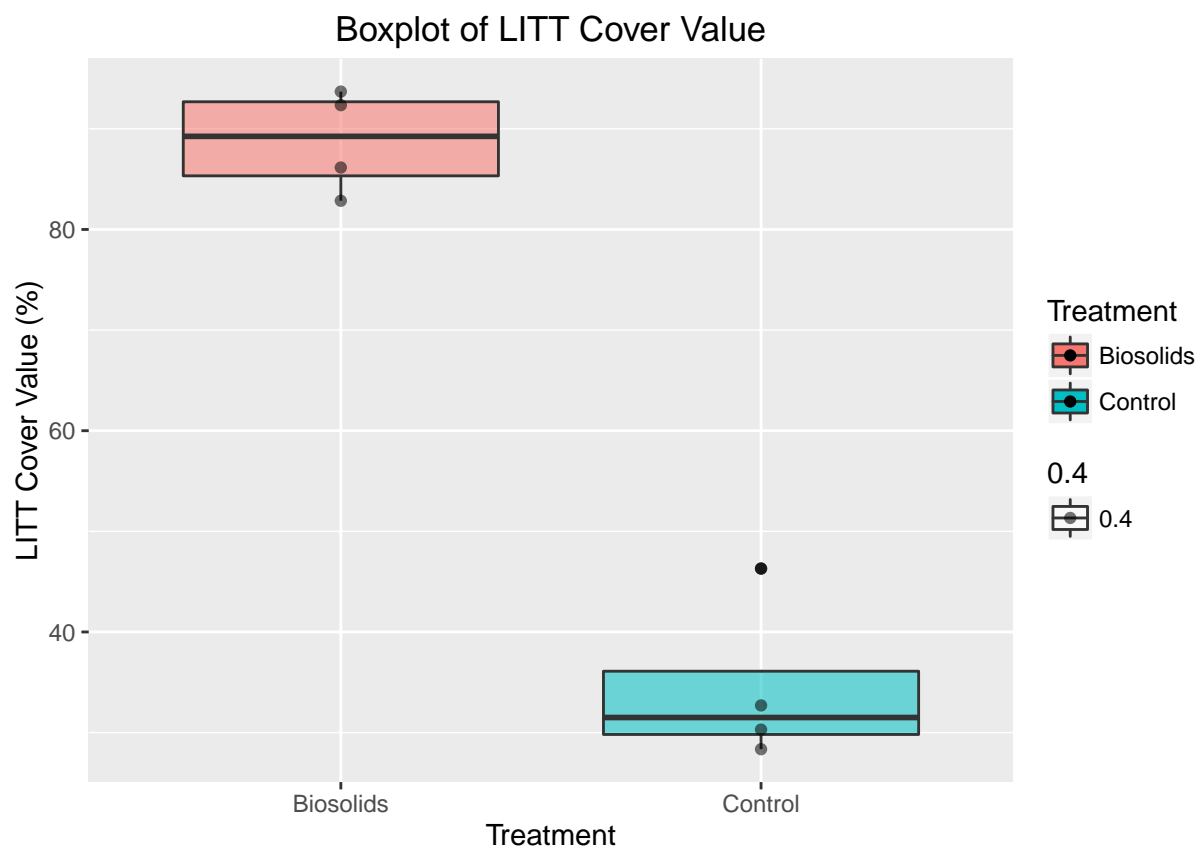
Histogram of cover value for KOMA


```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -3.062 -1.328 -0.700  1.359  3.487
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)         6.913      1.227   5.632  0.00134 **
## TreatmentBiosolids -4.988      1.736  -2.874  0.02829 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.455 on 6 degrees of freedom
## Multiple R-squared:  0.5792, Adjusted R-squared:  0.509
## F-statistic: 8.257 on 1 and 6 DF,  p-value: 0.02829


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```

Boxplot of KOMA Cover Value


```
## [1] "LITT"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1 Biosolids 93.70
## 2      1   Control 30.30
## 3      2 Biosolids 82.85
## 4      2   Control 28.35
## 5      3 Biosolids 92.35
## 6      3   Control 46.30
## 7      4 Biosolids 86.15
## 8      4   Control 32.70
```
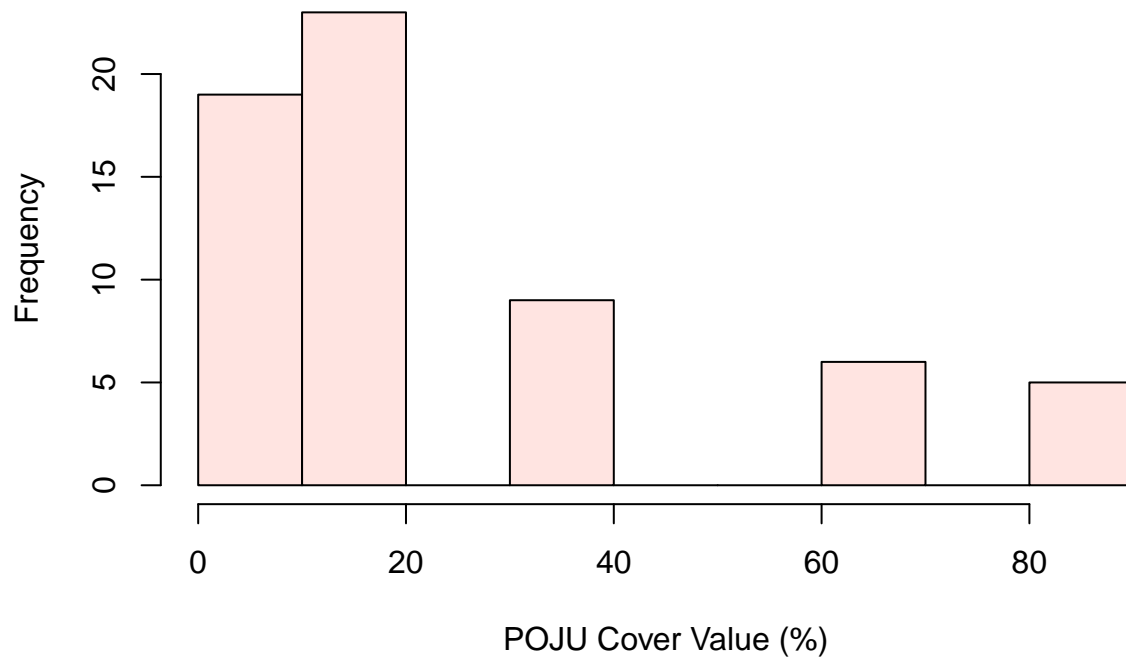
Histogram of cover value for LITT


```
## 
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
