

Joshua Richer

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Profile

I analyze high dimensional data, quantify what is known and deliver insights into that which is unknown. I develop robust machine learning methods for diagnostics and analysis pipelines for transcriptome profiling (RNA-Seq). A proficient Linux user and software developer at work and at home, I am active in open source projects and love learning new things about computing. See github (<https://github.com/joshuaar>) or linkedin (<https://linkedin.com/in/joshuaar>) for more details.

Experience

02.2014- **USDA Agricultural Research Service, Bioinformatics Specialist**, Maricopa, AZ.

- Present Run a small bioinformatics core facility focusing primarily on **RNA-Seq** transcriptomics in insects. Significant projects include:
- Antennal transcriptome profiling for olfactory receptors and odorant binding proteins (manuscript under preparation)
 - An analysis pipeline available on **Galaxy** for de-novo transcriptome **assembly, annotation, searching and visualization**. Used by three participating research groups.
 - Support and parallelization of FORTRAN code for radiative transfer atmospheric models.

2010-Present **Biodesign Institute, Research Associate**, Tempe, AZ.

- Conduct research projects involving high density **peptide microarrays**. Design experiments, **algorithms and software** geared toward turning this technology into a **universal disease diagnostic** called Immunosignaturing (<http://en.wikipedia.org/wiki/Immunosignature>).
- Designed and tested a system for rapidly mapping B-Cell epitopes from human sera and monoclonal antibodies. Includes a novel **statistical algorithm** for epitope determination from noisy sequence data (Manuscript submitted to Molecular and Cellular Proteomics).
 - Designed and built a rapid pattern search engine for biological sequences using **Apache Lucene and Scala**. It is over 100x faster than naive methods, and useful for identifying peptide motifs in large sequence databases. Includes **trigram index, pattern compiler, web interface**.
 - Wrote non-parametric (bootstrapping) validation procedures for a an immunosignature based Dengue Fever diagnostic. Includes **feature selection, SVM classification, cross validation, ROC analysis** and visualization. I packaged this into a command line application which became standard protocol in the lab.
 - Assorted infrastructure work - SQL schema design, data warehousing, organization and retrieval. **PostgreSQL Database** and web interface for storing, cleaning and retrieving **high throughput peptide microarray** data.

2009-2010 **Entech, Quality Control Engineer**, White Pigeon, MI.

- Directed quality control for a recycling plant specializing in tire rubber for artificial turf, molding and extrusion.
- Built and supported a database for QC results with **nightly backups to offsite storage**.
 - Wrote procedures creating formatted reports for management.
 - Technologies used: PostgreSQL, Python, Excel
 - Ensured data and product samples were available and accurate, which was important for occasional disputes over quality.

01.2009- **University of Notre Dame, Research Visitor**, Notre Dame, IN.

- 07.2009 Research internship at UND in the lab of Dr. Paul Helquist. Synthesized TSA analogs for treatment of Niemann-Pick disease, co-authoring two papers in peer reviewed journals.

Skills

Analytical Skills, Experience in supervised and unsupervised machine learning, RNA-Seq analysis, high dimensional data, multivariate and nonparametric statistics, data visualization in R and Python.

Languages, Python, R, Scala, Java, C++, Javascript.

Software/Libraries, Bioconductor, Lucene, Trinity (sequence assembly), Galaxy, Vim, sed/grep/awk/etc....

Education

2010-Present **Arizona State University, Ira. A. Fulton School of Engineering**, *Ph.D, Biological Design (conc. Bioinformatics)*, Tempe, AZ.

2005-2009 **Goshen College**, *B.A, Chemistry*, Goshen, IN.

2005-2009 **Goshen College**, *B.A, Mol. Biology*, Goshen, IN.

Quantitative Coursework (Selected).

- Nonparametric Statistics
- Linear Regression
- Statistical Computing
- Data Structures and Algorithms
- Theoretical Computer Science
- Operating Systems
- Assembly Language Programming

Publications

Josh Richer, Stephen Johnston, and Phillip Stafford. Epitope identification from fixed-complexity random-sequence peptide microarrays. *Molecular and Cellular Proteomics*, Manuscript Under Review.

Josh Richer, Xiao Wang, and Stephen Johnston. Immunosignatures for dengue diagnosis. Manuscript in Preparation.

Joe Hull, Josh Richer, and Jeffrey Fabrick. Sequencing and de novo assembly of the western tarnished plant bug (*lygus hesperus*) antennal transcriptome. Manuscript in Preparation.

Casey Cosner, Vijaya Bhaskara, Anamitra Chatterjee, John Markiewicz, Steven Corden, Joakim Lofstedt, Ankner Tobias, Joshua Richer, Tyler Hulett, Douglas Shauer, Olaf Wiest, and Paul Helquist. Evolution of concise and flexible synthetic strategies for trichostatic acid and the potent histone deacetylase inhibitor trichostatin a. *European Journal of Organic Chemistry*, 2013(1):162–172, 2013.

Anamitra Chatterjee, Joshua Richer, Tyler Hulett, Vijaya Bhaskara Reddy Iska, Olaf Wiest, and Paul Helquist. An efficient synthesis of (\pm)-trichostatic acid and analogues: A new route to (\pm)-trichostatin a. *Organic letters*, 12(4):832–834, 2010.

Contact

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