

GradAnalysis.r

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```
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
```

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

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

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

```
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
```

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

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

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

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

# Import the MWD data.
soil <- read.table('MWD.csv', sep=',', header=T)
soil.unreveled <- 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 ...
## $ Date : Factor w/ 2 levels "June 21, 2016",...: 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 ...
```

```
## $ 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 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 ...
```

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

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

```
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
```

```
#####
# 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 x 5 transects x 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
```

```
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
```

```
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 occurs 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.occuring.greater.than5 <- ifelse(test=(sum(dat.avg.try2$y.avg<5)==0),
                                       yes=1, no=0)

  all.greater.than5 <- is.in.all.combs * all.occuring.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
```

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

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

```
# Obtain the MWD averages (to be used in calculating the correlations).
```

```
a <- group_by(soil.unreveled, 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))
cor.vec <- rep(NA, times=length(species.vec))
for (ii in 1:length(species.vec))
{
```

```
  # 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() +
#      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]

#####
# Correlations:

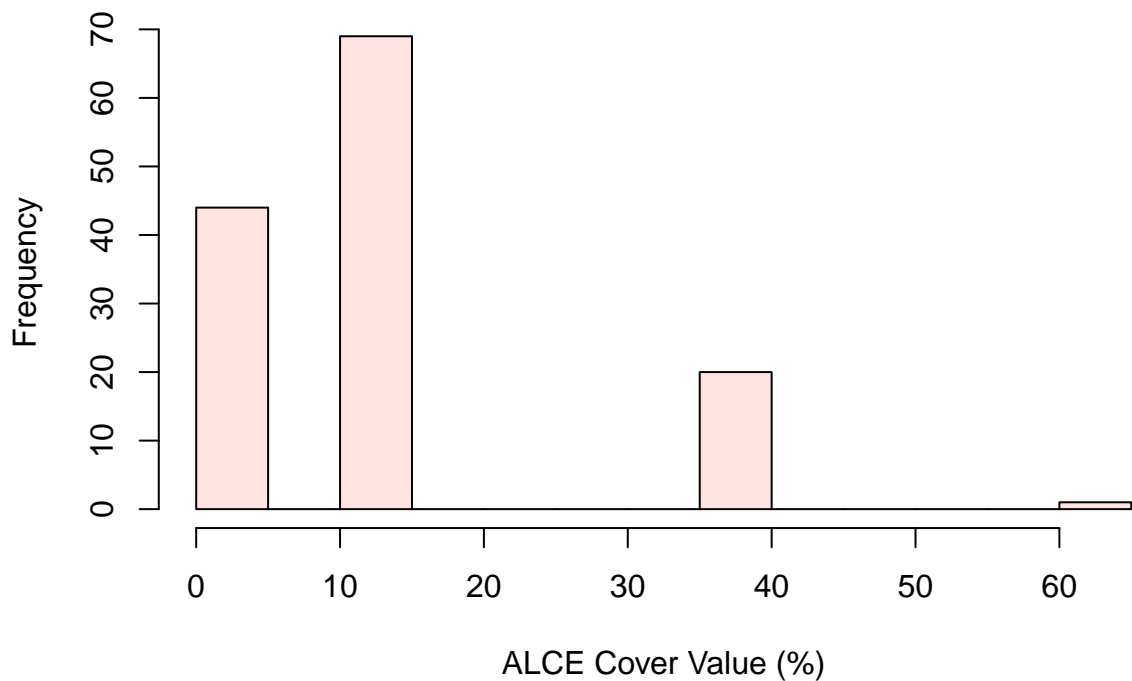
```

```
#####

# 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)
}
```

