***New box analysis***

commands in blue

example commands in green

PC commands in lilac

LL - 12/7/16 - changed instructions to reflect move from tier2 to dm11, and added command for use on a PC.

**Step 1: Copy files from computer to dm11**

1) Open **Terminal** application (make sure you are either on Secure wifi or plugged in to the network through ethernet)

2) Type ssh boxuser@flyolympiad Password is: b0xuser!

3) Type cd box

4) Type cd scripts

5) (optional) Type vim copy\_apollo\_experiments.sh or vim copy\_orion\_experiments.sh to check and edit the files

6) Run script by typing ./copy\_apollo\_experiments.sh and/or ./copy\_orion\_experiments.sh

./copy\_apollo\_experiments.sh && ./copy\_orion\_experiments.sh

This step takes a long time (over an hour).

* Once this script is run, the files should be copied from the PC in the room which runs the boxes to smb://dm11/groups/reiser/flyvisionbox/box\_data
  + from windows: \\dm11.hhmi.org\groups\reiser\flyvisionbox\box\_data
* each experiment folder should contain the following at this point of the analysis:
  + Two folders named 02\_5.34\_34 and 01\_5.34\_34
    - Each of these folders contains 4 avi files, 4 avi.mat files, one .seq file and two matlab files (.mat or .m)
  + Seven files:
    - Two .mat files titled 01\_Transition\_to\_5.34 and 02\_Transition\_to\_5.34
    - ROI.txt
    - TheBoxDefaultXmlFile\_last.xml
    - Experiment\_Name\_Metadata.xml
    - Experiment\_Name\_RunData.mat
    - Experiment\_Name.exp

**Step 1.5: Repair manually stopped runs**

Need to be repaired:

10/13 Orion SS33673

11/3 Orion SS28175

**Step 2: Track movies**

Once all of the files have been copied over, we want to track them

1) Type cd ../ if still in the scripts folder or cd ./groups/reiser/home/boxuser/box/

* Go into the manual pipeline folder for tracking box experiments
* The processing time of step2 may have timed you out of your login. If it can’t find this directory, login again following steps 1.1 and 1.2

cd ..

# (should now be in ~/box/)

2) Type cd ./00\_incoming

* Move into the 00\_incoming folder

cd 00\_incoming

3) Type ls

* List all of the items in the 00\_incoming folder. This should return nothing because 00\_incoming should be empty. If there are items in here, let me know...

ls

# List all of the items in the 00\_incoming folder. This should return nothing because 00\_incoming should be empty. If there are items in here, let me know...

4) Type ln -s <FULL PATH TO DATA IN DM11>/\* .

* Creates symbolic links of the experiment folders in the 00\_incoming folder
  + e.g.   ln -s /groups/reiser/flyvisionbox/box\_data/\*20170826\* . (note the space between the last asterisk and the period)

replace only the date between the asterisks.

20170929T143536

20171006T141951

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20170929\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171006\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171013\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171020\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171027\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171103\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171110\* .

5) Type cd ..

* Go back one folder

6) Type ./scripts/TubeSplitter/avi\_extract.sh

* Run the script to split 1 movie into 6, each containing a tube. **Don’t run the next step until this one is finished!**
  + You can check on the progress of this step by typing ‘bjobs’, which should just show you a bunch of jobs.
  + If you don’t have bjobs enabled on your computer yet, run the command
  + . /misc/lsf/conf/profile.lsf while logged in as the boxuser

Errors:

[flyolympiad - boxuser@e01u09]~/box>bjobs

bash: bjobs: command not found

. /misc/lsf/conf/profile.lsf

bjobs

* Once bjobs returns nothing, the process is complete
* In addition to the files and folders listed above, this step added the following:
  + Inside each of the 02\_5.34\_24 and 01\_5.34\_34 folders:
    - 24 new avi files and a file called “6”
  + A folder named “Logs”\

