

Matt Ralston

blend of bioinformatics and biochemistry

contact

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bioinformatics

Bowtie, Tophat, BWA
Blast, Blat, Clustal
Cufflinks, Trinity, Velvet
Samtools, Picard,
Bedtools
DESeq, MACS, Circos

programming

♥ Ruby/Rails, R
Bash, Python, Julia
Matlab, \LaTeX , Racket
MySQL, SQLite
JavaScript, CSS/HTML

laboratory

RNA-seq, qRT-PCR
Northern & Western
Spectrometry, HPLC
Immunofluorescence
Immunohistochemistry
Microscopy, HPLC
FACS, GC-MS
Mammalian cell culture
Anaerobic fermentation

summary

Combines a mechanistic mindset from a B.S. in Biochemistry with M.S. in Bioinformatics to produce and interpret 'omics datasets from Next Generation Sequencing (NGS) reflected by an academic research record. Enjoys research and development, from experimental design to analysis. Offers interdisciplinary expertise for teams of scientists, engineers, and analysts.

education

- 2012-2015 **Masters** of Bioinformatics and Computational Biology **3.97** University of Delaware
*Assembling Improved Gene Annotations in *Clostridium acetobutylicum* with RNA Sequencing.*
- 2008-2012 **Bachelors** of Biochemistry University of Delaware
Minor in Biochemical Engineering, Scholarship, Summer Research Fellowship

experience

- 2012-Now **DELAWARE BIOTECHNOLOGY INSTITUTE** Newark, DE
Graduate Research Assistant
Accomplishments:
 - Developed and utilized laboratory and computational workflows for first strand-specific deep RNA-seq and transcriptome assembly in *Clostridia*.
 - Built and launched a genome browser for research community.
- 2010-2012 **Center for Translational Cancer Research** Newark, DE
Undergraduate Research Fellow
Investigated the BMP-signaling pathway in colon cancer cells and tissue.

leadership

- 2014 **Bioinformatic Student Association** Newark, DE
President
Organized and led a UNIX and HPC student development workshop.
- 2013 **IGERT Business, Ethics, and Communication Project** Newark, DE
Project Manager
Won a proposal for a revision to Fraunhofer CMB's vaccine production process.

publications

- "Complex and extensive post-transcriptional regulation revealed by integrative proteomic and transcriptomic analysis of metabolite stress response in *Clostridium acetobutylicum*", contributing author. *BMC Genomics*. (2015). Accepted
- "Overexpression of the *L. plantarum* peptidoglycan biosynthesis murA2 gene increases the tolerance of *E. coli* to alcohols and enhances ethanol production", contributing author. *Applied Microbiology and Biotechnology* 98.19 (2014): 8399-8411.
- "The *Clostridium* small RNome that response to stress: the paradigm and importance of toxic metabolite stress in *C. acetobutylicum*", contributing author. *BMC Genomics*. 14.1 (2013): 849.