

Sean Maden

Bioinformatician; computationalist; Ph.D. candidate

Contact and connect

Phone:
Education
Oregon Health & Science UniversityAugust 2018 – May 2022 (expected) Computational Biology Program Department of Biomedical Engineering Portland, OR
Ph.D. Computational Biology, advisor Professor Abhinav Nellore Cross-study analyses of public DNA methylation array data; Metadata mapping, prediction and harmonization; Compilation of public genomics datasets; Experiment planning and independent validation; Programming tool development for biomedical research; Cross-platform workflows.
Reed CollegeSeptember 2007 – May 2011 Biology Department Portland, OR
B.A. Biology, advisor Professor Suzy Renn Rigorous science and humanities curriculum; emphasis on population evolution, statistics genetics; senior thesis quantifying genetic diversity in lab cichlids (<i>A. burtoni</i>) with microsatellites.
Selected research experience
Research Data Analyst AssistantOctober 2015 – June 2018 Fred Hutch, Seattle, WA Principal Investigators: Prof. William Grady, Dr. Ming Yu
Gastroesophageal cancer epigenetics research position; Preprocessing and analysis pipelines for methylation arrays, and next-generation data; Collaborations across disciplines; Coauthor or original research manuscripts; Intellectual contributions to grants; Lectures and posters are conferences and meetings; Used R, Python, and related software for data science, biostatistics.
Bioinformatics Research Intern
Laboratory Assistant
Analyzed clinical population and epidemiologic data; Quantified gene-environment interactions

Used programming workflows for next-generation data; Co-authored original research manuscript.

Software packages and selected programmatic resources

- Sean K. Maden, Reid F. Thompson, Kasper D. Hansen, Abhinav Nellore. recountmethylation: Utilities to obtain, query, and analyze cross-study compilations of DNAm array datasets from the Gene Expression Omnibus. Bioconductor/R package. DOI: 10.18129/B9.bioc.recountmethylation
- 2. **Sean K. Maden**, Reid F. Thompson, Kasper D. Hansen, Abhinav Nellore. recountmethylation_instance: Synchronize public DNAm array data. Snakemake workflow. https://github.com/metamaden/recountmethylation_instance

Scientific memberships, fellowships, and funding awards

Conference for statistical modeling hosted by University of Pittsburgh Dept. of Computer Science.

Affiliate Member, Fred Hutch, Seattle, WA.....June 2018 – September 2019 Collaborators: Grady Lab; Luebeck Lab

Affiliate Member of Fred Hutch, with ongoing collaborations with clinical epigenetics labs.

AAAS Member.....June 2018 – September 2019

Affiliation: OHSU Graduate School

American Association for the Advancement of Science (AAAS), nominated through OHSU.

2016 SAS-BWF Fellow, Fred Hutch, Seattle, WA......May 2016 – 2017 Advisors: Prof. Bill Grady, Dr. Ming Yu

Fellowship hosted and funded by SAS Institute and Burroughs Wellcome Fund. Contributed to ongoing research of epigenetics of colorectal cancer and biomarker discovery for clinical screening. Worked closely with JMP developers, recommended software features based on research needs.

Granted funding to extend research for undergraduate senior thesis studying genetic diversity of *A. burtoni* fishes (see Publications), awarded by Reed College Biology Department based on submission of original research overview.

Fischer Memorial Fellow, Reed College, Portland, OR......Summer 2010 Advisor: Prof. Robert Kaplan

Designed and conducted habitat field survey experiment of native at-risk frog *Rana aurora*, constructed breeding habitat and compiled a literature review of amphibian ecology. Authored and coauthored extensive reports presented as contributions to canon of Fisher Fellows.

Peer-reviewed scientific papers (+ : first author or co-first author)

- +1. **Sean K. Maden**, Reid F. Thompson, Kasper D. Hansen, Abhinav Nellore. *Comparing two major DNA methylation array platforms across studies and tissues.* (preprint in preparation)
- +2. **Sean K. Maden**, Reid F. Thompson, Kasper D. Hansen, Abhinav Nellore. *Human methylome variation across Infinium 450K data on the Gene Expression Omnibus*. NAR Genomics and Bioinformatics, Volume 3, Issue 2, June 2021, Igab025
- 3. Austin Nguyen, Julianne K David, **Sean K. Maden**, Mary A Wood, Benjamin R Weeder, Abhinav Nellore, Reid F Thompson. *Human leukocyte antigen susceptibility map for SARS-CoV-2*. Journal of Virology, Volume 94, No. 13, June 2020

