

SUPPLEMENTAL DATASET - GENETIC ARCHITECTURE OF FLOWERING-TIME VARIATION IN *BRACHYPODIUM DISTACHYON*

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Content of the supplemental dataset

Supplemental data includes:

- A folder called “Data,” which contains:
 1. Raw genotypic data.
 2. Raw phenotypic data.
 3. The genetic map (see Material and Methods section of Woods et al., 2016 for additional information).
 4. A file containing the position of annotated genes on the Brachypodium distachyon genome V2.1. Data from [Phytozome](#).
- The R script used for the QTL analysis (“Final_script.R”).
- A folder called “VCF” that includes the VCF (Variant Call Format) files of the genes presented in Fig. 6 (VRN1, PHYC, VRN2, and FD).

How to run the script?

The script was created in RStudio (R v3.3.0) for Mac OSX 10.11.6. The script was not tested under other system configurations, but it should work properly on different platforms with any R GUI.

One step is required to execute the analysis: **in the R script (“Final_script.R”), set the path (Line 18) to the folder containing the R script and the data.** For example, if the supplemental package is located on the desktop in OSX, the code

Line 18 will be:

```
path <- "/Users/johndoe/Desktop/Supplemental_dataset_woods_2016"
```

The packages required for the analysis should be installed automatically. The script will generate two additional folders (“Figure_results” and “Tables_produced”), in which the results will be stored, as well as a text file showing the parameters used in the analysis.

Users can change the parameters of the analysis by changing the assigned values between Line 24 and Line 56. By default, the “Perform_scantwo_permutation” is set to “NO”, as it takes hours to compute. If you are willing to perform such analysis, change this variable to “YES”. Also, you can run the permutation job on several clusters. To do so, turn the “Number_of_clusters” variable to the number of clusters you are willing to use (the number of available clusters on your computer depends on your CPU).

Contact

If you have questions or have troubles running the script, please contact me at fbouche@wisc.edu or through GitHub (fredericbouche)