**יש לי מספר מקומות שבהם אני יכולה להריץ: כל המקומות זה בפייתון.**  
1. בענן- כללים בדרייב.   
2. בויזואל סטודיו קוד. רץ על מערכת ההפעלה לינוקס. מריצים דרך הטרמינל. עם אובנטו.  
3. בויזואל סטודיו קוד. על מערכת הפעלה ווינדוס. אני יכולה דרך מחברת ג'ופיטר.  
ctrl+shift+p  
4. בויזואל סטודיו קוד. על ווינדוס. דרך הסקריפט הרגיל. שם אריץ דרך הטרמינל.

**Script:**

1. **merge\_meme\_files.py (2)**

take two meme’s file and marge them.  
need to open folder: analysis and logs.

1. **Unite\_motifs\_of\_biological\_condition.py (2)**after merge, this script combine motifs (look like “cluster to combine.csv” file)
2. **Compare combined motifs (3)**  
   we did it after merge meme.py and unite.py  
   check if the new motif constructed from some cluster from other samples.
3. **check if discriminatory motif in df (3)**take table from CSV/XLSX and compare to list of discriminatory features.we did it after marge meme.py and unite.py and compare\_combined\_motifs.ipynb
4. **Compare Motifs/ Compare peptides (3)** compare motifs or peptides from another source.
5. **depletion\_of\_sequences (3)**depletion list of peptides from one list to another list.
6. **Distinctive motif (2)**check if motifs are positive\negative\artifact\mix\ selection. Need csv file hits\values and features\_importance.txt (only features that in csv file too)
7. **quantify motif merge (3)**

check from how many and which samples a motifs is constructed. (to phi chart)

1. **rename\_files\_in\_folder (4)**change file`s name in folder
2. **rename\_folder (4)**change folder`s name
3. **shorten\_fastq\_file (3)**shorten fastq file
4. **depletion motifs-> deplete\_p\_loop\_faster (4)**depletion all the peptides that have specific motifs
5. **depletion motifs-> write\_number\_of\_p\_loop\_in\_file (4)**

write rpm factor to peptides that will be remove

1. **remove\_line (3)**remove line from exel file
2. **Frequency\_linker (3)**
3. **Compare list (3)**
4. **describe\_dataframe(4)**

python3 "C:\Users\JonathanG03\Dropbox\MotifAi\_Supplem\Supp\_scripts\_IgOme\_Profiling-main\describe\_dataframe.py" "C:\Users\JonathanG03\Dropbox\MotifAi\_Exercises\Sanofi\exp12\all\_data\rf\_all\_data12"

describe data in filder

1. **Frequency\_unique\_peptides\_rpm (3)**

Calculate DF

1. **Mypipeline->part II (3)**

Create table with linker and length

1. **Mtpipeline->part III (3)**

Create text tab file (because it is file to convert to fasta). Linker + “xxx” by length