E4 Results and Figures

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This code needs the following raw data file: e4_trimmedData.txt

This code does the following things:
* Analyzes variation in biomass and soil measurements in unplanted and monoculture pots * Analyzes variation in biomass and soil measurements in mixed community pots * Analyzes the relationship between Microstegium density treatment on the measured Microstegium abundance at harvest

This code produces the following items:
1. Unplanted and monoculture pots
+ summary table (aggregated by plant): mean, se, n = 'summary_monos.txt'
+ figure 2: resps v plant = 'fig2_monos.png'
+ lme4 model: resp<-plant+(1|bk) and test of fixed effects = 'termeffs_monos.txt'
2. Mixed community pots
a. summary tables (aggregated by (1) mvtrt, (2) comptrt, and (3) factorial trts): mean, se, n = 'summary_mixedcomm.txt'
b. plot parameters to determine if correlated: logtotal/mvtrt, logtotal/comptrt = 'param_correl.png'
c. figure 3: resps v mvtrt, resps v logtotal = 'fig3_mixedcomm.png'
3.Relationship between Microstegium density treatment on the measured Microstegium abundance at harvest
a. plot of mvabund v mvtrt, mvrelabund v mvtrt
b. lme4 models: mvabund/relmvabund<-mvtrt+(1|bk) and test of fixed effects = 'termeffs_abund_mixedcomm.txt'

Load libraries

```
library(doBy)
```

```
## Loading required package: survival
## Loading required package: splines
## Loading required package: MASS
```

```
library(lme4)
```

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

```
# library(coefplot2)# this no longer exists for R version 3.1.1
library(coefplot)# hopefully this has the same functionality...
```

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

```
require(data.table)
```

```
## Loading required package: data.table
```

Import data

```
data<-read.table('e4_trimmedData.txt',header=T)
```

Modify... Create a total aboveground biomass column by adding Microstegium biomass, Panicum biomass, Sorghum biomass per observation (pot). Make sure that block is coded as a factor. Create 'compabund' (aka Neighbor abundance) column by adding Panicum biomass and Sorghum biomass per observation (pot).

```
data$total<-data$Mvabund + data$pavi + data$sobi
data$bk<-as.factor(data$bk)
data$compabund<-data$pavi + data$sobi
```

Subset... Subset data based on whether it is a monoculture or mixture pot, also subset by the species identity (in the case of monocultures) or the neighbor treatment (in the case of the mixtures).

```
Empty<-data[data$type=='Empty',]
Mivi<-data[data$type=='Mivi',]
Pavi<-data[data$type=='Pavi',]
Sobi<-data[data$type=='Sobi',]
CompEmpty<-data[data$type=='CompEmpty',]
CompPavi<-data[data$type=='CompPavi',]
CompSobi<-data[data$type=='CompSobi',]
```