



Barbara Elizabeth Engelhardt

Professor (Research) of Biomedical Data Science and, by courtesy, of Statistics and of Computer Science

Department of Biomedical Data Science

Bio

BIO

Barbara E Engelhardt is a Senior Investigator at Gladstone Institutes and Professor at Stanford University in the Department of Biomedical Data Science. She received her B.S. (Symbolic Systems) and M.S. (Computer Science) from Stanford University and her PhD from UC Berkeley (EECS) advised by Prof. Michael I Jordan. She was a postdoctoral fellow with Prof. Matthew Stephens at the University of Chicago. She was an Assistant Professor at Duke University from 2011-2014, and an Assistant, Associate, and then Full Professor at Princeton University in Computer Science from 2014-2022. She has worked at Jet Propulsion Labs, Google Research, 23andMe, and Genomics plc. In her career, she received an NSF GRFP, the Google Anita Borg Scholarship, the SMBE Walter M. Fitch Prize (2004), a Sloan Faculty Fellowship, an NSF CAREER, and the ISCB Overton Prize (2021). Her research is focused on developing and applying models for structured biomedical data that capture patterns in the data, predict results of interventions to the system, assist with decision-making support, and prioritize experiments for design and engineering of biological systems.

ACADEMIC APPOINTMENTS

- Professor (Research), Department of Biomedical Data Science
- Professor (Research) (By courtesy), Statistics
- Professor (Research) (By courtesy), Computer Science
- Member, Bio-X

ADMINISTRATIVE APPOINTMENTS

- Senior Investigator, Gladstone Institutes, (2021- present)

HONORS AND AWARDS

- International Society for Computational Biology Fellow, International Society for Computational Biology (ICSB) (March, 2024)
- Overton Award, International Society for Computational Biology (ICSB) (2021)

Teaching

COURSES

2025-26

- Biomedical Data Science Student Seminar: BMDS 201A, BMDS 201B, BMDS 201C (Aut)
- Introduction to Biomedical Informatics Research Methodology: BIOE 212, BMDS 212, CS 272, GENE 212 (Spr)
- Workshop in Biomedical Data Science: BMDS 280A, STATS 260A (Aut)

2024-25

- Biomedical Data Science Student Seminar: BIOMEDIN 201 (Aut)
- Introduction to Biomedical Informatics Research Methodology: BIOE 212, BIOMEDIN 212, CS 272, GENE 212 (Spr)
- Workshop in Biostatistics: BIODS 260A, STATS 260A (Aut)

2023-24

- Biomedical Data Science Student Seminar: BIODS 201, BIOMEDIN 201 (Aut)
- Workshop in Biostatistics: BIODS 260A, STATS 260A (Aut)

2022-23

- Biomedical Informatics Student Seminar: BIODS 201, BIOMEDIN 201 (Aut)
- Workshop in Biostatistics: BIODS 260A, STATS 260A (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Karen Feng, Amber Hu, Christine Yiwen Yeh

Postdoctoral Faculty Sponsor

Ed Tam

Doctoral Dissertation Advisor (AC)

Luis Chumpitaz Diaz, Joshua Lazaro, Aishwarya Mandyam

Orals Evaluator

Aishwarya Mandyam

Doctoral Dissertation Co-Advisor (AC)

Esther Robb

Master's Program Advisor

Ming Sun

Doctoral (Program)

Bryan Bunning, Jordan Cahoon, Sohaib Hassan, Bridget Lin, Wendi Liu, Aishwarya Mandyam

Publications

PUBLICATIONS

- **Optimizing the design of spatial genomic studies.** *Nature communications*
Jones, A., Cai, D., Li, D., Engelhardt, B. E.
2024; 15 (1): 4987
- **Alignment of spatial genomics data using deep Gaussian processes.** *Nature methods*
Jones, A., Townes, F. W., Li, D., Engelhardt, B. E.
2023
- **Parts-based decomposition of spatial genomics data finds distinct tissue regions** *NATURE METHODS*
Townes, F., Engelhardt, B. E.
2023: 1-2
- **Sequential Gaussian Processes for Online Learning of Nonstationary Functions** *IEEE TRANSACTIONS ON SIGNAL PROCESSING*
Zhang, M., Dumitrascu, B., Williamson, S. A., Engelhardt, B. E.
2023; 71: 1539-1550

