Package Documentations-normfluodbf

NORM\_TIDY\_DBF (SHOULD HAVE BEEN NORM\_DIRTY\_DBF)

Title: Cleans and Normalizes ".dbf" data files obtained from experiments using the FLUOstar Omega (Ω) microplate reader (from [BMG LABTECH](https://www.bmglabtech.com/en/about-us/)).

Description: The simplest function utilization scenario entails an input of the path to a ".dbf" file obtained from the FLUOstar microplate (usually a 96-well microplate) reader; In a single step, this function will create a data frame, clean the data frame, normalize the data frame, append a "Cycle\_Number" attribute, perform an adjustment to the “time” attribute and return a data frame that is ready for analysis.

Since the initial publication of this package, several changes have been made to improve the user experience and to give the user more options to fine-tune the output from the package to meet the users’ aesthetic needs. Users who decide to move past the simplest utility scenario have been given more options to customize the output based on the users’ needs. Notably, several normalization sub-parameters have been provided in the package which yields different outputs based on what the user is used to seeing.

Just as the FLUOstar instrument is built to handle an array of assays, this function is designed to be multi-dimensional (meaning it can handle data with the same DBF extension from other assay types), on the condition that the data from assay types other than liposome flux assays follow the same data format this package was designed to handle. Of course, users of this package are advised to pre-analyze DBF files from other assay types to ensure they are compliant with this package (compliance in this scenario is simple meaning DBF files from other assays should be like DBF files from liposome flux assays).

Parameters: Not placed here. No need to eat up space. Proofread in the package.

Note:

* The default normalization sub-parameter outputs values in the 0-1 range. Unless a “norm\_scale” level is specified by the user, the default output is in the 0-1 range.
* The “norm\_scale” sub-parameter “decimal” is a machine-learning tool and should be avoided; it also provides no advantage for basic research analysis as its output operates on a sliding scale just like the raw data.
* Logarithmic transformation provides a minuscule advantage in data analysis and could/should be avoided.
* Backward compatibility is maintained in all updates, so there should be no issues with using the package the way the user was used to.
* The last NOTE is that if the user has no real clue how to analyze their data and just inputs a link to the dbf file, the program returns a 0-1 scale normalized data frame.
* Example (Check out in a more relaxing state as I enjoy the learning process)
* The favorite "norm\_scale" level is "z-score" since it divides the axis into negative and positive, thus facilitating interpretation.

Unique\_identifier function

Title: A function to append a unique identifier attribute to any data frame within the normfluodbf package.

Description: The function in the context of normfluodbf creates an attribute called Cycle\_Number and appends this attribute to the cleaned or wrangled data frame derived from the dirty DBF file.

Param: df A data frame with n number of rows

Return: A data frame with the Cycle\_Number attribute appended to the end of the data frame.

Note: The function operates in a closed system, meaning it is primarily designed to work with this package ONLY. Other use cases are simply a coincidence.