

Sean Davis

Curriculum Vita

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🌐 <http://seandavi.github.io/>

Google Scholar–i10-index: 92; h-index: 57; 28,530 citations

Education and Professional Experience

- 2021–Present **Professor and Rifkin Chair of Cancer Informatics**, Department of Medicine, University of Colorado Anschutz School of Medicine.
- 2021–Present **Deputy Director**, Center for Health Artificial Intelligence, University of Colorado Anschutz School of Medicine.
- 2017–2020 **Senior Associate Scientist**, Center for Cancer Research, National Cancer Institute.
- 2009–2016 **Staff Scientist**, Center for Cancer Research, National Cancer Institute.
- 2007–2008 **Research Fellow**, National Cancer Institute.
- 2005–2007 **Research Fellow**, National Human Genome Research Institute.
- 2002–2005 **Clinical Fellow**, Combined Johns Hopkins and National Cancer Institute Pediatric Hematology/Oncology Fellowship.
- 1999–2002 **Pediatric Resident**, Children’s Hospital and Regional Medical Center, University of Washington.
- 1993–1999 **MD**, University of Pittsburgh School of Medicine.
- 1995–1997 **PhD**, University of Pittsburgh Graduate School of Public Health.
Department of Human Genetics
- 1989–1993 **B.S.E.**, Princeton University, *With Honors*.
Mechanical and Aerospace Engineering

Professional Involvement and Service

- 2020–Present Member of NHGRI AnVIL project Executive Committee
- 2013–Present *Senior instructor*, Statistical Methods for Functional Genomics, Cold Spring Harbor Laboratory
- 2008–2020 *Bioconductor Technical Advisory Board*, shared responsibility for the ongoing technical leadership of the Bioconductor Project
- December, 2016–2020 *Founding Member*, NIH Data Science Special Interest Group (>600 members)
- 2012–2019 *Founding Member*, NIH High Performance and Scientific Computing Working Group
- May, 2019 *Co-organizer*, Artificial Intelligence for Data Reuse, an NSF-funded symposium, Carnegie Mellon University, Pittsburgh, PA
- May, 2018 *Co-organizer*, Renal Cell Cancer Hackathon, in collaboration with <https://sv.ai> and Google, San Francisco, CA
- 2017 *NIH Intramural Representative*, NIH Data Commons working group
- December, 2017 *Co-organizer*, NIH Hour of Code, Data Science Special Interest Group, NIH, Bethesda, MD

- November, 2017 *NIH Representative to US Department of Agriculture*, Blueprint for USDA Efforts in Agricultural Animal Genomics, Beltsville, MD
- August, 2017 *NIH Intramural Representative*, NIH Data Commons Review Committee
- February, 2017 *Organizer*, NIH/NIST Medical Devices Cybersecurity Workshop, Bethesda, MD
- January, 2017 *Organizer*, Cancer Moonshot Blue Ribbon Panel Implementation Working Group, National Cancer Data Ecosystem
- 2017-present
- January, 2017 *Organizer*, Globus Data Platform Hackathon and Workshop, NIH, Bethesda, MD
- January, 2017 *NCI Representative*, NHLBI TopMed Data Commons Planning Workshop
- July, 2016-July, 2017 *NCI Representative*, NIH Data Commons Reference Dataset Working Group
- July, 2016 *Co-organizer*, Frontiers of Predictive Oncology and Computing Symposium, Washington, DC
- June, 2016 *Organizer*, Bioconductor 2016 Annual Meeting and Developer Conference. Stanford, CA.
- April-November, 2016 Presidential Subcommittee on AI and Machine Learning, Cancer Moonshot Initiative
- December, 2015 *NCI representative and panel member*, FDA Informatics and Precision Medicine Workshop
- January, 2016 *Co-organizer*, NCBI Genomics and Bioinformatics Hackathon
- November, 2015-October, 2017 *Organizer*, NCI Cancer Cloud Pilot, Lead for Intramural Research Program evaluation and implementation
- July, 2015 *Organizer*, Bioconductor 2015 Annual Meeting and Developer Conference. Seattle, WA.
- May, 2015-present CCR Representative to CBIIT Strategic Planning Committee
- 2015 NCI Intramural Research Program Representative, NCI Cancer Cloud Initiative
- 2015 NCI Desktop Linux Working Group
- 2014-Present Software Carpentry Instructor
- 2014-2018 NIH and NCI Genomic Data Sharing Policy Implementation working groups
- July, 2014 *Organizer*, Bioconductor 2014 Annual Meeting and Developer Conference. Boston, MA.
- May 12-13, 2014 *Intramural NIH representative*, BD2K Software Development Conference
- January, 2014 *Organizer and Instructor*, Bioinformatics Summer Course, Riberão Preto Medical School, University of São Paulo, Brazil
- 2014 NCI Center for Cancer Genomics Genomic Data Commons (GDC) Review Committee
- July, 2013 *Organizer*, Bioconductor 2013 Annual Meeting and Developer Conference. Fred Hutchinson Cancer Research Center, Seattle, WA
- February, 2013 *NIH Representative*, Big Data Conference, Agricultural Research Service, USDA, Beltsville, MD
- 2012-2016 High Throughput Molecular Data Working Group, National Cancer Institute
- 2010-Present *Steering Committee*, NCI Center of Excellence in Integrative Cancer Biology and Genomics
- July, 2012 *Organizer*, Bioconductor 2012 Annual Meeting and Developer Conference. Fred Hutchinson Cancer Research Center, Seattle, WA
- 2011 NCI PacBio User Committee