- **Nonnegative spatial factorization applied to spatial genomics.** *Nature methods*
Townes, F. W., Engelhardt, B. E.
2022
- **Hierarchical Gaussian Processes and Mixtures of Experts to Model COVID-19 Patient Trajectories.** *Pacific Symposium on Biocomputing*
Pacific Symposium on Biocomputing
Cui, S., Yoo, E. C., Li, D., Laudanski, K., Engelhardt, B. E.
2022; 27: 266-277
- **A Poisson reduced-rank regression model for association mapping in sequencing data.** *BMC bioinformatics*
Fitzgerald, T., Jones, A., Engelhardt, B. E.
2022; 23 (1): 529
- **Telescoping bimodal latent Dirichlet allocation to identify expression QTLs across tissues.** *Life science alliance*
Gewirtz, A. D., Townes, F. W., Engelhardt, B. E.
2022; 5 (12)
- **CONTRASTIVE LATENT VARIABLE MODELING WITH APPLICATION TO CASE-CONTROL SEQUENCING EXPERIMENTS** *ANNALS OF APPLIED STATISTICS*
Jones, A., Townes, F., Li, D., Engelhardt, B. E.
2022; 16 (3): 1268-1291
- **Towards 'end-to-end' analysis and understanding of biological timecourse data.** *The Biochemical journal*
Jena, S. G., Goglia, A. G., Engelhardt, B. E.
2022; 479 (11): 1257-1263
- **Guiding Efficient, Effective, and Patient-Oriented Electrolyte Replacement in Critical Care: An Artificial Intelligence Reinforcement Learning Approach.** *Journal of personalized medicine*
Prasad, N., Mandyam, A., Chivers, C., Draugelis, M., Hanson, C. W., Engelhardt, B. E., Laudanski, K.
2022; 12 (5)
- **Brain kernel: A new spatial covariance function for fMRI data.** *NeuroImage*
Wu, A., Nastase, S. A., Baldassano, C. A., Turk-Browne, N. B., Norman, K. A., Engelhardt, B. E., Pillow, J. W.
2021; 245: 118580
- **A self-exciting point process to study multicellular spatial signaling patterns** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Verma, A., Jena, S. G., Isakov, D. R., Aoki, K., Toettcher, J. E., Engelhardt, B. E.
2021; 118 (32)
- **Joint analysis of expression levels and histological images identifies genes associated with tissue morphology** *NATURE COMMUNICATIONS*
Ash, J. T., Darnell, G., Munro, D., Engelhardt, B. E.
2021; 12 (1): 1609
- **Optimal marker gene selection for cell type discrimination in single cell analyses** *NATURE COMMUNICATIONS*
Dumitrascu, B., Villar, S., Mixon, D. G., Engelhardt, B. E.
2021; 12 (1): 1186
- **COP-E-CAT: Cleaning and Organization Pipeline for EHR Computational and Analytic Tasks**
Mandyam, A., Yoo, E. C., Soules, J., Laudanski, K., Engelhardt, B. E., ASSOC COMP MACHINERY
ASSOC COMPUTING MACHINERY.2021
- **Causal network inference from gene transcriptional time-series response to glucocorticoids** *PLOS COMPUTATIONAL BIOLOGY*
Lu, J., Dumitrascu, B., McDowell, I. C., Jo, B., Barrera, A., Hong, L. K., Leichter, S. M., Reddy, T. E., Engelhardt, B. E.
2021; 17 (1): e1008223
- **ACE inhibition and cardiometabolic risk factors, lung ACE2 and TMPRSS2 gene expression, and plasma ACE2 levels: a Mendelian randomization study.** *Royal Society open science*
Gill, D., Arvanitis, M., Carter, P., Hernández Cordero, A. I., Jo, B., Karhunen, V., Larsson, S. C., Li, X., Lockhart, S. M., Mason, A., Pashos, E., Saha, A., Tan, et al

