

RAZVAN IOAN PANEA

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Summary

- Initiative-taking individual with strong knowledge and experience in computer science and bioinformatics.
- Currently a PhD candidate in computational biology and bioinformatics at Duke University.
- Developed from scratch a cloud-based workflow management system for bioinformatics in Python.
- Led a group of software engineers to develop a complete cloud-based infrastructure using Kubernetes and Django.
- Processed a terabytes-scale dataset of Burkitt lymphoma tumor samples and analyzed the results in R.

Education

Expected: **Duke University | Durham, NC, USA**
05/2020 Ph.D. in *Computational Biology and Bioinformatics*
Research: *Cloud computing and cancer genomics*

09/2011 – **Jacobs University Bremen | Bremen, Germany**
06/2014 Bachelor of Science in *Applied and Computational Mathematics*
Specialization: *Bioinformatics and Computational Biology*

Research and Work Experience

08/2014 – **Duke University | Durham, NC, USA**
Present Ph.D. Candidate – Advisor: Sandeep Dave, MD
► Developed a cloud-based infrastructure for cancer genomics
Technologies used: *Python, Bash, Git, Docker, Kubernetes, Google Cloud, AWS, Apache libcloud*

- Developed CloudConductor, a cloud-based, modular, scalable, parallelizable and extensible workflow engine to generate and execute analysis pipelines. Available at github.com/labdave/CloudConductor
- Led a team of 5 software engineers and bioinformaticians to extend CloudConductor to a complete cloud-based infrastructure for bioinformatics analysis using Kubernetes and Django
- Improved CloudConductor to a platform-agnostic workflow engine using Apache libcloud
- Integrated and evaluated the workflow engine on Google Cloud Platform and Amazon Web Services
- Integrated 50+ bioinformatics tools using Docker and utilized them to analyze terabytes of genomics data

► Characterized the mutational patterns in Burkitt lymphoma subtypes
Technologies used: *R, Python, Bash*

- Sequenced the whole genome and transcriptome of 101 Burkitt Lymphoma cases of different subtypes
- Identified genetic alterations in the sequencing data using the newly developed cloud-based infrastructure
- Identified mutations in driver genes, such as *MYC*, *ID3* and *DDX3X*, the presence of the Epstein-Barr virus (EBV) in the samples, and translocations characteristic to Burkitt Lymphoma
- Identified associations between lymphoma subtypes and EBV status
- Work has been accepted and published in the *Blood* journal

06/2013 – **Max Planck Institute for Marine Microbiology | Bremen, Germany**
08/2013 *Software Developer* - Supervisor: Dr. Frank-Oliver Glöckner
► Improved features of the SILVA Project (www.arb-silva.de) software using Python and C++ binding
Technologies used: *C++, Python*

- Researched and tested SWIG, a software for Python and C++ binding
- Implemented SWIG in the project to bind and call methods implemented in Python on C++ objects

► Tested the performance and efficiency of a phylogenetic tree generating software
Technologies used: *C++*

- Benchmarked a new phylogenetic tree generator software
- Compared the performance and quality of the new tree generator software to the one currently used
- Deployed the new, more efficient software

03/2013 – **Jacobs University Bremen | Bremen, Germany**
06/2014 *Research Assistant* – Advisor: Dr. Georgi Muskhelishvili
► Determined the interaction between two neighboring genes in *E.coli*
Technologies used: *Java*

- Developed a software in Java to aggregate, analyze and report the expression levels of all neighboring genes at different time points in *E.coli* life cycle
- Identified a correlation between the differential expression between two neighboring genes and their transcriptional orientation to each other

Teaching Experience

01/2016 – **Duke University | Durham, NC, USA**
05/2016 *Teaching Assistant* – CompSci 260: Introduction to Computational Genomics

- Designed and graded course assignments
- Organized and presented tutorial sessions for programming in Python
- Held office hours to answer students' questions and provide supplemental instructions

09/2012 – **Jacobs University Bremen | Bremen, Germany**
06/2014 *Teaching Assistant* – NatSciLab Unit Computer Science I/II

- Assisted computer science professors in teaching courses based in C and Python
- Offered supplemental instruction and assisted students in planning their programming projects
- Assessed student progress and offered weekly reviews to help improve student performance

Publications

09/2019 **Panea R***, Love C*, Shingleton J*, Reddy A* et al., "The whole genome landscape of Burkitt lymphoma subtypes", *Blood*, 2019

02/2020 Shingleton J., [and 16 authors, including **Panea R.**] (2020). "Non-Hodgkin Lymphomas: Malignancies Arising from Mature B Cells". In M. Kharas, R. L. Levine, A. M. Melnick (Ed.), "Leukemia and Lymphoma: Molecular & Therapeutic Insights". Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, (In Press).

11/2019 Li X., [and 75 authors, including **Panea R.**], "Whole Exome and Transcriptome Sequencing in 1042 Cases Reveals Distinct Clinically Relevant Genetic Subgroups of Follicular Lymphoma" *Blood* (2019), (Manuscript in preparation).

Posters and Presentations

07/2018 **Google Next '18 | San Francisco, CA, USA**
Presentation and Panel Discussion
Title: Speeding up Research in Genomics
Link: <https://youtu.be/goBFt3B976A?t=11m31s>

06/2016 **Intelligent Systems for Molecular Biology | Orlando, FL, USA**
Poster Presentation
Title: Defining the Microbiome of Lymphomas

10/2017 **Duke Cancer Institute | Durham, NC, USA**
Poster Presentation
Title: A Cloud-Based Framework for Cancer Genomics

Skills

Programming: Python, R, Bash, C, Java, C++, SQL, Git
Libraries/Packages: Apache Libcloud, Plotly, Pandas, SQLAlchemy
Computing Platforms: Google Cloud, SLURM, Kubernetes, AWS
Operating Systems: Linux, Windows, OS X, Chrome OS
Softwares: PyCharm, Jupyter Notebook, RStudio, Adobe Illustrator