

BERNARD J. KOCH

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ABOUT ME: I am a computational social scientist (data scientist) interested in culture, the science of science, and the intersections of deep learning, causal inference, and network science. Before graduate school, I worked at NHGRI (the NIH genomics institute) doing bioinformatics/scientific programming, and at AAAS (publisher of *Science*) doing science education research and front-end development of science education tools.

EDUCATION:

- Ph.D. in Sociology, University of California Los Angeles, ABD (2022 expected), advised by Jacob Foster
- M.A. in Sociology, University of California Los Angeles, 2018
- B.A. in Biology with a Cognitive Science minor, Swarthmore College, 2013

GRANTS, FELLOWSHIPS, and HONORARIA:

- Templeton Foundation Education Development Grant, Primary Investigator, Jun 2019 (\$5,704)
- Templeton Foundation Diverse Intelligence Summer Institute, Travel/Housing Full Scholarship, 2019
- National Science Foundation Graduate Research Fellowship, 2018-2021 (\$138,000)
- University of California Graduate Research Mentorship Fellowship, 2017-2018 (\$38,000)
- University of California Graduate Summer Research Mentorship Fellowship, 2017 & 2018 (\$6,000)
- University of California Dean's Scholar Award, 2016-2021 (~14,000) (declined)
- University of California Dr. Ursula Mandel Scholarship, 2016 -2017 (\$15,000)
- Russell Sage Foundation Workshop for Social Science Genomics, Travel/Housing Full Scholarship, 2017

AWARDS:

- 2021 UCLA Sociology Sifton Undergraduate Research Mentorship Award
- 2018 California Workshop on Evolutionary Social Sciences Poster Award, 2nd Place
- 2014 NHGRI Genome Recognition of Employee Accomplishment and Talents Award (as member of a team)

PEER-REVIEWED PUBLICATIONS:

- Jiang S, **Koch BJ**, Sun Y. HINTS: time series prediction via dynamic heterogeneous information network embedding. *WWW*, 2021.
- Brand JE, Xu J, **Koch BJ**, Geraldo PE. Uncovering sociological effect heterogeneity using tree-based machine learning. *Sociological Methodology*, 2021..
- Gjesfjeld E, Silvestro D, Chang J, **Koch BJ**, Foster JG, Alfaro ME. A quantitative workflow for modeling diversification in technological systems. *PLoS One*, 2020 February 6;15(2): e0227579.
- Brand JE, **Koch BJ**, Xu J. Machine learning, in **SAGE Research Methods in the Social Sciences Foundation**. Paul Atkinson, Sara Delamont, Alexandru Cernat, Joseph W. Sakshaug, and Richard A. Williams. eds. 2020.
- Davidson PL, **Koch BJ**, Schnitzler CE, Henry JQ, Martindale MQ, Baxeavanis AD, Browne WE. The maternal-zygotic transition and zygotic activation of the *Mnemiopsis leidyi* genome occurs within the first three cleavage cycles. *Mol Reprod Dev.*, 2017 Oct 25;84: 1218–1229.

- Moreland RT, Nguyen AD, Ryan JF, Schnitzler CE, **Koch BJ**, Siewert K, Wolfsberg TG, Baxeavanis AD. A customized web portal for the genome of the ctenophore *Mnemiopsis leidyi*. **BMC Genomics**, 2014 Apr 15:316.
- Ryan JF, Pang K, Schnitzler CE, Nguyen A-D, Moreland RT, Simmons DK, **Koch BJ**, Havlak P, NISC Comparative Sequencing Program, Smith SA, Putnam N, Dunn CW, Wolfsberg TG, Mullikin JC, Martindale MQ, Baxeavanis AD. The genome of the ctenophore *Mnemiopsis leidyi*. **Science**, 2013 Dec 13;342(6164).
- **Koch BJ**, Ryan JF, Baxeavanis AD. The diversification of the LIM superclass at the base of the metazoa increased subcellular complexity and promoted multicellular specialization. **PLoS One**, 2012 March 15;7(3): e33261.