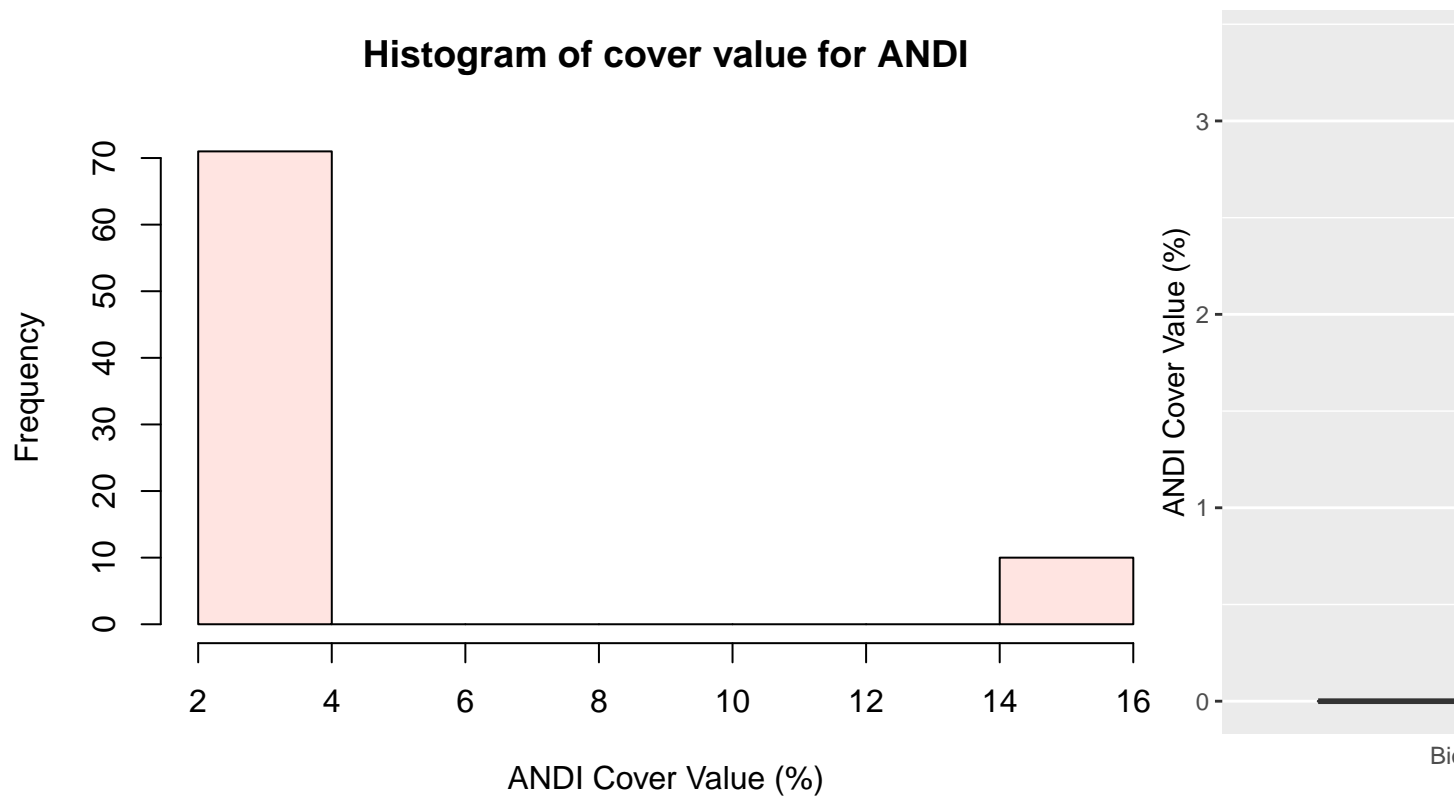
```
## [1] "ALCE"
## Source: local data frame [8 x 3]
## Groups: Block [3]
##
##   Block Treatment y.avg
##   (fctr)      (fctr) (dbl)
## 1      1 Biosolids 13.90
## 2      1  Control 19.70
## 3      2 Biosolids  2.75
## 4      2  Control  2.55
## 5      3 Biosolids  0.10
## 6      3  Control  0.10
## 7      4 Biosolids  0.00
## 8      4  Control  0.05
```

Histogram of cover value for ALCE



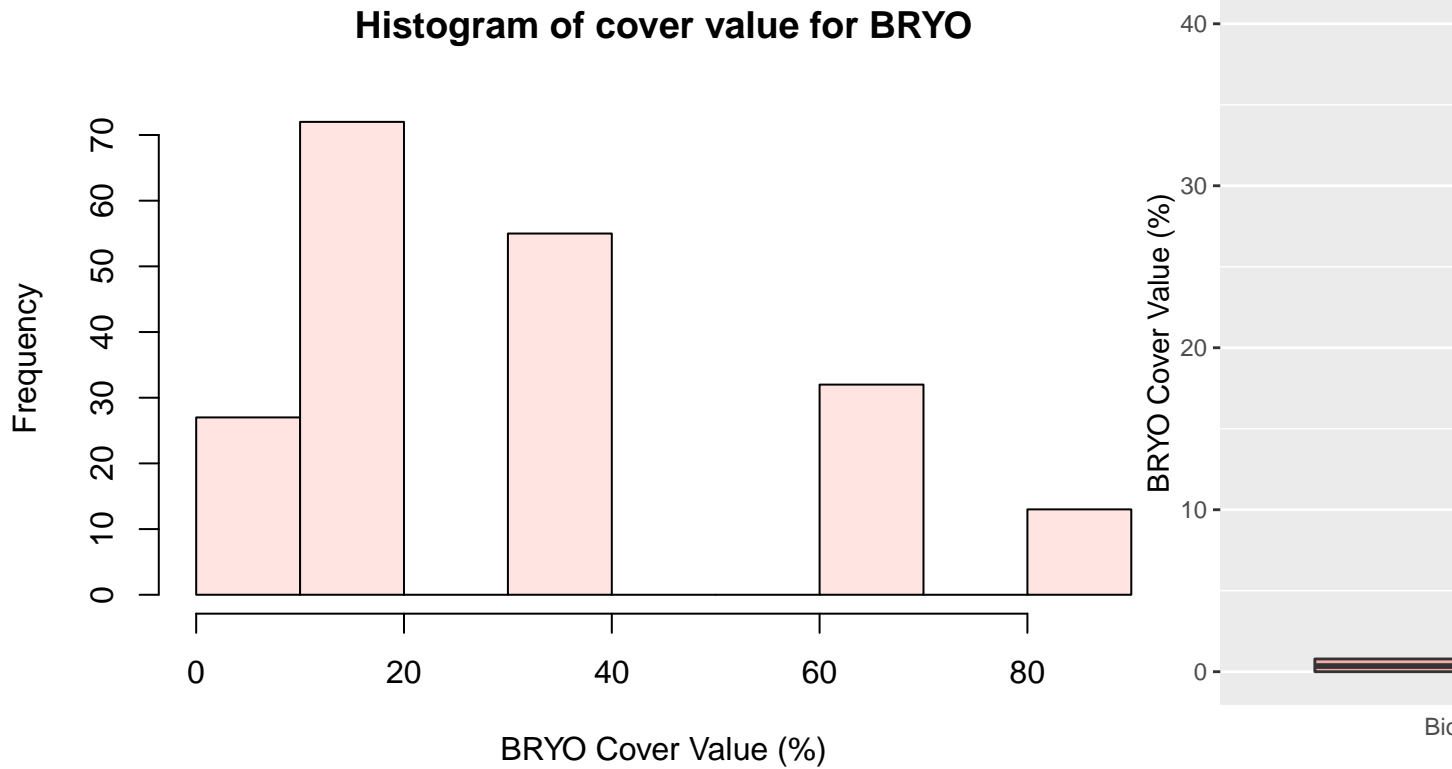
```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
```

```
##
## 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
##
## [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
```