## 
## Residuals:
##    Min     1Q Median     3Q    Max
## -6.062 -4.562 -2.163  3.925 11.887
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         34.413      3.397   10.13 5.38e-05 ***
## TreatmentBiosolids  54.350      4.804   11.31 2.85e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 6.794 on 6 degrees of freedom
## Multiple R-squared:  0.9552, Adjusted R-squared:  0.9478
## F-statistic:   128 on 1 and 6 DF,  p-value: 2.854e-05


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```
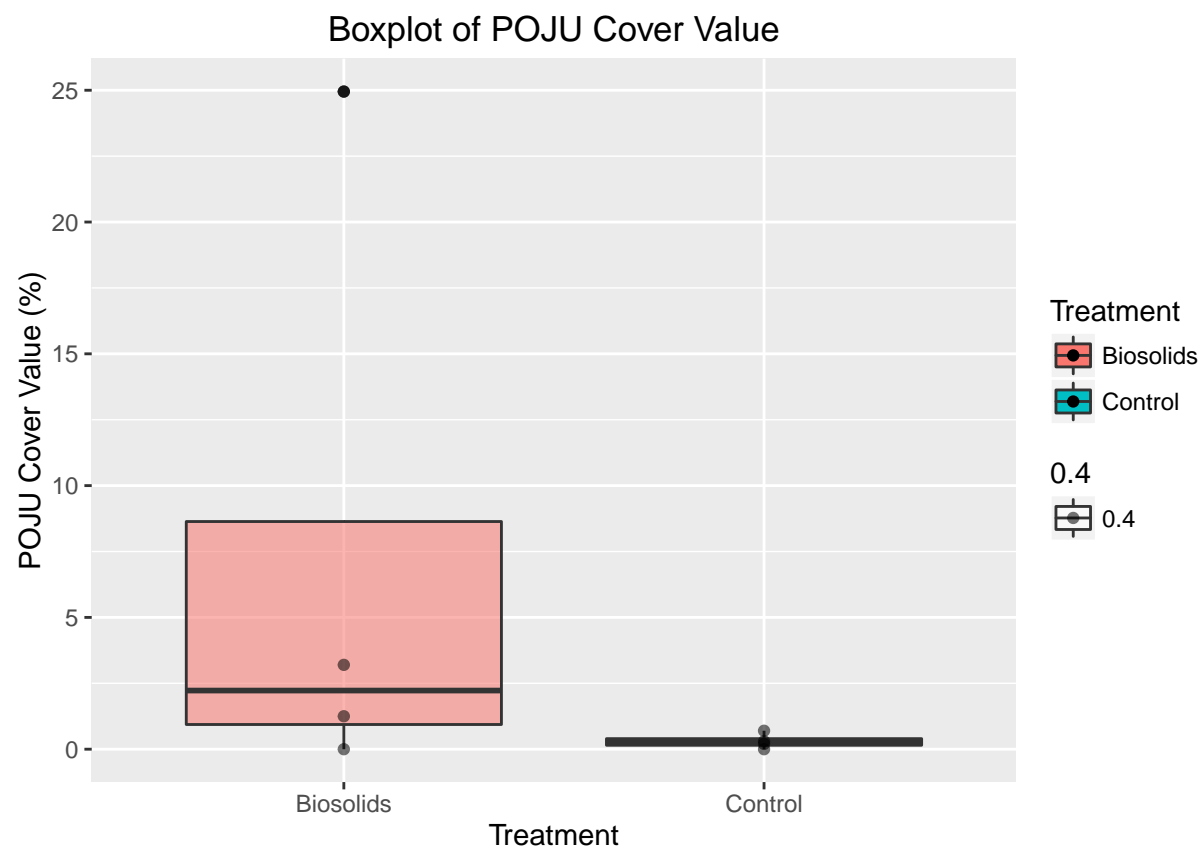
Boxplot of LITT Cover Value


```
## [1] "POJU"
## Source: local data frame [8 x 3]
## Groups: Block [4]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1 Biosolids  3.20
## 2      1   Control  0.30
## 3      2 Biosolids 24.95
## 4      2   Control  0.70
## 5      3 Biosolids  0.00
## 6      3   Control  0.20
## 7      4 Biosolids  1.25
## 8      4   Control  0.00
```
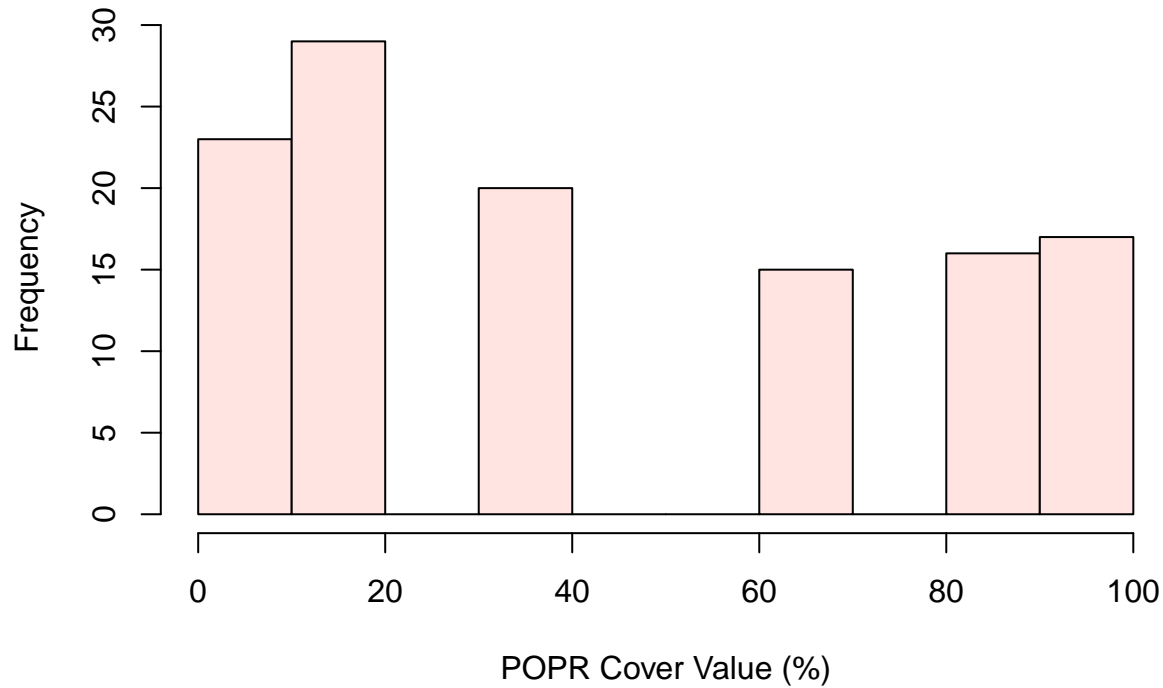
Histogram of cover value for POJU


```
## 
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
## 
## Residuals:
##    Min     1Q Median     3Q    Max
## -7.350 -4.638 -0.200  0.100 17.600
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.300      4.176   0.072    0.945