WORKS IN PROGRESS:

- **Koch BJ**, Silvestro D, Foster JG. The evolutionary dynamics of cultural change (as told through the birth and brutal, blackened death of Metal music) ([under review at the American Journal of Sociology](#)).
- **Koch BJ**, Sainburg T, Geraldo PE, Jiang S, Foster JG, Sun Y. A review of deep learning of potential outcomes.
- **Koch BJ**, Dasgupta K, Panofsky A. White supremacy in an academic forest: does anyone hear it?
- Koch BJ, Denton E, Hanna A, Foster JG. The genealogy of data and genesis of fields in machine learning research (*authorship order TBD*).

INVITED TALKS:

- “*Modeling the Dynamics of Cultural Diversification*” Cultural Evolution Society/National Institute for Mathematical and Biological Synthesis, virtual, November 2020.

CONFERENCE PRESENTATIONS:

- Koch BJ, Sainburg T, Jiang S, Foster JG, Sun Y. Deep Learning of Potential Outcomes. American Sociological Association, Main Session on Methodology, San Francisco CA (virtual), August 2020.
- Koch BJ, Silvestro D, and Foster JG. Evolutionary Dynamics of Cultural Change. American Sociological Association, Main Session on Culture, San Francisco CA (virtual), August 2020.
- Koch BJ, Silvestro D, and Foster JG. The Birth and Death of Cultural Things: Explaining Cultural Evolution Through Bayesian Analysis of Diversification Rates. American Sociological Association, Main Session on Computational Sociology, New York NY, August 2019.
- Koch BJ, Silvestro D, and Foster JG. The Birth and Death of Cultural Things: Explaining Cultural Evolution Through Bayesian Analysis of Diversification Rates. International Conference for Computational Social Science, Amsterdam NL, July 2019.
- Koch BJ, Silvestro D, and Foster JG. The birth and (brutal, blackened) death of cultural things: a macroevolutionary history of metal music 1968-2000. Cultural Evolution Society, Tempe AZ, October 2018.
- Koch BJ, Roseman JE. Understanding Speciation at the High School Level: An NGSS-Aligned Mental Model and Relevant Misconceptions. Accepted for presentation at National Association For Research in Science Teaching Annual International Conference, Baltimore MD, April 2016.

POSTERS:

- Koch BJ, Dasgupta K, Panofsky A. White Supremacy in an Academic Forest: Does Anyone Hear It? Pre-ASA Workshop on Computational Sociology, Palo Alto CA (virtual), August 2020.
- Koch BJ, Silvestro D, Foster JG. The Evolution of Cultural “Things:” Diversity Dependence Among Metal Bands (1968-2000). California Workshop for the Evolutionary Social Sciences, Santa Barbara CA, May 2018.
- Koch BJ, Glassman SE, Roseman JE, DeBoer GE. A Case Study in the Evaluation of Alignment to the Next Generation Science Standards using the EQuIP Rubric. The National Association For Research in Science Teaching Annual International Conference, Chicago IL, April 2015.

- Koch BJ, Schnitzler CE, Gildea, DE, Henry JQ, Martindale MQ, Baxeavanis AD, Browne WE. Differential Gene Expression During Early Embryogenesis in the Ctenophore *Mnemiopsis leidyi*. The Society for Integrative & Comparative Biology Annual Meeting, Austin TX, January 2014.
- Koch BJ, Ryan JF, Baxeavanis AD. The Diversification of the LIM Superclass at the Base of the Metazoa Increased Subcellular Complexity and Promoted Multicellular Specialization. Swarthmore College Sigma Xi Poster Session, Bethesda MD. October 2011.
- Koch BJ, Ryan JF, Baxeavanis AD. Evolution of the LIM Domain Superclass throughout Metazoa. NIH Spring Research Festival, Bethesda MD. May 2011.
- Koch BJ, Bilke S, Davis SR, Meltzer PS. Retrovirus Detection in Next Generation Sequence Data and a Bioconductor Package for the NCBI Entrez EUtils API. NIH Summer Poster Session, Bethesda MD. August 2010.
- Koch BJ, Pianka AR, Weir MP. Effects of Secondary Structure on Alternative Translation Initiation in *Saccharomyces cerevisiae*. Wesleyan University Summer Research Presentation, Middletown CT. August 2009.

