

Matthew Ralston

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EDUCATION

UNIVERSITY OF DELAWARE

MS IN BIOINFORMATICS

Feb 2015 | Newark, DE

Cum. GPA: 3.97

BS IN BIOCHEMISTRY

June 2012

Minor in Biochem. Engineering

COURSEWORK

Databases • Biostatistics

Metabolic Engineering

Systems Biology • Biochem • Mol. Bio.

Genetics • Microbiology • Virology

PChem • OChem • Technical Writing

SKILLS

BIOINFORMATICS

Hisat2 • Tophat • BWA • Blast • Blat

Fastqc • Samtools • Picard • Bedtools

Cuffdiff • DEseq2 • Bioconductor • Circos

PROGRAMMING

♥ Python • R • NodeJS • Emacs • Ruby

Haskell • D3 • Linux • Perl • bash • grep/sed

Matlab • \LaTeX • AWS • Mongo • PostgreSQL

LABORATORY

RNA-seq library prep • Northern & Western

Spectrometry • Microscopy • qRT-PCR

IF • IHC • FACS • GC-MS • HPLC

Human cell culture • Anaerobic fermentation

LINKS

OPEN-SOURCE

Github://Kmer.JS

Github://Curam (AUR)

Rubygems://NGS-CI beta

SOCIAL

Github:// MatthewRalston

LinkedIn:// matthewralston

Blog:// NotVeryHumerus

Rosalind.info://mrals89

Stackoverflow://TheWaterAndWind

Spotify://TheWaterAndWind

EXPERIENCE

BRISTOL MYERS SQUIBB | RESEARCH SCIENTIST II

May 2015 - May 2019 | Lawrenceville NJ

- Galaxy bioinformatics server administrator, sequencer automation, NGS QC pipeline and large sample (20+) summary reports (Comp Bio)
- Built deduplicated dataset version control system, git expertise (Comp. Bio)
- Built a mirrored chemical database, structural and UID deduplication. (CADD)
- Expanded a multi-platform theoretical chemistry framework to enumerate all protomers, tautomers, and rotamers/conformers (2D->3D enumeration) (CADD)
- Parameter optimization and scalability investigation of the framework across multiple chemotypes, SMARTS filters for implausible substructures. (CADD)

PAPOUTSAKIS LABORATORY | GRADUATE RESEARCH ASSISTANT

Dec 2012 - May 2015 | Newark, DE

- Batch anaerobic fermentation for strand-specific Illumina RNA-seq expression readouts of small-molecule stress response over time
- Constructed a bioinformatics pipeline to process, align, and assess 1.5 billion paired-end Illumina reads.
- Produced and corrected a transcriptome assembly from a range of culture conditions.
- Designed a custom genome browser with D3JS to visualize assembly and *in silico* genomic features
- Validated several transcription start-sites with Northern blots.

RESEARCH

KMER.JS | K-MER PROPERTIES OF NUCLEIC ACIDS

Feb 2018 - Present | Ewing NJ

Developed a tool to generate k-mer profiles from streamed or locally stored large fasta/fastq files. Working on the Markov-chain probability of a new sequence given the profile. Assessing scalability and accuracy of the k-mer profile from real world and simulated data.

NGS-CI | NEXT GENERATION SEQUENCING COMPLEXITY INDEX

December 2014 - Present | Hockessin, DE

Designed a novel per-base sequencing complexity metric for assembly troubleshooting and expression estimates. Proper assembly often depends on the number of reads at the end of a transcript or contig. Poor sequencing complexity can reflect library quality issues or even alternative transcription start sites.

PUBLICATIONS

- Ralston, Matthew *et al.* "RNAseq-based transcriptome assembly of *Clostridium acetobutylicum* for functional genome annotation and discovery", *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.