How to use track_analyzer

2017/11/21 Y. Iino

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<Outline>

track_analyzer.r is a GUI-based program to read and analyze the outputs of multiworm tracker (LuCaM Tracker), which are text files. It can also output the data in csv format, which can be read and processed by Microsoft Excel.

<Installation>

Install R in the PC on which track_analyzer.r is to be run.

From here

https://cran.ism.ac.jp/bin/windows/

or

https://cran.ism.ac.jp/bin/macosx/

Launch R and install gWidgets or gWidgets2. For example, to use gWidgetsRGtk2, input

install.packages("gWidgetsRGtk2", dep=TRUE)

then all necessary components will be installed.

Please note, however, that if RGtk+ is not already installed, a message saying that dll file is not found will be shown when you use the library for the first time, and you are asked whether to install Gtk+. Answer Yes and it will be installed. Now you are ready to run track_analyer.r.

<Execution>

Place the data to be read by track_analyzer in subfolders (for example “data ..... dustless.txt”, and optionally contour.data and/or something like “time12345z1.txt” in case you use chemical gradient data), then launch R (R console) (see Note below).

Run the program by either “Read R code source” in the menu bar or enter

source(“(folder¥)track_analyzer1.x.r”)

from the console. The track_analyzer window will open. Then press appropriate buttons to read and process the data (see below). Windows that open for each command can be closed by pressing the close button in the top corner once the command has been executed.

Although you can execute all regular commands by pressing the command buttons, you can also type in commands from the R console. For example, if you enter ls(), all objects (variables and other objects) will be shown. Enter an object name and then the content of that object will be shown. You can also use any standard commands in R, such as

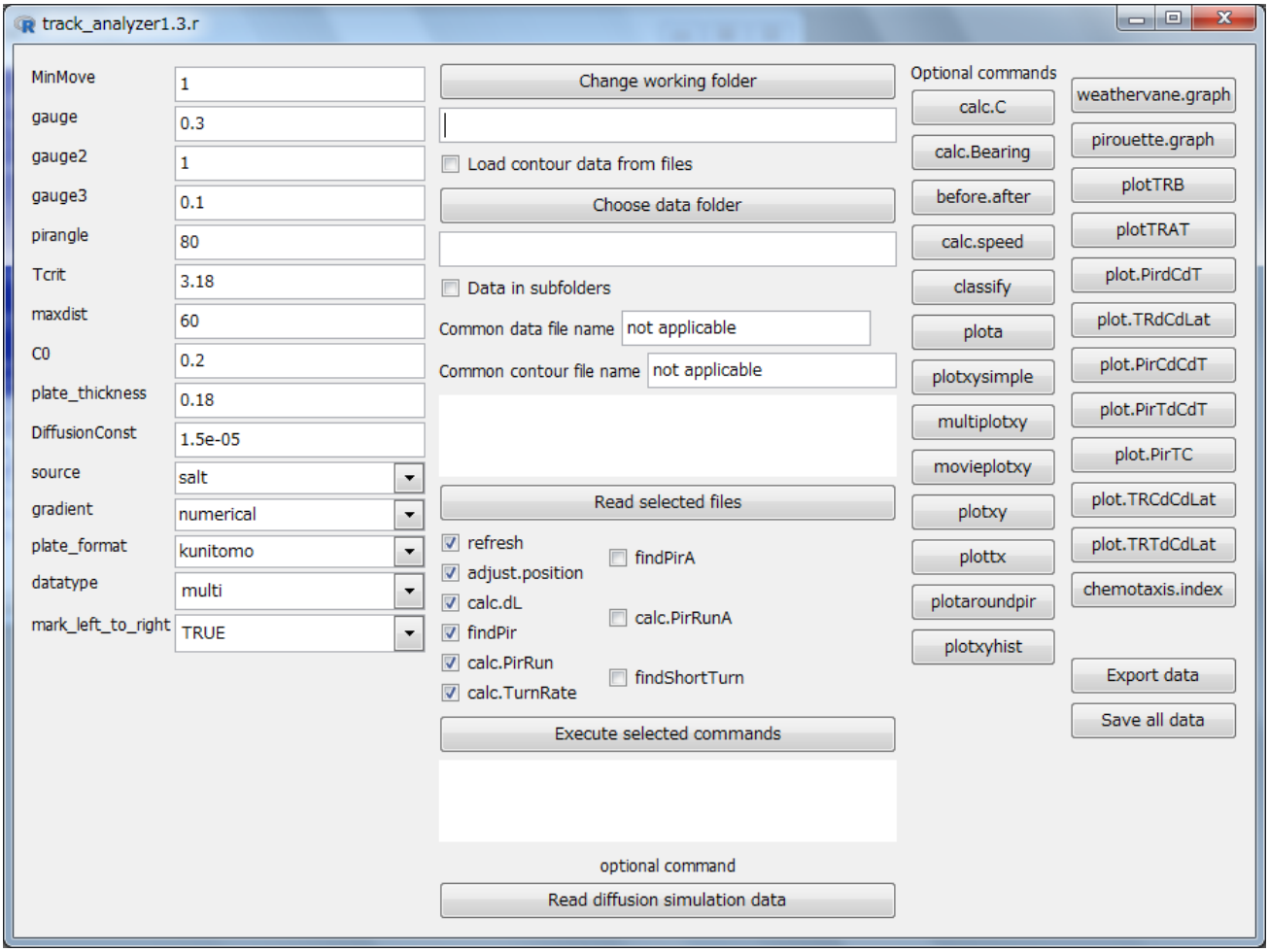
exists(“variable name”) : to see whether the variable exists,

