

Sean K. Maden

Senior researcher/analyst, open-access developer, nature-lover

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Education

Oregon Health & Science University, August 2018 – May 2022
Department of Biomedical Engineering,
Portland, OR

Ph.D. Computational Biology, Advisor: Prof. Abhinav Nellore,

Dissertation title: *Applications of public omics data*

Compiled public DNA methylation array data; published recountmethylation Bioconductor package; characterized epigenetic variation across tissues; performed novel cross-study analyses; conducted independent validation of biomarker candidates; studied retained introns in long-read and short-read RNA-seq data; quantified splice junction expression in cancer and normal tissues; mined and plotted population HLA allele frequencies related to SARS-CoV-2 risk

Reed College, September 2007 – May 2011
Biology Department,
Portland, OR

B.A. Biology, Advisor: Prof. Suzy Renn

Rigorous science and humanities curriculum; research focus in evolution, statistics, and population genetics; fellowship in field and ecology survey research; thesis quantifying genetic diversity with microsatellite molecular markers.

Research experience

Postdoctoral research fellow June 2022 – June 2024

Dept of Biostatistics

Johns Hopkins Bloomberg School of Public Health

Baltimore, MD

Advisor: Prof. Stephanie Hicks

Gene expression in normal and diseased brain cells; single-cell sequencing; spatial transcriptomics; development of analytical tools for research; development of open-access documents for data science and analysis; utilization of public sequencing data from the Sequence Read Archive for independent validation; collaborations with the Lieber Institute.

Research Data Analyst Assistant October 2015 – June 2018
Fred Hutch, Seattle, WA

Principal Investigators: Prof. William Grady, Dr. Ming Yu

Epigenetic markers of gastroesophageal cancer risk and progression; preprocessing and analysis of DNA methylation arrays; integrative analysis of epigenetics and RNA-seq data; wrote R scripts to conduct research; made a shiny dashboard to analyze epigenetic data and genome annotations.

Bioinformatics Research Intern April – September 2015 Fred Hutch,
Seattle, WA

Principal Investigator: Prof. William Grady; Postdoc project lead: Dr. Ming Yu Analysis of colorectal cancer epigenetics; trained data science and R programming.

Laboratory Assistant January – October 2013

Principle Investigator/Advisor: Prof. Gail Jarvik

University of Washington Medical Genetics

Analyzed clinical population and epidemiologic data; Quantified gene-environment interactions; Used programming workflows for next-generation data; Co-authored original research manuscript.

Awards

Grad Student Travel Stipend May 2019

MOMACS Modeling the World's Systems 2019

Washington, DC

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

2016 SAS-BWF Fellow, Fred Hutch, Seattle, WA May 2016 – May 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.

AACR Associate Member, Fred Hutch, Seattle, WA Jan 2016 – 2017 Recognized and supported by Association for Cancer Research (AACR) as promising early-career cancer investigator. AACR is one of the largest cancer research organizations in the US, and it hosts numerous annual meetings and workshops to network and learn from colleagues.

Undergraduate Research Grant, Reed College, Portland, OR Winter 2010

Advisor: Prof. Suzy Renn

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 Fischer Fellows.

Skills and expertise

R/Bioconductor (recountmethylation)	Statistical tests (lm, ANOVA, cor.test, Chi)
Python for analysis (pandas, numpy, scipy)	Model training (SVM, LASSO, AIC)
R for data science (data.table, dplyr)	Machine learning (neural networks, tensors)
Plots for publication (ggplot2, UpsetR)	Biomarker discovery (ROC, AUC, precision)
Data dashboards (shiny and plotly)	DNA methylation arrays (HM450K, EPIC)
Version control (git, GitHub)	RNA-seq analysis (long-read, short-read)
Public omics data (GEO, SRA, Entrez)	Relational databases (MySQL, SQLite)
Omics consortia (TCGA, CCLE, GTEx)	Data engineering (PostgreSQL, XML, JSON)

Peer-reviewed journal publications (* first-author)

