RAZVAN IOAN PANEA

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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*
Cumulative GPA: 3.5

Research and Work Experience

08/2014 –
Present
Duke University | Durham, NC, USA
Ph.D. Candidate – Advisor: Sandeep Dave, MD
► Developed CloudConductor: a cloud-based framework for cancer genomics analysis
• Lead a group of 5 people to develop CloudConductor, a modular, scalable, elastic, parallelizable and extensible framework to generate different analysis pipelines
• Researched cloud-based services for optimizing and improving the performance of analysis pipelines
• Integrated over 50 bioinformatics tools into the newly developed framework
• Integrated and tested the framework on Google Cloud Platform and currently working to make the framework platform-agnostic
• Extended CloudConductor to a complete infrastructure using Kubernetes for automatic deployment and Django for user interface
• Available on GitHub: github.com/labdave/CloudConductor

► Characterized the mutational patterns in Burkitt lymphoma
• 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 framework
• 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 –
08/2013
Max Planck Institute for Marine Microbiology | Bremen, Germany
Software Developer - Supervisor: Dr. Frank-Oliver Glöckner
► Improved features of the main software from the SILVA Project (www.arb-silva.de) software using Python and C++ binding
• Researched and tested SWIG, a software for Python and C++ binding
• Implemented SWIG interfaces in the SILVA Project to bind and call methods implemented in Python on C++ objects

► Tested the performance and efficiency of a phylogenetic tree generating software
• Benchmarked a new phylogenetic tree generator software
• Compared the performance and quality of the new tree generator software to the one used in the SILVA Project
• Deployed the new, more efficient software

03/2013 – 06/2014	**Jacobs University Bremen | Bremen, Germany**

Jacobs University Bremen \| Bremen, Germany
Research Assistant – Advisor: Dr. Georgi Muskhelishvili
► Determined the interaction between two neighboring genes in *E.coli*, by comparing their temporal expression level with their transcriptional orientation
• Developed a software in Java to aggregate and analyze 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

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03/2016 –
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
• Aide computer science professors in teaching courses based in C and Python
• Offer supplemental instruction and assist students in planning their programming projects
• Assess student progress and offer weekly reviews to help improve student performance

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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).

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07/2018

Google Next '18 \| San Francisco, CA, USA
Breakout Session
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

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