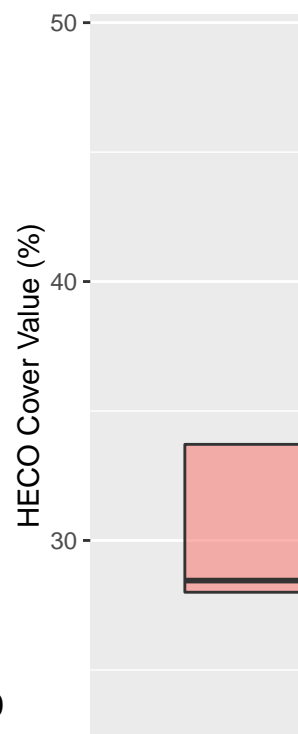
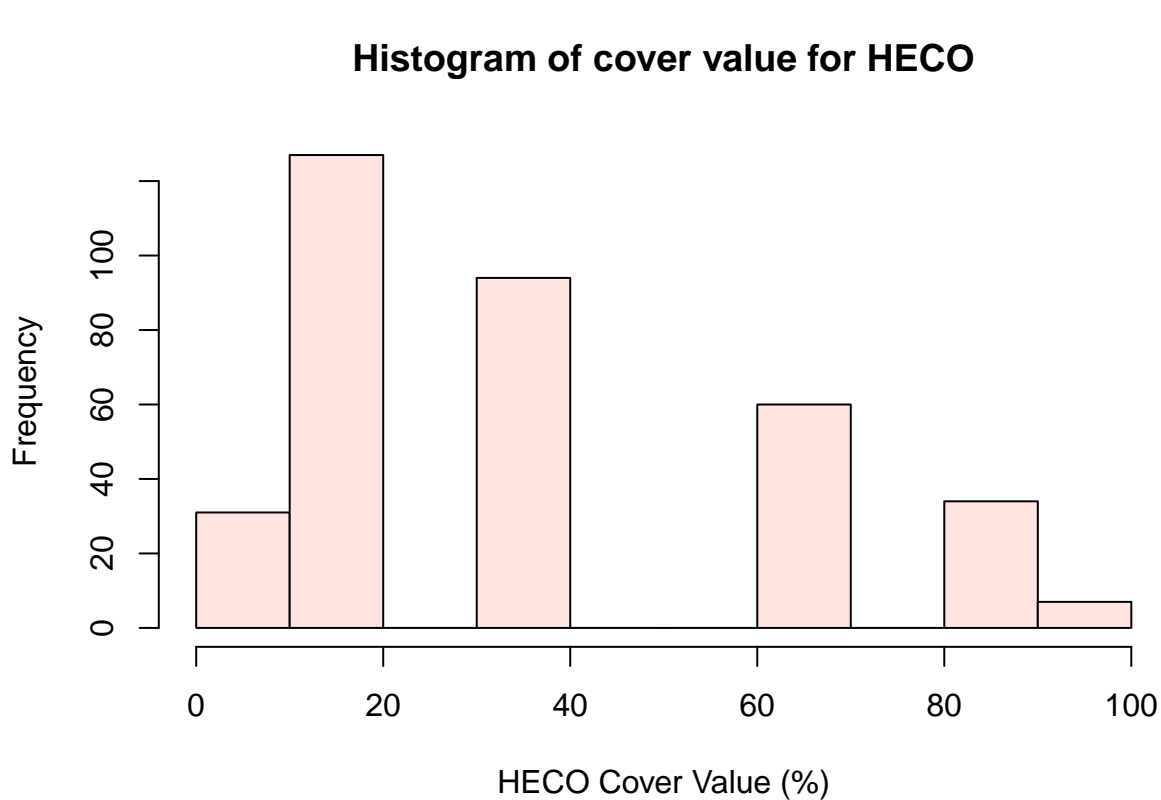
```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8375 -0.4500  0.0000  0.0000  1.7625
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.6375     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
##
## [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
```