7) Type ./scripts/SBFMFConversion/avi\_sbfmf\_conversion.sh

* **Again, don’t run the next step until this one is finished** — you can check on all of these jobs with ‘bjobs’.
* This converts the movies from .avi to .sbfmf.
* After this script is run, the following changes are made inside each of the 02\_5.34\_24 and 01\_5.34\_34 folders:
  + the 24 avi files made in the last step are gone
  + 6 new sbfmf folders appear, one for each tube
  + Each of the 6 new sbfmf folders created contains 9-11 files: four .sbfmf, three-five .log, one .summary, and one .pickle

./scripts/SBFMFConversion/avi\_sbfmf\_conversion.sh

bjobs

# this step also takes a long time

8) Type ./scripts/FlyTracking/fotrak.sh

* This tracks the movies.
* After this script is run, the following changes are made to the contents of each experiment:
  + The folder Output\_1.1\_1.7 is created.
    - Inside this folder are 2 other folders called 02\_5.34\_24 and 01\_5.34\_34
    - Inside each of those folders will be 24 additional folders
    - Each of the 24 folders contains 11 files: 5 .mat, 4 .bmp, 1 .xls, & 1 .txt

9) When that’s done, type cd ./02\_fotracked

* Go into the output folder

10) Type ls

* This checks to make sure your files made it through the pipeline! If they’re all there, move onto the next step. If they’re not there, something went wrong somewhere.

11) Type rm ./\*

* Remove the symbolic links from the pipeline folders

**Step 3: Analysis**

Now that the movies have been copied and tracked, we can do analysis

1) Make sure you are connected to the server smb://dm11.hhmi.org/flyvisionbox (not flyvisionbox/box\_data) on your computer. If not, and you’re on a Mac, go to Finder> Go> Connect to server. If not, and you’re on a PC, map network drive \\dm11.hhmi.org\flyvisionbox

2) In the terminal application, type cd .. if still in the box folder and then cd /dm11/flyvisionbox/box\_data

        -on a PC: do this in GitShell instead:

               cd  //dm11.hhmi.org/flyvisionbox/box\_data

* depending on the amount of time it takes to complete step2, you may need to sign in  again before trying this step by typing ssh boxuser@flyolympiad . Password is: b0xuser!

3) Type ls and copy all of the folder names in case they are needed later

4) Log out of boxes by typing logout in the terminal.

5) To make sure you’re using the most up-to-date matlab files for analysis:

a. If this is the first time you’re using git, you must first copy the “repository” somewhere you can use it. For example:

i. cd Documents/MATLAB/Box

ii. git clone https://github.com/JaneliaSciComp/flyvisionbox analysis-code

b. Navigate to the analysis-code folder in the terminal.

E.g. cd Documents/MATLAB/Box/analysis-code

c. Type git pull

6) Open MATLAB. cd into the analysis-code folder mentioned above. Execute the command modpath to add all the needed code to your Matlab path. For example:

a. cd Documents/MATLAB/Box/analysis-code

b. modpath

7) In batch\_analysis.m, make sure the flyvisionbox\_folder\_path directory (lines 14-21) is correct.

* For example, if you’re on a Mac, in most cases it should read ‘/Volumes/flyvisionbox/box\_data’

8) Open the MATLAB function “update\_boxdata\_mat\_file.m”. This compiles all experiments into a struct and classifies them by various features.

9) Check to make sure the control genotypes listed from lines 34 to 42 are correct.

10) Determine the first argument to batch\_analysis().

* *If you wish to analyze all the experiments from a given date* (most common), then call batch\_analysis like this: batch\_analysis(‘20170810’)
* I*f you need to analyze individual experiment from disparate dates*, then call batch\_analysis like this: batch\_analysis({'pBDPGAL4U\_shi\_Apollo\_20160610T102049' 'pBDPGAL4U\_shi\_Orion\_20160610T090339'} I.e. pass it a list of the file names you want to analyze

11) *If your experiments require the gal4 controls* instead of the split control, give a second argument to batch\_analysis, like this: batch\_analysis(‘20170810’, ‘gal4’). If the split control, use only one argument, or use ‘split’ for the second argument.

