

E4 Visualization

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Filename: e4_vis_md.Rmd

A. This code needs the following files:

1. 'e4_potData.txt' in 'e4DataPackage_092614' folder
2. 'e4_potData_dictionary.txt' in 'e4DataPackage_092614' folder
3. 'e4_cleanCode.R' in 'e4CodePackage_100614' folder
4. 'e4_calcsiCode.R' in 'e4CodePackage_100614' folder

B. This code does the following things:

1. Clean raw dataset (run external code)
2. Plot
 - Fig2. Mv density treatment vs plant biomass
 - Fig3. Monoculture type vs soil meas at harvest (s1)
 - Fig4. Mixture plant biomass vs soil meas (s1) or soil meas diff relative to the baseline (s1s0)
3. Fit models
 - A. To predict s1s0 using mivi biomass, compabund, and total
 - B. To predict s1 using mivi biomass, compabund, and total

C. This code produces the following items:

1. NA

1. Clean raw dataset (run external code)

```
source('e4CodePackage_100614/e4_cleanCode.R')
#str(data)
```

2. Plot

- Load libraries

```
library(ggplot2)
library(reshape2)
```

Fig2. Mv density treatment vs plant biomass

- Remove unnecessary cols
- Reshape so that plant biomass values are all in one column (biomval), with an identifier column to identify what type of biomass that value represents (biommeas)
- Plot Mv treatment vs biomass measures

Fig3. Monoculture type vs soil measure at harvset (s1)

- Remove unnecessary cols
- Reshape so that plant biomass values are all in one column (biomval), with an identifier column to identify what type of biomass that value represents (biommeas)
- Plot monoculture type vs soil measures (s1)

Fig4. Mixture plant biomass vs soil measure (s1) or soil measure difference relative to the baseline (s1s0)

