Natalie R. Davidson, Ph.D.

Assistant Professor

Division of Reproductive Sciences, Department of Obstetrics & Gynecology

University of Colorado Anschutz Medical Campus

Aurora, Colorado

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Research Program

The Davidson Laboratory develops machine learning methods for precision oncology by integrating transcriptomic, imaging, and clinical data, with a focus on high-grade serous ovarian cancer (HGSC). We develop computational approaches to characterize tumor heterogeneity, predict therapeutic response, and identify clinically actionable biomarkers.

Our work bridges artificial intelligence, computational biology, image processing, and cancer genomics through close collaboration with experimental scientists and clinicians. By combining methodological innovation with biological validation, we develop computational tools that can be translated into clinical decision-making and improved ovarian cancer care.

Academic Appointments

2024–Present	Assistant Professor, Division of Reproductive Sciences, Department of Obstetrics & Gynecology, University of Colorado Anschutz Medical Campus
2020–2024	Postdoctoral Fellow, Department of Biomedical Informatics, University of Colorado Anschutz Medical Campus
2019–2020	Postdoctoral Fellow and Lecturer, Department of Computer Science, ETH Zürich
2013–2019	Graduate Research Assistant, Tri-Institutional Program in Computational Biology and Medicine, Weill Cornell Medicine

Education

2019	Ph.D., Computational Biology and Medicine, Weill Cornell Medicine
2013	M.S., Computer Science (Computational Biology), University of California, Los Angeles
2011	B.S., Computer Science; Minor in Applied Mathematics, University of California, Santa Barbara

Honors and Awards

- 2026 – University of Colorado Cancer Center Collaborative Pilot Grant (co-Principal Investigator)
- 2026 – Golfers Against Cancer Pilot Grant Finalist (Principal Investigator)
- 2026 – Cancer League of Colorado Research Grant (Principal Investigator)
- 2023 – NIH NHGRI Pathway to Independence Award (K99/R00)
- 2023 – University of Colorado Anschutz Postdoctoral Association, Postdoc of the Month
- 2021 – Rocky Mountain Bioinformatics Conference, Best Poster Award
- 2020 – Swiss Institute of Bioinformatics, Recognition of Remarkable Output

Research Funding

University of Colorado Cancer Center Collaborative Pilot Grant
2026–2028 Principal Investigator
Award Amount: $99,910
Inferring Multiplex Immunofluorescence from H&E to Predict Treatment Response in Ovarian Cancer.

Cancer League of Colorado Research Grant
2026–2027 Principal Investigator
Award Amount: $60,000
Beyond Genomic Scarring: Modeling Dynamic Changes in DNA Repair Pathways.

NIH NHGRI R00HG012945
2024–2027 Principal Investigator
Award Amount: $746,999
Domain adaptation approaches to unify established and emerging sequencing technologies.

NIH NHGRI K99HG012945
2023–2024 Principal Investigator
Award Amount: $268,778
Domain adaptation approaches to unify established and emerging sequencing technologies.

Patent

- Patent 2024-302: Domain adaptation for cell-free DNA fragmentomics using variational autoencoders.

Invited Lectures and Scientific Presentations

Invited Seminars

2025 Human Genetics and Genomics Faculty Seminar
2025 Computational Biosciences Program Seminar
2024 Reproductive Sciences Seminar, University of Colorado Anschutz Medical Campus
2024 University of Colorado Ovarian Cancer Think Tank

Selected Conference Presentations

2024 ISMB — Domain adaptation for cell-free DNA fragmentomics
2023 Quantitative Cell and Molecular Biology Summer School — *BuDDI: Bulk Deconvolution with Domain Invariance*
2023 University of Colorado Biomedical Informatics Retreat — *BuDDI: Bulk Deconvolution with Domain Invariance*
2022 ISMB — Analysis of science journalism reveals gender and regional disparities in coverage
2020 ICML Workshop on Machine Learning for Global Health — Anonymous Survey System and Methodology to Enable COVID-19 Surveillance
2018 RECOMB Computational Cancer Biology — Integrating Diverse Transcriptomic Alterations to Identify Cancer-Relevant Genes

Research Mentorship

Postdoctoral Fellows

Stephanie Tanis	Postdoctoral Fellow (2025–present) Recipient, University of Colorado Postdoctoral Travel Fellowship (2026).

Graduate Students

Samantha Lopez Alvarez	Graduate Student (2025–present) Recipient, ISMB Travel Fellowship (2026); selected for an oral presentation at ISMB 2026.
Saloni Dixon	Graduate Student (2026–present) Recipient, University of Colorado Computational Biosciences T15 Fellowship.
Raymond Lesiyon	Graduate Student (2026–present).