## TreatmentBiosolids   7.050      5.905   1.194    0.278
## 
## Residual standard error: 8.351 on 6 degrees of freedom
## Multiple R-squared:  0.1919, Adjusted R-squared:  0.05727
## F-statistic: 1.425 on 1 and 6 DF,  p-value: 0.2776


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```
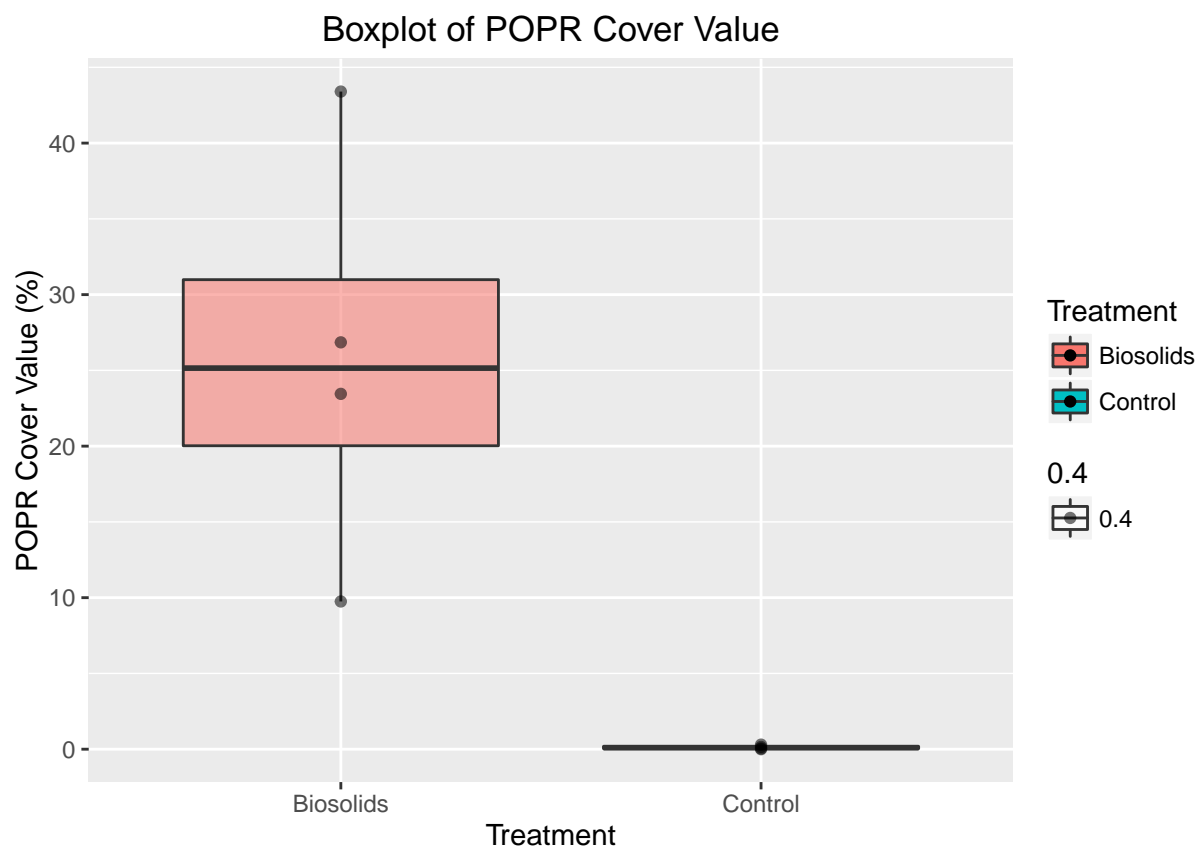
Boxplot of POJU Cover Value


```
## [1] "POPR"
## Source: local data frame [8 x 3]
## Groups: Block [2]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1 Biosolids 23.45
## 2      1   Control  0.15
## 3      2 Biosolids  9.75
## 4      2   Control  0.00
## 5      3 Biosolids 26.85
## 6      3   Control  0.05
## 7      4 Biosolids 43.40
## 8      4   Control  0.30
```

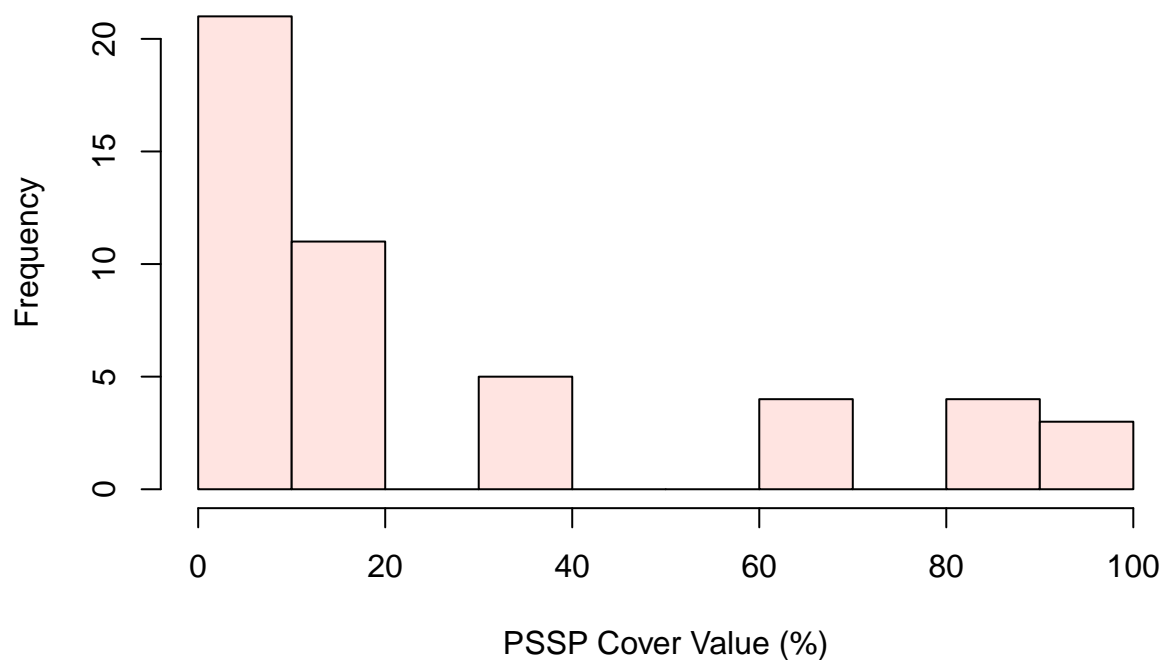## Histogram of cover value for POPR


```
## 
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
## 
## Residuals:
##      Min      1Q   Median      3Q      Max
## -16.1125  -0.6969  -0.0250   0.3781  17.5375
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.125      4.891   0.026  0.98044
