Samuel Kopelev

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(484) 797 - 8227

EDUCATION

Rochester Institute of Technology, Rochester NY
B.S.: Bioinformatics and Computation Biology
Minor - Applied Statistics

Expected 2027

- Honors: RIT Presidential Scholar
- Relevant Courses: Bioinformatics, Discrete Mathematics, Organic Chemistry, Molecular Biology

SUMMARY

Seeking to gain programming and data analytic skills in various fields with computational modeling. Proficient in managing multiple projects simultaneously with precision and efficiency. (4+ Years of Professional Experience)

PROFESSIONAL EXPERIENCE

RIT GOSNELL SCHOOL OF LIFE SCIENCES (SCHULZE LAB), ROCHESTER NY

STUDENT RESEARCHER (DATA AGGREGATION) — 01/2024 - 04/2024

- Extracted instrumental and experimental metadata from various public databases (PRIDE, ProteomXChange, PeptideAtlas, JASPAR, PDB) for the bacterial pathogen Pseudomonas aeruginosa.
- Prepared Python scripts for the large-scale re-analysis of proteomic datasets.

STUDENT RESEARCHER (DATA ANALYSIS) — 06/2024 - 08/2024

- Worked in a collaborative team overseeing the processing of MS data and peptide identification for the computational analysis of Pseudomonas aeruginosa data.
- Assisted in the analysis of proteomic data of protein glycosylation in Pseudomonas aeruginosa by employing computational techniques and pattern recognition using Python.

STUDENT RESEARCHER (PIPELINE DEVELOPMENT) — 09/2024 - 12/2024

- Developed a Python pipeline for analyzing mass spectrometry-based peptide data, significantly reducing computational runtime by thousands of hours

CHEMICAL LABORATORY TECHNICIAN (INTERNSHIP) PHYTOGENX, — 09/2021 – 01/2022 MORGANTOWN PA

- Analyzed over fifty chemical samples to guarantee required quality control standard for further research and development.
- Tested products under various conditions to ensure compliance with manufacturing standards.

INDEPENDENT RESEARCH & PROJECTS

Molecular Pathway Analysis and Python based coding

- Used various visualization and analytical tools such as CHIMERA, MEGA for the analysis of extracted Frovatriptan succinate hydrate signaling pathway from databases such as KEGG.
- Wrote multiple Python scripts for the statistical analysis of the chromosomal attributes of the completed yeast genome.

SKILLS

- Data Pipelines (Aggregation, Integration, Analysis)
- Computing (Database Management, Python, Bash, R)
- Data Processing (Sequence Alignment, Proteomic Data)