Teaching and Professional Service

Teaching

- Lecturer, *Computational Biomedicine*, ETH Zürich (2019–2020)
- Lecturer, *Digital Medicine*, ETH Zürich (2020)
- Teaching Assistant, *Learning and Intelligent Systems*, ETH Zürich (2017–2019)
- Teaching Assistant, *Introduction to Machine Learning*, ETH Zürich (2017–2019)

Professional Service

Journal Reviewer

- Nature Methods
- Nature Communications
- Genome Biology
- Bioinformatics
- PLOS Computational Biology
- PLOS Genetics
- NAR Genomics and Bioinformatics
- GigaScience

Departmental Service

- Reproductive Sciences Seminar Committee (2026–present)
- Department of Biomedical Informatics Seminar Committee (2023–2024)
- Postdoctoral Search Committee Chair, Greene Lab (2023)
- Postdoctoral Search Committee, Pividori Lab (2023)
- Postdoctoral Search Committee Chair, Way Lab (2021)

Conference Reviewing

- Intelligent Systems for Molecular Biology (ISMB)
- Machine Learning for Health (ML4H)

Professional Profiles

- Google Scholar: profile
- ORCID: 0000-0002-1745-8072
- Email: natalie.davidson@cuanschutz.edu

Software

BuDDI
Bulk Deconvolution with Domain Invariance: a deep learning framework for estimating cell-type-specific perturbations from bulk transcriptomic data.
Publication: [8]
GitHub: https://github.com/NDavidsonLab/buddi

ssPATHS
Bioconductor package for single-sample pathway scoring and pathway-level analysis of transcriptomic datasets.
Publication: [27]
Bioconductor: https://www.bioconductor.org/packages/release/bioc/html/ssPATHS.html

pmVAE
Interpretable pathway module variational autoencoder for representation learning in single-cell transcriptomics.
Publication: [28]
GitHub: https://github.com/ratschlab/pmvae

Selected Publications

[1] E. Ehimiaghe, H. Dimmick, D. Spinosa, F. Ireigbe, M. D. Post, R. J. Wolsky, A. Clauset, S. Orsulic, S. Taylor, E. W. Hsieh, et al. "Ovarian cancer think tank: the use of integrated artificial intelligence and computational biology in ovarian cancer diagnosis and treatment." In: *European Journal of Gynaecological Oncology* 47.1 (2026), p. 15.

[2] A. Ivich, L. Grieshober, N. R. Davidson, G. Y. Akatsu, L. C. Peres, S. C. Hicks, J. R. Marks, J. M. Schildkraut, J. A. Doherty, and C. S. Greene. "Deconvolved tumor adipocyte proportions and high grade serous ovarian carcinoma survival". In: *bioRxiv* (2026), pp. 2026–01.

[3] S. Tanis, M. Lixandrão, A. Ivich, L. Grieshober, K. A. Lawson-Michod, L. J. Collin, L. C. Peres, L. A. Salas, J. R. Marks, B. G. Bitler, et al. "Transcriptomic subtypes in high-grade serous ovarian cancer are driven by tumor cellular composition". In: *bioRxiv* (2026).

[4] H. A. Townsend, K. R. Jordan, R. J. Wolsky, L. B. Van Kleunen, N. R. Davidson, K. Behbakht, M. J. Sikora, R. D. Dowell, A. Clauset, and B. G. Bitler. "Cross-assay RNA modeling reveals cancer biomarkers". In: *bioRxiv* (2026), pp. 2026–04.

[5] B. G. Bitler, J. Lang, D. Nunez-Avellaneda, K. Behbakht, N. R. Davidson, E. R. Woodruff, and F. R. Villagomez. "Claudin-4 as a dual regulator of genome stability and immune evasion in high grade serous ovarian cancer". In: *Scientific Reports* 15.1 (2025), p. 39257.

[6] R. Casanova, S. Xu, P. Bost, S. Sivapatham, A. Jacobs, S. Engler, T. P. Consortium, R. Aebersold, M. Ak, F. S. Al-Quaddoomi, et al. "Standardization of Suspension and Imaging Mass Cytometry Single-Cell Readouts for Clinical Decision Making". In: *Cytometry Part A* 107.6 (2025), pp. 390–403.

