Meta R Script/Analysis File

R Script Meta Info

* All script used to process data files, prep for Figure generation, and analyses are included here.
* Scripts are separated into section by the corresponding subheading from Hostetler et al., 2021
* Analyses are ordered in the order they appear in the results section
* Processed files are exported as Figure files and used in Figure generation (Hostetler\_et\_al\_2021-FigureGeneration.R)

Genotype determines root lodging susceptibility

Input:

* LodgingData\_2020\_long\_02162021.csv - 2020 lodging data, all plant replicates
  + Raw data file (no prep needed)
* Unique\_55Genotypes\_Plots.csv
  + Meta file (no prep required)
* LodgingData\_2020.csv - 2020 lodging data, plot averages
  + Raw data file (no prep needed)

Output:

* Figure2A-B\_04122021.csv
  + Figure 2
* TableS4\_LodgingData.csv
  + Table S4 info for root lodging susceptibility and root lodging severity

Brace root phenotypes vary between genotypes  
Input:

* 2019\_root\_photo\_data\_filtered.csv – 2019 pheno data, all replicates
  + Raw data file (no prep needed)
* Inbred\_Subpop\_2Years\_Broot\_Ratio.csv – 2018 and 2019 ratio data, all replicates
  + Raw data file (no prep needed)
* Inbred\_Subpop\_2Years\_EI\_All.csv – 2018 and 2019 EI data, all replicates
  + Raw data file (no prep needed)
* 2019PC\_Height.csv – 2019 height data, all replicates
  + Raw data file (no prep needed)

Output:

* Averaged2019\_Pheno\_and\_Combined\_Mech\_Data\_04132021.csv  
  \*File w/ 2019 phenotype data (phenotypic profiles), EI data, Ratio data, and height data; converted to cm
  + File for Figure S8
  + File for “Brace root phenotypes predict root lodging”
* TableS4\_PhenotypeData.csv
  + Table S4 info for plant phenotypes

Brace root phenotypes predict root lodging

Input:

* Inbred\_Subpop\_2Years\_EI\_All.csv – 2018 and 2019 EI data, all replicates
  + Raw data file (no prep needed)
* Inbred\_Subpop\_2Years\_Broot\_Ratio.csv – 2018 and 2019 ratio data, all replicates
  + Raw data file (no prep needed)
* LodgingData\_2020\_long\_02162021.csv - 2020 lodging data, all plant replicates
  + Raw data file (no prep needed)
* Averaged2019\_Pheno\_and\_Combined\_Mech\_Data\_04132021.csv – 2019 phenotype data for all reps
  + Prepped in previous analysis (see above)
* LodgingData\_2020.csv - 2020 lodging data, plot averages
  + Raw data file (no prep needed)

Output:

* Inbred\_Subpop\_2Years\_EI\_Processed.csv
* Inbred\_Subpop\_2Years\_Broot\_Ratio\_Processed.csv
* Table1\_03292021.csv
  + File for Table 1
* Note: save Mean Decrease in Gini from each model in external excel file for figure prep

Brace root phenotypes predict plant biomechanics

Input:

* Inbred\_Subpop\_2Years\_EI\_Processed.csv – 2018 and 2019 Biomechanics (EI)
  + Prepped in previous analysis (see above)
* Inbred\_Subpop\_2Years\_Broot\_Ratio\_Processed.csv – 2018 and 2019 Biomechanics (Ratio)
  + Prepped in previous analysis (see above)
* Averaged2019\_Pheno\_and\_Combined\_Mech\_Data\_04132021.csv
  + Prepped in a previous analysis (see above)

Output:

* TableS4\_RatioData.csv
  + Table S4 info for plant biomechanics none/all ratio
* TableS4\_EIData.csv
  + Table S4 info for plant biomechanics EI
* Note: save Mean Decrease in Gini from each model in external excel file for figure prep

Inclusion of plant biomechanics improves the prediction accuracy of root lodging

Input:

* Inbred\_Subpop\_2Years\_EI\_Processed.csv – 2018 and 2019 Biomechanics (EI)
  + Prepped in previous analysis (see above)
* Inbred\_Subpop\_2Years\_Broot\_Ratio\_Processed.csv – 2018 and 2019 Biomechanics (Ratio)
  + Prepped in previous analysis (see above)
* LodgingData\_2020\_long\_02162021.csv - 2020 lodging data, all plant replicates
  + Raw data file (no prep needed)
* LodgingData\_2020.csv - 2020 lodging data, plot averages
  + Raw data file (no prep needed)
* Averaged2019\_Pheno\_and\_Combined\_Mech\_Data\_04132021.csv
  + Prepped in a previous analysis (see above)

Output:

* Figure5A\_03182021.csv
  + Figure 5A
* Note: save Mean Decrease in Gini from each model in external excel file for figure prep