Matt**Ralston**
blend of bioinformatics and biochemistry

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

data-science
Multivariate/GLM/OLS
ANOVA MLE
power-analysis
Machine Learning
PCA/UMAP AI/DNN
R/bioconductor

programming
♥ Python R Rust
Linux 💜 Emacs/vi
AWS/Docker/k8s bash
MySQL PostgreSQL
Matlab LaTeX NodeJS
Perl 💙 Ruby Julia
Javascript CSS/HTML

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

open-source
GitHub
kmerdb
NGS-CI
Portfolio

summary

Combines experiences in pharma R&D, translational cancer research, and microbial genomics to biochemical problems including Illumina sequencing and data science/analysis. Offers interdisciplinary expertise for teams of scientists, engineers, and researchers.

experience

2021-Current TERRA INFORMATICS LLC *Founder*- Newark, DE

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

2020 BAYER CROP SCIENCES *Genomics Research Scientist* - St. Louis, MO

- AWS StepFunctions production metagenomics pipeline of 24 steps

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

- LevTech Innovation Award team member for a large dataset version-control system (like git-lfs).
- Early-stage antibody-discovery sequencing informatics.
- Cheminformatics ligand enumeration software.

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

- 150x fold-coverage RNAseq with DGE/assembly of *C. aceto* found 24 novel RNAs spanning 15kb, agreed and validated prior 5'-RACE and Northern results, with novel species confirmed by Northern blot.

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

- TGF-β/BMP pathway - IHC/IF, FACS, RNAseq

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"**, 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.