12) Run batch\_analysis, giving it appropriate arguments for your use-case.

13) To collect all the comparison summaries into one folder in the flyvisionbox, go back to your terminal and sign in by typing ssh boxuser@login1 Password is: b0xuser!

14) type cd /../groups/reiser/flyvisionbox

15) type ./copy\_cs.sh

16) To plot duplicates on the same graphs, run the function “plotduplicates” found in the Analysis.git folder in MATLAB

* This function will not plot anything for which a graph already exists in the folder. I.e. if you run it and a sample had two runs, it will not plot the third one run on a later date. The original graph will need to be deleted from the folder in order to run this function again and get all three runs plotted on one graph

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171020\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171027\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171103\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171110\* .

# ln -s /groups/reiser/flyvisionbox/box\_data/\*20171117\* . ?

1 batch\_analysis.m

2 copy\_cs.sh

**Additional Notes for Troubleshooting**

# Need to be repaired:

# 10/13 Orion GMR\_SS33673

# 11/3 Orion GMR\_SS28175

# find the runs:

# find . -regex 'GMR\_SS33673.\*' -type d

# GMR\_SS33673\_shi\_Orion\_20171013T125853

# JHS\_K\_85321\_shi\_Orion\_20171013T153903

# FULLNameOfStalledExperiment=GMR\_SS33673\_shi\_Orion\_20171013T125853

# NameOfStalledExperiment=GMR\_SS33673\_shi\_Orion

# FULLNameOfCompletedExperiment=JHS\_K\_85321\_shi\_Orion\_20171013T153903

# NameOfCompletedExperiment=JHS\_K\_85321\_shi\_Orion

cd GMR\_SS33673\_shi\_Orion\_20171013T125853

cd 02\_5.34\_34

cp ../../JHS\_K\_85321\_shi\_Orion\_20171013T153903/02\_5.34\_34/\*.mat .

cp ../../JHS\_K\_85321\_shi\_Orion\_20171013T153903/02\_5.34\_34/sequence\_details\_JHS\_K\_85321\_shi\_Orion.m .

cp ../../JHS\_K\_85321\_shi\_Orion\_20171013T153903/02\_5.34\_34/5.34.seq .

mv sequence\_details\_JHS\_K\_85321\_shi\_Orion.m sequence\_details\_GMR\_SS33673\_shi\_Orion.m

vim sequence\_details\_GMR\_SS33673\_shi\_Orion.m

:%s/JHS\_K\_85321/GMR\_SS33673/g

# shift + zz

# GMR\_SS28175\_shi\_Orion\_20171103T130227

# JHS\_K\_85321\_shi\_Orion\_20171103T153927

# FULLNameOfStalledExperiment=GMR\_SS28175\_shi\_Orion\_20171103T130227

# NameOfStalledExperiment=GMR\_SS28175\_shi\_Orion

# FULLNameOfCompletedExperiment=JHS\_K\_85321\_shi\_Orion\_20171103T153927

# NameOfCompletedExperiment=JHS\_K\_85321\_shi\_Orion

cd GMR\_SS28175\_shi\_Orion\_20171103T130227

cd 02\_5.34\_34

cp ../../JHS\_K\_85321\_shi\_Orion\_20171103T153927/02\_5.34\_34/\*.mat .

cp ../../JHS\_K\_85321\_shi\_Orion\_20171103T153927/02\_5.34\_34/sequence\_details\_JHS\_K\_85321\_shi\_Orion.m .

cp ../../JHS\_K\_85321\_shi\_Orion\_20171103T153927/02\_5.34\_34/5.34.seq .