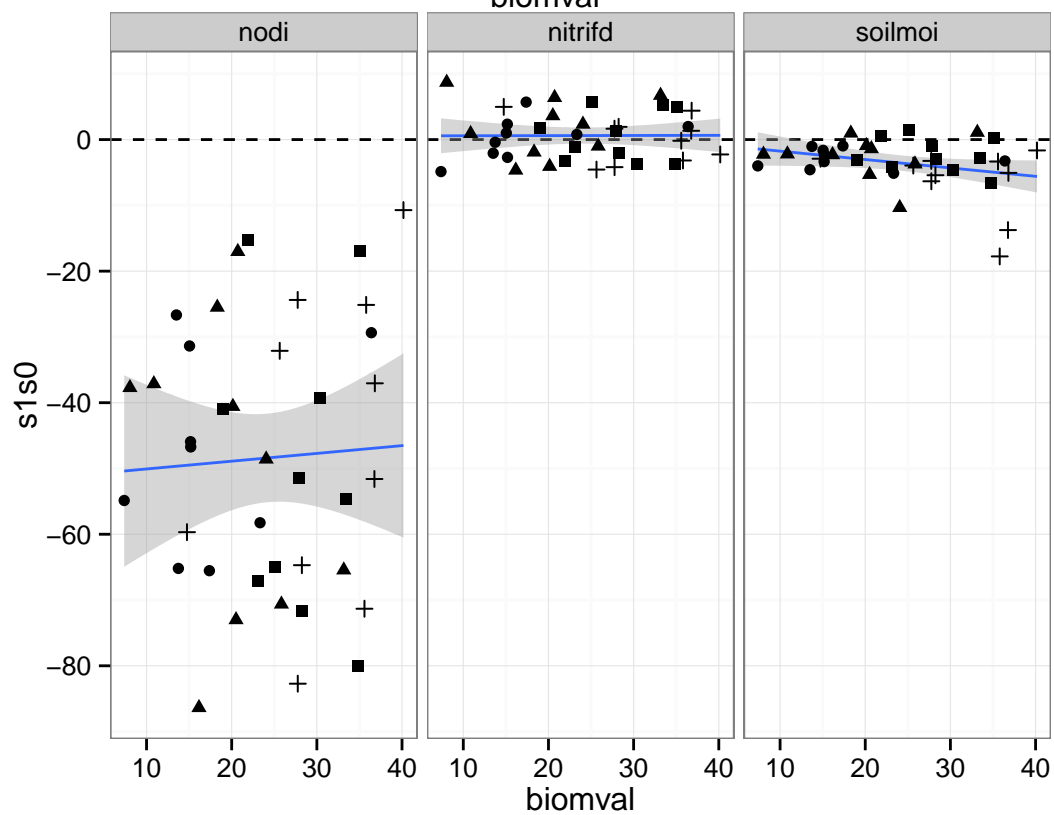
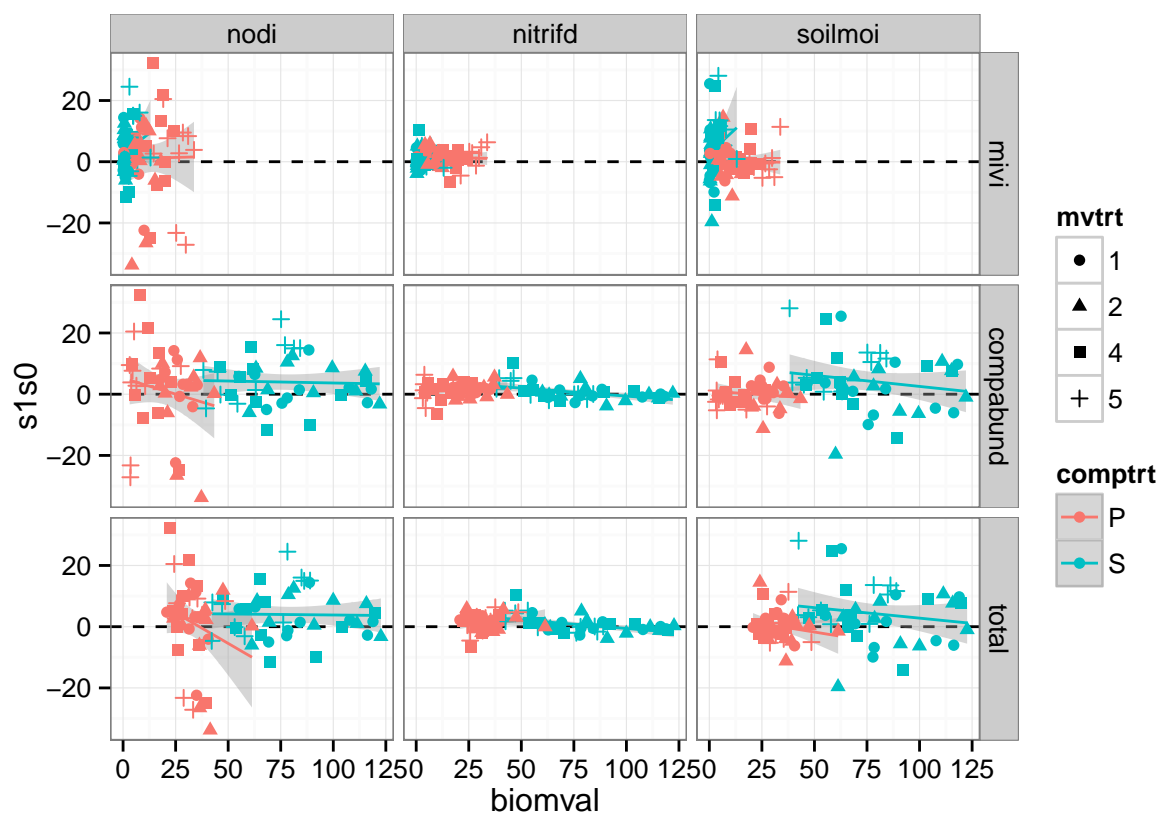
- Calculate 'Si', the soil property impact in response to the presence of Mv and create a new dataframe with this info (run external code)

```
source('e4CodePackage_100614/e4_calcsiCode.R')
```

