Sean K. Maden, PhD

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Summary

- Collaborative and interdisciplinary senior research leader with skills and experience in computation and genomics
- Led collaborative research, resulting in 11 (4 first-author) peer-reviewed publications including high-impact journals
- Deep understanding of data formats, analysis pipelines, and workflows for RNA-seq and microarray platforms
- Self-motivated, problem-solving, and critical thinking scientist with excellent communication and presentation skills

Research Experience

Computational biology

Postdoctoral Research Fellow, Johns Hopkins School of Public Health, Baltimore, MD **June 2022 to present**

- Modeled brain cell marker gene expression in human dorsolateral prefrontal cortex single-nucleus RNA-seq data
- Analyzed multi-omics data normalization impact on deconvolution accuracy with orthogonal cell size scale factors
- Conducted thorough review of reference-based transcriptomics deconvolution algorithm and benchmark literature

Bioinformatics analyst

Data Analyst Assistant, Fred Hutch, Seattle, WA **October 2015 to June 2018**

- Performed molecular epigenetic subtyping from multi-dimensional cluster analysis of multi-replicate microarrays
- Discovered and assessed biomarkers of cancer risk and progression using cross-validation and AUC/ROC methods
- Affymetrix ChIP-seq, correlation and categorical analysis collaboration
- Training/Validation of DNA methylation biomarker candidates (HM450K, EPIC/HM850K)
- Managed multi-omics data, including epigenetics (DNAm), genetic variant (SNP), transcriptomics (RNA-seq)

Bioinformatics Intern, Fred Hutch, Seattle, WA **April to October 2015**

- Analyzed epigenetic molecular markers, pathologist tissue compositions, and clinical record data in CRC patients
- Quantified nested batch effects, bias correction impacts, and normalization pipeline efficacy for microarray datasets

Genetic epidemiology

Laboratory Assistant, University of Washington Medical Genetics, Seattle, WA **January to October 2013**

- Linear modeling of Paraoxonase (PON)-1 enzyme activity, genetic variants, and patient conditions from clinical records
- Analyzed genetic variant microarray data by preprocessing using PLINK and visualizing with Q-Q and Manhattan plots

Education

Ph.D., Computational Biology, Oregon Health & Science University, Portland, OR **June 2018 to June 2022**

Machine learning course, scalable DNA methylation microarray analysis. Dissertation: Applications of public omics data
Relevant coursework:

1. **BMI 550/650: Bioinformatics and Computational Biology I: Algorithms**
2. **CS 545: Machine Learning**
3. **PHG 536: Bioinformatics and Sequence Analysis (transferred from UW SPH)**
4. **PHG 513: Pharmacogenetics and Toxicogenomics (transferred from UW SPH)**
5. **PHG 511: Genetic Epidemiology (transferred from UW SPH)**
6. **EPI 512/513: Epidemiological Methods I and II (transferred from UW SPH)**
7. **BIOSTAT 517/518: Applied Biostatistics I and II (transferred from UW SPH)**

B.A., Biology, Reed College, Portland, OR **September 2007 to May 2011**

Rigorous liberal arts and sciences, population genetics and ecology focus. Thesis topic: microsatellite genetic diversity
Relevant coursework:

1. **MATH 111: Calculus**
2. **MATH 112: Intro to Analysis**
3. **PHIL 201: Logic**
4. **BIOL 366: Population Ecology and Evolution**

Awards

- **MOMACS Grad Student Travel Stipend (May 2019)** Modeling the World's Systems conference, Washington, D.C.
- **SAS-BWF Fellow (May 2016-2017)** Collaborative colorectal cancer biomarker research, Fred Hutch, Seattle, WA
- **AACR Associate Member (January 2016-2017)** Early-career cancer researcher, Fred Hutch, Seattle, WA

- **Undergraduate Research Grant (January to March 2010)** Genetics research for thesis, Reed College, Portland, OR
- **Fischer Memorial Fellow (May to September 2010)** Amphibian habitat survey research, Reed College, Portland, OR

Software

Software libraries and applications authored

1. **Sean K. Maden** and Stephanie C. Hicks. lute: Cell size normalization for RNA-seq deconvolution. Bioconductor (2023), language: R/Bioconductor.
2. Julianne David and **Sean Maden**. intronomer: Retained intron detection in long-read RNA-seq data. GitHub (2022). language: Python.
3. **Sean Maden**. recountmethylation: Public DNA methylation microarray analysis utilities. Bioconductor (2021). language: R/Bioconductor.
4. **Sean Maden**. cgmappeR: Interactive gene feature visualization using Gviz and UCSC GB data. GitHub (2018). language: R/Bioconductor.

