Sean Maden

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Summary

- Accomplished senior researcher and advanced developer with a collaborative and interdisciplinary approach, adept in analysis, computation, and biomedical research methods.
- Guided collaborative research efforts at widely acclaimed institutions, leading to the publication of over 14 peer-reviewed manuscripts (including 7 as first author) and published articles in prestigious genomics journals.
- Proficient in data formats, analysis pipelines, and workflows for clinical research, patient records, and genomics data platforms. Published open-access software packages, dashboards, workflows, and database.
- Driven scientist with a self-motivated approach, great problem-solving skills, and a strong foundation in critical thinking. Excellent communicator with polished presentation abilities.

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

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

Experience

Postdoctoral Research Fellow, Johns Hopkins School of Public Health, Baltimore, MD **June 2022 to present**
- Modeled brain cell marker gene expression in human prefrontal cortex single-nucleus RNA-seq data
- Analyze cell size scale factors in integrative multi-omics dataset
- Conducted literature review of bulk transcriptomics deconvolution methods and algorithms

Data Analyst Assistant, Fred Hutch, Seattle, WA **October 2015 to June 2018**
- Molecular subtyping from clustering analysis on DNA methylation microarray data
- Gastroesophageal cancer risk and progression biomarker discoveryand panel AUC/ROC critical assessment
- Management of complex integrative epigenetics, gene variant, and clinical condition datasets with multiple replicates

Bioinformatics Intern, Fred Hutch, Seattle, WA **April to October 2015**
- Colorectal cancer epigenetic and clinical condition statistical analyses
- Nested batch effect quantification, and correction of bias and noise from microarray datasets

Laboratory Assistant, University of Washington Medical Genetics, Seattle, WA **January to October 2013**
- Linear modeling of Paraoxonase (PON)-1 enzyme activity, genetic variants, and clinical conditions
- Genetic variant microarray data preprocessing with PLINK and Manhattan plot visualizations

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

Programming

- **lute (2023, coauthor: Stephanie Hicks, language: R/Bioconductor)** Data transformation & experiment framework.
- **cellScaleFactors (2023, language: R/Bioconductor)** Mined/scraped cell size bias-correction factors & metadata.
- **intronomer (2022, coauthor: Julianne David, language: Python)** Long-read retained intron detection and analysis.
- **recountmethylation (2021, language: database, R/Bioconductor)** High-throughput QC and analysis of public data.
- **recountmethylation (2021, language: Python, SQL, HDF5)** Epigenetics microarray data server and database.
- **cgageR (2018, language: R/Bioconductor)** Ensemble age prediction from multiple machine learning models.
- **cgmappeR (2018, language: R/shiny)** Query and visualize genome ideograms, sequences, and sample data.

Skills

Compute environments: Slurm, SGE, AWS, Azure, Linux, Unix, Ubuntu, Windows, OSX, Conda, Docker
Developer software: Visual Studio, RStudio, PyCharms, SublimeText, BioRender, Microsoft Office
Programming languages: R/Bioconductor, Python, Bash/Shell, Conda, HTML, CSS, JavaScript, NextFlow, SQL, JSON
Data engineering: Relational (SQL), Document (MongoDB), Graph (PostgreSQL), Sparse (HDF5), ETL, high-throughput
Statistics: Machine learning, decomposition, cluster analysis, transformation, bias correction, ROC/AUC
Software development: Version control (Git), data servers (Synapse, NCBI), APIs, dependencies, open-access

Publications (*first author)

Peer-reviewed preprint and journal publications

1. **Maden SK***, Huuki-Myers LA, Kwon SH, Collado-Torres L, Maynard KR, Hicks SC. “lute: estimating the cell composition of heterogeneous tissue with varying cell sizes using gene expression.” bioRxiv. 2024.
2. Huuki-Myers LA*, Montgomery KD*, Kwon SH, Cinquemani S, **Maden SK**, Eagles NJ, Kleinman JE, Hyde TM, Hicks SC, Maynard KR, Collado-Torres L. “Benchmark of cellular deconvolution methods using a multi-assay reference dataset from postmortem human prefrontal cortex.” bioRxiv. 2024.
3. **Maden SK***, Kwon SH, Huuki-Myers LA, Collado-Torres L, Hicks SC, Maynard KR. “Challenges and opportunities to computationally deconvolve heterogeneous tissue with varying cell sizes using single-cell RNA-sequencing datasets.” Genome Biol 24, 288. 2023.
4. **Maden SK*** , Walsh B, Ellrott K, Hansen KD, Thompson RF, Nellore A. “Recountmethylation enables flexible analysis of public blood DNA methylation array data.” Bioinformatics Advances 3, 1. 2023.
5. David JK*, **Maden SK***, Wood MA, Thompson RF, Nellore A. “Retained introns in long RNA-seq reads are not reliably detected in sample-matched short reads.” Genome Biology 23, 240. 2022.
6. **Maden SK***, Thompson RF, Hansen KD, Nellore A. “Human methylome variation across Infinium 450K data on the Gene Expression Omnibus.” NAR Genomics and Bioinformatics 3, lqab025. 2021.
7. David JK*, **Maden SK**, Weeder BR, Thompson RF, Nellore A. “Putatively cancer-specific exon–exon junctions are shared across patients and present in developmental and other non-cancer cells.” NAR Cancer 2, zcaa001. 2020.
8. Nguyen A*, David JK, **Maden SK**, Wood MA, Weeder BR, Nellore A, Thompson RF. “Human Leukocyte Antigen Susceptibility Map for Severe Acute Respiratory Syndrome Coronavirus 2.” Journal of Virology 94, e00510–20. 2020.
9. Wang T*, **Maden SK**, Luebeck GE, Christopher LI, Newcomb PA, Ulrich CM, Joo JE, Buchanan DD, Milne RL, Southey MC, Carter KT, Willbanks AR, Luo Y, Yu M, Grady WM. “Dysfunctional epigenetic aging of the normal colon and colorectal cancer risk.” Clinical Epigenetics 12, 5 (2020).
10. Luebeck GE*, Hazelton WD, Curtius K, **Maden SK**, Yu M, Carter KT, Burke W, Lampe PD, Li CI, Ulrich CM, Newcomb PA, Westerhoff M, Kaz AM, Luo Y, Inadomi JM, Grady WM. “Implications of Epigenetic Drift in Colorectal Neoplasia.” Cancer Research 79, 495–504. 2019.
11. Yu M*, **Maden SK***, Stachler MS*, Ayers AMJ, Guo Y, Carter KT, Willbanks A, Heinzerling TJ, O’Leary RM, Xu S, Bass A, Chandar AK, Chak A, Elliott R, Willis JE, Markowitz SD, Grady WM. “Subtypes of Barrett’s oesophagus and oesophageal adenocarcinoma based on genome-wide methylation analysis.” Gut 68, 389–399. 2019.
12. Smith J*, **Maden SK***, Lee D*, Buie R, Peddu V, Shean R, Busby B. “Consensus Machine Learning for Gene Target Selection in Pediatric AML Risk.” bioRxiv. 2019.
13. Luebeck GE*, Curtius K, Hazelton WD, **Maden S**, Yu M, Thota PN, Patil DT, Chak A, Willis JE, Grady WM. “Identification of a key role of widespread epigenetic drift in Barrett’s esophagus and esophageal adenocarcinoma.” Clinical Epigenetics 9, 113. 2017.
14. Kim DS*, **Maden SK**, Burt AA, Ranchalis JE, Furlong CE, Jarvik GP. “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.