E4 manuscript Results - Using ggplot

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Filename: e4_ms_results.Rmd'

A. This code needs the following files:

1. *'e4Data' folder*

- 'e4_potData.txt'
- 'e4_potData_dictionary.txt'

2. *'e4Code' folder*

- 'e4_cleanCode.R'
- 'e4_calcsiCode.R'
- 'mytheme.R'
- 'statFxns.R'
- 'e4_Fig2stats.R' and 'e4_makeFig2.R' –> both reference –> 'e4_prepdfFig2.R'
- 'e4_Fig3stats.R' and 'e4_makeFig3.R' –> both reference –> 'e4_prepdfFig3n4.R'
- 'e4_Fig4stats.R' and 'e4_makeFig4.R' –> both reference –> 'e4_prepdfFig3n4.R'
- 'e4_Fig5stats.R' and 'e4_makeFig5.R' –> both reference –> 'e4_prepdfFig5.R'

B. This code does the following things:

1. Clean raw dataset (run external code)
2. *'e4Output_figures' folder* has Results section figures
   - Fig2. Species' biomass
   - Fig3. Soil measures vs Pot monoculture type
   - Fig4. Soil measures vs M.v. biomass w/o neighbors
   - Fig5. Soil measures vs M.v. biomass w/ neighbors, vs relative Mv abundance, vs total biomass
3. *'e4Output_tables' folder'* has txt tables that hold anova results and mean values

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1. Clean raw dataset (run external code)

```
source('e4Code/e4_cleanCode.R')
#str(data)

### Read-in all the custom functions for doing stats ###
source('e4Code/statFxns.R')
```

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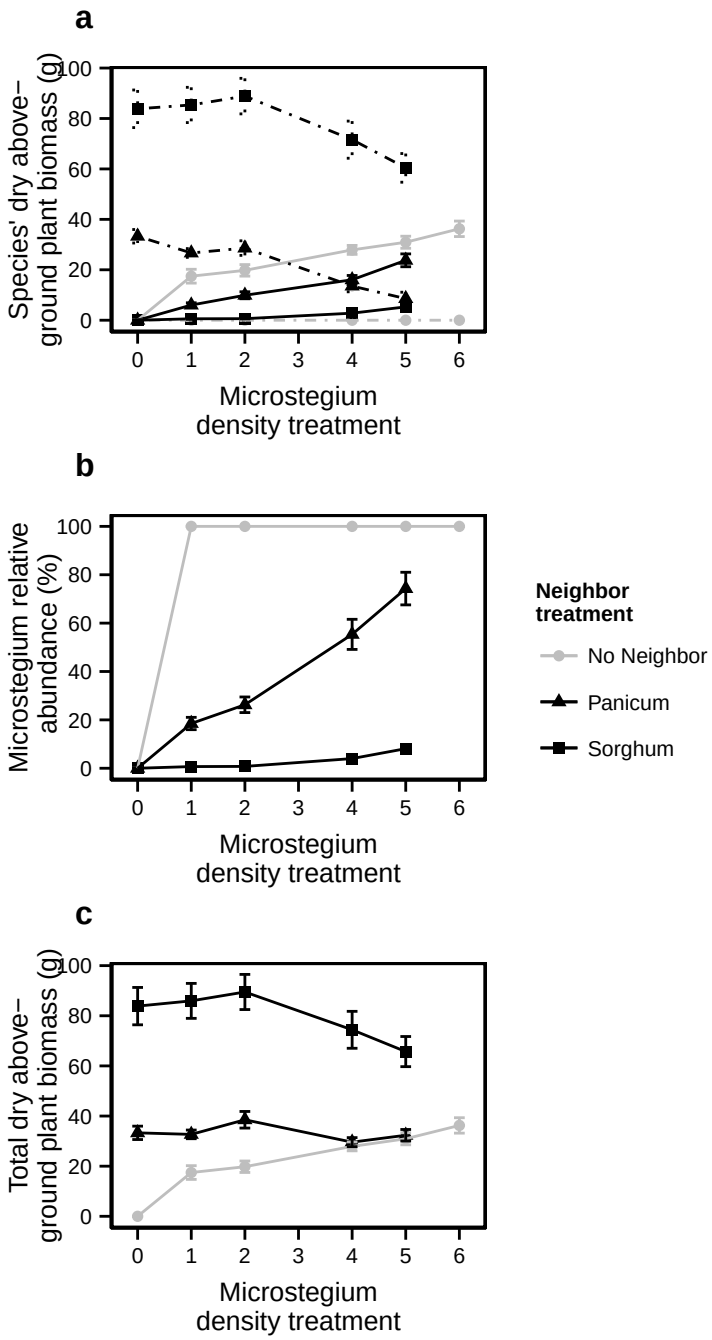
2. Plot

