# Joshua Richer

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## Profile

I'm a scientist with training in **computer science, statistics, and biology**. I've worked with high dimensional data on clustering, classification, modeling and software engineering problems in both academic and industry settings. I seek a team that values independent contributions and encourages new ideas. See github (https://github.com/joshuaar) or linkedin (https://linkedin.com/in/joshuaar) for more details.

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## Skills

**Analytical Skills**, Experience in **supervised and unsupervised machine learning**, genomics data analysis, high dimensional data, multivariate and nonparametric statistics, statistical modeling, data visualization in R and Python, database design, object oriented programming, functional programming, web development.

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

**Software/Libraries**, Linux, ElasticSearch, Apache Spark, Apache Lucene, Vim, Git, Illustrator, AWS: EC2, S3.

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## Experience

**12.2014-Present** **Orion Health**, *Intermediate Software Engineer (Analytics)*, Scottsdale, AZ.
Designing analytics systems using **Spark, Scala and Elasticsearch** to solve population health problems.
- Designed, validated and reported on a **statistical model** aimed at **predicting hospital readmission risk** given certain clinical variables found in claims data.
- Designed and wrote **Spark Jobs** for indexing millions of patient records in a data warehouse based on Elasticsearch.
- Automated **Spark cluster** deployment to **Amazon Web Services**.
- Regularly present machine learning topics to a group of engineers.

**01.2014-12.2014** **USDA Agricultural Research Service**, *Bioinformatics Specialist*, Maricopa, AZ.
**Fixed-term appointment** to set up and ran a small informatics core facility focusing primarily on **RNA-Seq transcriptomics** in insects.
- Designed a **statistical analysis pipeline** for de-novo transcriptome assembly, annotation, hypothesis testing and visualization for three participating research groups.

**08.2010-12.2014** **Biodesign Institute**, *Research Associate*, Tempe, AZ.
**Designed experiments** and performed analysis on large, high dimensional datasets.
-Used **Python** to **clean, munge and wrangle** large amounts of experimental data.
- Designed and validated an **end-to-end method** for Dengue Fever diagnosis using data collected from blood samples. This included **feature selection, SVM classification, cross validation, and ROC analysis**.
- Built and published a novel **statistical method** for epitope determination from noisy sequence data.
- Designed and built a trigram index based search engine for biological sequences based on Apache Lucene that is over 100x faster than naive methods.

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: MySQL, Python, Excel

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 resulting in two co-authored papers in peer reviewed journals.

## Education

2010-2014 **Arizona State University, Ira. A. Fulton School of Engineering**, *Ph.D, Biological Design (conc. Bioinformatics)*, Tempe, AZ.

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

**Quantitative Coursework (Selected)**.
- Nonparametric Statistics
- Multivariate 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*, 14(1):136–47, 2015.

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

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 Chaterjee, 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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