M. Cyrus Maher, PhD, MS, MPH
Physiosigns Inc.

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SUMMARY

I am the **machine learning lead** at a **healthcare startup**. I have experience **creating breakthrough big data products**, including a **deep learning-based classifer** that **correctly predicts twelve times more heart attacks** than existing clinical models. I have rigorous training in **statistical genetics, machine learning, chemical biology,** and **epidemiologic methods**. I **finished my PhD in three years**, and have completed a total of **eight lead author manuscripts** and **two software packages**.
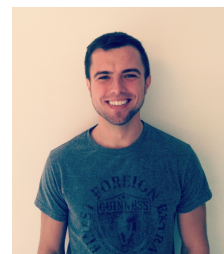
SKILLS

Performance computing: Python, R, C, Julia, Unix, SQL, AWS EC2, distributed computing (e.g. hadoop), pandas, sklearn, matplotlib, seaborn, bokeh.

Statistics/Machine Learning: Probability theory, classification (neural networks, gradient boosting, etc.) regression, clustering, feature selection, visualization.

Genetics/Clinical informatics: Whole-genome sequencing, other high throughput experimental data (RNAseq, proteomics, etc.), disease modeling, drug design, clinical trials.

WORK EXPERIENCE

Physiosigns Inc. *Machine Learning Lead*   **May 2016 to Present**
Built end-to-end machine learning pipeline. Leveraged deep learning to increase the number of heart attacks detected by twelve-fold. Designed interactive presentation of results to patients and doctors that includes accurate probabilities, quantified uncertainty, key personalized risk factors, and projected trends over time.

Human Longevity Inc. *Data Scientist*   **November 2014 to May 2016**
Spearheaded an interdisciplinary team of PhDs to achieve breakthroughs in forensic genomics. Invented the most sensitive method to-date for detecting contamination in next-generation sequencing data. Applied software and wet-lab experience to propose $6 million per year reduction in sequencing costs.

Francis I. Proctor Foundation *Software Engineer*   **June 2010 to May 2011**
Built high-performance probabilistic disease model to quantify cost of antibiotic resistance in *S. pneumoniae* using a system of over 23,000 differential equations. Calculated timeline for competitively eliminating resistance.

SOFTWARE PACKAGES

MOSAIC, a method for discovering, e.g. the genetic basis of human-specific diseases
http://pythonhosted.org/bio-MOSAIC
CauseMap, a tool for establishing causality in complex non-linear systems
http://cyrusmaher.github.io/CauseMap.jl

LEADERSHIP

- Led fourteen PhD scientists to complete work forms the foundation for a possible $1 billion forensics business.
- Mentored two graduate students. One mentee's findings have improved HLI's use of metabolomic data. The other won an NSF scholarship based on our work.
- Taught five semesters of General and Organic Chemistry at UC Berkeley, in addition to years of tutoring and volunteer experience.

EDUCATION | **University of California, San Francisco**, San Francisco, CA
PhD, Statistical Genetics, 2011–2014

University of California, Berkeley, Berkeley, CA
MPH, Statistics and Epidemiologic Methods, 2009–2011
MS, Chemical Biology, 2007–2009

Pomona College, Claremont, CA
BA, Chemistry, 2002–2006

GRADUATE
COURSEWORK
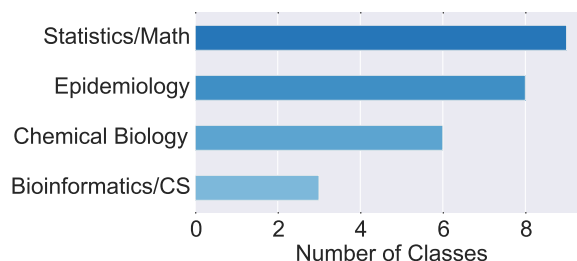
GRADUATE
RESEARCH

UC San Francisco *Graduate Student*   **June 2011 to November 2014**
Projects included: statistical methods development and deployment, scoring and integration of complex experimental data, investigation of genetic basis of human disease.

UC Berkeley *Research Scientist*   **June 2009 to June 2010**
Conducted a comprehensive literature review of cost-effectiveness of influenza vaccination. Combined with own disease modeling to quantify economic cost of influenza.

UC Berkeley *Graduate Student*   **Sept. 2007 to May 2009**
Leveraged computational tools to design improved inhibitors against tuberculosis. Approaches included molecular simulation, isosteric ligand design, and molecular docking.

AWARDS &
HONORS

Ruth L. Kirschstein National Research Service Award, 2013 to 2014.
Lloyd M. Kozloff Fellowship, 2013 to 2014.
National Merit Scholarship, 2002 to 2006.
Rensselaer Medal, 2001 ($100K value, awarded to best student in math and science).

LEAD AUTHOR
PUBLICATIONS

Maher MC[*], Lippert C[*], Sabbatini R, Garst P, Lee S, Park E, Yocum K, Wong T, Roby R, Venter JC, Och F. Prediction of human traits from genome and voice. *Science. In review.*

Deyle E[*], **MaherMC**[*], Basu S, Hernandez R, Sugihara G. Global Environmental Drivers of Influenza. *Proceedings of the National Academy of Sciences. Accepted with minor revision.*

Maher MC and Hernandez RD. CauseMap: Fast inference of causality from complex time series. *PeerJ.* 3:824. 2015.

Maher MC and Hernandez RD. Rock, paper, scissors: harnessing complementarity in ortholog detection methods improves comparative genomic inference. *Genes, Genomes, and Genetics.* 5(4):629-38. 2015.

Maher MC[*], Uricchio LH[*], Torgerson DG, RD Hernandez. Population genetics of rare variants and complex diseases. *Human Heredity*, 74:3-4. 2012.

Maher MC, Alemayehu W, Lakew T, Gaynor BD, Haug S, Cevallos V, Keenan JD, Lietman TM, Porco TC. The fitness cost of antibiotic resistance in Streptococcus pneumoniae: insight from the field. *PLoS One*, 7(1):e2907. 2012.

† Walsh J and **Maher MC**, The cost-effectiveness of influenza vaccination. In R. Rappuoli & G. Del Giudice (Eds.). <u>Influenza Vaccines for the Future</u>. Birkhauser Publications, Boston. 2010.

† Steinmetz WE and **Maher MC**, Magnetic resonance imaging in the undergraduate laboratory, *J. Chem. Ed.*, 84: 1830-1831. 2007.

† Steinmetz WE and **Maher MC**, Magnetic resonance imaging on an NMR spectrometer: an experiment for the Physical Chemistry laboratory, *Concepts in Magn. Reson.*, 30A:133-139. 2007.

These authors contributed equally to this work.
† *By convention in the field, equivalent to first author publication.*

HOBBIES   Meditation, snorkeling, skydiving, rock climbing. Also, dog walking, talking science on Twitter.