SKILLS:

- **Programming:** Python/pandas, R (fluent), Javascript, SQL, Bash (intermediate)
- **Deep Learning:** Tensorflow2, Pytorch (intermediate)
- **Supervised Machine Learning:** Standard models (LR, NB, SVM, RF, XGBoost, etc...)
- **Unsupervised Machine Learning:** Standard models (PCA, t-SNE, UMAP, Struct. topic models, Word vecs)
- **Network Science:** GNNs, Community detection, ERGMs, Centrality analyses
- **Bayesian Statistics:** Simple MCMCs with Gibbs Sampling
- **Causal Inference:** DL models for CI, Causal Trees/Forests, interpreting DAGs, other methods for obs. data
- **Regression:** GLMs, Mixed effect models
- **Languages:** English (fluent), Spanish (intermediate)

PREVIOUS EMPLOYMENT/RESEARCH EXPERIENCE:

American Association for the Advancement of Science, Washington DC Spring 2014-Spring 2016

Position: Research Assistant

- Designed and validated assessments to measure high school students' understanding of evolution
- Managed random controlled trial study of biochemistry curriculum over a cohort of ~1000 students
- Co-wrote & programmed instructional [web app](#) using 80+ years of NOAA weather data and Google Maps API
- Researched criteria for the evaluation of curricula in the context of national science education standards

National Human Genome Research Institute/NIH, Bethesda MD Summer 2013-Winter 2014

Position: Post-baccalaureate Fellow

- Quantified gene expression in embryos to find evolutionarily important developmental pathways
- Worked on assembly of animal genomes and algorithmic identification of genomic features

Sars International Centre for Marine Molecular Biology, Bergen, Norway Summer 2012

Position: Howard Hughes Medical Institute Undergraduate Summer Research Grantee

- Wrote user-friendly Python program for selection of statistical models of evolution for phylogenetics
- Studied the developmental genes of animals to understand how evolutionary innovations occurred

National Human Genome Research Institute/NIH, Bethesda MD Fall 2010-Fall 2011

Position: Student Fellow

- Worked with a team of scientists on algorithmic identification of features in a newly sequenced genome
- Co-taught and organized introductory "Python Programming for Biologists" course for NHGRI fellows

- Chronicled evolution of protein structures throughout animal history using Hidden Markov Models
- Provided scientific programming support to non-computational laboratories

National Cancer Institute/NIH, Bethesda MD Summer 2010

Position: NIH Summer Intern

- Worked on unpublished Bioconductor package to import biomedical publication metadata into R
- Developed techniques for detecting virus contamination in genomic sequencing data

Wesleyan University, Middletown CT Summer 2009

Position: Howard Hughes Medical Institute Undergraduate Summer Research Grantee

- Used information theory to identify alternative gene start sites in yeast genomes

METHODS WORKSHOPS (lead/co-lead and organized):

- Summer Institute in Computational Social Science (SICSS) at UCLA, 2 weeks, sponsored by California Center for Population Research (CCPR) and SICSS, Jun 2020.
- Summer Institute in Computational Social Science at UCLA, 2 weeks, sponsored by CCPR and SICSS, Jun 2019.
- UCLA Computational Social Science Bootcamp, 1 week, sponsored by UCLA Sociology, Sep 2018.
- Word Embeddings for Social Science, 4 hr, UCLA BRITE Center, retreat, Sep 2018.
- Introduction to Text Analysis, sponsored by UCLA Library, 2hr, 2018.
- Introductory Programming for Text Analysis, UCLA Sociology, 2hr, May 2018 & Oct 18.
- Python Programming for Biologists, National Human Genome Research Institute, weekly, Spring 2011.

MENTORSHIP:

- Brandon Grayson (Undergraduate Thesis in Sociology) 2020-2021
- Cheng Yi (Krystal) Xu (Undergraduate Research in Statistics) 2017-2018
- Jordan Jurczyk (Undergraduate Thesis in Sociology) 2018-2019
- Vinay Kumar (Undergraduate Research in Biology) 2018-2019
- Shawn Schwartz (Undergraduate Research in Biology) 2018-2019
- Brandon Grayson (Undergraduate Thesis in Sociology) 2020-2021

SERVICE:

- UCLA Graduate Student Association Social Sciences Council, VP of Communications 2017-2019
- UCLA Sociology Graduate Association Treasurer & Social Sciences Council Representative 2016-2019

REVIEWER:

- *American Sociological Review*
- *Poetics*

INTERESTS:

- Sound Design/Music Composition
- Cycling