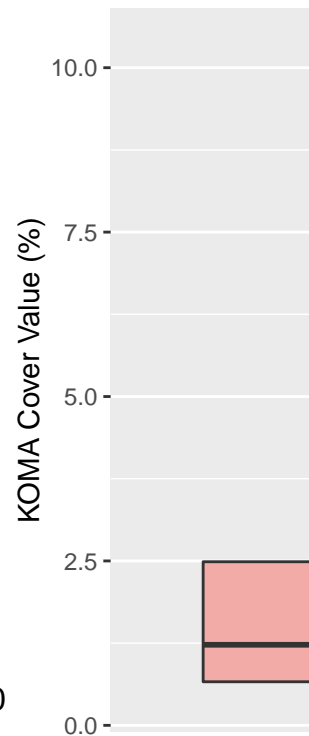
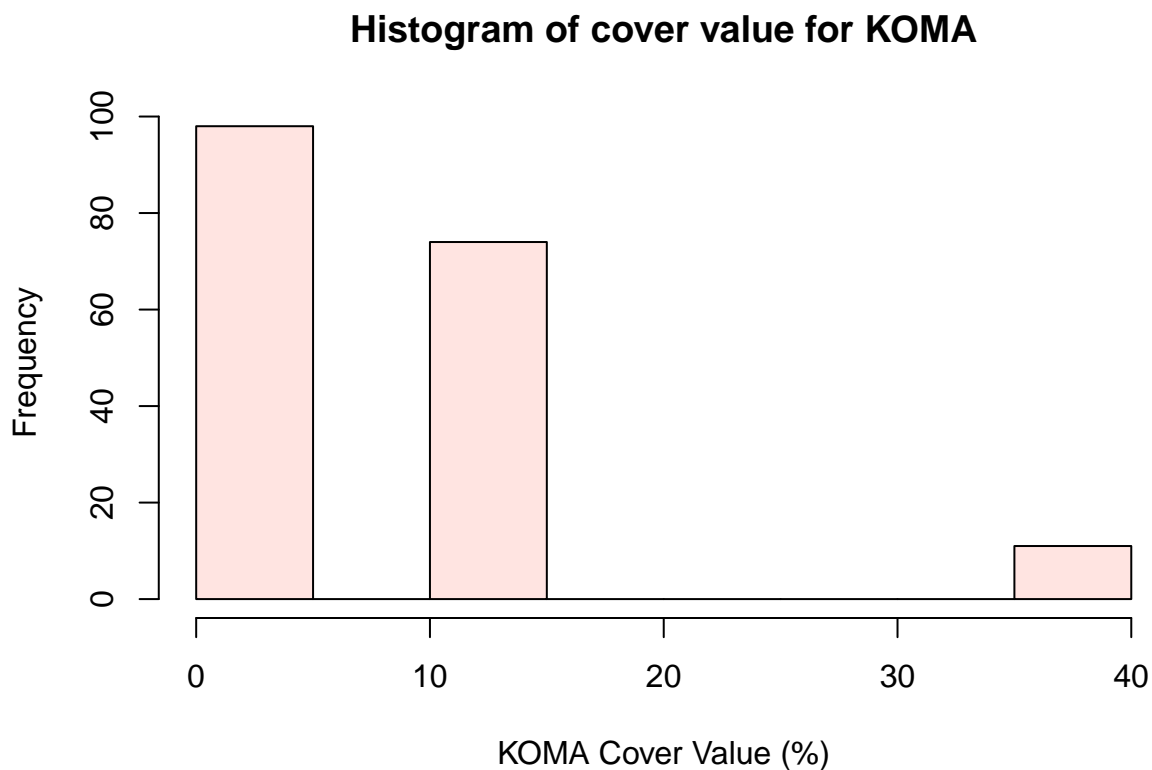
```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.3875 -0.8500 -0.2125  0.3500  9.4625
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      31.137      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
##
## [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
```



```
##
## 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
## ---
```