mv sequence\_details\_JHS\_K\_85321\_shi\_Orion.m sequence\_details\_GMR\_SS28175\_shi\_Orion.m

vim sequence\_details\_GMR\_SS28175\_shi\_Orion.m

:%s/JHS\_K\_85321/GMR\_SS28175/g

# should say 18 substitutions on 18 lines

# shift + zz

**A note for A Stalled Experiment:**

* Every now and then, the experiment will finish, but the robot does not terminate the run and it must be manually terminated.
* When this happens, certain .mat files will not be included in the folder. We can copy them from another experiment on the same day, since they mostly contain the same information, and then change the name from the good experiment to the stalled experiment.
* Navigate to the folders missing files
  + Type ssh boxuser@flyolympiad Password: b0xuser!
  + Type /Y:/
  + cd /groups/reiser/flyvisionbox/box\_data/
  + Type cd FULLExperimentName
    - Example cd JHS\_K\_85321\_Kir21DL\_Orion\_20160916T140039
  + Type cd 02\_5.34\_34
* Copy files from another experiment run on Orion and run the same day (note the space and periods after each command)
  + Type cp ../../FULLNameOfCompletedExperiment/02\_5.34\_34/\*.mat .
  + Type cp ../../FULLNameOfCompletedExperiment/02\_5.34\_34/sequence\_details\_NameofComplete.m .
  + Type cp ../../FULLNameOfCompletedExperiment/02\_5.34\_34/5.34.seq .
    - Example
      * cp ../../JRC\_SS03760\_Kir21DL\_Orion\_20160916T125558/02\_5.34\_34/\*.mat .
      * cp ../../JRC\_SS03760\_Kir21DL\_Orion\_20160916T125558/02\_5.34\_34/sequence\_details\_JRC\_SS03760\_Kir21DL\_Orion.m .
      * cp ../../JRC\_SS03760\_Kir21DL\_Orion\_20160916T125558/02\_5.34\_34/5.34.seq .
* Rename files
  + Type mv sequence\_details\_NameofComplete.m sequence\_details\_NameofIncomplete.m
    - Example mv sequence\_details\_JRC\_SS03760\_Kir21DL\_Orion.m sequence\_details\_JHS\_K\_85321\_Kir21DL\_Orion\_20160916T140039.m
  + Type vim sequence\_details\_NameofIncomplete.m
    - Example  vim sequence\_details\_JHS\_K\_85321\_Kir21DL\_Orion\_20160916T140039.m
  + Hit the esc key to enter a mode where you can give commands in the vim editor. When you start typing the next line, the cursor will appear at the bottom of the page
  + Type :%s/Name\_of\_Complete/Name\_of\_Incomplete/g
    - Example :%s/JRC\_SS03760/JHS\_K\_85321/g
    - the colon indicates you are giving a command
    - The %s indicates you want substitutions to be made for the entire file
    - The g indicates global substitution. Without g, it will only replace the first instance in each line
  + hold shift key while typing z z to exit vim mode

**A Note for Removing Files from Flyvisionbox**

* Files cannot be removed manually from flyvisionbox because this requires special permission
* Sometimes, experiment runs have errors and must be removed so they do not affect analysis.
* Navigate to the folders you want to remove
  + Type ssh boxuser@flyolympiad Password: b0xuser!
  + Type cd /tier2/flyvisionbox/box\_data
  + Type rm -rf /tier2/flyvisionbox/box\_data/FULLExperimentName
    - e.g.  rm -rf /tier2/flyvisionbox/box\_data/GMR\_SS01596\_shi\_Orion\_20160212T094937

**A Note for Moving files in Flyvisionbox**

* Files cannot be moved manually around flyvisionbox because this requires special permission
* Sometimes, experiment runs have errors and must be removed so they do not affect analysis.
* To make a new folder:
  + Navigate to the directory you want to add it to
    - e.g. cd /tier2/flyvisionbox/box\_data
    - mv GMR\_SS33673\_shi\_Orion\_20170915T133244 bad\_experiments
  + Type mkdir NameOfNewFolder
* To move folders into a different folder:
  + Type mv NameOfFile NameOfNewFolder
    - e.g. cd /groups/reiser/flyvisionbox/box\_data/\*20170826\* .
  + Or if moving several files with a common string in their names, you can use:
    - mv NameOfFile\* NameOfNewFolder

