

EVGENIIA CHIKINA

I am Bioinformatic Master student who previously graduated from Medical University. I use all my medical and biological knowledge to combine with the world of computer science. At the moment I have especially good knowledge and skills in analyzing RNA sequencing data. Now and in the future I try to develop and gain knowledge in various aspects of bioinformatics, in particular in such areas as: data science and machine learning, multi-omics data analysis.



EDUCATION

Current
|
2020



M.S., Applied Mathematics and Informatics, Bioinformatics and System Biology

ITMO University

📍 Saint-Petersburg, Russia

- Thesis: Metabolic Modules Identification in Single-Cell Data
- Course Project: Identifying Metabolic Modules in TCGA Datasets
- Semester Project: Effects of Background RNA Noise on Differential Expression Results in scRNA-seq

2020
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2014



Specialist, Medicine, Pediatrics

Saint-Petersburg State Pediatric Medical University

📍 Saint-Petersburg, Russia

- Pediatrician



RESEARCH PROJECTS

Current
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2021



Metabolic Modules Identification in Single-Cell Data

ITMO University

📍 Saint-Petersburg, Russia

- Thesis
- Main goal of the project is to extend applications of the GAM-clustering tool on the *single-cell RNA-seq* data. In order to find optimal **clustering** algorithm performed and analysed multiple clustering strategies for the single-cell RNA-seq data. Used **trajectories** and **gene set enrichment** analysis for biological interpretation of the results. Involved in the *modification of the tool*.

2021
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2021



Identifying Metabolic Modules in TCGA Datasets

ITMO University

📍 Saint-Petersburg, Russia

- Course Project
- With previously developed GAM-clustering algorithm analyzed TCGA datasets (LUSC) - *bulk RNA-seq* data. Identified metabolic modules and performed biological analysis of them. During work was involved in the *modification of the tool and testing*.

View and download this CV with links at <https://github.com/JaneChik/cv> or [here](#)

CONTACT

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🐙 github.com/JaneChik

in [evgenia_chikina](#)

SKILLS

R

Python

Linux

Bash

LANGUAGES

Russian


English

German

Made with the R package
[pagedown](#).


The source code is available on
github.com/nstrayer/cv. Modified
source code for this CV is available
[here](#)

Last updated on 2022-03-03.


- 2020
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2020
- **Effects of Background RNA Noise on Differential Expression Results in scRNA-seq**
ITMO University  Saint-Petersburg, Russia
 - Performed standart analysis of the single-cell data with Seurat pipeline and integration of multiple samples using SCTransform intgration. With help of DropletUtils R package identified ambient RNA and tried to estimate the impact of it on the differential expression results.



ACHIEVEMENTS

- 2021
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2021
- **NGSprint Hackaton**
[NGSchool](#)  Discord, online
 - Project: Data Visualization in Bioinformatics
 - Result: ShinyApp¹
 - Certificate by the link²

2021
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2021

 - **Bioinformatics Contest 2021**  Stepik, Online
 - Participant³



COURSES

- 2020
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2020
- **Molecular biology of the cell (ru)**
Bioinformatics Institute  Stepik, Online
 - <https://stepik.org/cert/353448>

2019
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2019

 - **Programming in Python (ru)**
Bioinformatics Institute  Stepik, Online
 - <https://stepik.org/cert/209363>



LINKS

1. https://github.com/JaneChik/NGSprint_Hackathon-TCGA_RShinyApp
2. https://drive.google.com/file/d/1PS_joxoZYsNmJzZyqR5xkMqH9ZiE5UrO/view?usp=sharing
3. https://drive.google.com/file/d/1SEgIqYqY7m2tne_XPy9rAscXteFH957N/view?usp=sharing