Matt**Ralston**

blend of bioinformatics and biochemistry

contact

Matt Ralston
1170 Old Wilmington Rd
Hockessin DE, 19707

Phone: 610-470-8028
mrals89@gmail.com
matthewralston.github.io
LinkedIn:matthewralston

bioinformatics

Bowtie2
RNAseq/WGS/WES
BAM/VCF
Samtools/Picard

data-science

Linear Regression
ANOVA/f-test, t-test
PCA, R/bioconductor

programming

♥ Python, R, Rust
Javascript, CSS/HTML
AWS/Docker, bash
MySQL, PostgreSQL
Linux, 💜 Emacs/vi
Matlab, LaTeX, NodeJS
Perl, 💙 Ruby, Julia

laboratory

Human cell culture
UV-Vis spectrometry
GLP, BSL2
RNA-seq, qRT-PCR
Northern & Western
IF/IHC, HPLC
Microscopy, FACS
GC-MS, LC-MS
Organic synthesis

open-source

kmerdb
Kmer.JS
NGS-CI
GitHub

summary

Combines experiences in pharmaceutical discovery, biofuel engineering, and translational cancer research to diverse biochemical problems including Illumina sequencing and analysis. Offers interdisciplinary expertise for teams of scientists, engineers, and analysts.

experience

2021-Current **Terra Informatics** — Newark, DE
Founder and P.I.

- Data-science, HPC, kubernetes/Docker, and research informatics.

2020 **Bayer Crop Sciences** — St. Louis, MO
Genomics Research Scientist

- Used AWS to prototype a metagenomics pipeline of 24 steps

2015–2020 **BRISTOL MYERS SQUIBB** — Lawrenceville, NJ
Research Scientist II

- Developed a large dataset version-control system.
- Early-stage antibody-discovery sequencing informatics.

2012–2015 **DELAWARE BIOTECHNOLOGY INSTITUTE** — Newark, DE
Graduate Research Assistant

- Culture and RNAseq of *C. aceto* 8244. Diff. exp. analysis

2010-2012 **HELEN F. GRAHAM CANCER RESEARCH CENTER** — Newark, DE
Undergraduate Research Fellow

education

2012-2014 **M.S.** Bioinformatics and Computational Biology **3.97** — University of Delaware

2008–2012 **B.S.** Biochemistry — University of Delaware
Minor in Biochemical Engineering; Research Fellowship; Merit Scholarships

publications

- **"Assembling improved gene annotations in Clostridium acetobutylicum with RNA sequencing"**, Masters thesis. University of Delaware.
- **"RNAseq based transcriptome assembly of C acetobutylicum for functional genome annotation and discovery."**, First author. *AIChE Journal* 64.12 (2018): 4271-4280.
- **"Complex and extensive post-transcriptional regulation revealed by integrative proteomic and transcriptomic analysis of metabolite stress response in Clostridium acetobutylicum"**, contributing author. *Biotechnology for biofuels*. 8.1 (2015): 81.
- **"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 responds to stress: the paradigm and importance of toxic metabolite stress in C. acetobutylicum"**, contributing author. *BMC Genomics*. 14.1 (2013): 849.