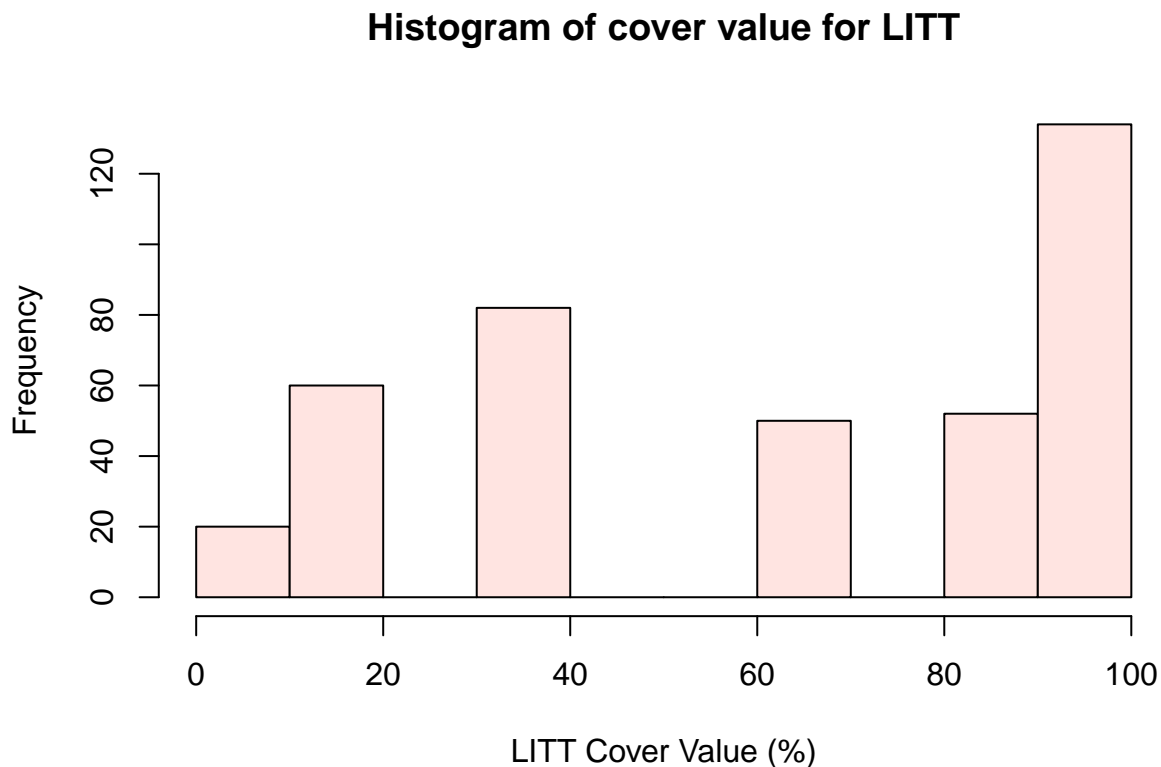
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.624 on 6 degrees of freedom
## Multiple R-squared:  0.0199, Adjusted R-squared:  -0.1435
## F-statistic: 0.1218 on 1 and 6 DF,  p-value: 0.739
##
## [1] "KOMA"
## Source: local data frame [8 x 3]
## 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
```



```
##
## 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
##
## [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
```



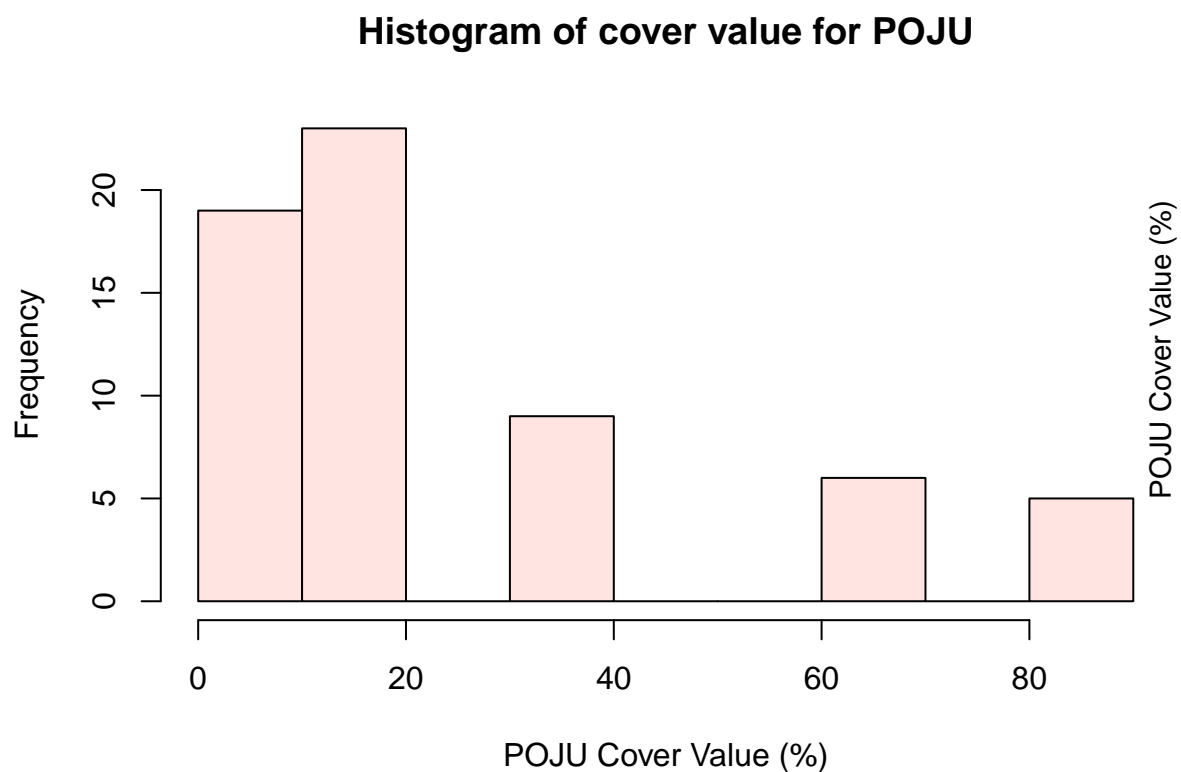