- July, 2011 *Organizer*, Bioconductor 2011 Annual Meeting and Developer Conference. Fred Hutchinson Cancer Research Center, Seattle, WA
- 2010-2012 Scientific Liaison, Center for Cancer Research Bioinformatics Core
- 2009-2010 *Chair*, Center for Cancer Research Bioinformatics Planning and Implementation Committee
- September, 2010 *NIH Representative*, NIFA, USDA, Genomics and Bioinformatics Workshop, Washington, DC
- 2009-2016 Sequencing Facility Steering and Review Committee, Center for Cancer Research, NCI
- 2009 *Team Leader*, Advanced Biomedical Computing Center Review Committee
- April, 2008 *Organizer*, European Bioconductor Developer Conference, Lausanne, Switzerland

Invited Presentations, Teaching, and Short Courses

- September 22, 2021 Bio-IT World
- November 2021 Supercomputer
- September, 2020 *sars2pack: A open software package providing fit-for-use COVID-19 data resources*, Cornell Weill School of Medicine, New York, NY
- July, 2018 *Cloud computing approaches to genomic data science*, American Statistical Association, Joint Statistical Meeting, Vancouver, Canada
- July, 2018 *Leveraging Public Data using R and Bioconductor—a hands-on workshop*, Bioconductor Conference, Victoria College, University of Toronto, Toronto, Canada
- June, 2018 *Cloud Scale Genomics—a Hands-on Tutorial*, Big Data Training for Translational Omics Research, Purdue University
- June, 2018 *Machine Learning and Artificial Intelligence in Biomedicine*, Big Data Training for Translational Omics Research, Purdue University
- April, 2018 *R and Bioconductor for Genomic Data Science*, Wake Forest School of Medicine, Winston-Salem, NC
- January, 2018 *A Data Ecosystem for Biomedical Big Data*, Grand Rounds, Wake Forest School of Medicine, Winston-Salem, NC
- November, 2017 *Thoughts on Components of an Agricultural Data Ecosystem*, Blueprint for USDA Efforts in Agricultural Animal Genomics, Beltsville, MD
- July, 2017 *What can I do with my data?*, National Institute of Nursing Research, BigData Bootcamp, Bethesda, MD
- July, 2017 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY
- June, 2017 *Cloud-scale genomics with the Cancer Genomics Cloud Pilots and Machine Learning in Biomedicine*, Purdue University, West Lafayette, IN
- January, 2017 *A cloud-based data ecosystem for cancer research*, Dana Farber Cancer Institute, Boston, MA
- January, 2017 *Open APIs with R and Bioconductor*, Harvard/Boston R/Bioconductor Meetup, Boston, MA
- October, 2016 *Big data science careers in Government*, University of California, Riverside, CA
- October, 2016 *Democratizing access to Big Cancer Data*, Midatlantic Bioinformatics Conference, University of Pennsylvania, Philadelphia, PA

