

IO17 | Large Scale Bioinformatics for Immuno-Oncology

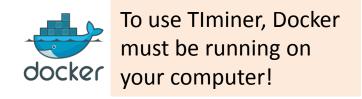
Neoantigens: exercise 4 - Solution

Francesca Finotello, Federica Eduati, and Pedro L. Fernandes

GTPB | The Gulbenkian Training Programme in Bioinformatics
Instituto Gulbenkian de Ciência, Oeiras, Portugal | Sept 19th-22nd, 2017



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

Neoantigen prioritization: Python code

```
from TIminer import TIminerAPI

TIminerAPI.filterNeoantigenFile(
    neoantigenInputFile="../Output/Patient_1_NetMHCpan_binders.txt",
    geneExpressionInputFile="../Input/Patient_1_normalized_expression.txt",
    filteredNeoantigenOutputFile="../Output/Patient_1_candidate_neoantigens.txt",
    expressionThreshold=1)
```

Neoantigen prioritization: questions

1) How many peptides are select by Tlminer for Patient 1 after the filtering (Exercise 4)?

154

Neoantigen prioritization: questions

2) When running neoantigen filtering for patient 1 (Exercise 4), a warning message reports that the mutated gene KMT2D is not present in the file of normalized expression.

Sometimes, genes are not missing from expression data, but are saved with different gene symbols/names/IDs.

Search for "KMT2D" on the website of the HUGO Gene Nomenclature Committee (HGNC) and retrieve synonyms (i.e. alternative symbols that have been used to refer to the KMT2D gene) and previous symbols (i.e. previous symbols used for KMT2D the gene that have now been dismissed): http://www.genenames.org.

Then, look for these alternative symbols in the file of normalized expression to extract the **expression of KMT2D**.

According to its normalized expression, would KMT2D have passed the **threshold** for neoantigen filtering?

Previous symbol: MLL2 \rightarrow log2(TPM+1)=18.87 > 1 TPM \rightarrow Yes