Yogesh Saletore

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objective

Data Scientist with a background in Computational Biology and Computer Science, interested in using advanced algorithms and machine learning to integrate multi-omic data for the improvement of patient quality of life.

work experience

Agios, Inc.   Cambridge, MA

Mar 17-   Contract Data Scientist, Metabolism. Developed applications to annotate, compare, and visualize mass spectrometry data. Designed and implemented a database to store raw data and application output. Implementing a Bayesian method for annotating untargeted mass spectrometry data.

Seven Bridges Genomics, Inc.   Cambridge, MA

Jun 16-Jan 17   R & D Engineer. Implemented pipelines to benchmark Graph Genome Aligner and variant calling. Further developed Graph Genome Aligner to support additional types of data.

Sep 15-Jun 16 Bioinformatics Scientist, Department of Customer Projects. Worked directly with customers to architect and implement bioinformatics solutions that met client needs, including whole genome/exome variant calling and RNA-Seq alignment. Implemented a custom workflow for identifying RNA editing sites from RNA-Seq data.

Amazon.com, Inc.: Promotions Team Software Development Engineer Intern   Seattle, WA

Jul-Sep,2009   Designed & delivered the front-end for Vendor Central in Perl Mason, Javascript, HTML, and CSS

Jun-Sep,2008   Developed and tested Java software to process NTIA vouchers for the DTV program.

Jun-Sep,2007   Designed & developed a landing web page and implemented a new promotion type for retail transactions

education

2010-2015   **Ph.D.** in Computational Biology: **"The functional role of methyl-6-Adenosine"**   New York & Ithaca, NY

Tri-Inst. Training Program in Comp. Biol. & Medicine: Weill Cornell Medical College and Cornell Univ. Christopher Mason Lab: Developed protocols and computational methods to identify and understand the functional significance of the RNA modification methyl-6-adenosine (m6A). Performed RNA-Seq extraction, MeRIP-Seq protocol, Illumina sample prep, RNA-Seq alignment, and implemented Java tool, MeRIPPeR, for identifying putative m6A sites.

2005-2010   **B.S. Honors** in **Computer Science, B.S.** in **Bioengineering**   Seattle, WA
University of Washington

Languages   Java, C/C++, R, Python, Perl, HTML/CSS, SQL, JavaScript, LaTeX

publications

[1] Yogesh Saletore, Kate Meyer, Jonas Korlach, Igor D Vilfan, Samie Jaffrey, and Christopher E Mason. The birth of the Epitranscriptome: deciphering the function of RNA modifications. Genome Biology, 175(October), 2012.

[2] Yogesh Saletore, Selina Chen-Kiang, and Christopher E Mason. Novel RNA regulatory mechanisms revealed in the epitranscriptome. RNA biology, 10(3):1–5, February 2013.

[3] Kate D Meyer, Yogesh Saletore, Paul Zumbo, Olivier Elemento, Christopher E Mason, and Samie R Jaffrey. Comprehensive Analysis of mRNA Methylation Reveals Enrichment in 3' UTRs and near Stop Codons. Cell, 149(7):1635–46, June 2012.

References available upon request.