**A Note for Removing Files from BoxData**

* When running the script getboxdata, information is stored in a .mat file in the flyvisionbox drive
* Occasionally, files need to be removed because of errors, but this will not change or replace the information already stored in BoxData.mat and may affect future experiments or analysis
* Find the entry in the BoxData.mat for the file you want to remove. Load the file into matlab from /tier2/flyvisionbox/box\_data
  + Type find(strcmp({BoxData.experiment\_name},’Full\_experiment\_name'))
    - E.g. find(strcmp({BoxData.experiment\_name},'GMR\_SS02427\_shi\_Orion\_20160222T134359’))
  + This will give you a number. Double check it is the correct entry by typing BoxData(#)
    - E.g. BoxData(345)
  + If it is correct, replace the entry with an empty array by typing BoxData(#)= [ ] ;
    - E.g. BoxData(345) = [ ];
    - Note, the brackets in matlab will not have a space between them. I added it here because in this font you couldn’t tell they were brackets without the space
  + Save your changes by typing save('/Volumes/flyvisionbox/BoxData.mat','BoxData’)

**A note for “Connection refused” error**

* From time to time, the IP address of the computers change. This will affect the ./copy\_apollo\_experiments.sh and ./copy\_orion\_experiments.sh
  + The error when you try to run this script will say e.g. " ssh: connect to host 10.102.32.49 port 22: Connection refused"
  + As of now, the scripts say the Orion IP address is 10.102.32.52 and Apollo IP address is 10.102.32.50
* To find the new IP address:
  + go to the computer and in windows click Start>run
  + When the new window opens, type cmd and click OK
  + when the new window pop up, type ipconfig and press enter
* To change the script to have the correct IP address:
  + Make sure you are logged in as boxuser and in box/scripts (see instructions in Step 1 above)
  + on the command line, type sed -i ’s/oldIP/newIP/g’ FULLFileName
    - e.g.  sed -i 's/10.102.32.50/10.102.32.52/g' copy\_orion\_experiments.sh
    - sed call the stream editor
    - -i: realtime works with file
    - s: substitute
    - g: global (or it will only replace the first one it sees on a line)

