1. To run epiTCR, go to its main folder in “C:\Users\amita\Downloads\local\_runs\_softwares\ epiTCR-main\ epiTCR -main”. So go to miniconda terminal, cd to the above folder, then activate conda environment epitcr-env and finally run the code with input output arguments

* cd C:\Users\amita\Downloads\local\_runs\_softwares\ epiTCR-main \ epiTCR-main
* Conda activate epitcr-env
* python predict.py --testfile test.csv --modelfile models/rdforestWithMHCModel.pickle --chain cem > output.csv

The results will be in output.csv file in the main directory

1. Main github lnk: <https://github.com/ddiem-ri-4D/epiTCR>
2. MHC Allele sequences are copied from available test files corresponding to the same alleles

Got these warnings:

1. UserWarning: Trying to unpickle estimator DecisionTreeClassifier from version 1.2.0 when using version 1.1.2. This might lead to breaking code or invalid results. Use at your own risk. For more info please refer to:
2. https://scikit-learn.org/stable/model\_persistence.html#security-maintainability-limitations
3. warnings.warn(
4. C:\Users\amita\miniconda3\envs\epitcr-env\lib\site-packages\sklearn\base.py:329: UserWarning: Trying to unpickle estimator RandomForestClassifier from version 1.2.0 when using version 1.1.2. This might lead to breaking code or invalid results. Use at your own risk. For more info please refer to:
5. https://scikit-learn.org/stable/model\_persistence.html#security-maintainability-limitations