```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-6.062	-4.562	-2.163	3.925	11.887

```
##
## Coefficients:
```

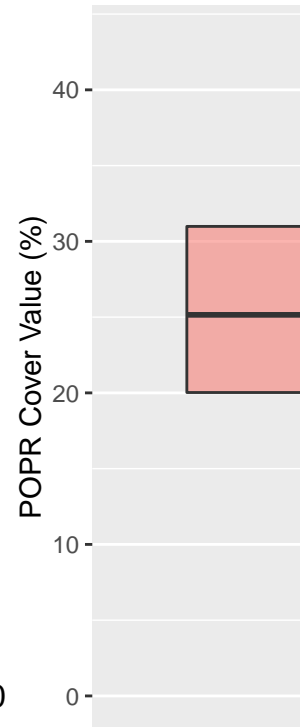
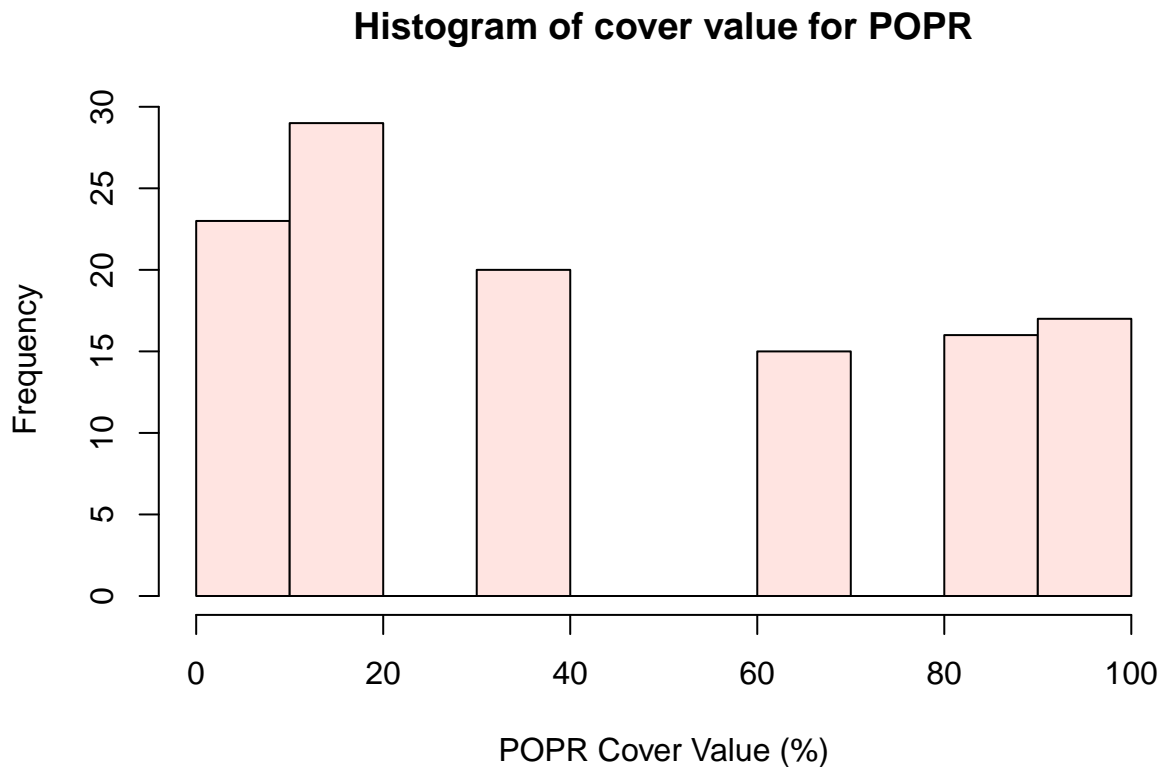
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	34.413	3.397	10.13	5.38e-05 ***
TreatmentBiosolids	54.350	4.804	11.31	2.85e-05 ***

```
## ---
## 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
##
## [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
```



