SEAN CORBETT, Ph.D.

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LinkedIn | Personal Site

I'm a computational biologist with deep expertise in multi-omics integration and analysis, population genetics, and data infrastructure and design. I've led analytical strategy across projects throughout the drug development process, and I thrive in bridging the gaps in multidisciplinary scientific teams. I'm passionate about uniting experimental science with scalable computational methods, including emerging machine learning and generative models, towards accelerating the process of therapeutic innovation.

EMPLOYMENT HISTORY

Biohaven Pharmaceuticals April 2024– Present
Principal Investigator Cambridge, MA

I am the lead computational biologist for Biohaven's Discovery group. I work in close collaboration with a wide range of scientists and physicians on projects throughout the drug development cycle, from early discovery to subgroup analysis of clinical trial data.

- Develop genetic patient stratification strategies for therapeutics in a wide range of modalities.
- Integrate population genetics, multi-omic, and clinical data from cohorts such as the UK Biobank and All Of Us to identify and prioritize novel targets for early drug programs.
- Provide indication selection and prioritization from a molecular perspective for projects in Biohaven's antibody-drug conjugate portfolio.

Tessera Therapeutics August 2022 – April 2024
Senior Scientist Somerville, MA

Collaborate with teams across Tessera's various gene therapy platforms and pre-clinical therapeutic projects, analyzing multi-omics datasets encompassing genotoxicity, editing efficiency, and basic biology.

- Designed, coordinated, and analyzed data for experiments to identify key mechanistic features of Tessera's RNA writer technology
- Characterized the range of structural alterations associated with Tessera's pre-clinical RNA rewriter technology to de-risk potential genotoxicity
- Created infrastructure for and analyzed data from a wide variety of datasets spanning a wide array of 'omics modalities, including long- and short-read DNA/RNA sequencing, high-throughput compound screening, and FACS data.

Agios Pharmaceuticals June 2019 – June 2022
Associate Scientist (2019-2020), Scientist (2020-2022) Cambridge, MA

Provided cross-functional computational biology support to a diverse variety of early-to-late stage drug projects. Catalyzed the modernization of the digital infrastructure behind Agios' 'omics platform.

- Leveraged flux balance analysis models of mitochondrial metabolism to provide mechanistic insights into potential drug targets
- Designed a novel FACS-enabled genome-wide CRISPR screening series to optimize hit identification for primary mitochondrial dysfunction indications

- Coordinated experimental design, and conducted data ingestion, normalization, pipeline creation and analysis of RNA-seq, single cell RNA-seq, TCR-seq metabolomics, proteomics, and FACS data in drug projects spanning immuno-oncology, mitochondrial dysfunction, and benign hematology indications

Broad Institute of MIT and Harvard August 2012-May 2014
Software Engineer Cambridge, MA

Wrote software to support high-throughput small molecule screening in the Broad's Center for the Science of Therapeutics.

Tufts University Medical School May 2011- July 2012
Programmer / Analyst Boston, MA

Project lead on an effort to internationalize TUSK, Tufts University Medical School's course management system for medical student training in collaboration with Translators Without Borders.

EDUCATION

Boston University (M.S., Ph.D. Bioinformatics) 2014-2019 Boston, MA

Clark University (B.A., Computer Science & Music) 2007-2011 Worcester, MA

ACADEMIC RESEARCH EXPERIENCE

Boston University Fall 14 – Spring 19
Doctoral Candidate – Spira-Lenburg Lab, Boston University Medical Center
Currently studying the molecular pathogenesis of pulmonary disease through the lens of high throughput sequencing and gene expression technologies.

- Developed *CELDA,* a novel method for identifying novel cell subpopulations in single-cell RNA-seq data.
- Analyst for several of the Spira-Lenburg lab's exposures projects, characterizing the genomic effects and clinical implications of inhaled exposures such as diesel exhaust, formaldehyde, and electronic cigarette vapor.
- Collaborate with the CMap team at the Broad Institute on the "Lung Connectivity Map," a project aimed at improving therapeutics discovery and development for pulmonary disease.

HONORS AND AWARDS

- **NIH T32 Training Grant Fellowship (2017-2019),** *"Biology of the Lung: A Multidisciplinary Program"* (T32 HL007035)
- **American Thoracic Society 2016:** Environmental and Occupational Population Health Abstract Scholarship
- **Boston University Student Organized Symposium 2016**: 2nd Place Poster Award

PATENTS & SELECT PUBLICATIONS

- Listed inventor on 4 confidential provisional patent applications filed by Tessera Therapeutics, involving novel genome editing technologies (2024-2025)

S. E. Corbett*, M. Nitzberg*, E. Moses, E. Kleerup, T. Wang, C. Perdomo, C. Perdomo, G. Liu, S. Zhang, H. Liu, D. A. Elashoff, D. R. Brooks, G. T. O'Connor, S. M. Dubinett, A. Spira†, Marc E Lenburg†*" Gene Expression Alterations in the Bronchial Epithelium of Electronic Cigarette Users"* CHEST, Elsevier, May 2022

S. Yang, **S. E. Corbett,** Y. Koga, Z. Wang, E. Johnson, M. Yajima, J. Campbell, *"Decontamination of ambient RNA in single-cell RNA-seq with DecontX."* Genome Biology, BioMed Central, December 2020

Zhe Wang, Shiyi Yang, Yusuke Koga, **Sean E Corbett**, Conor V Shea, W Evan Johnson, Masanao Yajima, Joshua D Campbell *"Celda: A Bayesian model to perform co-clustering of genes into modules and cells into subpopulations using single-cell RNA-seq data"* NAR Genomics and Bioinformatics, Oxford University Press, September 2022

Complete publication list available on Google Scholar