1. Unzip the Plasticty\_Workshop.zip. The Zip file contains three folds, two R scripts, and this document.

######## Top\_dir

######## |----0MaizeG2F

######## | |--8Envs\_envParas\_DAP80.txt

######## | |--Env\_meta\_table.txt

######## | |--Trait\_records.txt

######## | |--Genotype.txt

######## |----1Sorghum

######## | |--7Envs\_envParas\_DAP122.txt

######## | |--Env\_meta\_table.txt

######## | |--Trait\_records.txt

######## | |--Genotype.txt

######## |----2Rice

######## | |--9Envs\_envParas\_DAP80.txt

######## | |--Env\_meta\_table.txt

######## | |--Trait\_records.txt

######## | |--Genotype.txt

######## |----CERIS\_ Workshop.r

######## |----Sub\_functions\_Workshop.r

######## |----Readme.docx

2. We suggest running the first 18 lines in ‘CERIS\_Workshop.r’ to install the required R packages before the Workshop.

3. Within each crop fold, there are three essential files for:

* Observations (Trait\_records.txt), which stores the phenotypic values for each accession (line\_code) in each environment (env\_code);
* Genotype (Genotype.txt), which stores the marker information, if running genomics prediction to predict performance for new genotype is desired;
* Environmental (Either Env\_meta\_info.txt or xxEnv\_envParas\_Dapx~.txt).

4. To practice each crop, please modify line 32 & 34 correspondingly.

|  |  |
| --- | --- |
| Crop | Traits |
| 0MaizeG2F | DTA, PH, or YLD |
| 1Sorghum | FTgdd |
| 2Rice | FTdap |

And run to the line 91, then modify line 95-96 based on the searching results