MWT analysis manual

for Alcohol Worm Team

Conny Lin

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Generals

Remember to eject the hard drive safely each time you switch computers, tidy up the cables, and return it to Conny's desk after you are done.

Reporting

1. The Beethoven Analysis program will create a folder called "Matlab Analysis" under your Beethoven folder.
2. Upload the Matlab Analysis folder onto your dropbox folder you have shared with Conny. Rename the Matlab Analysis folder to the name of your experiment (i.e. 10sISI_20132523C_NG) so Conny knows which experiment this analysis file refers to.
3. Email the "GraphCombine.tif" file to Conny. In the email copy and paste your experiment folder name.
4. If you are reporting in the lab meeting, copy and paste the .tif file into Powerpoint.

Step1: Organize And Prepare Data

Standard

Program name: MWTorgfiles(pFun,pExp)

Before you start:
Your Experiment folder should contain a list of zipped or unzipped MWT files like "20130708_122206". Do not group the folders. If you have, you must ungroup them before you start. If you don't see your folder under Student_Folder, you don't have an experimenter code assigned in this program so this program will not work for you. Please talk to Conny to a personal folder. Make sure the EACH of your MWT run files are named correctly. If not, please see trouble shoot section to correct for the naming.

1. Transfer MWT files to Hard drive "Flame" (the red lego one on Conny's desk), under "Student_Folders/[Your Name]".
2. Go to a Mac computer in the lab. Double click Matlab program to open it
3. Drag experiment folder into Command Window, you will see this:

```
EDU>> cd('/Users/connylinlin/MatLabTest/Orgfiles/PersonalFolders/Nicole
Gehring/20130523A_NG_100s30x10s10s')
```

4. Enter

```
pExp=cd
```

5. Drag the matlab function folder called "Step1_MWTOrgFiles" in Command Window, you will see this after you dragged it in. You must drag the experiment folder and then Matlab program folder. Otherwise, Matlab will not run.

```
EDU>> cd('/Users/connylinlin/Documents/Lab/Methods &
Database/Analysis/MatlabProgramming/Program_Coding/PublishReady/Step1_MWT
OrgFiles_v20130719P')
```

1. Enter

```
pFun=cd
```

2. Copy and paste into the Command Window, then press enter:

```
MWTorgfiles(pFun,pExp);
```

3. You will see a warning message as below. Follow the instruction as below:

```
This program only works with ungrouped MWT files...
Please enter(1) to stop the program if your data is grouped,
otherwise, enter any key to continue:
```

4. If the files are zipped, the program will start unzipping so it can access information in the MWT files. This will take some time. You will see message like this below:

```
unzipping files, please wait...
```

5. The program will generate unique group code from your MWT runs. (This is why correct naming is extremely important). You will see below. Enter the name of your groups as prompted. For example, group a can be N2, group b can be N2_400mM

```
'a'
'b'
'c'
'd'
type in the name of each group as prompted...
name of group a:
```

6. Once you finish entering all of the names, you will see below. Enter 1 to confirm and 0 to re-enter.

```
name of group a: N2
name of group b: N2_400mM
name of group c: KP1580
name of group d: KP1580_400mM
    'a'    'N2'
    'b'    'N2_400mM'
    'c'    'KP1580'
    'd'    'KP1580_400mM'

is this correct? (y=1,n=0)
```

7. Sometimes the sequence you'd like your groups to appear on the graph is not the same as the sequence your groups are named. Enter 0 if you'd like to change the sequence.

```
    [1]    'a'    'N2'
    [2]    'b'    'N2_400mM'
    [3]    'c'    'KP1580'
    [4]    'd'    'KP1580_400mM'

is this the sequence to be appeared on graphs (y=1 n=0): 1
```

8. If you choose to change the sequence of your groupings, you will see below. Enter the desired sequence such as "2 3 1 4" with space in between (no space at the end!!!).

```
Enter the index sequence to appear on graphs separated by space...
```

9. If you enter "2 3 1 4", you will see something like this. Enter 1 if it is correct, enter 0 if you'd like to change it.

```
Enter the index sequence to appear on graphs separated by space...
2 3 1 4
    [2]    'b'    'N2_400mM'
    [3]    'c'    'KP1580'
    [1]    'a'    'N2'
    [4]    'd'    'KP1580_400mM'
is this correct(y=1 n=0):
```

10. The file transferring and copying will take some time. When the program completed, you will see below. In your personal folder, you will have a copy of zipped files, a Groups*.mat file. Your data will be backed-up in Raw_Data, and another copy in Conny's folder. Please proceed to Beethoven analysis using the experiment folder in your personal folder.

```
File organization done, proceed to Beethoven analysis...
```

Manually group folder

1. Group your MWT files into experimental groups (i.e. N2, N2_400mM), put it all under a folder called "Raw_Data".
2. Zip all MWT files within each folder
3. Transfer your whole experiment folder to your personal folder in the Flame hard drive
4. Make a copy of "Raw_Data" called "Beethoven" under the same experiment folder

Step2: Choreography Analysis (Extracting Data)

Beethovenv3_v20130712P

This is the most current version (2013/07/12). Please use this code for analysis unless otherwise specified.

