Plethysmography is used to measure respiratory functions in both human and lab animal. Respiratory waveforms, air analysis, temperature and electrophysiology are recorded into data sets. Currently, we use LabChart to record data. We will pick up data set manually and transfer the data to excel sheet and MATLAB for further analysis. This process is time consuming and artificial.

To get more consistent results, I use "Plethysmography.py" to automated analyze multiple input files (.txt) and produce figures.

To run the "Plethysmography.py", simply enter the folder of the program by type "cd <path." and the type "python ./Plethysmography.py".

Experimental conditions are required by user inputs and are saved as "MUID.csv" under subfolder "/ExpInfo".

Experimental data inputs are converted by LabChart to "MUID.txt" and "MUID_comment.txt". (MUID indicate the experimental ID of each mouse)

Each mouse data will be saved as "MUID_data.csv" and will be summarized into "MUID.csv" under subfolder "/MUID"

Figures will be then generated and saved as "Title.tif" under subfolder "/figures")

Title includes 8 different parameters we are looking at: Respiratory Rate, Tidal Volume, Tidal Volume (Body Weight normalized), Minute Ventilation, Oxygen Consumption, Carbon Dioxide, Minute Ventilation normalized to Oxygen Consumption, and Temperature.

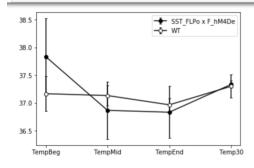
Packages required: os, numpy, scipy, pandas, matplotlib, datetime, csv, neurokit

Examples:

input:	Out	put:	
M27699_comment	>	Explnfo	
M27699.txt			
M28041_comment		figures	
M28041.txt	>	MUID	
M28042_comment		M27699_data.csv	
M28042.txt		M28041_data.csv	
M28043_comment			
M28043.txt		M28042_data.csv	
M28045_comment		M28043_data.csv	
M28045.txt		M28045_data.csv	
M28641_comment			
M28641.txt		M28641_data.csv	
main()			
Start a new project? (y/n): y			
<pre>ExpCon, Treatment, GenoGroups, Dose = NewProj()</pre>			
Experimental Conditions (hypoxia or hypercapnia): hypoxia CNO? (y/n): y Dose (mg/kg): 1 List all the genotypes in this project (separate by ;): SST_FLPo x F_hM4De;WT			

path, files = LoadFiles() The path of file:/Users/huananshi/Documents/Graduate school/Second year /Python/project File (MUIDs) names (separate by ;):M27699;M28041;M28042;M28043;M28045;M28641 file2, Stat = ExpInfo(files,path) M27699 Sex (m/f): m Genotype: SST_FLPo x F_hM4De Group (Exp or Con): Exp Body Weight (g):25.4 Beginning Temperature (C): 39.2 Middle Temperature(C): 36.4 End Temperature (C): 36.1 Post 30 min Temperature (C): 37.2 Room Temperature(F): 69.5 Barometric Pressure (inHg): 29.58 Experiment Date (mm/dd/yy): 11/18/17 Birth Date (mm/dd/yy): 9/22/17 M28041 Sex (m/f): f Genotype: WT Group (Exp or Con): Con Body Weight (g):21 Beginning Temperature (C): 37.7 Middle Temperature(C): 37 End Temperature (C): 36.9 Post 30 min Temperature (C): 37.7 Room Temperature(F): 67 Barometric Pressure (inHg): 29.7 Experiment Date (mm/dd/yy): 1/15/18 Birth Date (mm/dd/yy): 10/25/17 DAQ(files,path) %%%%% M27699 done%%%%% %%%%% M28041 done%%%%% %%%%% M28042 done%%%%% %%%%% M28043 done%%%%% %%%%% M28045 done%%%%% %%%%% M28641 done%%%%%

Report(path, Stat, Treatment, ExpCon, CompiledData, CompiledTemp, GenoGroups)



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