2020; 7 (11): 200958

- **The GTEx Consortium atlas of genetic regulatory effects across human tissues** *SCIENCE*
Aguet, F., Barbeira, A. N., Bonazzola, R., Brown, A., Castel, S. E., Jo, B., Kasela, S., Kim-Hellmuth, S., Liang, Y., Parsana, P., Flynn, E., Fresard, L., Gamazon, et al
2020; 369 (6509): 1318+
- **A robust nonlinear low-dimensional manifold for single cell RNA-seq data.** *BMC bioinformatics*
Verma, A., Engelhardt, B. E.
2020; 21 (1): 324
- **Sparse multi-output Gaussian processes for online medical time series prediction.** *BMC medical informatics and decision making*
Cheng, L. F., Dumitrascu, B., Darnell, G., Chivers, C., Draugelis, M., Li, K., Engelhardt, B. E.
2020; 20 (1): 152
- **The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution.** *Cell*
Rozenblatt-Rosen, O., Regev, A., Oberdoerffer, P., Nawy, T., Hupalowska, A., Rood, J. E., Ashenberg, O., Cerami, E., Coffey, R. J., Demir, E., Ding, L., Esplin, E. D., Ford, et al
2020; 181 (2): 236–49
- **Measuring the predictability of life outcomes with a scientific mass collaboration.** *Proceedings of the National Academy of Sciences of the United States of America*
Salganik, M. J., Lundberg, I., Kindel, A. T., Ahearn, C. E., Al-Ghoneim, K., Almaatouq, A., Altschul, D. M., Brand, J. E., Carnegie, N. B., Compton, R. J., Datta, D., Davidson, T., Filippova, et al
2020
- **netNMF-sc: leveraging gene-gene interactions for imputation and dimensionality reduction in single-cell expression analysis.** *Genome research*
Elyanow, R., Dumitrascu, B., Engelhardt, B. E., Raphael, B. J.
2020; 30 (2): 195-204
- **The impact of sex on gene expression across human tissues.** *Science (New York, N.Y.)*
Oliva, M. n., Muñoz-Aguirre, M. n., Kim-Hellmuth, S. n., Wucher, V. n., Gewirtz, A. D., Cotter, D. J., Parsana, P. n., Kasela, S. n., Balliu, B. n., Viñuela, A. n., Castel, S. E., Mohammadi, P. n., Aguet, et al
2020; 369 (6509)
- **An Optimal Policy for Patient Laboratory Tests in Intensive Care Units.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Cheng, L. F., Prasad, N., Engelhardt, B. E.
2019; 24: 320-331
- **Statistical tests for detecting variance effects in quantitative trait studies.** *Bioinformatics (Oxford, England)*
Dumitrascu, B., Darnell, G., Ayroles, J., Engelhardt, B. E.
2019; 35 (2): 200-210
- **SEX DIFFERENCES AT THE MOLECULAR LEVEL: LESSONS FROM THE HUMAN TRANSCRIPTOME**
Stranger, B., Oliva, M., Gamazon, E., Reverter, F., Wucher, V., Balliu, B., Dumitrascu, B., Parsana, P., Payne, A., Jo, B., Montgomery, S., Battle, A., Ardlie, et al
ELSEVIER.2019: 1034
- **Fast Moment Estimation for Generalized Latent Dirichlet Models.** *Journal of the American Statistical Association*
Zhao, S., Engelhardt, B. E., Mukherjee, S., Dunson, D. B.
2018; 113 (524): 1528-1540
- **Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding.** *Genome research*
McDowell, I. C., Barrera, A., D'Ippolito, A. M., Vockley, C. M., Hong, L. K., Leichter, S. M., Bartelt, L. C., Majoros, W. H., Song, L., Safi, A., Koçak, D. D., Gersbach, C. A., Hartemink, et al
2018; 28 (9): 1272-1284
- **Bayesian nonparametric discovery of isoforms and individual specific quantification.** *Nature communications*
Aguiar, D., Cheng, L. F., Dumitrascu, B., Mordelet, F., Pai, A. A., Engelhardt, B. E.