## TreatmentBiosolids  25.738      6.916   3.721  0.00984 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 9.781 on 6 degrees of freedom
## Multiple R-squared:  0.6977, Adjusted R-squared:  0.6473
## F-statistic: 13.85 on 1 and 6 DF,  p-value: 0.009838


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```
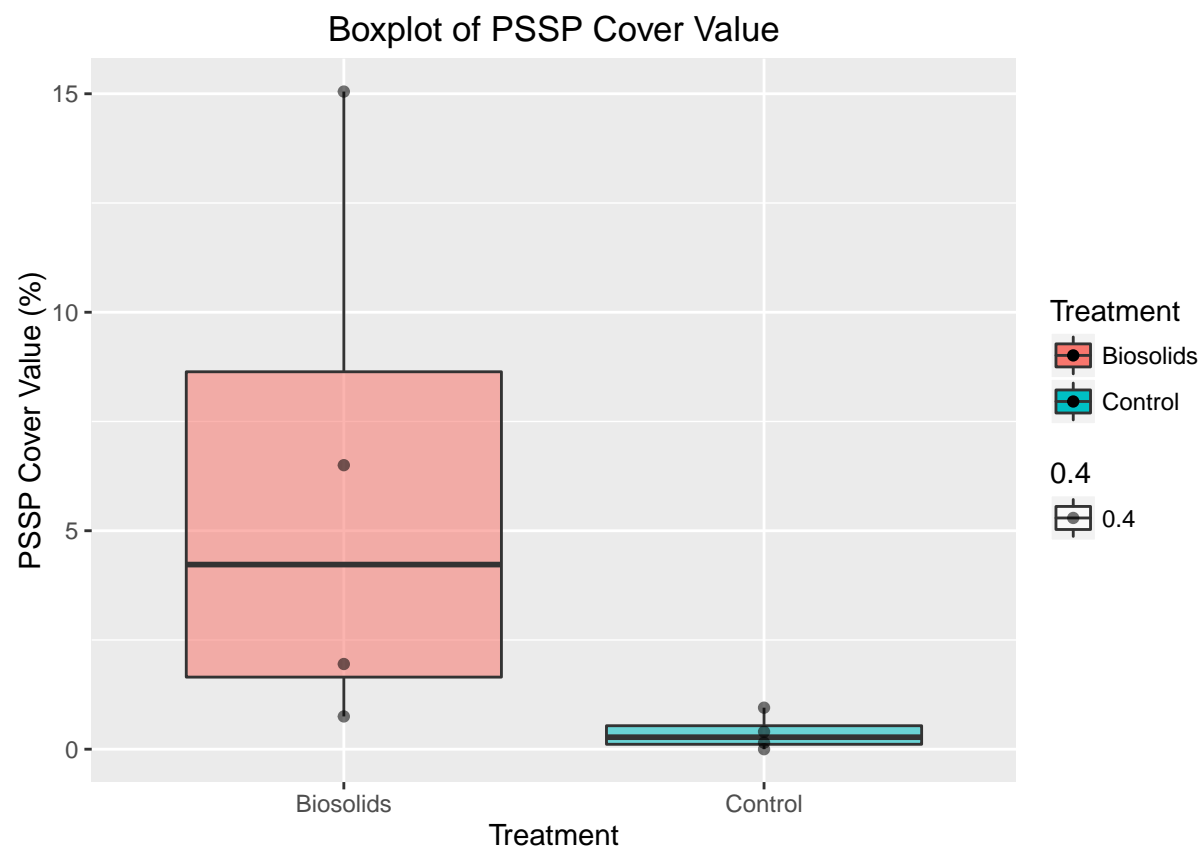
Boxplot of POPR Cover Value


```
## [1] "PSSP"
## Source: local data frame [8 x 3]
## Groups: Block [3]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1     1 Biosolids 15.05
## 2     1   Control  0.95
## 3     2 Biosolids  6.50
## 4     2   Control  0.15
## 5     3 Biosolids  0.75
## 6     3   Control  0.00
## 7     4 Biosolids  1.95
## 8     4   Control  0.40
```

Histogram of cover value for PSSP
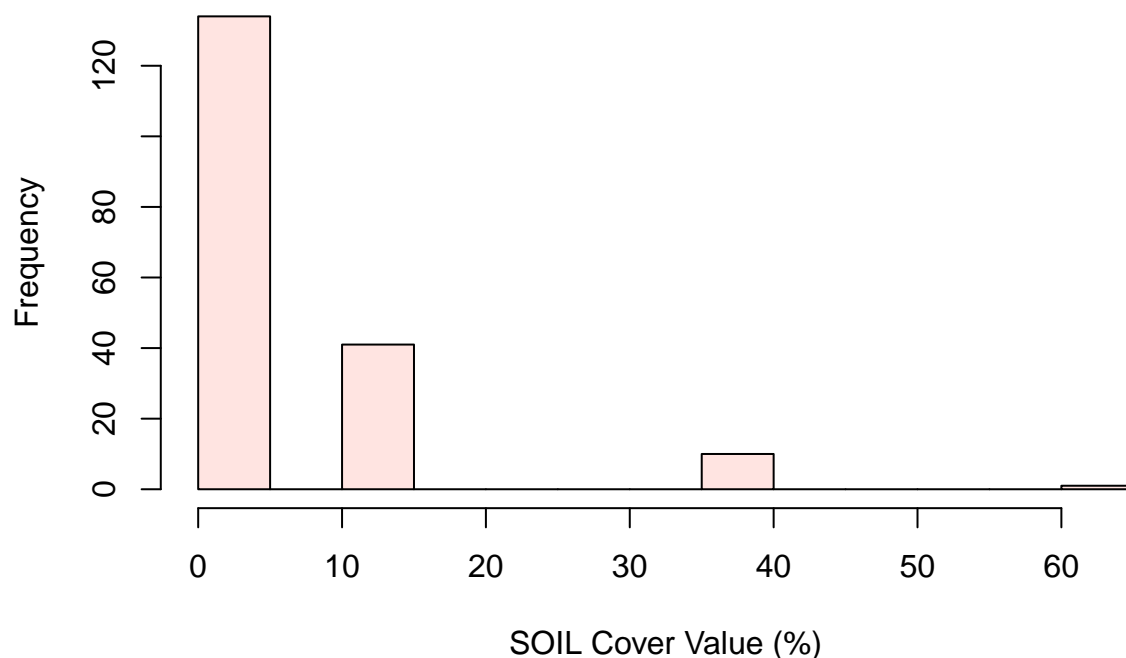


```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -5.3125 -1.3094 -0.1000  0.4719  8.9875
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.375      2.297   0.163    0.876
## TreatmentBiosolids   5.688      3.248   1.751    0.131
##
## Residual standard error: 4.594 on 6 degrees of freedom
## Multiple R-squared:  0.3382, Adjusted R-squared:  0.2278
## F-statistic: 3.066 on 1 and 6 DF,  p-value: 0.1305


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```
