This readme.txt file was generated on 2020-12-15 by Isaiah Taylor

The files included in the "R_analysis" directory include the code and data required to reproduce the statistical analysis in Taylor and Lehner, et al, "Mechanism and function of root circumnutation" (doi: https://doi.org/10.1101/2020.05.04.075127).

GENERAL INFORMATION

1. Title of Dataset: Data and scripts from: Mechanism and function of root circumnutation

2. Author Information

A. Principal Investigator Contact Information

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3. Date of data collection (single date, range, approximate date): 2018-2020

SHARING/ACCESS INFORMATION

1. Licenses/restrictions placed on the data: Data available under a CC0 waiver

2. Links to publications that cite or use the data: Taylor and Lehner, et al, "Mechanism and function of root circumnutation" (doi: https://doi.org/10.1101/2020.05.04.075127)

DATA & FILE OVERVIEW

1. File List:

Each folder is a separate analysis included an Rproj file which can be loaded. The scripts directory contains a runner script that will use the "here" library to find the data in the "data" directory for seamless loading. The exception is the "05_gene_expression" folder which only contains gene expression count matrices for RNA-Seq experiments.

METHODOLOGICAL INFORMATION

1. Description of methods used for collection/generation of data:

See preprint at https://doi.org/10.1101/2020.05.04.075127 for methodological description.

2. Methods for processing the data:

See preprint at https://doi.org/10.1101/2020.05.04.075127 for data processing description.

3. Instrument- or software-specific information needed to interpret the data:

R, version > 3.7

 Libraries: ggplot2, here, splines, readxl, aod,

DATA-SPECIFIC INFORMATION FOR: All data files are described below

all_tip_tracking_combined.csv - used as the input data for 02, 03

Column definitions:

plant = experiment number and the specific plant

BX and BY = Tip coordinates

range = the frames after germination recorded (1_192 means frames 1-192, and since each frame represents 1/4 of an hour, 192*1/4=48 hours of measurements)

uid = unique identifier corresponding to the plant and the range

line = experiment number

01_root_length folder

data file: wt_mutant_length_position.csv

Column definitions:

plant = individual root measurements

root_length = root length in mm

genotype = genotype

x_beg = x coordinate in image (pixel) of the base of root

x_end = x coordinate in image (pixel) of the tip of root

y_beg = y coordinate in image (pixel) of the base of root

y_end = y coordinate in image (pixel) of the tip of root

04_cell_length

data files: Analysis_MUT_final_graphs.xlsx, Analysis_WT_final_graphs.xlsx

We create a dataframe with the following columns:

midline_distance = distance of the cell along the middle path of the root where the cell is located (um)

length = length of the cell (um)

side = inner or outer

root = root, numbered 1-9

angle = the measured angle of the root

angle_start = the distance along the midline that is considered the maximal bend.

05_gene_expression

data files: hk1_plus_minus_tZ_CPM_edgeR.csv, WT_hk1_CPM_edgeR.csv

06_surface_exploration

data file: logistic_data.csv

Column definitions:

Y_success = success or failure in growing through within 72 hours of striking the surface

Genotype = wildtype or hk1 mutant

Spacing = distance between holes in platform= 5, 7, 9, or 11 mm

07_nutation_robot

data file: angles.csv

Column definitions:

type = "off" (non-nutating) or "on" (nutating)

angle = angle of the robot upon striking peg

success = 1 (success) or 0 (failure)

08_gravel_penetration

data file: gravel_success.csv

Column definitions:

box = specific experiment number

genotype = genotype

germinated = number of seeds that germinated

thru_72hr_pg = number of seeds that successfully passed through the gravel

expt = experimental replicate