

March 26 2017

Right now I'm working on a script that will take CSV data that I download from IEDB, and add it to a Python pickle. This pickle will consist of a dictionary mapping the HLA allele name to a list of tuples. Each tuple maps a peptide to its Kd. I'm calling this script "iedb.py".

Here's the text of the help function:

```
[jforce@jforce TrainingSystems]$ python iedb.py -h
usage: iedb.py [-h] [--listHLA] [--addHLA hla_name csv_file]
               [--showIEDBFilters] [--setIEDBFilters IEDBFilters]
               dataPickle
```

Manipulate the storage of HLA allele data

positional arguments:

dataPickle Give us the name of the pickle we are working with. If it doesn't exist, then I will create it.

optional arguments:

-h, --help show this help message and exit

--listHLA Lists the HLA alleles that are already in the pickle (default: False)

--addHLA hla_name csv_file Adds the HLA with NAME and CSV data to the pickle

--showIEDBFilters Prints out the IEDB filters that were used to collect data (other than the HLA allele) (default: False)

--setIEDBFilters IEDBFilters Sets the IEDB filters that were used to collect the data. Simply pass in a string with quotes around it. Do not pass the HLA allele name to this

Start	End	Time	Activity
10:15 a.m.	2:30 p.m.	4:15	Filled out as much of the TA application as possible, emailed Swapna and Maifi
2:30 p.m.	4:07 p.m.	1:37	Finished genomics homework
4:45 a.m.	5:50 a.m.	1:05	Worked on thesis
5:50 a.m.	6:00 a.m.	0:10	Emailing and facebooking