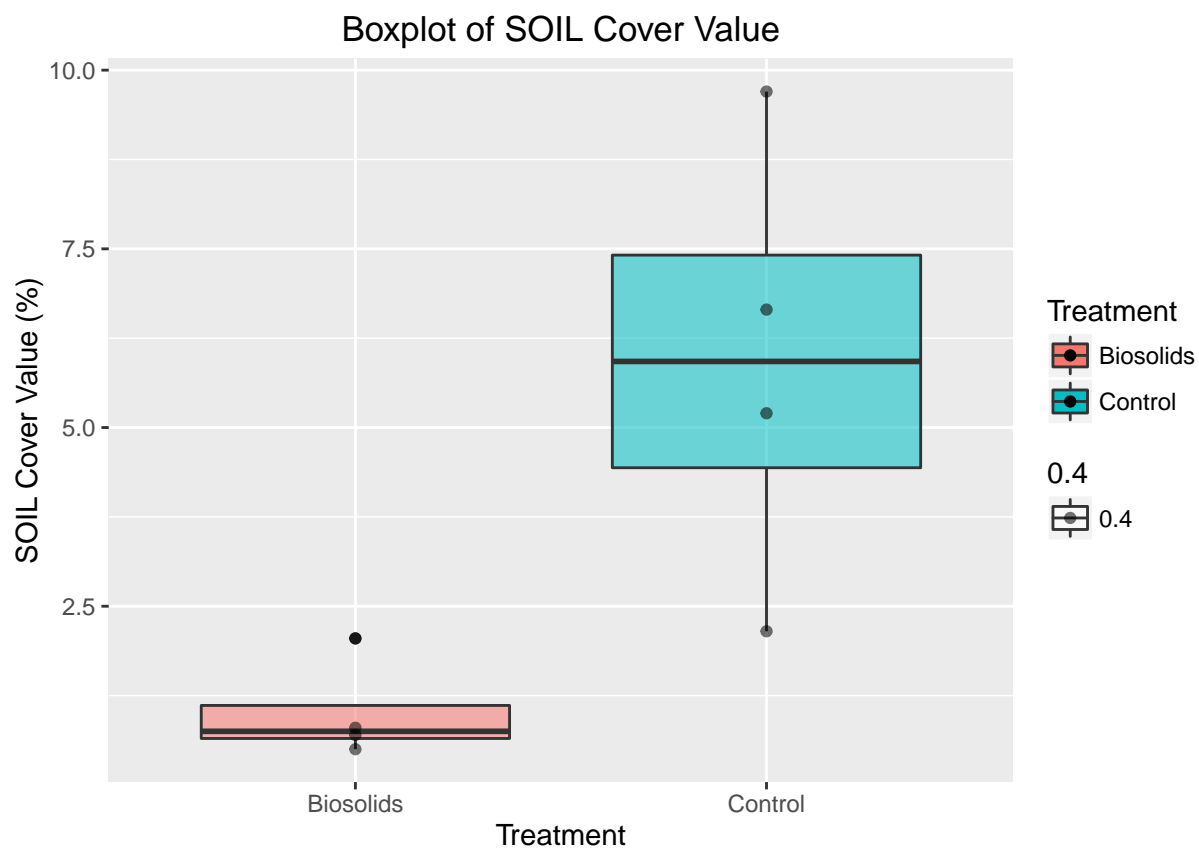
Boxplot of PSSP Cover Value


```
## [1] "SOIL"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##    Block Treatment y.avg
##   (fctr)    (fctr) (dbl)
## 1      1 Biosolids  0.70
## 2      1   Control  5.20
## 3      2 Biosolids  2.05
## 4      2   Control  9.70
## 5      3 Biosolids  0.80
## 6      3   Control  2.15
## 7      4 Biosolids  0.50
## 8      4   Control  6.65
```

Histogram of cover value for SOIL
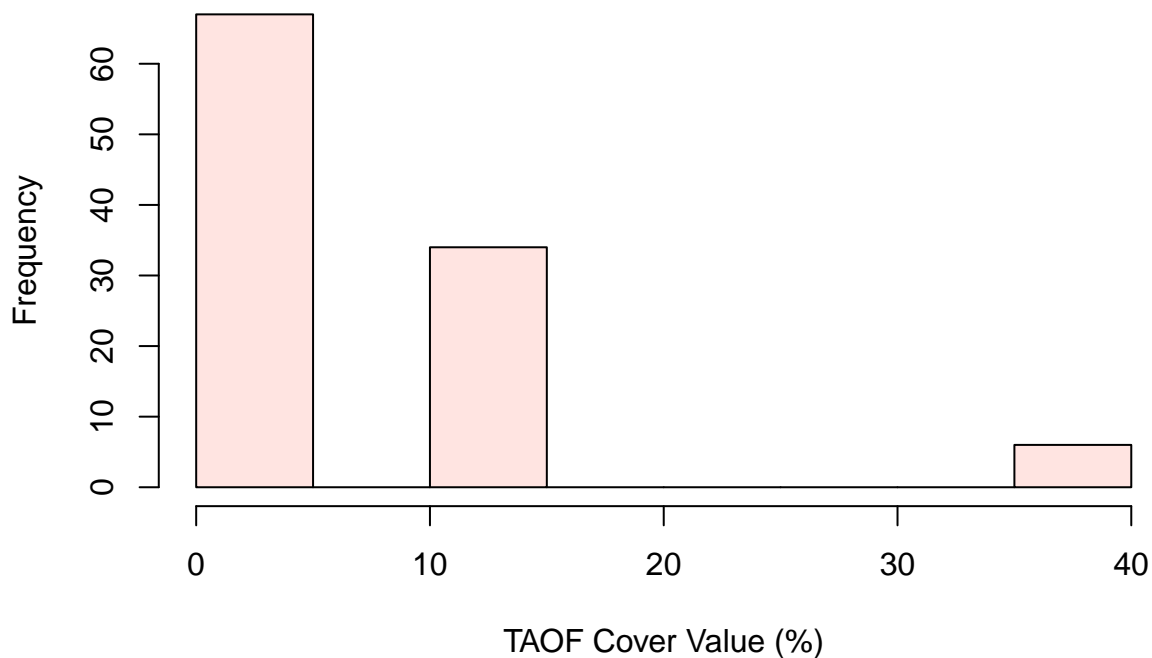


```
## 
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.7750 -0.5656 -0.2625  0.8031  3.7750
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          5.925      1.137   5.210  0.00199 **
## TreatmentBiosolids  -4.913      1.608  -3.055  0.02238 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.274 on 6 degrees of freedom
## Multiple R-squared:  0.6086, Adjusted R-squared:  0.5434
## F-statistic: 9.331 on 1 and 6 DF,  p-value: 0.02238


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```

Boxplot of SOIL Cover Value



```
