

**IO17** | Large Scale Bioinformatics for Immuno-Oncology

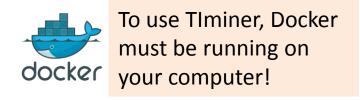
Neoantigens: exercise 4

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## Exercise 4: neoantigen prioritization



We have predicted a list of candidate neoantigens, i.e. mutated peptides binding to the patients HLA-A molecule: Patient\_1\_NetMHCpan\_binders.txt

We also have access to normalized RNA-seq expression data from the same patient (assume the data are already in the format required by Tlminer, i.e. log2(TPM+1)): Patient\_1\_normalized\_expression.txt

Use Timiner (function TiminerAPI.filterNeoantigenFile) to filter only the peptides arising from genes with TPM > 1.

Once you get the results, answer the questions related to this exercise at: <a href="https://b.socrative.com/login/student/">https://b.socrative.com/login/student/</a>

## Filtering candidate neoantigens with Timiner

from TIminer import TIminerAPI

TIminerAPI.filterNeoantigenFile (...)

### From Timiner documentation

http://icbi.i-med.ac.at/software/timiner/doc/index.html

TIminer.TIminerAPI.filterNeoantigenFile(neoantigenInputFile, geneExpressionInputFile, filteredNeoantigenOutputFile=None, expressionThreshold=2) ¶

This function considers a file of candidate neoantigens and a file of normalized gene expression levels, computed as log2(TPM+1), to select neoantigens arising from expressed genes.

- Parameters: neoantigenInputFile (str) Path to the neoantigen input file as generated by the Netmhcpan, containing binding peptides as possible neoantigen canditates (see the output files section for details).
  - geneExpressionInputFile (str) Path to the gene expression file: a tab-separated file containing the list of HGNC gene symbols inside the first column and their gene expression, as log2(TPM+1), inside the second column. The output file of Kallisto expression.txt can be used directly as input file (see the format in the output files section).
  - filteredNeoantigenOutputFile (str) Path to the output file (optional, default = inputfilename neoantigens.txt).
  - expressionThreshold (int) The expression threshold in TPM. Neoantigens arising from genes with an expression lower than the threshold are discarded (optional, default = 2).

# How to access the questions on Socrative (1)

- Access Socrative with student access at: <a href="https://b.socrative.com/login/student/">https://b.socrative.com/login/student/</a>
- 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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