1. **Sean K. Maden***, et al. *Recountmethylation enables flexible analysis of public blood DNA methylation array data*. Bioinformatics Advances 3, no. 1 (January 1, 2023).
2. Julianne K. David*, **Sean K. Maden***, et. al. *Retained introns in long RNA-seq reads are not reliably detected in sample-matched short reads*. Genome Biol 23, 240 (2022).
3. **Sean K. Maden***, et al. *Human methylome variation across Infinium 450K data on the Gene Expression Omnibus*. (2021) NAR Genomics and Bioinformatics, Volume 3, Issue 2.
4. Julianne K. David*, **Sean K. Maden**, et al. *Putatively cancer-specific exon–exon junctions are shared across patients and present in developmental and other non-cancer cells*. (2019) NAR Cancer, Volume 2, Issue 1.
5. Ting Wang*, **Sean K. Maden**, et. al. *Dysfunctional epigenetic aging of the normal colon in association with colorectal adenoma and cancer risk*. (2020) Clin Epigenet 12, 5.
6. Yuna Guo*, Kelly Carter, Ming Yu, **Sean K. Maden**, et. al. *Senescence-associated tissue microenvironment promotes colon cancer formation through the secretory factor GDF15*. (2019) Aging Cell e13013.
7. Georg E. Luebeck*, William D. Hazelton, Kit Curtius, **Sean K. Maden**, et. al. *Implications of epigenetic drift in colorectal neoplasia*. (2019) Cancer Res. 1;79(3):495-504.
8. Ming Yu*, **Sean K. Maden***, Matthew Stachler*, et. al. *Subtypes of Barrett's esophagus and esophageal adenocarcinoma based on genome-wide methylation analysis*. (2019) Gut 68:389.
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**, et. al. *Discovery of methylated circulating DNA biomarkers for comprehensive non-invasive monitoring of treatment response in metastatic colorectal cancer*. (2017) Gut, 67(11):1995-2005.
10. Georg E. Luebeck*, Kit Curtius, William D Hazelton, **Sean Maden**, et. al. *Identification of a key role of widespread epigenetic drift in Barrett's esophagus and esophageal adenocarcinoma*. (2017) Clinical Epigenetics.
11. Kit Curtius*, et. al. *A molecular clock infers heterogeneous tissue age among patients with Barrett's esophagus*. PLoS Comput Bio. (May 11, 2016, acknowledgement).
12. Daniel S. Kim*, **Sean K. Maden**, et. al. *Dietary fatty acid intake is associated with paraoxonase 1 activity in a cohort-based analysis of 1,548 subjects*. (2013) Lipids in Health and Dis., 2, 183

Additional articles (preprints, lay press pieces, etc.)

1. **Sean K. Maden***, et al. *Challenges and opportunities to computationally deconvolve heterogeneous tissue with varying cell sizes using single cell RNA-sequencing datasets*. arXiv preprint arXiv:2305.06501, 2023.
2. Jenny Smith*, **Sean K. Maden***, David Lee*, et. al. *Consensus machine learning for gene target selection in pediatric AML risk*. (2019) BioRxiv, 632166.

3. Anne-Sophie Kuhlman*. *Esophageal adenocarcinoma: when DNA methylation informs the treatment*. (2018) Fred Hutch Science Spotlight. (acknowledgement).

Selected scientific presentations

1. (abstract) **Sean K. Maden**, Stephanie C. Hicks. *lute*, a new framework for bulk transcriptomics deconvolution experiments. Bioc2023, Boston, MA.
2. (poster/abstract) **Sean K. Maden**, Kasper D. Hansen, Abhi 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, Abhinov 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
5. (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.
10. (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 coursework

Ph.D. Computational Biology (completed)

June 2022-June 2024

Biomedical Engineering

Oregon Health & Science University, Portland, OR

BMI 550/650: Bioinfo. and Comp. Biol. I

CS 545: Machine Learning

CONJ 650: Practice and Ethics of Science

BME 601: Prequalifying PhD Research

M.Sc. Genetic Epidemiology (no degree obtained)
Public Health Genetics
University of Washington, Seattle, WA

Fall 2012 – Winter 2013

PHG 536: Bioinformatics and Seq.
BIOSTAT 517/518: Applied Biostat.
EPI 512/513: Epidemiological Meth.
PHG 512: Law and Ethics in PHG
PHG 513: Pharmacogen. and Toxicogen.
BIOST 580: Biostatistics Seminar

EPI 583: Epidemiology Seminar
GENOME 525: Topics in Human Genetics
PHG 511: Genetic Epidemiology
PHG 521: Culture and Societal Genomics
PHG 523: Genetics and the Law

Undergraduate coursework

Biotechnology Lab Specialist (no degree obtained)
Shoreline Community College, Shoreline, WA

Fall 2014 - Winter 2015

BIOL 270: Molecular Biology
BIOL 285: Basics of Bioinformatics
BIOL 286: Molecular Diagnostics

BIOL 265/266: Solution and Media Prep
BIOL 275: Recombinant DNA

B.A. Biology (completed)

Fall 2007 - Spring 2011

Biology Department

Reed College, Portland, OR

MATH 111: Calculus
MATH 112: Intro. to Analysis
PHYS 100: General Physics I
HIST 315: Mediv. Sci. and Religion
BIOL 332: Vasc. Plant Diversity
BIOL 101/102: Intro. Biology
CHEM 101/102: Intro. Chem.
BIOL 361: Genetics
BIOL 431: Sem: Evol.Plant-Hum. Int.

BIOL 358: Microbiology
BIOL 366: Population Ecology and Evol.
CHEM 201/202: Organic Chem.
PHIL 201: Logic
BIOL 351: Dev. Biology (lecture)
BIOL 431: Seminar: Chrom. Structure
PHIL 316: Philosophy of Science
BIOL 431: Seminar: Gene Overexpr.