## [1] "TAOF"
## Source: local data frame [8 x 3]
## Groups: Block [2]
##
##    Block Treatment  y.avg
##   (fctr)    (fctr)  (dbl)
## 1      1 Biosolids   3.05
## 2      1   Control   0.10
## 3      2 Biosolids   0.20
## 4      2   Control   0.00
## 5      3 Biosolids  11.30
## 6      3   Control   0.10
## 7      4 Biosolids   3.20
## 8      4   Control   0.10
```

Histogram of cover value for TAOF


```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -4.237 -1.275 -0.025  0.025  6.862
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.075      1.690   0.044    0.966
## TreatmentBiosolids   4.362      2.389   1.826    0.118
##
## Residual standard error: 3.379 on 6 degrees of freedom
## Multiple R-squared:  0.3571, Adjusted R-squared:   0.25
## F-statistic: 3.333 on 1 and 6 DF,  p-value: 0.1177


## Warning in wilcox.test.default(x = dat.avg.this.species
## $y.avg[dat.avg.this.species$Treatment == : requested conf.level not
## achievable
```

Boxplot of TAOF Cover Value
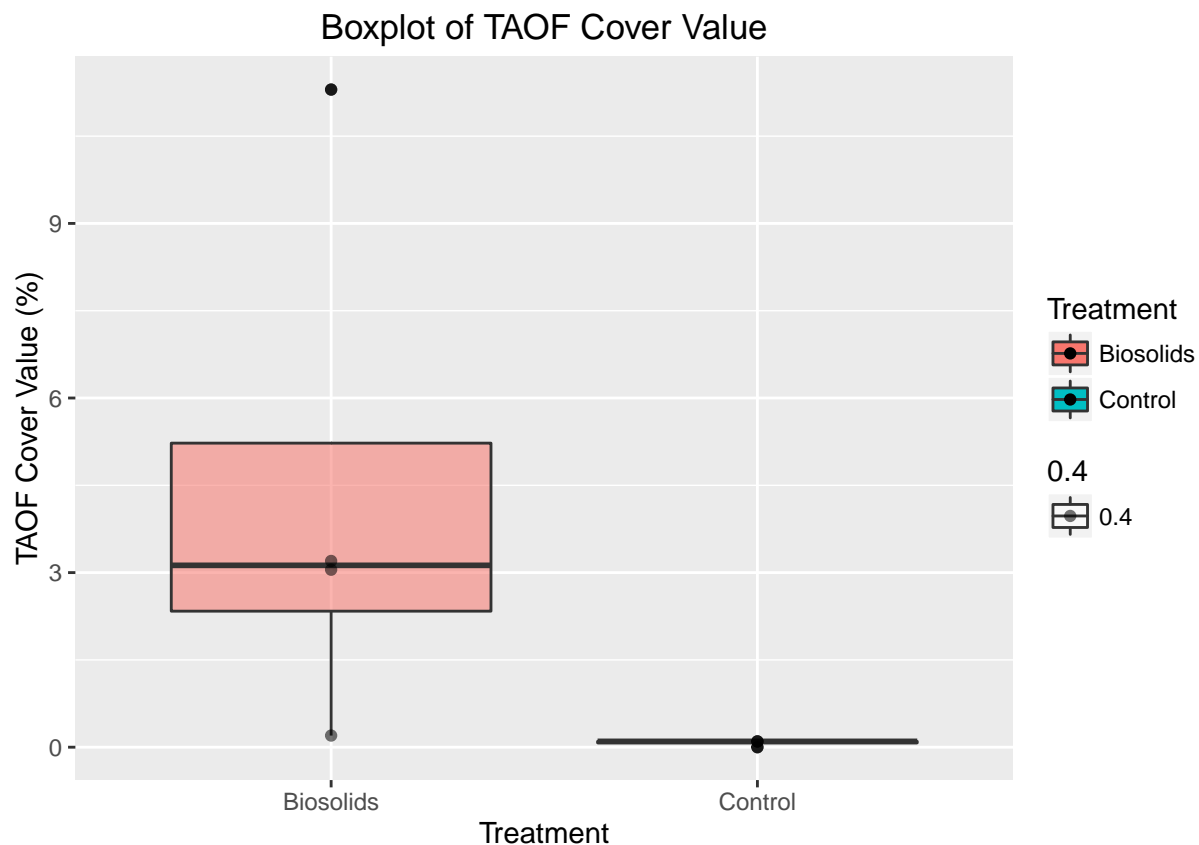

```r
# Print the linear regression p-values and coefficients for each species.
cbind(species.vec, p.vals.vec, coefs.vec)
