

TheraMe! Bioinformatics homework

Your task will be to analyze perturbation RNAseq data. The RNAseq data is from HEK293 cells treated with Interferon gamma for 4 hours. Sequencing data (single-ended, non-stranded) is available from the [SRA](#) (suggest using [ENA](#) for faster download). The samples are as follows:

| SRA ID | Cell line | Treatment | Dose | Time |
|------------|-----------|------------------|------------|------|
| SRR5458657 | HEK293 | BSA (control) | - | 4 h |
| SRR5458658 | HEK293 | BSA (control) | - | 4 h |
| SRR5458661 | HEK293 | Interferon gamma | 50 ng / ml | 4 h |
| SRR5458662 | HEK293 | Interferon gamma | 50 ng / ml | 4 h |

If you need some other information about the experimental design, the data is coming from [Schubert et. al 2019](#).

Your tasks are the following:

- (Pseudo)align the samples to human transcriptome
- Create analysis report about the quality of the alignment
- Perform a Differential Expression analysis
- Get biological insight about the effect of the perturbation using pathway analysis / gene set enrichment tools
- Visualize your results

Please provide your code and create documentation about your work (alternatively you can work in some notebook environment, and submit your final notebook).