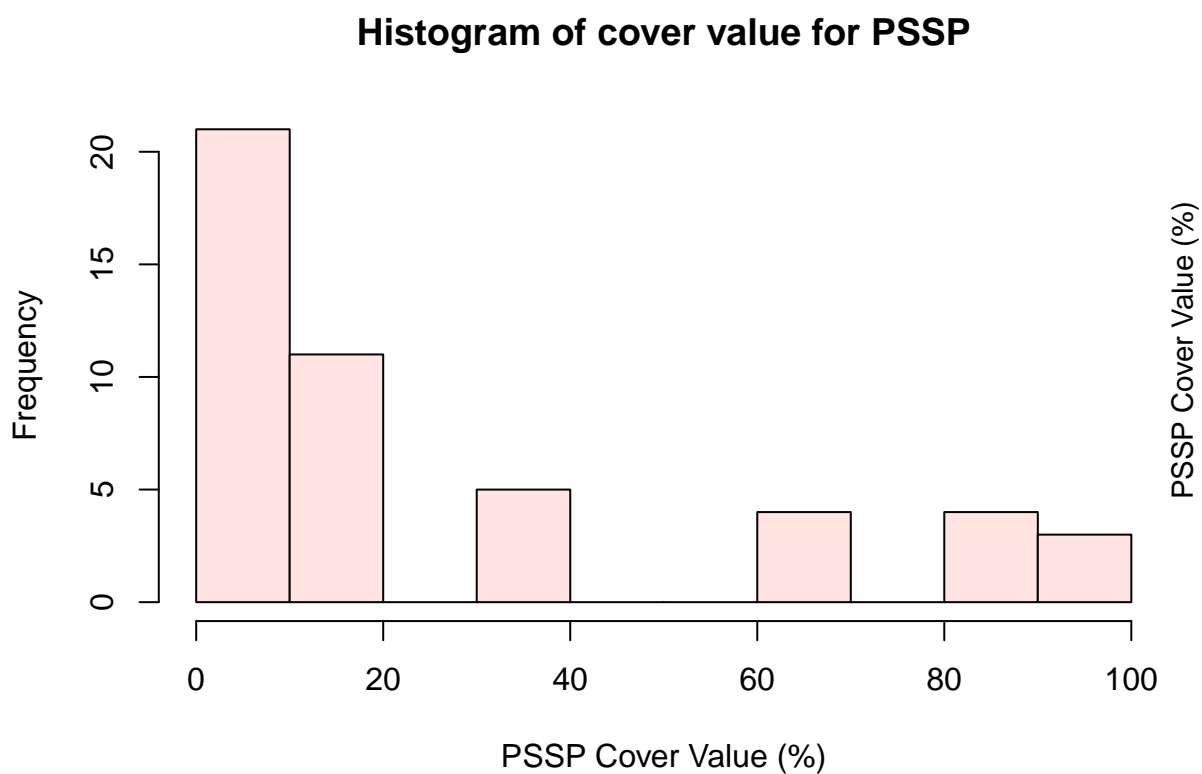
```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.350  -4.638  -0.200   0.100  17.600
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.300      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
##
## [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
```



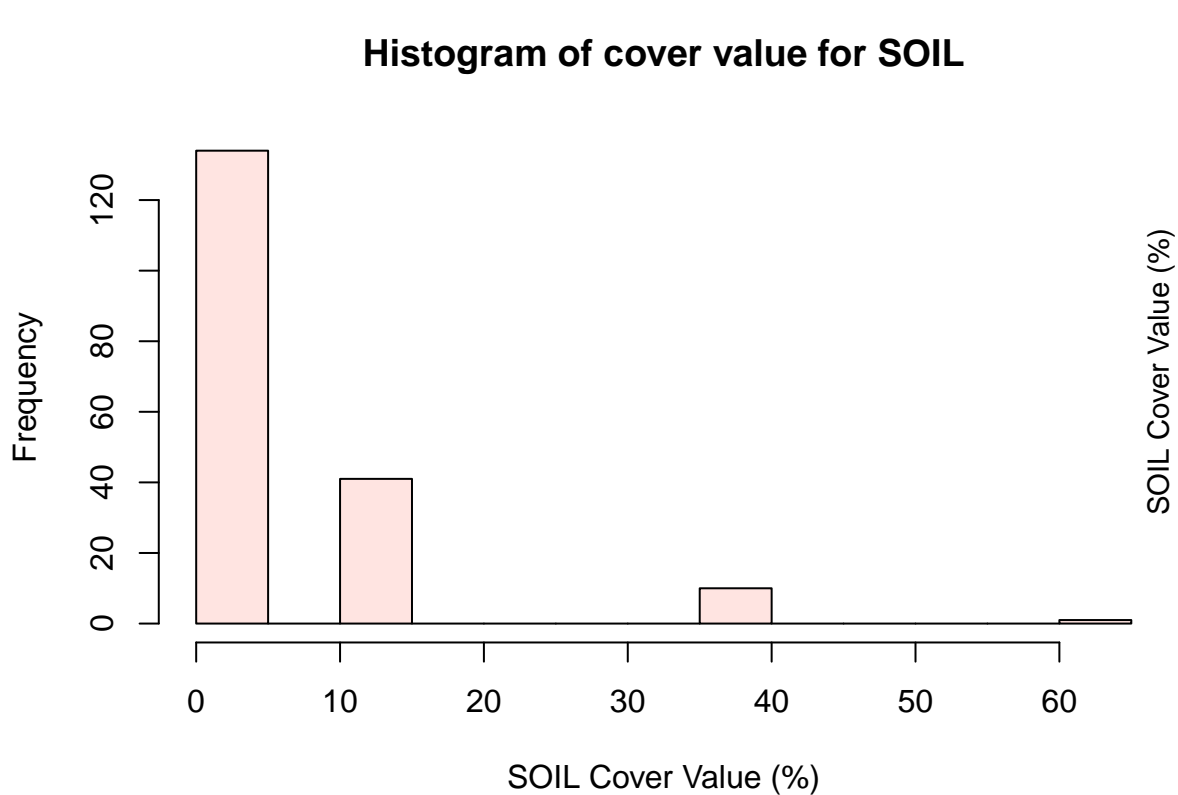
```
##
## Call:
## lm(formula = as.numeric(y.avg) ~ Treatment, data = dat.avg.this.species)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -16.1125  -0.6969  -0.0250   0.3781  17.5375
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.125      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
##
## [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
```



```
##
## 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
```

