Rina Thesis Hardware:

In the main folder "Research Dr Lior" you can find the following folders:

1. **Dataset** – includes the all raw data sorted in folders:

All – includes neurons with all the neurites reconstruction and SSP.

no axons reconstruction - includes neurons with no axons reconstruction but with SSP.  
no axons reconstruction+SP - includes neurons with no axons reconstruction and no axon SSP.  
no axons SP - includes neurons with all the neurites reconstruction and but no axon SSP.  
no reconstruction - includes neurons with SSP but no reconstruction.  
no SP- includes neurons with all the neurites reconstruction and but no SP.  
no SP + no axons reconstruction - includes neurons with no axons reconstruction and no SSP.

Outliers – includes outliers reconstruction.  
  
Each neuron folder contains the raw data of its whole cell as well as its zoom in sections. In addition it contains a pptx file with the SSP annotation, a doc file "הערות" with comment regarding the number of time points and soma depth and another folder called "SNT" which has:   
\*a tif file for reconstruction.   
\*a trace file of the reconstructed cell using SNT plugin.   
\*snapshot of top\side view of the reconstructed cell.   
\*movies of the reconstructed cell.

1. **Swc dataset files** – in this folder there are folders with all swc files of our dataset and the other datasets sorted in folders.

Our dataset - includes all the swc files from all the neurons we have reconstructed (also the outliers). In addition, it includes matrices of the data in csv files;

* Mergedatall! – all the neuroanatomical data of all the neurons.
* All\_dataset2 – all the SSP data for all the neurons.
* Merged\_alldatset!!! – all the data of neuroanatomy and SSP for each neuron (not includes the outliers cells).
* Merged\_alldatset reduce! – all the data of neuroanatomy without SSP for comparing with the other datasets.
* Correlation – all the correlations we found in our dataset and their p values.
* Correlation all\_datset – correlations of significants p\_values.
* *All the files that ends with " –r "; it means reduced parameters (for datasets comparing)*
* Correlation\_p – the matrices for p colormaps.
* Correlation\_r – the matices for r colormap
* P\_fdr – the matrices for q colormap
* Fdr correction2 – all the correlation with the p values and the q values from Nitza.
* Parameters key – like the parameter list in the thesis.
* Depth\_groups – a matrix file in which we define the most superficial and the most deep neurons depth as the number 1 and 2 to compare between them relative to the other parameters by ttest. The results are in the files ttest by depth (.xlsx/.doc)

In adittion there are pdf files that were created from the python scripts. You can   
 understand what they mean from their names.   
 Also there are folders (correlation fdr, correlation 0.05 fdr) – with pdf files of   
 regression figures of significant correlations.

For the other datasets (the folders of: Human L2/3, Mouse L2/3, Rat L2/3, Rat L5 and RatIN) you can find:   
\* swc files of the cells. In most of the folders the relevant swc will be in a sub-folder called "trial". In this folder will be also;  
\* matrices of the neuroanatomy data that called: "merged\_trial reduce" (mouse L2/3), "trial\_human reduce", "mergedratL23 reduce", "ratIn", "ratL5 reduce".   
\* "FDR\_\_\_" – the p values and the q values for each correlation that we got from Nitza.  
\*p\_fdr – a matrix of q values for q colormap  
\*mse data \_\_\_\_ - the p value of the mse comparing between our data and the specific dataset (the similarity is the not significant p-values)  
\* pdf files that you can understand what they mean from their names. And from looking at them.   
\*In some datasets there is a folder with the name "corr" which has pdf files of   
 regression figures of significant correlations. (I am not sure if the siginicant correlations figures are before or after the fdr correction)  
  
Beside the folders of all the datasets there are 2 files:  
Datasets size – a summary of all the datasets amount and sizes.  
Datasets comparing – a pptx file with all kinds of comparing between the datasets.

1. **Images for Elad -** top and side view of reconstructed cells (not all of them), that I sent to Elad.
2. **SP correlation –**

"Dataset.xlsx" – Has 5 tabs:

1. Database – all information about each section in every neuron, includes section depth and soma depth. Each neuron's name colored by different color which represents the folder he came from (for example neurons from "all" colored by purple). The rows that colored with blue represent the average for all sections in each neuron neurite.
2. Formula – In this tab there are formulas that helped me to insert the numbers of arrows in the annotation and to calculate density, gain, loss and turnover rate.
3. SP – all the data SSP (average of sections) of neurons which have SSP.
4. SP vs somD – same as SSP + column with soma depth.
5. SP vs segD – all the data SSP (no average) + segment depth for each segment.

"SP.csv" – this is the matrix for SSP data of all 46 neurons with SSP (also with Gain and Loss).

"sp for corr.csv" - this is the matrix for SSP data of all 46 neurons with SSP including segment depth and distance.

"sp corr table.docx" – a table of our results of correlations SSP with depth.

Pdf files of regression correlations from data of "sp for corr".

1. **Job-** contains files of instructions for annotation and reconstruction.
2. **מאמרים ליאור כהן-** pdf files of articles we used for the proposal and thesis and also 2 folders (proposal and thesis) which has all the relevant summaries, presentations and figures.
3. **Scripts –** in this folder you can find Matlab and Python scripts for extracting parameters and creating figures from the swc files and matrices.

* Python scripts - Here is .py files with explanation of the code (it is a little bit messy).  
    
  1. "hncUtility.py" – this is a scripts with many functions that has been called by the other scripts. when you see 'hnc.\_\_\_\_' it means that we called for a fucntion from this script.

2. "rina\_neurom\_features\_3.py" – In this script you put a folder with relevant swc files and create a matrix of neuroanatomy parameters from neuroM. (the matrix is csv file, but you need to arrange it by hand after creation (to delete irrelevant parameters, to change the order of parameters that will fit the parameters list and to remove blank rows.

3. "rina\_merge\_1.py – This script is used to merge the matrix of SSP data with the matrix of neuroanatomy data.

4. "parameters distribution.py" – Script to create the figure of parameters distribution

5. "sp correlation" – Script to create color maps for r and p values between depth and ssp parameters.

6. "ttest for depth" – a file we used to test if there siginificant difference between features by their depth (we used the matrix file "depth\_groups" in the folder "our dataset").

7. "remove outliers" – In this script you take a matrix with neuron's data and mark each parameter's outliers with the sign '^'. So you can recognize them in the matrix.

8. "p\_value mse map" – In this script you create to colormap of significant\not significant MSE difference between our dataset to another dataset. You should use the matrices that Nitza send us with the p-values differences between the MSE's.

9. "mse map" – In this script you can create a color map of mse ratio between our dataset and another dataset or a matrix with the values of MSEs and number of neuron in each parameter group (this matrix we send to Nitza in order to calculate the p values between MSEs).

10. "correlation\_final2" – This script was designed for many targets.. You can "comments" the unnecessary lines. The script takes a matrix of neuroanatomy and SSP (if there is) dataset and making matrices of the correlations values (p, q, r, r\_square etc.). It cans save them and/or use them for creating correlation figures or color maps figures.

**Matlab figures –** in this folder there are script to create correlation figures and specific   
 data for the significant correlations in my thesis.

**(Rina) Matlab –** scripts that you sent me for extracting neuroanatomy parameters, and   
 the beginning of cluster analysis.

Pdf files for learning Python and Matlab.

1. **קבצים לסטטיסטיקאי-** Files that we made for our meetings with Nitza.
2. **Other –** doc and pptx files that you already have. There is 2 time reconstructions tables and figures. File with parameters list. Cell sheets. Presentations that you sent me etc….