Fig2 : Plant biomasses vs density trt

```
source('e4Code/e4_Fig2stats.R')
source('e4Code/e4_makeFig2.R')
fig2
```



e4Output_tables/fig2_means.txt – **Figure 2 Means**

e4Output_tables/fig2_lme_anova.txt – **Microstegium biomass, relative abundance, and total plant biomass were shaped by the density treatment, neighbor treatment, and their interaction**

Microstegium biomass and relative abundance were X to X times lower in the presence of Sorghum than Panicum across density treatments (Fig 2)

```
##   INNERID XgreaterthanNP XgreaterthanPS
## 1       1       2.905826      10.505245
## 2       2       1.997375      16.128664
## 3       4       1.738686       5.727240
## 4       5       1.301545       4.490833
```

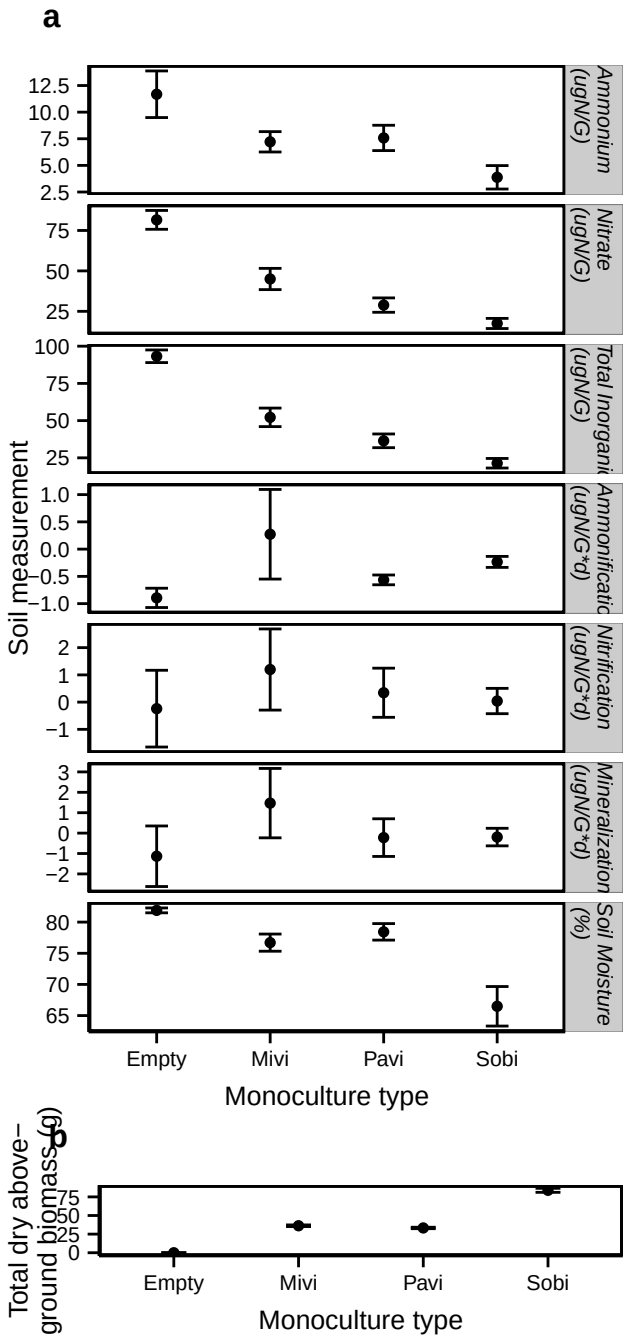
```
##   INNERID XgreaterthanNP XgreaterthanPS
## 1       1             NA      26.287253
## 2       2             NA      34.473152
## 3       4             NA      13.815379
## 4       5             NA       9.167698
```

Pots with Sorghum also had X to X times more total plant biomass than those given the Panicum neighbor treatment and X to X times more total plant biomass than the no neighbor treatment (Fig 2)

```
##   INNERID XgreaterthanPN XgreaterthanSP
## 1       1       1.871588       2.629804
## 2       2       1.946967       2.323700
## 3       4       1.060591       2.515111
## 4       5       1.045528       2.032164
```