- July, 2016 *Bioconductor: Where Biology and Software Meet*, National Institute of Nursing Research, Bethesda, MD
- July, 2016 *The Central Role of Data in Biomedical Research*, Purdue University, West Lafayette, IN
- June, 2016 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY
- April, 2016 Software Carpentry, National Institute on Aging, Baltimore, MD
- March, 2016 Using the NCI Cancer Genomics Cloud, a Hands-on Tutorial, NIH
- February, 2016 Introduction to RNA-Seq Data Analysis, NCI
- January, 2016 Introduction to Bioconductor: Code and Practice, DataCommunityDC, Washington DC
- October, 2015 *Course organizer and faculty*: Harvard School of Engineering and Applied Science: CS290 Extreme Computing
- September, 2015 BioIT: A Symbiotic Relationship Between Biological Research and IT Infrastructure, Converged IT Summit, San Francisco, CA
- June, 2015 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY
- May, 2015 Beyond the Promise of Precision Medicine, Health 2.0 Meetup, Bethesda, MD
- April, 2015 Relational Databases and R: a Powerful Combination for Science, NCI, DCEG
- February, 2015 Introduction to RNA-Seq Data Analysis, NCI
- January, 2015 Introduction to R and Bioconductor, NCI
- December, 2014 Introduction to R for Data Manipulation and Visualization, NIH
- June, 2014 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY
- February, 2014 One-day course on RNA-seq data analysis and visualization, CIT, NIH
- February, 2014 Reproducible research using the Snakemake workflow toolkit on Biowulf, CIT, NIH
- January, 2014 *Course Organizer*, Bioinformatics Summer Course, Riberão Preto Medical School, University of São Paulo, Brazil
- July 19, 2013 Accessing Public Genomics Data Using R and Bioconductor, Bioconductor Conference, Fred Hutchinson Cancer Research Center, Seattle, WA
- June, 2013 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY
- February 6, 2013 Planning for High Performance and Scientific Computing at the NIH, Agricultural Research Service, USDA, Beltsville, MD
- November 6, 2012 Introduction to Next Generation Sequencing Technologies, Bioinformatics Training and Education Program, CCR, NCI
- July 24, 2012 Accessing Public Genomics Data Using R and Bioconductor, Bioconductor Conference, Fred Hutchinson Cancer Research Center, Seattle, WA
- June, 2012 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory, NY. Topics taught: public data access and data integration lab
- 2005-2012, except 2008 AACR Molecular Biology in Clinical Oncology (one-week course), Aspen & Snowmass, CO
- March 28, 2012 Featured Speaker, Bioinformatics for Medical Genetics Symposium, American College of Medical Genetics, Charlotte, NC

- February 27-28, 2012 Advanced R and Bioconductor Workshop on High-Throughput Genetic Analysis, Fred Hutchinson Cancer Research Center, Seattle, WA
- January 13, 2012 Introduction to Next-Generation Sequencing: Mapping and Counting, Center of Excellence in Integrative Cancer Biology and Genomics Seminar Series, NCI
- November 18, 2011 High-resolution Views of the Cancer Genome Using Next-Generation Sequencing Approaches, Lombardi Cancer Center, Georgetown University
- July, 2011 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory. Topics taught: exome sequencing, methylation arrays, comparative genomic hybridization, public data access, and data integration lab
- March, 2011 Introduction to Next-Generation Sequence Data Analysis, Center for Information Technology
- January 28, 2011 Complete Genomics Data Tutorial, Center for Cancer Research, NCI
- October 22, 2010 BioConductor: Tools for the Comprehension of Genomic Data, Translational Genomics Conference, Center of Excellence in Integrative Cancer Biology and Genomics annual meeting
- October 22, 2010 Bioinformatics at the Center for Cancer Research, An Update, Center of Excellence in Integrative Cancer Biology and Genomics annual meeting
- September 9, 2010 Potential Applications of Genomics in Agriculturally Important Species, NIFA, U.S. Department of Agriculture
- Spring, 2010 Microarray Data Analysis Using R and Bioconductor, Department of Biostatistics, Bioinformatics, and Biomathematics, Georgetown University
- February 23, 2010 Genomic Technologies for Viewing the Cancer Genome, Georgetown University
- July, 2010 *Course Organizer*, Statistical Analysis of Genomic Data, Cold Spring Harbor Laboratory
- November 18, 2009 Structural Variant Discovery in Short Read Sequencing using R and Bioconductor, Fred Hutchinson Cancer Research Center, Seattle, WA
- November 18-20, 2009 Instructor, High throughput sequence analysis tools and approaches with Bioconductor, Fred Hutchinson Cancer Research Center, Seattle, WA
- March 17, 2009 High-resolution Views of the Cancer Genome: Tools for examining the genome in a high-throughput way, Case Western Reserve University, Cleveland, OH
- February 12, 2009 Genomics for the Pediatrician: An Overview of Genomics Technologies, Pediatric Grand Rounds, Oklahoma University Health Sciences Center, Oklahoma City, OK