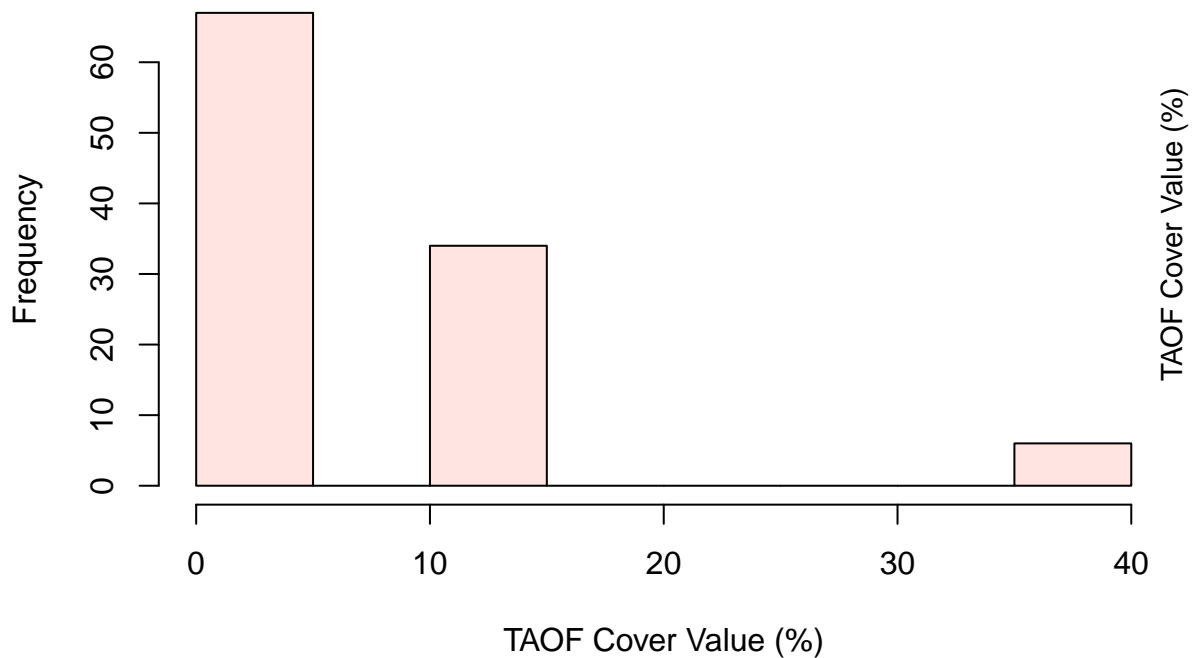
```
## F-statistic: 3.066 on 1 and 6 DF, p-value: 0.1305
##
## [1] "SOIL"
## Source: local data frame [8 x 3]
## Groups: Block [?]
##
##   Block Treatment y.avg
##   (fctr)   (fctr) (dbl)
## 1     1 Biosolids  0.70
## 2     1  Control  5.20
## 3     2 Biosolids  2.05
## 4     2  Control  9.70
## 5     3 Biosolids  0.80
## 6     3  Control  2.15
## 7     4 Biosolids  0.50
## 8     4  Control  6.65
```



```
##
## 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
##
## [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
```

```
# Print the linear regression p-values 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"
```

```
# 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"
```