- 4. Julianne K. David, **Sean K. Maden**, Benjamin R. Weeder, Reid F. Thompson, Abhinav Nellore. *"Cancer-specific" exon-exon junctions appear in embryological and other normal cells.* 2019. NAR Cancer, Volume 2, Issue 1, March 2020, zcaa001
- 5. Ting Wang, **Sean K. Maden**, Georg Luebeck, Chris Li, Polly Newcomb, Cornelia Ulrich, Kelly Carter, Michael Luo, Ming Yu, William M. Grady. *Dysfunctional epigenetic aging of the normal colon in association with colorectal adenoma and cancer risk.* 2019 (under review).
- Yuna Guo, Kelly Carter, Ming Yu, Sean K. Maden, Darwin Edmonds, Polly Newcomb P, Christopher Li, Neli Ulrich, William M. Grady. Senescence-associated tissue microenvironment promotes colon cancer formation through the secretory factor GDF15. 2019 Aging Cell.
- 7. Georg E. Luebeck, William D. Hazelton, Kit Curtius, Sean K. Maden, Ming Yu, Kelly T. Carter, Wynn Burke, Paul D. Lampe, Christopher I. Li, Cornelia M. Ulrich, Polly A. Newcomb, Maria Westerhoff¹¹, Andrew M. Kaz, Yanxin Luo, John M. Inadomi, William M. Grady. *Implications of epigenetic drift in colorectal neoplasia*. 2019 Cancer Res. 1;79(3):495-504
- +8. Ming Yu*, **Sean K. Maden***, Matthew Stachler*, Andrew M. Kaz, Tai J. Heinzerling, Rachele M O'Leary, Xinsen Xu, Adam Bass, Amitabh Chak, Joseph E. Willis, Sanford D. Markowitz, William M. Grady. Subtypes of Barrett's Esophagus and Esophageal Adenocarcinoma Based on Genome-wide Methylation Analysis. 2019 Gut 68:389-399 *co-first authors.
- 9. Ludovic Barault, Alessio Amatu, Giulia Siravegna, Agostino Ponzetti, Sebastian Moran, Andrea Cassingena, Benedetta Mussolin, Chiara Falcomatà, Alexandra Binder, Carmen Cristiano, Daniele Oddo, Carlotta Cancelliere, Sara Bustreo, Katia Bencardino, Sean Maden, Alice Vanzati, Patrizia Zavattari, Mauro Truini, William M. Grady, Patrizia Racca, Karin B. Michels, Salvatore Siena, Manel Esteller, Alberto Bardelli, Andrea Sartore-Bianchi, Federica Di Nicolantonio. Discovery of methylated circulating DNA biomarkers for comprehensive non-invasive monitoring of treatment response in metastatic colorectal cancer. 2017 Gut; PMCID: PMC5897187.
- 10. Georg E. Luebeck, Kit Curtius, William D Hazelton, **Sean Maden**, Ming Yu, Prashanthi N Thota, Deepa T Patil, Amitabh Chak, Joseph E Willis, William M Grady. *Identification of a key role of widespread epigenetic drift in Barrett's esophagus and esophageal adenocarcinoma*. 2017 Clinical Epigenetics; PMCID: PMC5644061.
- 11. (**Acknowledgement**) Kit Curtius, Chao-Jen Wong, William D. Hazelton, Andrew M. Kaz, Amitabh Chak, Joseph E. Willis, William M. Grady, Georg E. Luebeck. *A Molecular Clock Infers Heterogeneous Tissue Age Among Patients with Barrett's Esophagus*. May 11, 2016 PLoS Comput Bio.; PMID: 27168458
- 12. Daniel Seung Kim, **Sean K. Maden**, Amber A Burt, Jane E Ranchalis, Clement E Furlong and Gail P Jarvik. *Dietary fatty acid intake is associated with paraoxonase 1 activity in a cohort-based analysis of 1,548 subjects*. 2013 Lipids in Health and Disease; PMCID: PMC3878825.
- +13. **Sean Maden**, Advisor: Suzy P Renn. *Observed Declines in Genetic Diversity Across Successive Generations of a Captive Astatotilapia burtoni Lineage, Using Microsatellite Molecular Markers*. Senior Thesis, 2011 Reed College.

Scientific lay press works

1. (**Acknowledgement**) Anne-Sophie Kuhlman. *Esophageal adenocarcinoma: when DNA methylation informs the treatment*. Fred Hutch Science Spotlight July 16, 2018.

Selected bioinformatics skills and interests

Scientific software development

R, Python, and Bash coding languages;

Python and Bioc software libraries;

Dply, data.table, data coercion

Graphics with ggplot2, ComplexHeatmap;

Shiny apps, reactive programming;

GitHub, version control;

Nix and Windows operating systems;

Embarrassingly parallel processing;

TCGA, GEO, and public genomics datasets;

MySQL, PostgreSQL, MongoDB databases;

Statistical modeling and regression;

Statistical prediction;

Machine learning;

ROC and AUC analysis;

Biomarker discovery;

DNA methylation array analysis;

Epigenetic regulation;

Enhancers, insulators, super-enhancers;