**A Note for Changing Line Name of Effector Name of experiments**

* If the incorrect name is selected during the experiment, or if we change the name of a line at a later point, it is useful to know how to go into the box data and alter the information in the files
* Navigate to the folder you wish to alter the name of
  + Type ssh boxuser@flyolympiad Password: b0xuser!
  + Type cd /tier2/flyvisionbox/box\_data
  + Rename the file in boxdata by typing mv OldFullExperimentName NewFullExperimentName
    - Example mv GMR\_SS02404\_Kir21DL\_Apollo\_20160916T145007 GMR\_SS02404\_UAS\_Shi\_ts1\_UAS\_Kir21\_Apollo\_20160916T145007
  + Navigate into the folder to change internal folders and files
    - Type cd FULLExperimentName
    - Example cd GMR\_SS02404\_UAS\_Shi\_ts1\_UAS\_Kir21\_Apollo\_20160916T145007
  + Do a search and replace within all files to change the name. This may take a while. Be patient. When the command line returns, it is done. If it takes more than 10min, something went wrong.
    - Type grep -lr ‘oldword' . | xargs sed -i 's/oldword/newword/g'
    - Examples
      * grep -lr 'DL\_UAS\_GAL80ts\_Kir21\_23\_0010' . | xargs sed -i 's/DL\_UAS\_GAL80ts\_Kir21\_23\_0010/UAS\_Shi\_ts1\_UAS\_Kir21/g’
      * grep -lr 'Kir21DL' . | xargs sed -i 's/Kir21DL/UAS\_Shi\_ts1\_UAS\_Kir21/g'
    - grep: searches for text in files recursively in a directory.
    - The -l flag for grep tells it to only output file names when it finds a word match. (lowercase L)
    - The -r flag tells grep to search recursively in the directory, i.e. it will also look in subfolders if applicable.
    - The dot (.) tells grep to look in the current directory. You can change that to a directory path, a specific file, or an asterisk (\*) if you want to search files in the current directory non-recursively.
    - The pipe (|) tells xargs to operate on the output of the grep command.
    - xargs tells sed to use the output of grep.
    - Sed calls the substitution editor
    - The i means “in place”, meaning the original file is modifed without ccreating a copy
    - s means substitute
    - g means  globally (otherwise it will just change the first instance on each line)
  + This last command will change the name within files, but not file names or folder names themselves.
    - Open each folder of your experiment using the cd and ls commands. Any incorrectly named files or folders can be renamed with the mv command
    - Example of an experiment getting all folder/file names replaced
      * cd GMR\_SS02404\_UAS\_Shi\_ts1\_UAS\_Kir21\_Apollo\_20160916T145007
      * ls
      * mv  GMR\_SS02404\_Kir21DL\_Apollo\_20160916T145007.exp GMR\_SS02404\_UAS\_Shi\_ts1\_UAS\_Kir21\_Apollo\_20160916T145007.exp
      * mv  GMR\_SS02404\_Kir21DL\_Apollo\_Metadata.xml  GMR\_SS02404\_UAS\_Shi\_ts1\_UAS\_Kir21\_Apollo\_Metadata.xml
      * mv  GMR\_SS02404\_Kir21DL\_Apollo\_RunData.mat  GMR\_SS02404\_UAS\_Shi\_ts1\_UAS\_Kir21\_Apollo\_RunData.mat
      * cd 01\_5.34\_34
      * ls
      * mv sequence\_details\_GMR\_SS02404\_Kir21DL\_Apollo.m sequence\_details\_GMR\_SS02404\_UAS\_Shi\_ts1\_UAS\_Kir21\_Apollo.m
      * cd ..
      * cd 02\_5.34\_34/
      * mv sequence\_details\_GMR\_SS02404\_Kir21DL\_Apollo.m sequence\_details\_GMR\_SS02404\_UAS\_Shi\_ts1\_UAS\_Kir21\_Apollo.m
        + Note that sometimes the time stamp is included in the "sequence details names", and sometimes not. Be sure to copy the name precisely

**A note for moving the entire project to a different disk location.**

* Update copy scripts
  + Open **Terminal** application (make sure you are either on Secure wifi or plugged in to the network through ethernet)
    - Type ssh boxuser@flyolympiad Password is: b0xuser!
    - Type cd box/scripts
  + Make backup copies of copy\_apollo\_experiments.sh and copy\_orion\_experiments.sh
  + Edit files
    - Type vim copy\_apollo\_experiments.sh or vim copy\_orion\_experiments.sh to edit the files
    - Replace old folder locations with new ones in the  3 lines after the "then".

---------------------------------------------------------------------------------------------------------------------------------------------

#!/bin/bash

ssh\_host="olympiad@10.102.32.52"

for line in `ssh $ssh\_host ls /cygdrive/e`

    do

        if ssh $ssh\_host "ls /cygdrive/e/$line/\*.exp 1> /dev/null 2>&1;"

            then

                scp -r $ssh\_host:/cygdrive/e/$line /tier2/flyvisionbox/box\_data/ && ssh $ssh\_host rm -rf cygdrive/e/$line

                chmod 755 $(find /tier2/flyvisionbox/box\_data/$line -type d)

                chmod 644 $(find /tier2/flyvisionbox/box\_data/$line -type f)

         fi

done

---------------------------------------------------------------------------------------------------------------------------------------------

* + If permission is denied for executing the file, use chmodugo+x <script name>  (e.g. chmodugo+x copy\_apollo\_experiments.sh )
* Update SBFMF conversion script