```

```
##       species.vec p.vals.vec             coefs.vec
##  [1,] "ALCE"      "0.814834091762861"    "-1.4125"
##  [2,] "ANDI"      "0.0330367117716462"   "-1.6375"
##  [3,] "BRYO"      "0.00012709185740304"  "-30.7"
##  [4,] "HECO"      "0.739008763957111"    "2.375"
##  [5,] "KOMA"      "0.0282943011554642"   "-4.9875"
##  [6,] "LITT"      "2.85417772499923e-05" "54.35"
##  [7,] "POJU"      "0.27759694571899"     "7.05"
##  [8,] "POPR"      "0.00983752836594799"  "25.7375"
##  [9,] "PSSP"      "0.130533801218531"    "5.6875"
## [10,] "SOIL"      "0.0223759429659092"   "-4.9125"
## [11,] "TAOF"      "0.117683262573748"    "4.3625"
```

```r
# Print the non-parametric p-values and estimates for each species.
cbind(species.vec, nonparam.p.vals.vec, nonparam.coefs.vec)
```

```
##       species.vec nonparam.p.vals.vec nonparam.coefs.vec
##  [1,] "ALCE"      "0.789268026134281" "-2.29405540546612"
##  [2,] "ANDI"      "0.125"             "-1.1875"
##  [3,] "BRYO"      "0.125"             "-30.3625"
##  [4,] "HECO"      "0.625"             "2.375"
##  [5,] "KOMA"      "0.125"             "-4.6625"
##  [6,] "LITT"      "0.125"             "54.2375"
```

