

Paul Ryvkin, PhD

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Experience

10x Genomics

Pleasanton, CA

May 2015 – present: Senior Scientist, Computational Biology

- Computational biology lead for groundbreaking single-cell RNA-sequencing product – team of 3 computational biologists.
- Developed single-cell RNA-seq statistical methods and analysis software.
- Designed extensive models and simulations to set product specifications and support biochemistry development.
- Designed nucleic acid assays to quantify biochemical processes
- Provided company-wide support for analysis of high-throughput sequencing data.

Guardant Health

Redwood City, CA

February 2015 – May 2015: Senior Bioinformatics Scientist

- Improved variant calling algorithms in and infrastructure surrounding liquid biopsy bioinformatics software.
- Streamlined clinical bioinformatics processes in order to scale sample throughput.
- Analyzed high-throughput DNA sequencing data in support of research, clinical operations, and marketing.
- Acted as liaison between bioinformatics, clinical software, marketing, and clinical lab teams.

Ariosa Diagnostics (acquired by Roche Molecular Systems Jan. 2015)

San Jose, CA

February 2015: Data Scientist II

July 2014 – January 2015: Data Scientist

August 2013 – July 2014: Statistician / Software Engineer

- Led development of production bioinformatics software for non-invasive prenatal testing (NIPT) products
- Developed statistical algorithms using R and re-implemented them in C#.
- Leveraged historical data in order to improve lab quality and genetic testing performance.
- Developed tools for automated visualization and analysis of data to streamline regulatory compliance in a CLIA-certified laboratory.

University of Pennsylvania Perelman School of Medicine

Philadelphia, PA

2007 – 2013: PhD Candidate, Genomics and Computational Biology

- Authored 10 peer-reviewed journal articles, 2 book chapters, & 2 conference proceedings covering topics including RNA-sequencing, DNA structure, and comparative genomics.
- Solved genomics research problems using statistical algorithms (C++, R, Ruby, & Python).
- Implemented 2 web applications using PHP and Javascript in a team environment.
- Processed tissue samples & performed high-throughput RNA sequencing experiments.

University of Connecticut**Storrs, CT****2004 – 2007: Research Specialist**

- Authored 2 peer-reviewed journal articles & 2 conference proceedings describing models of molecular evolution in gene duplication.

Dominion, Millstone Nuclear Power Plant**Waterford, CT****Jun 2004 – Aug 2004: Engineering Intern**

- Designed schema & user interfaces for engineering databases.

University of Connecticut**Storrs, CT****2002 – 2004: Applications Developer**

- Designed & developed the front- & back-end of an appointment-scheduling web application (>1,000 users) using PHP, MySQL, HTML, & Javascript.

Education

Ph.D., Genomics and Computational Biology**2007 – 2013**

University of Pennsylvania Perelman School of Medicine

B.S.E.E, Electrical Engineering and B.S.E., Computer Engineering**2002 – 2006**

University of Connecticut

Technical Skills

Programming Languages

Expert in C++, R, Python, Awk, Bash
Competent in C, Rust, C#, Java, Ruby, Perl, PHP, JS/HTML/CSS, SQL
Familiar with Go, D
Github profile: <https://github.com/pryvkin>

Biological

Expert in High-throughput sequencing, RNA biology, Comparative genomics

Mathematical

Expert in Machine Learning & Data Mining, Statistics & Statistical Modeling

Publications

A complete list can be found at <https://scholar.google.com/citations?user=KcB4muUAAAAJ>