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Viacheslav Ivanov

05/28/1997

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EDUCATION

Moscow Institute Of Physics And Technology, Weighted GPA: 9.43/10; top 5% of the university Bachelor of Science, Applied Mathematics & Computer Science 08.2016 - 08.2020

Relevant courses: Bayesian statistics, applied statistics, optimization, machine learning, deep learning, stochastic processes, algorithms and data structures, concurrent programming, distributed programming

RESEARCH EXPERIENCE

Research Internship, Computational Biology, DKFZ/EMBL Heidelberg, 01.07.2019 – 01.01.2020 Supervisors: Dr Oliver Stegle (group leader); Dr Hana Susak, Dr Nicola Casiraghi, Dr Yuanhua Huang

- Under supervision of Dr Yuanhua Huang (EMBL-EBI, Cambridge), I designed and implemented XClone, graphical Bayesian model capable of integrating single-cell genomes, transcriptomes, ATAC-seq, mitochondrial DNA. It's a modification of Cardelino model, a tool for clonal structure inference from scRNA-seq, but based on CNV and other sources of allele specificity observed in multiple modalities. We used variational inference to ensure that our model scales to the state-of-the-art datasets. We also implemented a method for sampling realistic cells from expression profiles obtained from G&T data.
- Under supervision of Dr Casiraghi, I worked with nuclei, PDX and G&T datasets coming from the patient with medulloblastoma brain cancer in children. I had hands-on experience with 10x Genomics software stack, in particular with CellRanger and its CNV-kit. We used Nanopore-seq for accurate read phasing and significantly reduced sparsity of scRNA-seq dataset by aggregating allele-specific expression information over SNPs sharing same CNV state and covered by particular haplotype block.
- Under supervision of Dr Susak, I worked on a method for inferring clonal tumour tree structure from scDNA/scATAC. We came up with a modification of Levenstein distance based on genomic rearrangements.
 We constructed a minimal spanning tree with cells as nodes and defined clones as clusters in that tree.
- At the same time, I've done a lot of data preparation myself in Python and C++. Given size and complexity of single-cell datasets, I had to written highly optimized code capable of making the most out of the resources of the dedicated HPC cluster. I also learned about the best practices of reproducible research (snakemake pipelines, environment isolation) and applied those in my projects.

Mutual analysis of interaction networks and quantitative trait loci for yeast, 2018-present: «Modern Combinatorics and Network Science» Lab of Prof A. Raigorodsky, MIPT. Supervisor: Yuri Pritykin, PhD (Princeton), Research Scholar at MKSCC Detailed project description is available on GitHub.

- Implemented different approaches to QTL mapping in yeast, from basic to state-of-the-art
- Integrated PPINs into QTL analysis. Implemented statistical tests using igraph package.
- Carried out GWAS on NGS expression data. Learned how to tackle domain-specific difficulties arising from large-scale hypothesis testing using FDR-correction techniques (especially qvalue).
- Learned how to write fast and memory-efficient scientific code using numpy, scipy and pandas.
- Practiced parallel programming, interprocess communication and data persistency in Python.
- Utilized MIPT supercomputing capabilities, learned how to use SLURM.
- Worked with GeneOntology and KEGG API and related Python/R tools.

HONORS

- Abramov Scholarship For Academic Excellence 2nd term 6th term Earned by top 10% students by cumulative GPA in their academic program in academic terms 2-6.
- Russian Government Scholarship For International Students 2016 2026 Was selected to become one of 3 Ukrainians to receive the full-coverage scholarship to study CS at the best Russian universities and got enrolled to MIPT directly, without entrance examination.
- Governor of the Moscow Region Scholarship For Academic Excellence Autumn 2017

 Awarded termly to excellent students for promising achievements in scientific activities.
- Future Biotech Winter Retreat "Genome function, editing and therapy" Winter 2019
 Became one of 70 young researchers selected to participate in top biotech winter school in Russia sponsored by companies like AstraZeneca, Biocad, GE Healthcare etc.

- Summer School in Bioinformatics by Russian Bioinformatics Institute Summer 2017

 Became one of 50 CS majors selected to participate. Was a member of a hackathon-winning team.
- Moscow International Workshops in Competitive Programming Autumn 2016, Spring 2017 Two-times participant of the leading Russian competitive programming bootcamp.
- ACM ICPC Moscow Subregional Contest (1/4 World Finals)

 Autumn 2017

 Our team ranked 17 among 301 participating teams and 7th at home university.
- All-Ukrainian Chemistry Olympiad double awardee, triple winner of regional stage
- All-Ukrainian Tournament of Young Chemists 2nd place

TEACHING EXPERIENCE

- TA at «Theory and practice of concurrent programming» course at MIPT Spring term 2019 My responsibilities included weekly code reviews on GitLab and knowledge assessment sessions.
- TA at «Mathematical statistics» and «Applied statistics» courses at MIPT Fall term 2019
 Authored learning materials for a primer on scientific computing for data scientists: see on GitHub (WIP).
 Topics included: environment setup, Jupyter ecosystem, efficient Python programming (JIT, Cython, data persistence, parallel and distributed computing), advanced visualizations (IPyWidgets, bokeh, bqplot), reproducible workflows (SnakeMake, pachyderm), cloud services (Google Colab, Amazon AWS). Also was responsible for code base maintenance and student knowledge evaluation.
- TA at «Algorithms and data structures» course at MIPT Weekly code reviews on GitLab (code style, correctness).

Fall term 2019

REFERENCES

Dr Oliver Stegle, group leader at EMBL, EMBL-EBI and DKFZ Dr Yuri Pritykin (thesis supervisor), research scholar at MSKCC Federal Prof. Andrei Raygorodsky, head of department at MIPT

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