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The future of electrophysiology

KlustaSuite spike sorter installation

Step 1: Spike extraction and automated spike sorting → 'Klusta'

1. Install Miniconda with a proper Python version (3.6.) https://conda.io/miniconda.html
2. Download the environment file for klusta (klusta.yml) – It's in the zip file.
3. Start Anaconda prompt from start menu
4. Navigate to the directory where the previously downloaded 'klusta.yml' file is saved.
5. Type: '*conda env create -f klusta.yml*' . This creates an environment within Miniconda, called 'klusta'
6. Once it finishes installing everything, activate the newly created environment by typing: '*activate klusta*'
7. Installation is done at this point. To start the process you need basically three files.
    a. The .dat file you recorded, let's say 'myfilename.dat'
    b. A .prb file that describes the geometry and channel list of the recording electrode you used (one prb file per recording SHANK is required)
    c. A .prm file that sets the parameters for spike sorting

    You can edit the latter two by using a text editor. You need to set the followings in the prm file:
    - experiment_name: this will be the base name of your newly created files. Let's use 'myfilename_sh1' for processing shank 1, etc.
    - raw_data_files: put here the full name of your dat file, e.g.: 'myfilename.dat'
    - prb_file: put here the filename of your probe definition file. (It is practical to have a separate prb file for each experiment/animal with a name that uniquely identifies it.)
    - nchannels: the number of channels saved in the dat file. (You can check the .meta file if unsure).
8. If you have all of these files in one directory, type '*klusta yourfile.prm*' at the Anaconda prompt, which will do the spike sorting job.
9. For later uses, start the Anaconda prompt, and repeat from step 6.

Step 2: Manual spike sorting (refining the results of the automated step). → 'Klustaviewa'

10. (If not done yet in step 1, Install Miniconda with a proper Python version (3.6.))
11. Download the environment file for klustaviewa (klustaviewa.yml) – It's in the zip file.
12. Start Anaconda prompt from start menu
13. Navigate to the directory where the previously downloaded 'klustaviewa.yml' file is saved.
14. Type: '*conda env create -f klustaviewa.yml*' . This creates an environment within Miniconda, called 'klustaviewa'
15. Once it finishes installing everything, activate the newly created environment by typing: '*activate klustaviewa*'
16. Type '*klustaviewa*' to launch the manual sorting environment.
17. Open your .kwik file created by klusta by navigating to the directory where the results of your previous automated clustering is located
18. For later uses, start the Anaconda prompt, and repeat from step 15.
19. For help see: https://github.com/klusta-team/klustaviewa/blob/master/docs/manual.md