בס"ד

**Installation instructions - TCR2Rep pipeline:**

**Step 1:**Click [here](https://www.anaconda.com/products/distribution) to download the latest version of Anaconda.

**Step 2:** Install Anaconda.

**Step 3:**From the Start menu, search for and open "Anaconda Prompt".

**Step 4:**From "Anaconda Prompt" install git by typing:

* ***conda install -c anaconda git***

**Step 7:**download TCR2Rep pipeline by typing:

* **git clone https://github.com/morhavap/tcR2Rep.git**

**Step 6:**get into "TCR2Rep" folder:

* **cd TCR2Rep**

**Step 8:** Click [here](https://ncbi.github.io/igblast/cook/How-to-set-up.html) to download and install IGBlast for windows.

(Important - Save your IgBlast download directory.)

Move "igblast-1.21.0 " folder into "TCR2Rep" folder.

(you can find "TCR2Rep" path by typing: "pwd" in "Anaconda Prompt").

**Step 8:**At "TCR2Rep" folder you can find "database" folder, please move this folder into

"igblast-1.21.0" folder.

Note: "database" folder contains IMGT VDJ TCR data base. It is important to update this folder once in a while according to the changes published [here](https://www.imgt.org/IMGT_vquest/data_releases).

How to update? (You can get a more extensive explanation [here](https://www.imgt.org/vquest/refseqh.html#VQUEST))

1. Delete all the files in "database" folder by typing:

* Cd TCR2Rep\NCBI\igblast-1.21.0\database
* rm TCR2Rep\NCBI\igblast-1.21.0\database\\*

1. Create 3 new txt file at "database" folder. (right button -> new -> text document)

Save the files with this names: "imgt\_human\_TRV","imgt\_human\_TRD","imgt\_human\_TRJ".

1. Go here, and copy all v genes (one after the other) of TCR into "imgt\_human\_TRV" file, all v genes of TCR into "imgt\_human\_TRV" file and all v genes of TCR into "imgt\_human\_TRV" file. Ex: for
2. For each file perform this 2 commands: (change just the gene segment V\D\J)

* <your\_puth\_to\_bin\_dir>/edit\_imgt\_file.pl "imgt\_human\_TRV" > "human\_TRV"
* <your\_puth\_to\_bin\_dir>/makeblastdb -parse\_seqids -dbtype nucl -in "human\_TRV"

**Step 10:**create the environment for TCR2Rep in "Anaconda Prompt" by typing:

* **conda env create -f TCR2Rep.yml** -> just for the first time running.
* **conda activate TCR2Rep**

**Step 8:** Run TCR2Rep pip:

***bash "<your/tcR2Rep\_pipeline\_folder/path>Run\_all\_TCR\_pip.bash"*** *<fastq\_file\_path> <sample\_name> <length\_threshold> <quality\_threshold> <output\_path> <igblastn\_path> <igblast\_dir\_path> <tcR2Rep\_pipeline\_folder\_path>*

|  |  |  |
| --- | --- | --- |
| 1 | <fastq\_file\_path> | הקובץ שמכיל את כל רצפי ה- TCR |
| 2 | <sample\_name> | שם דגימה ייחודי לבחירתך שיתווסף לקבצי הפלט |
| 3 | <length\_threshold> | בחר סך אורך מינימלי [ default- 240] |
| 4 | <quality\_threshold> | בחר סף איכות מינימלי [ default- 25] |
| 5 | <output\_path> | בחר כתובת יעד עבור כל קבצי הפלט |
| 6 | <igblastn\_path> | העתק את הכתובת של קובץ **igblastn** |
| 7 | <igblast\_directory\_path> | העתק את הכתובת של תיקיית **igblast** |
| 8 | <tcR2Rep\_pipeline\_folder\_path> | העתק לכאן את הכתובת של תיקיית TCR2Rep שייצרת. |

**Step 8:**From the Start menu, search for and open "Anaconda Prompt."

BiocManager::install("GenomicAlignments")

conda install -c "conda-forge/label/gcc7" r-igraph

conda install -c r r-openxlsx