Fig3 : Monocultures vs total biomass and soil measurements

```
source('e4Code/e4_Fig3stats.R')
source('e4Code/e4_makeFig3.R')
fig3
```


a
Ammonium (ugN/G)
Nitrate (ugN/G)
Total Inorgani (ugN/G)
Ammonificatic (ugN/G*d)
Nitrification (ugN/G*d)
Mineralization (ugN/G*d)
Soil Moisture (%)
Soil measurement
Empty
Mivi
Pavi
Sobi
Monoculture type
b
Total dry above−ground biomass (g)
Empty
Mivi
Pavi
Sobi
Monoculture type

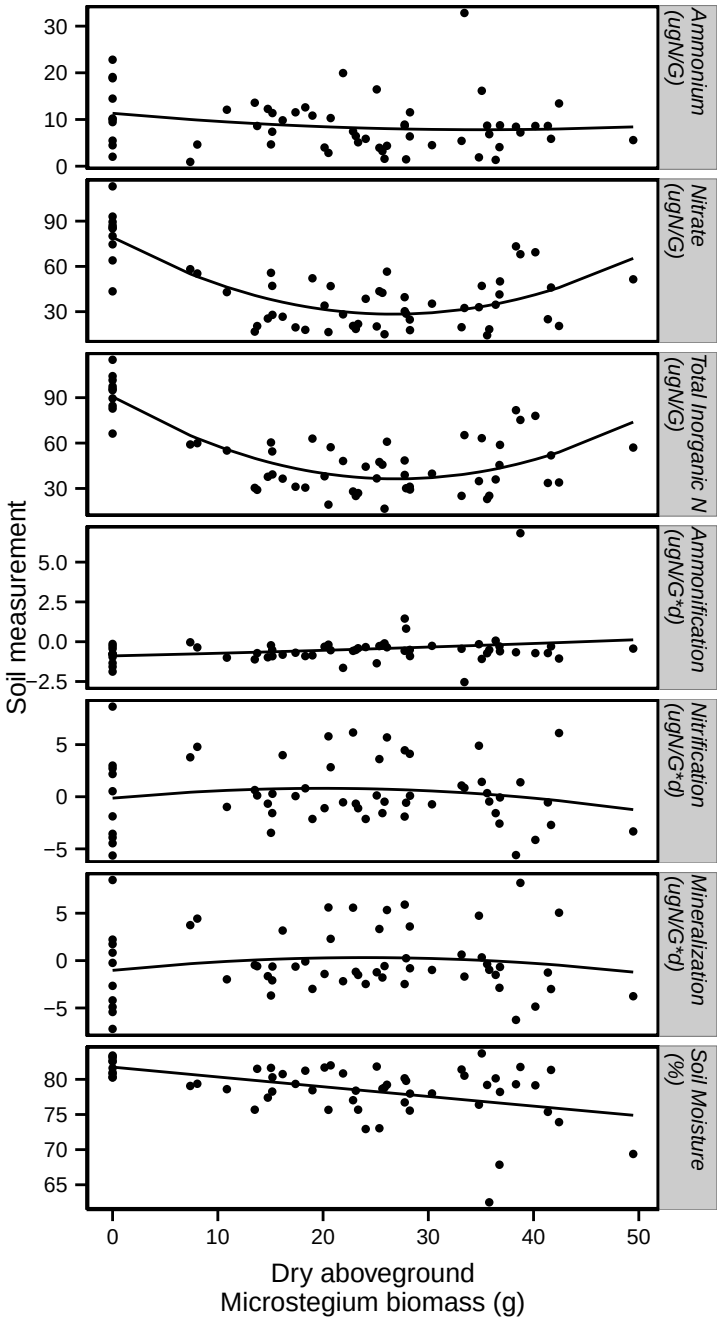
e4Output_tables/fig3a_means.txt – **Figure 3a Means**

e4Output_tables/fig3b_means.txt – **Figure 3b Means**

e4Output_tables/fig3_lme_anova.txt – **Soil measures and total biomass were shaped by the plant type**

Fig4 : Mivi biomass vs soil measures w/o neighbors

```
source('e4Code/e4_Fig4stats.R')
source('e4Code/e4_makeFig4.R')
fig4
```