This analysis use java code (Beethoven_v3):

```
java -jar '/home/crankin/Desktop/Beethoven_v2.jar'
/home/crankin/Desktop/Chore_1.3.0.r1035.jar' -p 0.027  -s 0.1 -t 20 -M 2
--shadowless -S –o
1nee#e*ss#s*SS#S*ll#l*LL#L*ww#w*aa#a*mm#m*MM#M*kk#k*bb#b*pp#p*dd#d  --
plugin Reoutline::exp  --plugin Respine  --plugin
MeasureReversal::tap::dt=1::collect=0.5::postfix=trv
```

1. Go to Linux analysis computer
2. Go to “places” click on “computer” and then your external hard drive
3. Open java
4. Copy and paste code above:

```
java -jar '/home/crankin/Desktop/Beethoven_v2.jar'
/home/crankin/Desktop/Chore_1.3.0.r1035.jar' -p 0.027  -s 0.1 -t 20 -M 2
--shadowless -S –o
1nee#e*ss#s*SS#S*ll#l*LL#L*ww#w*aa#a*mm#m*MM#M*kk#k*bb#b*pp#p*dd#d  --
plugin Reoutline::exp  --plugin Respine  --plugin
MeasureReversal::tap::dt=1::collect=0.5::postfix=trv
```

5. Press enter
6. Enter time range
    a. For 10sISI, enter 90:410
    b. For 60sISI, enter 90:1960
    c. For other set up, enter the experiment total duration after “90:”. For example, if your experiment duration is 3000 seconds, enter 90:3000
7. Enter number of folders to be analyzed. If you have a folder of ungrouped MWT folders, you can just enter 1.
8. Drag in first group folder under your “Beethoven” folder, press enter. Drag in second group folder, press enter. Drag in the subsequent folders and press enter after each drag
9. When asked whether you would like to standardize, answer “n”
10. When asked whether you like to generate Combined group, answer “n”
11. Press enter and wait for analysis program to complete. If your analysis is successful, you will see a combined graph generated under “Beethoven” folder.

Traditional Beethoven Analysis

This will generate you Beethoven Tap_Freq.dat and Tap_Dist.dat summary files. You may run this with grouped or ungrouped data. Beethoven only process .zip files and does not tolerate file names with space in it.

1. Go to Linux analysis computer

2. Go to “places” click on “computer” and then your external hard drive
3. Open java
4. Type in **java –jar** (space between java and –jar and a space after). Drag Beethoven_V2.jar into the java window. Click on the java window to return to it. Then press enter.
5. Enter time range
    a. For 10sISI, enter 90:410
    b. For 60sISI, enter 90:1960
    c. For other set up, enter the experiment total duration after “90:”. For example, if your experiment duration is 3000 seconds, enter 90:3000
6. Enter number of groups to be analyzed
7. Drag in first group folder under your “Beethoven” folder, press enter. Drag in second group folder, press enter. Drag in the subsequent folders and press enter after each drag
8. When asked whether you would like to standardize, answer “N”
9. When asked whether you like to generate Combined group, answer “Y”
10. Press enter and wait for analysis program to complete. If your analysis is successful, you will see a combined graph generated under “Beethoven” folder

Step 3: Graphing data for individual experiments

Current release: Step3_AnalysisOne_R20130719
This program uses function AnalysisOne(pExp,pFun,ID). ID defines which analysis to use.

Analysis ID	What can this be used for
'Raw1'	Use this if your MWT folders were grouped into folders when you do Beethoven v3 analysis.
'Raw2'	Ungrouped MWT data analyzed by Beethoven v3
'G1'	You have already analyzed this set of data before (i.e. analyzed using 'Raw1' and have a import.mat file created from previous Raw analysis
'G2'	You have already done Raw analysis and have import.mat file in your experiment folder. This analysis produces standard habituation graphs in distance and probability

Standard habituation curve analysis (G2)

1. Go to a Mac computer with Matlab. Double click Matlab program to open it
2. Drag experiment folder into Command Window, you will see this:
   ```
   EDU>> cd('/Users/connylinlin/MatLabTest/Orgfiles/PersonalFolders/Nicole Gehring/20130523A_NG_100s30x10s10s')
   ```
3. Enter
   ```
   pExp=cd
   ```
4. Drag the matlab function folder called "Step1_MWTOrgFiles" in Command Window, you will see this after you dragged it in. You must drag the experiment folder and then Matlab program folder. Otherwise, Matlab will not run.
   ```
   EDU>> cd('/Users/connylinlin/Documents/Lab/Methods & Database/Analysis/MatlabProgramming/Program_Coding/PublishReady/Step1_MWT OrgFiles_v20130719P')
   ```
5. Enter
   ```
   pFun=cd
   ```
6. Type in
   ```
   AnalysisOne(pExp,pFun,'G2');
   ```
7. Follow on screen instructions.

Combining multiple experiments

Statistical analysis

Trouble shooting

Correct file names

Program name: correctMWTname_mat

This can be done after running

1. Drag your folder

Program name: CorrectMWTname_v20130705

You must start with unzipped files

1. Drag file into Matlab command window
2. Run

```
Name to be fixed is...
N2_3x4_l96h20C_100s30x10s10s_A0519cb
N2_3x4_l96h20C_100s30x10s10s_A0519cb
new name: N2_3x4_l96h20C_100s30x10s10s_A0519cb
Is this Correct (1=yes, 0=no): 0
N2_3x4_l96h20C_100s30x10s10s_A0519cb
    [ 1]    'full name'
    [ 2]    'Strain'
    [ 3]    '# worms used to sync'
    [ 4]    'length of sync (hr)'
    [ 5]    'Synchronize code'
    [ 6]    'Age of worms (hh)'
    [ 7]    'culturing temperature'
    [ 8]    'preplate (s)'
    [ 9]    'number of taps'
    [10]    'ISI'
    [11]    'time(s) > last tap'
    [12]    'tracker code'
    [13]    'date of sync'
    [14]    'group code'
    [15]    'plate code'

Which of the above code do you want to fix? 1
Enter correct full name: KP1097_3x4_l96h20C_100s30x10s10s_A0519cb

KP1097_3x4_l96h20C_100s30x10s10s_A0519cb
Is this correct (1=yes, 0=no)? 1
name is corrected to...
KP1097_3x4_l96h20C_100s30x10s10s_A0519cb
```