Awards and Honors

- 2018 National Institutes of Health Director's Award
- 2016 & 2017 National Cancer Institute Technology Transfer Award
- 2016 United States Department of Health and Human Services Director's Award
- 2015 National Institutes of Health Director's Award
- 2012 Staff Scientist/Staff Clinician Travel Award, Center for Cancer Research, NCI
- 2002-2007 NIH General Loan Repayment Program
- 2002 Family-Centered Care Award, University of Washington, Childrens Hospital of Seattle
- 1995 W.M. Keck Fellowship for Advanced Scientific Computing
- 1989 National Merit Scholar
- 1989 National Honor Society Scholarship

- 1988 Pennsylvania Governor's School for Science
1988 Young Humanitarian of the Year, Pennsylvania Association for Gifted Education

Funding and grants

Current

- 07/01/2019–
06/30/2024 *Exploiting Public Metagenomic Data To Uncover Cancer-Microbiome Relationships*
U01 CA230551
PI: Levi Waldron
The human microbiome is implicated in the development and response to treatment of some cancers, including infectious agents estimated to be responsible for 18% of the global cancer burden. This project improves the ability to identify new roles of the human microbiome in cancer by 1) enabling comprehensive comparisons of microbiome studies to previously published results and known microbial physiology, 2) developing higher-resolution approaches to identifying viruses and bacterial strains from metagenomic shotgun data, and 3) making all methods and resources easily usable by a broad research community.
Role: Co-Investigator
- 06/01/2019–
06/01/2020 *BigRNA: Accelerating Research By Increasing Access and Use of Public Transcriptomic Data*
Amazon Research Grant
PI: Sean Davis
The BigRNA project reprocesses and distributes publicly available transcriptomic data, including data that are controlled-access, to facilitate data reuse, reanalysis, and machine learning applications.
Role: PI
- 09/17/2019–
08/31/2024 *Big Data Training For Cancer Research*
R25 CA233429
PI: Min Zhang
Cancer big data is a collection of high-density information from a variety of sources, and it requires sophisticated statistical and computational tools to analyze and extract knowledge. Built on a previous big data training program designed for general biomedical researchers, this new training program is aimed at helping cancer researchers develop the necessary analytical skills to work with big data, and translate big data into knowledge to facilitate precision cancer medicine.
Role: Co-Investigator
- 2020/01/30–
2021/01/29 *Increasing the value of public transcriptomic data through harmonized processing and metadata*
XSEDE (PSC) MCB200027
PI: Sean Davis
Startup allocation to prototype using XSEDE resources to perform large-scale, harmonized omics data processing, including transcriptomics and metagenomics.
Role: PI

Trainees

- 2015-2018 Vincent Laufer, University of Alabama, PhD thesis committee member. Graduation 2018.
- Summer, 2016 Rosa Choe, computer science, UC Berkeley, graduation 2019
- Summer, 2015 Olivia Zhang, computer science, Princeton University, graduation 2020

Summer, 2013 Peter Hansen, biology, Cornell University, graduation 2018

Editorial Responsibilities

2015-Present Editor, F1000Research Bioconductor Channel
2010-Present Associate Editor, BMC Bioinformatics
2009 Book reviewer, CRC Press, 2009
Peer Reviewer

- Bioinformatics
- BMC Bioinformatics
- Breast Cancer Research
- Cancer Research
- Clinical Cancer Research
- Database
- Endocrine-Related Cancer
- EURASIP Journal on Bioinformatics and Systems Biology
- Genetic Epidemiology
- Genomics
- Genome Research
- Gigascience
- Molecular Carcinogenesis
- Molecular Cancer Research
- Nature Methods
- Nucleic Acids Research
- Pigment Cell & Melanoma Research
- PLoS Computational Biology
- PLoS One
- Transactions on Computational Biology and Bioinformatics

References

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- [2] Ludwig Geistlinger, Gergely Csaba, Mara Santarelli, Marcel Ramos, Lucas Schiffer, Nitesh Turaga, Charity Law, Sean Davis, Vincent Carey, Martin Morgan, Ralf Zimmer, and Levi Waldron. “Toward a gold standard for benchmarking gene set enrichment analysis”. In: *Briefings in Bioinformatics* 22.1 (Mar. 2020), pp. 545–556. ISSN: 1477-4054. DOI: 10.1093/bib/bbz158. eprint: https://academic.oup.com/bib/article-pdf/22/1/545/35935075/supplement/_bbz158.pdf.
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