Publications (*first author)

Peer-reviewed publications

1. **Maden, S.K.***, S.H. Kwon, L.A. Huuki-Myers, L. Collado-Torres, S. C. Hicks, K. R. Maynard. Challenges and opportunities to computationally deconvolve heterogeneous tissue with varying cell sizes using single-cell RNA-sequencing datasets. Genome Biol 24, 288 (2023). https://doi.org/10.1186/s13059-023-03123-4
2. **Maden, S. K.*** , B. Walsh, K. Ellrott, K. D. Hansen, R. F. Thompson, A. Nellore. Recountmethylation enables flexible analysis of public blood DNA methylation array data. Bioinformatics Advances 3, no. 1 (January 1, 2023): vbad020. https://doi.org/10.1093/bioadv/vbad020.
3. David, J. K.*, **S. K. Maden***, M. A. Wood, R. F. Thompson, A. Nellore. Retained introns in long RNA-seq reads are not reliably detected in sample-matched short reads. Genome Biology 23, 240 (2022).
4. **Maden, S. K.***, R. F. Thompson, K. D. Hansen, A. Nellore. Human methylome variation across Infinium 450K data on the Gene Expression Omnibus. NAR Genomics and Bioinformatics 3, lqab025 (2021).
5. David, J. K.*, **S. K. Maden**, B. R. Weeder, R. F. Thompson, A. Nellore. Putatively cancer-specific exon–exon junctions are shared across patients and present in developmental and other non-cancer cells. NAR Cancer 2, zcaa001 (2020).
6. Nguyen, A.*, J. K. David, **S. K. Maden**, M. A. Wood, B. R. Weeder, A. Nellore, R. F. Thompson. Human Leukocyte Antigen Susceptibility Map for Severe Acute Respiratory Syndrome Coronavirus 2. Journal of Virology 94, e00510–20.
7. Wang, T.*, **S. K. Maden**, G. E. Luebeck, L. I. Christopher, P. A. Newcomb, C. M. Ulrich, J. E. Joo, D. D. Buchanan, R. L. Milne, M. C. Southey, K. T. Carter, A. R. Willbanks, Y. Luo, M. Yu, W. M. Grady. Dysfunctional epigenetic aging of the normal colon and colorectal cancer risk. Clinical Epigenetics 12, 5 (2020).
8. Luebeck, G. E.*, W. D. Hazelton, K. Curtius, **S. K. Maden**, M. Yu, K. T. Carter, W. Burke, P. D. Lampe, C. I. Li, C. M. Ulrich, P. A. Newcomb, M. Westerhoff, A. M. Kaz, Y. Luo, J. M. Inadomi, W. M. Grady. Implications of Epigenetic Drift in Colorectal Neoplasia. Cancer Research 79, 495–504 (2019).
9. Yu, M.*, **Maden, S. K.***, Stachler M. S.*, A. M. J. Ayers, Y. Guo, K. T. Carter, A. Willbanks, T. J. Heinzerling, R. M. O'Leary, X. Xu, A. Bass, A. K. Chandar, A. Chak, R. Elliott, J. E. Willis, S. D. Markowitz, W. M. Grady. Subtypes of Barrett's oesophagus and oesophageal adenocarcinoma based on genome-wide methylation analysis. Gut 68, 389–399 (2019).
10. Luebeck, G. E.*, K. Curtius, W. D. Hazelton, **S. Maden**, M. Yu, P. N. Thota, D. T. Patil, A. Chak, J. E. Willis, W. M. Grady. Identification of a key role of widespread epigenetic drift in Barrett's esophagus and esophageal adenocarcinoma. Clinical Epigenetics 9, 113 (2017).
11. Kim, D. S.*, **S. K. Maden**, A. A. Burt, J. E. Ranchalis, C. E. Furlong, G. P. Jarvik. Dietary fatty acid intake is associated with paraoxonase 1 activity in a cohort-based analysis of 1,548 subjects. Lipids in Health and Disease 12, 183 (2013).

Preprint publications

1. Smith, J.*, **S. K. Maden***, D. Lee*, R. Buie, V. Peddu, R. Shean, B. Busby. Consensus Machine Learning for Gene Target Selection in Pediatric AML Risk. 632166 https://www.biorxiv.org/content/10.1101/632166v1 (2019) doi:10.1101/632166.

Technical Skills and Experience

Programming languages: R/Bioconductor, Python, Bash/Shell, conda
Database formats and syntax: MySQL/SQLite, PostgreSQL, MongoDB, HDF5, DelayedArray
Statistics: Generalized Linear Models, Machine learning, Analysis of Variance, Decomposition, Batch effects, ROC/AUC
Developer and workflow software: Git, GitHub, Synapse, LaTeX, Markdown, Jupyter, Plotly/Shiny, Snakemake, NextFlow
Interactive dashboards: Shiny, plotly, reactive scripting, genome visualization, text search for assays