

IO17 | Large Scale Bioinformatics for Immuno-Oncology

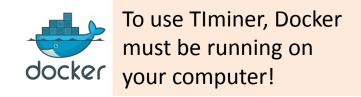
Neoantigens: exercise 3

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Exercise 3: peptide-MHC binding prediction



From Patient_1's data, we have:

- Predicted the HLA types: Patient_1_HLA.txt
- Annotated the mutations: *Patient_1_VEP_37_mutations.txt*
- Predicted the sequences of the mutated proteins:
 Patient_1_VEP_37_proteins.txt

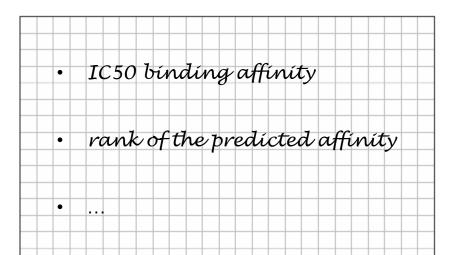
Predict the mutated peptides, **8-11 amino acid** long, which bind to the patient's HLAs with Timiner (function TiminerAPI.executeNetmhcpan), considering a **IC**₅₀ cut-off of 500 nM for the binding affinity.

Important note: To reduce the computational time, we will consider only the first HLA-A type, namely a tab-delimited text file with the same format of the output file of Input/Patient 1 HLA.txt, but with all HLA types equal: *Patient 1 HLA-A.txt*.

Brainstorming: prioritization of candidate neoantigens

This computation will take a while...

While you are waiting for the results, discuss in pairs what might be the features to consider for prioritizing tumor neoantigens for experimental validation.



Questions on peptide-MHC binding prediction

Once you get the results of exercise 3, answer the questions related to this exercise at:

https://b.socrative.com/login/student/

How to access the questions on Socrative (1)

- Access Socrative with student access at: https://b.socrative.com/login/student/
- 2. Join the IO17 room



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How to access the questions on Socrative (2)

3. Enter your name and click "done" to start the quiz

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