```
## [7,]  "POJU"         "0.25"                "2.4875"
## [8,]  "POPR"         "0.125"               "25.7375"
## [9,]  "PSSP"         "0.125"               "5.15"
## [10,] "SOIL"         "0.125"               "-4.9125"
## [11,] "TAOF"         "0.125"               "3.0625"
```

```
# Print the correlations between MWD and each species' cover value.
cbind(species.vec, cor.vec)
```

```
##       species.vec cor.vec
## [1,]  "ALCE"      "-0.0979609271355758"
## [2,]  "ANDI"      "-0.408243567137178"
## [3,]  "BRYO"      "-0.408826660600364"
## [4,]  "HECO"      "-0.436327732101949"
## [5,]  "KOMA"      "-0.375468054869239"
## [6,]  "LITT"      "0.619357051173369"
## [7,]  "POJU"      "0.615528658610572"
## [8,]  "POPR"      "0.644724082434805"
## [9,]  "PSSP"      "0.421947867236044"
## [10,] "SOIL"      "-0.405705525751975"
## [11,] "TAOF"      "0.0317200333125193"
```

```
# Save the outputs.
out.mat <- cbind(species.vec, p.vals.vec, coefs.vec, nonparam.p.vals.vec,
                 nonparam.coefs.vec, cor.vec)
#save(out.mat, file='OutMat.RData')
```