## Study of transcriptome during intense exercises in highlands

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This project aimed to study differential gene expression of 19 sportsmen during physical and psychological stress before and after running in extreme highlands conditions (2450-3450 m, Elbrus m.) and also in "start" point before arrival at the competition (Saint Petersburg).

We processed RNA-seq data of 19 sportsmen in 3 condition types, which means we had 57 samples. Reads were mapped to the human reference genome (hg38) using STAR. The genes and isoforms expression count was conducted with RSEM. The gene differential expression analysis was performed using DESeq2. We also did two parallel analyses using gene expression data and isoforms one. There were fewer differential expressing genes in isoforms results, so we thought that using isoforms data can give better resolution.

We found that second and third conditions differ less than other pairs of conditions, so we can propose that acclimatization shows the highest impact on the quantity of differential expressed genes.

Then we used MSigDB to determine functional groups in lists of differentially expressed genes. We found about 25 groups of genes, among which the most interesting was the group responsible for neurodegenerative diseases. It is well known that organisms can take energy from the brain during stress and high physical activity so it may be the reason for this result, but we are going to check this group in detail in the future.

All our results are in the GitHub repository:

https://github.com/Kate-Cher/Skyrunners.