2018; 9 (1): 1681

- **Clustering gene expression time series data using an infinite Gaussian process mixture model.** *PLoS computational biology*
McDowell, I. C., Manandhar, D., Vockley, C. M., Schmid, A. K., Reddy, T. E., Engelhardt, B. E.
2018; 14 (1): e1005896
- **Co-expression networks reveal the tissue-specific regulation of transcription and splicing.** *Genome research*
Saha, A., Kim, Y., Gewirtz, A. D., Jo, B., Gao, C., McDowell, I. C., Engelhardt, B. E., Battle, A.
2017; 27 (11): 1843-1858
- **Expandable factor analysis.** *Biometrika*
Srivastava, S., Engelhardt, B. E., Dunson, D. B.
2017; 104 (3): 649-663
- **Detecting differential growth of microbial populations with Gaussian process regression.** *Genome research*
Tonner, P. D., Darnell, C. L., Engelhardt, B. E., Schmid, A. K.
2017; 27 (2): 320-333
- **Genetic effects on gene expression across human tissues.** *Nature*
Battle, A. n., Brown, C. D., Engelhardt, B. E., Montgomery, S. B.
2017; 550 (7675): 204-13
- **Context Specific and Differential Gene Co-expression Networks via Bayesian Biclustering.** *PLoS computational biology*
Gao, C., McDowell, I. C., Zhao, S., Brown, C. D., Engelhardt, B. E.
2016; 12 (7): e1004791
- **Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium.** *Behavior genetics*
van den Berg, S. M., de Moor, M. H., Verweij, K. J., Krueger, R. F., Luciano, M., Arias Vasquez, A., Matteson, L. K., Derringer, J., Esko, T., Amin, N., Gordon, S. D., Hansell, N. K., Hart, et al
2016; 46 (2): 170-82
- **Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder.** *JAMA psychiatry*
de Moor, M. H., van den Berg, S. M., Verweij, K. J., Krueger, R. F., Luciano, M., Arias Vasquez, A., Matteson, L. K., Derringer, J., Esko, T., Amin, N., Gordon, S. D., Hansell, N. K., Hart, et al
2015; 72 (7): 642-50
- **Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements.** *Genome biology*
Zhang, W., Spector, T. D., Deloukas, P., Bell, J. T., Engelhardt, B. E.
2015; 16: 14
- **Genetic variation associated with euphorogenic effects of d-amphetamine is associated with diminished risk for schizophrenia and attention deficit hyperactivity disorder.** *Proceedings of the National Academy of Sciences of the United States of America*
Hart, A. B., Gamazon, E. R., Engelhardt, B. E., Sklar, P., Kähler, A. K., Hultman, C. M., Sullivan, P. F., Neale, B. M., Faraone, S. V., de Wit, H., Cox, N. J., Palmer, A. A.
2014; 111 (16): 5968-73
- **A statin-dependent QTL for GATM expression is associated with statin-induced myopathy.** *Nature*
Mangravite, L. M., Engelhardt, B. E., Medina, M. W., Smith, J. D., Brown, C. D., Chasman, D. I., Mecham, B. H., Howie, B., Shim, H., Naidoo, D., Feng, Q., Rieder, M. J., Chen, et al
2013; 502 (7471): 377-80
- **Integrative modeling of eQTLs and cis-regulatory elements suggests mechanisms underlying cell type specificity of eQTLs.** *PLoS genetics*
Brown, C. D., Mangravite, L. M., Engelhardt, B. E.
2013; 9 (8): e1003649
- **Stability selection for regression-based models of transcription factor-DNA binding specificity.** *Bioinformatics (Oxford, England)*
Mordelet, F., Horton, J., Hartemink, A. J., Engelhardt, B. E., Gordân, R.
2013; 29 (13): i117-25

- **Genome-wide association study of d-amphetamine response in healthy volunteers identifies putative associations, including cadherin 13 (CDH13).** *PLoS one*
Hart, A. B., Engelhardt, B. E., Wardle, M. C., Sokoloff, G., Stephens, M., de Wit, H., Palmer, A. A.
2012; 7 (8): e42646
- **Genome-scale phylogenetic function annotation of large and diverse protein families.** *Genome research*
Engelhardt, B. E., Jordan, M. I., Srouji, J. R., Brenner, S. E.
2011; 21 (11): 1969-80
- **Understanding mechanisms underlying human gene expression variation with RNA sequencing.** *Nature*
Pickrell, J. K., Marioni, J. C., Pai, A. A., Degner, J. F., Engelhardt, B. E., Nkadori, E., Veyrieras, J. B., Stephens, M., Gilad, Y., Pritchard, J. K.
2010; 464 (7289): 768-72
- **Protein molecular function prediction by Bayesian phylogenomics.** *PLoS computational biology*
Engelhardt, B. E., Jordan, M. I., Muratore, K. E., Brenner, S. E.
2005; 1 (5): e45