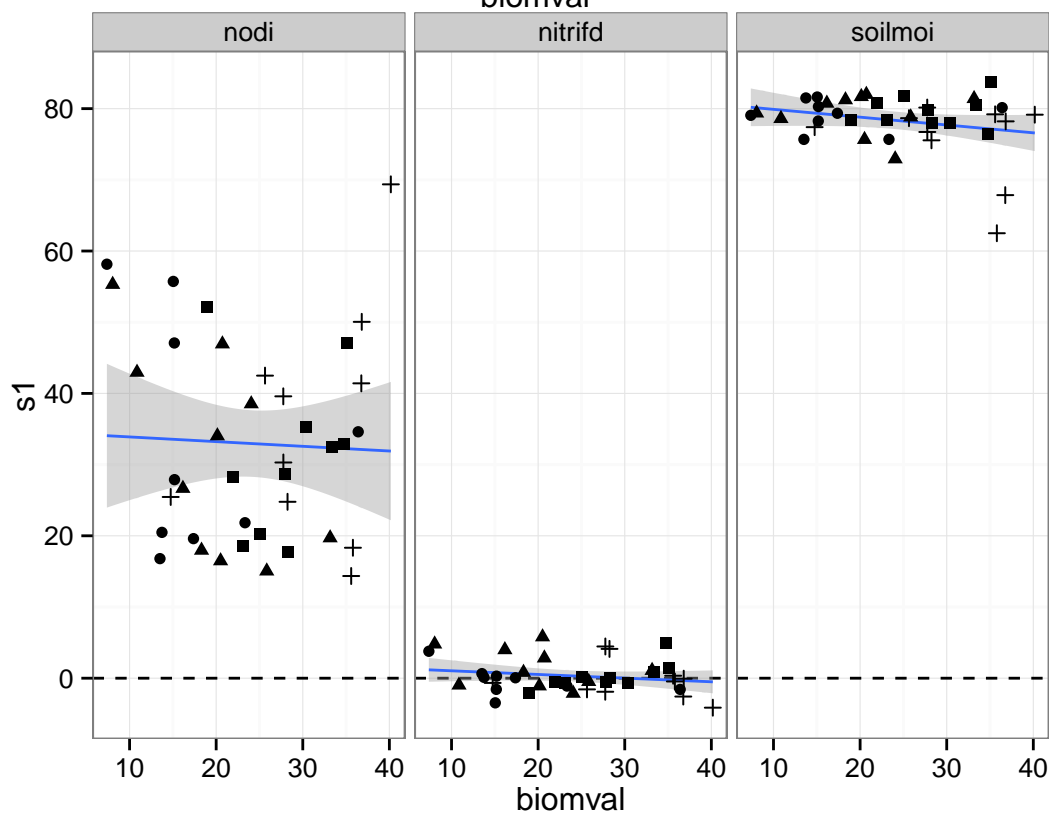
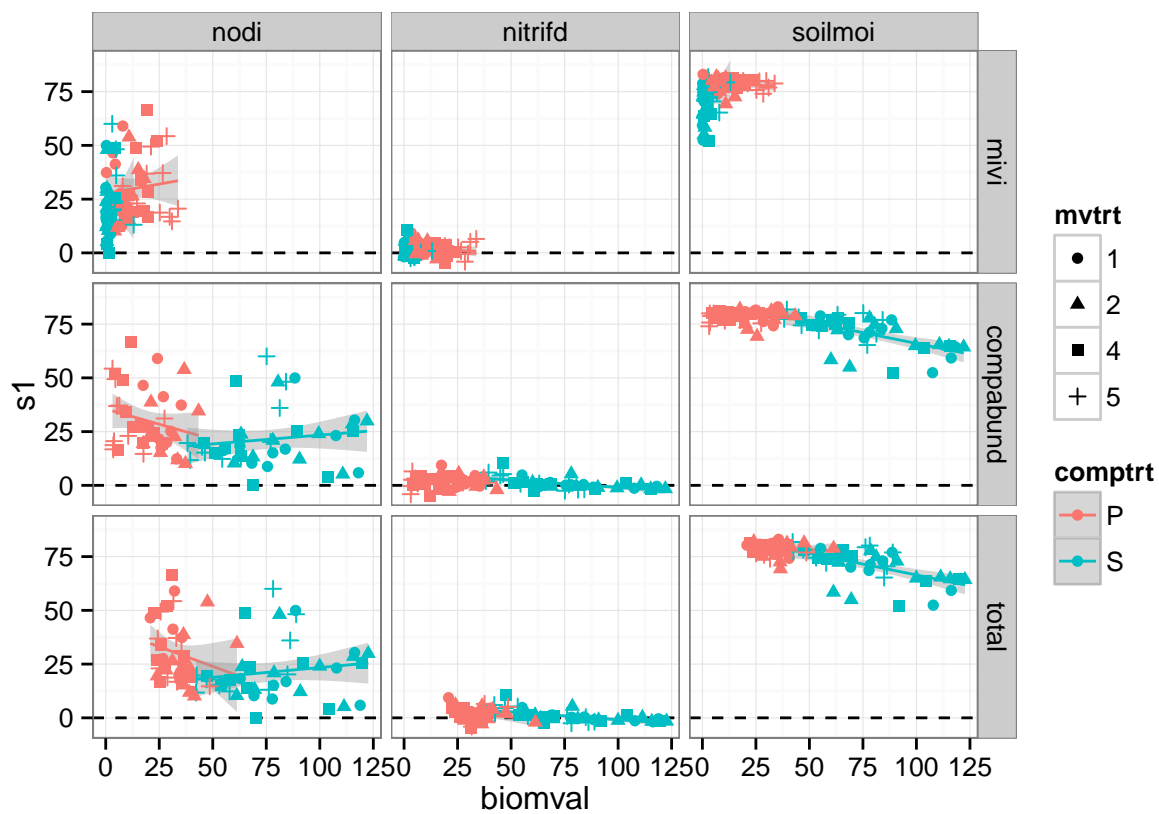
```
## Warning: number of columns of result is not a multiple of vector length
## (arg 340)
```

```
#str(datas)
```

