# E4 Visualization

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- A. This code needs the following raw data files: All are located in 'e4DataPackage\_092614' folder
  - 1. 'e4\_potData.txt'
  - 2. 'e4 potData dictionary.txt'
- B. This code does the following things:
  - 1. Cleans raw dataset.
  - 2. Creates dataframes where y = soil property impact to the presence of Mv
  - 3. Produces 1 multipanel figure for each soil property impact (soil moisture, nitrate, nitrification... others).
  - Panel rows will be (a) Mv only, (b) Mv + Panicum, (c) Mv + Sorghum
  - Panel cols will be (a) Mv biomass/Relative biomass, (b) Neighbor biomass/Relative biomass, (c) total biomass
- C. This code produces the following items:
  - 1. Multi-panel figures described above

## 1. Clean raw dataset

#### Import data and check it out

- Check out dataframe; Note that...
  - 'potid' and 'bk' columns need to be re-classified as factors
  - 'mivi', 'pavi', 'sobi' have NA values ... If these are pots without that species planted, then these values should be zero. If these are missing values, then the rows need to be excluded
  - there are notes that may mean some rows need to be excluded

#### Remove rows with NAs

- Change 'NAs' to 0s in 'mivi', 'pavi', and 'sobi' columns according to the treatment type. In other words, NA should be changed to 0 if the species' biomass is missing because it wasn't planted there in the first place due to its treatment assignment.
- Remove rows with an 'NA' in any column (other than 'notes')

## [1] 159 18

• Remove the row with the note about the nh and no outliers

## [1] 158 18

# Calculate aggregate biomass columns

- Create a total aboveground biomass column by adding Microstegium biomass, Panicum biomass, Sorghum biomass per observation (pot).
- Create 'compabund' (aka Neighbor abundance) column by adding Panicum biomass and Sorghum biomass per observation (pot).

# 2. Create dataframes where y = soil property impact in response to the presence of Mv

Calculate the impact of invader presence on soil properties (Si1 - Si1) and create new df for this info

- Start by creating a column to subset the data by neighbor treatment.
- Within each bk \* neighbor treatment, subtract the Si0 from each Si1.
- Re-structure the resulting dataset
- Order df by s1pid and remove rows with s1pid == NA
- Finally, subtract s1 s0, populate s1s0 column with the resulting values. Re-name the dataframe.

3. Produce 1 multipanel figure for each soil property impact (soil moisture, nitrate, nitrification...others).