Katerina Oleynikova

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MAIN SKILLS

Bioinformatics - more than 2.5 years of experience, Python - 1.7 years of experience, R - 1 year of experience

EDUCATION

Ufa State Petroleum Technological University   Oufa, Russia
BSc in Engineering   June 2018

Skolkovo Insitute of Science and Technology   Moscow, Russia
MSc in Engineering and Computer Science   July 2020

HSE   Moscow, Russia
MSc in Bioinformatics   -

WORK EXPERIENCE

FMBA   Moscow, Russia
Bioinformatician, Deparment of Medical Genomics   October, 2020 − currently

- Integrated several biotools in the genome analysis pipeline (in particular, for STRs, Transposons, HLAs identification).
- Created several scripts for genome analysis.
- Had deal with bio data (DNA/RNA) [human genome, viral genome (SARS-CoV2)] possibly for all the file formats such as .bam, .sam, .bcl, .fastq, .fasta, .json, etc.
- Constructed several pipelines to annotate a genome.
- Performed Genome-Wide Association Studies.
- Worked with bio databases (NCBI, EMBL-EBI GWAS Catalog, ClinVar).
- Worked with raw data (demultiplication, alignment, sorting, indexing, etc).

PROJECT WORK

Single-cell RNA Sequencing as a Method to Early Reveal CD19-negative Relapsing Patients
Biomedical Entrepreneurship   December, 2018
- The method for companion diagnostics to CD19 CAR-T treatment of B- cell was conceptually developed.
- The project was defended and finally reviewed by experts in the biomedical industry.

Estimating IQ of Bacteria *Bioinformatics, Skolkovo Institute of Science and Technology*   October, 2019
- Aestuariivita boseongensis was chosen for the IQ calculation. To achieve it, identification how many signaling proteins in the genome and the total number of the proteins was required. It was concluded finally that the IQ of Aestuariivita boseongensis is characterized as the pretty averaged one.

Genome Annotation of the Bacterium *Bioinformatics, Skolkovo Institute of Science and Technology*   November, 2019
- In the project, the fragment of genomic DNA of Tepidiforma bonchosmolovskayae gen. nov., sp. nov. was considered and the following tasks were solved: Annotating all coding and non-coding genes. Finding the functions for coding genes. Describing the operon structure. Finding the genes that were obtained by this bacteria through HGT. Finding genes associated with secondary metabolites. Visualisation part.

Multivariate Genetic Analysis of Human Blood N- glycome Project *The course "Models and methods of quantitative genetics", MIPT/Institute of Cytology and Genetics*   November, 2020
- The aim of the project - to discover novel genetic loci influencing the glycosylation of human blood plasma N-glycome while performing a multivariate genome-wide association study (GWAS) of total blood plasma N-glycome and using published summary statistics of association.

SKILLS

Biology: Genomics, Genetics [the deep knowledge in STRs, MEs, HLAs, DNA methylation processes, Longevity or Aging]
Programming: Python [pandas, seaborn, scikit-learn, mongo; Biopython], R, Statistics, bash [working with biotools, genome analysis pipeline, development tools, etc.]
Others: Github(lab), LaTeX, English (7.0), German (B2), Russian (native).