- Remove unnecessary cols
- Reshape so that plant biomass values are all in one column (biomval), with an identifier column to identify what type of biomass that value represents (biommeas)
- Plots where $y = S1 - S0$



- Plots where $y = S1$



3. Fit models

A. To predict s1s0 using mivi biomass, compabund, and total

- Set up model fxns (run external code)

```
source('e4CodePackage_100614/e4_fitmodCode.R')
#ModFxn1
#ModFxn2
#ModFxn3
```

- Set up generic fxn to pull out info from each fitted model
- Fit the models
- Organize fitted model results into tables; view the fitted model results
- Significant model terms

Model 1. $s1s0 = (mivi * beta)$

```
## $pval2
## [1] "soilmoi_N 0.0601"
```

Model 2. $s1s0 = (mivi * beta) + (compabund * beta2) + ((mivi * compabund) * beta3)$

```
## $pval2
## [1] "nodi_P 0.0934"      "totdi_P 0.0588"    "soilmoi_N 0.0601"
##
## $pval3
## [1] "nhdi_S 0.0777"      "nodi_P 0.0536"     "totdi_P 0.0433"
## [4] "ammonifd_S 0.0979" "nitrifd_S 0.0293"  "minzd_S 0.0347"
## [7] "minzd_P 0.0777"
##
## $pval4
## character(0)
```

Model 3. $s1s0 = (total * beta)$

```
## $pval2
## [1] "nhdi_S 0.0153"      "ammonifd_S 0.0235" "nitrifd_S 0.0015"
## [4] "minzd_S 0.0018"     "soilmoi_N 0.0601"
```

B. To predict s1 using mivi biomass, compabund, and total

- Set up model fxns (run external code)

```
# source('e4CodePackage_100614/e4_fitmodCode.R') #this was already loaded above...
#ModFxn1
#ModFxn2
#ModFxn3
```

- Set up generic fxn to pull out info from each fitted model
- Fit the models
- Organize fitted model results into tables; view the fitted model results
- Significant model terms

Model 1. $s1s0 = (mivi * beta)$

```
## $pval2
## [1] "soilmoi_N 0.0601"
```

Model 2. $s1s0 = (mivi * beta) + (compabund * beta2) + ((mivi * compabund) * beta3)$

```
## $pval2
## [1] "nodi_P 0.0934"      "totdi_P 0.0588"    "soilmoi_N 0.0601"
##
## $pval3
## [1] "nhdi_S 0.0777"      "nodi_P 0.0536"      "totdi_P 0.0433"
## [4] "ammonifd_S 0.0979"  "nitrifd_S 0.0293"   "minzd_S 0.0347"
## [7] "minzd_P 0.0777"
##
## $pval4
## character(0)
```

Model 3. $s1s0 = (total * beta)$

```
## $pval2
## [1] "nhdi_S 0.0153"      "ammonifd_S 0.0235"  "nitrifd_S 0.0015"
## [4] "minzd_S 0.0018"     "soilmoi_N 0.0601"
```