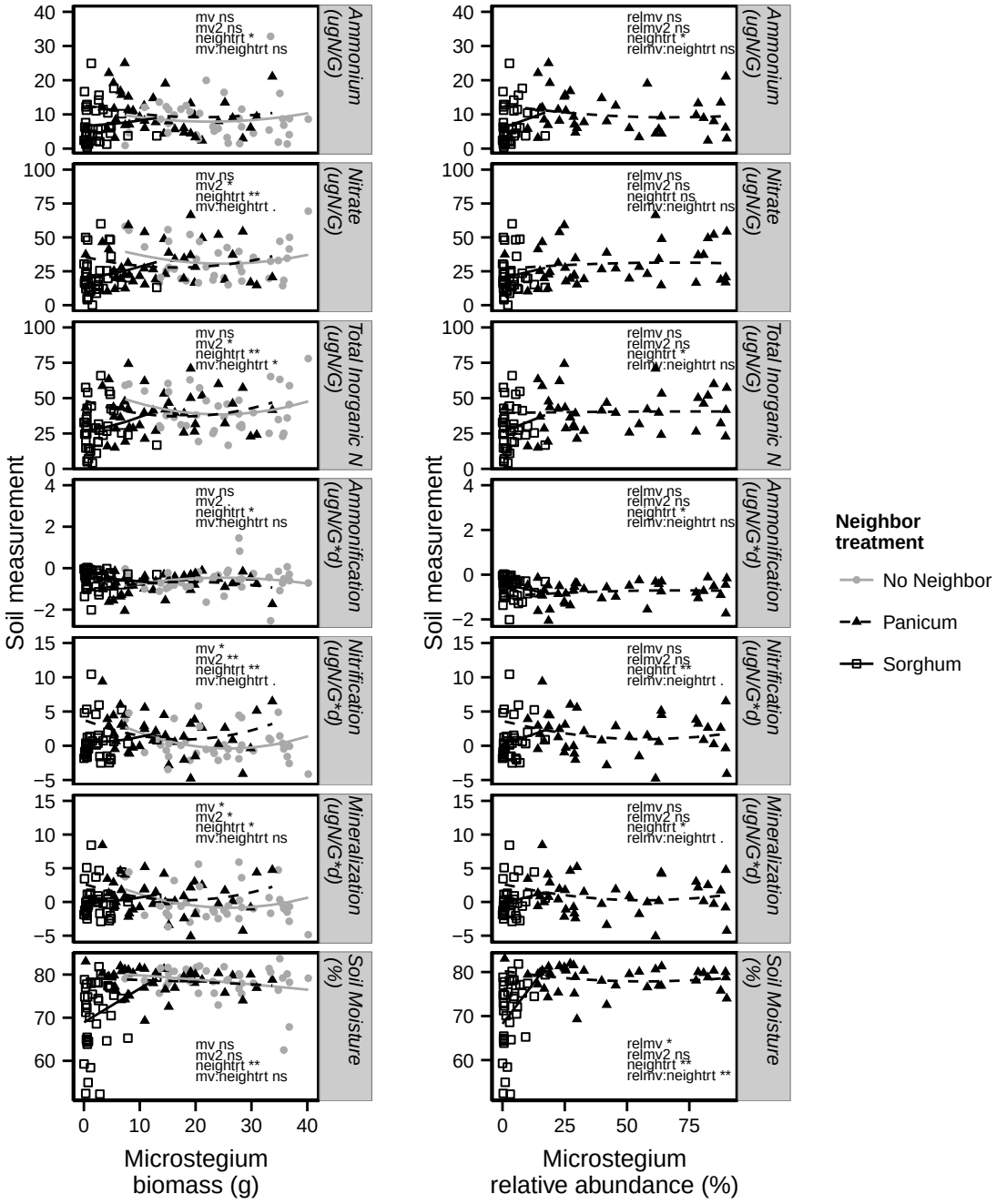


***e4Output_tables/fig4_lme_anova.txt* and *e4Output_tables/fig4_lme_fe.txt* – Soil measures varied by Mivi**

Fig5. Mixture plant biomass vs soil measures

- Exclude pots without 2 species present

```
source('e4Code/e4_Fig5stats.R')
source('e4Code/e4_makeFig5.R')
fig5
```



e4Output_tables/fig5_lme_mivi_anova.txt – **Soil measures varied by Mivi and comptrt**

e4Output_tables/fig5_lme_relmivi_anova.txt – **Soil measures varied by RelMivi and comptrt**

e4Output_tables/fig5_lme_total_anova.txt – **Soil measures varied by Total**

e4Output_tables/fig5_means.txt – **Mean soil measurement values by comptrt in mvtrt=1,2,4,5**