Metadata mining and cleaning

Selected science presentations

- 1. (workshop/package demo) **Sean K. Maden**, Reid F. Thompson, Kasper D. Hansen, Abhinav Nellore. *Accessing, querying, and analyzing public DNAm array data compilations with recountmethylation*. Bioc2021, August 4, 2021 (upcoming)
- 2. (poster/abstract) **Sean K. Maden**, Kasper D. Hansen, Abhinav Nellore. *Human methylome variation across Infinium 450K raw data on the Gene Expression Omnibus.* 2019 CEEHRC/IHEC Annual Meeting, Banff, AB.
- 3. (poster/abstract) **Sean K. Maden**, Kasper D. Hansen, Abhinav Nellore. *Comprehensive Reanalysis of DNA Methylation Array Data.* 2019 MOMACS Modeling the World's Systems Conference, Washington, DC.
- 4. (poster) Mitra Barahimi, **Sean Maden**, et. al. Sa1617-Discovery and Validation of Potential Field Cancerization Molecular Markers that Associate with Metachronous Polyp Formation. Gastro. 154 (6), S-331
- (poster) Erik J. Snider, E. Georg Luebeck, Ming Yu, Kelly T. Carter, Sean K. Maden, et. al. Medication effects on methylation-related biological aging in Barrett's esophagus. 2018. Gastroenterology 156 (6), S-509
- 6. (lecture) **Sean Maden**. "Recount Methylation: A generalizable platform for re-analysis of array-based epigenetic data". Biophysics Journal Club meeting, October 2018.
- 7. (poster) Mitra Barahimi, **Sean Maden**, et. al. *Discovery and Validation of Potential Field Cancerization Molecular Markers That Associate With Metachronous Polyp Formation*. Presented at 2018 Digestive Disease Week.
- 8. (lecture) **Sean Maden**. *Identification of Novel Molecular Characteristics of Methylation Subtypes in Esophageal Adenocarcinoma by Integrated Analysis*. Cancer Epigenetics Affinity Group meeting. Fred Hutch campus. Nov. 7, 2017.
- 9. (poster) **Sean Maden*** and Georg Luebeck*, et. al. *first authors. *Scope and Significance of Epigenetic Drift in Barrett's Esophagus*. Cancer Systems Biology Consortium (CSBC) Annual Meeting, Broad Institute MIT, Cambridge, MA. Oct 3, 2017.
- (lecture) Sean Maden. Spatial and temporal epigenetic pattern gradients differentiate normal and progressed tissues in esophagus. Cancer Intervention and Surveillance Modeling Network (CISNET) 2017 meeting, Esophageal Cancer projects, June 6, 2017.
- 11. (poster) **Sean Maden***, Ming Yu*, Matthew Stachler*, et. al. (*first authors). *Genome-wide methylation analysis reveals methylator subtypes of Barrett's esophagus and esophageal adenocarcinoma*. 2016 AACR Annual Meeting.

Graduate level scientific coursework completed

Oregon Health & Science University, Ph.D. Computational Biology, Biomedical Engineering Summer 2018 – Spring 2021 (expected)

BMI 550/650: Bioinformatics and CONJ 650: Practice and Ethics of Science BME 601: Prequalifying PhD Research

CS 545: Machine Learning

University of Washington, M.Sc. Genetic Epidemiology, Public Health Genetics Fall 2012 - Fall 2013 (no degree obtained)

PHG 536: Bioinformatics and PHG 513: Pharmacogenetics and

Sequence Analysis Toxicogenomics

BIOSTAT 517/518: Applied BIOST 580: Biostatistics Seminar EPI 583: Epidemiology Seminar

EPI 512/513: Epidemiological GENOME 525: Topics in Human Genetics

Methods I and II PHG 511: Genetic Epidemiology

PHG 512: Law and Ethics in Public PHG 521: Culture and Societal Genomics

Health Genetics PHG 523: Genetics and the Law

Undergraduate level scientific coursework completed

Shoreline Community College, Biotechnology Lab Specialist Certificate

Fall 2014 - Winter 2015 (no degree obtained)

BIOL 270: Molecular Biology BIOL 265/266: Solution and Media

BIOL 285: Basics of Bioinformatics

Prep I and II

BIOL 286: Molecular Diagnostics

BIOL 275: Recombinant DNA

Reed College, B.A. Biology, Fall 2007 - Spring 2011

MATH 111: Calculus

BIOL 358: Microbiology

MATH 112: Intro to Analysis

PHYS 100: General Physics I

BIOL 366: Population Ecology and Evolution

HIST 315: Medieval/Renaissance CHEM 201/202: Organic Chemistry I

Structure

BIOL 431: Seminar: Chromosome

Science and Religion and II

BIOL 332: Vascular Plant Diversity
BIOL 101/102: Introductory Biology
BIOL 351: Developmental Biology

CHEM 101/102: Introductory (lecture only)

Chemistry

BIOL 361: Genetics

BIOL 431: Seminar: Ecology and PHIL 316: Philosophy of Science

Evolution of Plant-Human BIOL 431: Seminar: Gene

Interactions Duplication/Overexpression

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