length(“variable name”) or dim(“variable name”): to see the size of that variable

For details, refer to “How to use wt0.1.pdf”.

Note) gWidgets seems to have a poor compatibility with RStudio and therefore R console is recommended over RStudio.

<Usage>



<< Arrangement of data files>>

In ver1, default arrangement was to place track data (“dustress-result.txt”, the output of LuCamTracker) from all experiments in one folder (e.g. “data folder”). However, in ver1.3, standard arrangement is to put data in separate subfolders, one for each experiment. In this case, names of data files should be common, which should be entered in the ”Common ... file name” box. Check ”Data in subfolders”. Choose the parent folder by the ”Choose data folder” button, then a list of subfolders will be shown in the window.

Worm contour data （contour.data as output of LuCamTracker) can be read in ver1.3. In this case check ”Load contour data from files”. Place the contour data along with “dustress-result.txt” in each subfolder for each experiment. Do not place the files in lower levels.

When all data are put in a common folder, each pair of files (with extensions .txt and .data) must have the same names differing only in the extensions.

1. Click “Change working folder” button and change the working folder if you need to change it from the default.
2. Click “Choose data folder” and choose the folder with the outputs of multiworm tracker (such as ”data ..... dustless.txt”) or the parent folder. The content of the folder will be shown in the box below.
3. Click “Read selected files” button and read data. If you have selected some files or folders selected files/folders will be read, otherwise all files/folders will be read.
4. Process the data by checking the commands you need to execute (if you need to change the selection from default) and click “Execute selected commands” button. Note that findPir() will take considerable time to execute. The process of execution is monitored in R console and when all commands are finished “All completed” will be shown.
5. (Optional) when you want to use the result of diffusion simulator, click “Read diffusion simulation data” button, select the appropriate data files (in sequential numbers) and read the data.
6. When you have read the salt concentration gradient data, click calc.c, then concentration information will be calculated.
7. If you want to calculate the bearing of chemical peak relative to worm locomotion direction (Bearing） click calc.Bearing.
8. Click before.after when you want to calculate the locomotion direction before and after pirouette.
9. If you want to calculate mean speed in intervals based on V or dV (instaneous speed) then click calc.speed.
10. For other calculation/plot commands, see “Figures in wt and track_analyzer.pdf”. In these cases, if you need to specify parameters, use “ ” for texts and do not use “ ” for other values.
10. If you want to export data and process the data by Excel, click the “Export data” button. In the window that opens, select the variables to write to the file, put the name of output file and select the directory to write the file in.
11. To save all current data in R data format, click “Save all data”. Data will be saved in R data format (usually with the extension “.RData”), which can be opened by double click or “read working space” from R command bar, then you can continue processing.
12. Finish track_analyzer by clicking X in the upper corner of track_analyzer window.