RAZVAN IOAN PANEA

Contact: contact@razvanpanea.com | (917) 755-6090
Website: razvanpanea.com
GitHub: github.com/ripanea
LinkedIn: linkedin.com/in/rpanea

Summary

- Initiative-taking with strong knowledge and experience in computer science and bioinformatics.
- 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 genomics dataset of Burkitt lymphoma and performed analysis using R.

Education

Expected:
05/2020

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

09/2011 –
06/2014

Jacobs University Bremen | Bremen, Germany
Bachelor of Science in *Applied and Computational Mathematics*
Specialization: *Bioinformatics and Computational Biology*

Research and Work Experience

08/2014 –
Present

Duke University | Durham, NC, USA
Ph.D. Candidate – Advisor: Sandeep Dave, MD
► Developed a cloud-based infrastructure for cancer genomics
Technologies used: *Python, Bash, Git, SQL, 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 throughout the SDLC process to extend CloudConductor to a complete cloud-based infrastructure for bioinformatics analysis
- 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, SQL*

- 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 published in the *Blood* journal (*Panea et al., Blood, 2019*)

06/2013 –
08/2014

Max Planck Institute for Marine Microbiology | Bremen, Germany
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 – 06/2014	**Jacobs University Bremen | Bremen, Germany** *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 – 05/2016	**Duke University | Durham, NC, USA** *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 – 06/2014	**Jacobs University Bremen | Bremen, Germany** *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.**], "Non-Hodgkin Lymphomas: Malignancies Arising from Mature B Cells", Cold Spring Harbor Perspectives in Medicine, 2020
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
Development Software: PyCharm, Jupyter Notebook, RStudio, MySQL Workbench, Adobe Illustrator
Bioinformatics Tools: BWA, Samtools, BCFtools, VCFtools, GATK, Picard, STAR, RSEM, Trimmomatic, Diamond, Annovar, BEDtools