[7] L. J. Collin, C. E. Johnson, N. Davidson, C. S. Greene, J. M. Schildkraut, and J. A. Doherty. "Validation of the ovarian tumor tissue analysis consortium stratified prognosis of ovarian tumors score using RNAseq and among Black women". In: *Cancer Research* 85.8_Supplement_1 (2025), pp. 981–981.

[8] N. R. Davidson, F. Zhang, and C. S. Greene. "BuDDI: Bulk Deconvolution with Domain Invariance to predict cell-type-specific perturbations from bulk". In: *PLoS computational biology* 21.1 (2025), e1012742.

[9] A. Ivich, N. R. Davidson, L. Grieshober, W. Li, S. C. Hicks, J. A. Doherty, and C. S. Greene. "Missing cell types in single-cell references impact deconvolution of bulk data but are detectable". In: *Genome biology* 26.1 (2025), p. 86.

[10] C. E. Johnson, X. Ran, J. Wrobel, N. R. Davidson, C. S. Greene, M. P. Epstein, J. R. Marks, L. C. Peres, J. A. Doherty, and J. M. Schildkraut. "An analytic pipeline to obtain reliable genetic ancestry estimates from tumor-derived RNA sequencing data". In: *Cancer Epidemiology, Biomarkers & Prevention* 34.9 (2025), pp. 1593–1599.

[11] K. A. Lawson-Michod, C. E. Johnson, M. E. Barnard, N. R. Davidson, L. J. Collin, D. A. Nix, C. D. Huff, A. Berchuck, L. A. Salas, C. S. Greene, et al. "Homologous recombination deficiency and survival in ovarian high-grade serous carcinoma by self-reported race". In: *Cancer Epidemiology, Biomarkers & Prevention* 34.11 (2025), pp. 2007–2014.

[12] K. A. Lawson-Michod, J. R. Marks, L. J. Collin, D. A. Nix, N. R. Davidson, C. D. Huff, Y. Yu, A. Atkinson, C. E. Johnson, L. A. Salas, et al. "Genomic characterization of high-grade serous ovarian carcinoma reveals distinct somatic features in Black individuals". In: *Cancer research* 85.9 (2025), pp. 1725–1737.

[13] C. Litchfield, R. Nienhold, A. Wicki, M. Schmid, D. Aguilera-Garcia, V. H. Koelzer, R. Aebersold, M. Ak, F. S. Al-Quaddoomi, S. I. Albert, et al. "Integrating Formalin-Fixed, Paraffin-Embedded–Derived Whole-Genome Sequencing into Routine Molecular Pathology: Validation and First Experiences in Metastatic Melanoma". In: *The Journal of Molecular Diagnostics* 27.8 (2025), pp. 722–735.

[14] N. R. Davidson, M. E. Barnard, A. A. Hippen, A. Campbell, C. E. Johnson, G. P. Way, B. K. Dalley, A. Berchuck, L. A. Salas, L. C. Peres, et al. "Molecular subtypes of high-grade serous ovarian cancer across racial groups and gene expression platforms". In: *Cancer Epidemiology, Biomarkers & Prevention* 33.8 (2024), pp. 1114–1125.

[15] N. R. Davidson and C. S. Greene. "Analysis of science journalism reveals gender and regional disparities in coverage". In: *Elife* 12 (2024), RP84855.

[16] K. Lawson-Michod, M. E. Barnard, N. Davidson, L. J. Collin, C. Johnson, L. A. Salas, C. Greene, J. R. Marks, L. Peres, J. M. Schildkraut, et al. "Characterization of germline and somatic homologous recombination deficiency features in high-grade serous ovarian cancer among Black individuals". In: *Cancer Research* 84.6_Supplement (2024), pp. 6127–6127.

[17] S. Lin, L. L. Nguyen, A. McMellen, M. S. Leibowitz, N. Davidson, D. Spinosa, and B. G. Bitler. "Leveraging multi-omics to disentangle the complexity of ovarian cancer". In: *Molecular diagnosis & therapy* 29.2 (2024), p. 145.

[18] C. Calabrese, N. R. Davidson, D. Demircioglu, N. A. Fonseca, Y. He, A. Kahles, K.-V. Lehmann, F. Liu, Y. Shiraishi, C. M. Soulette, et al. "Genomic basis for RNA alterations in cancer (vol 578, pg 129, 2020)". In: *NATURE* (2023).

[19] I. Cortés-Ciriano, J. J.-K. Lee, R. Xi, D. Jain, Y. L. Jung, L. Yang, D. Gordenin, L. J. Klimczak, C.-Z. Zhang, D. S. Pellman, et al. "Author Correction: Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing". In: *nature genetics* 55.6 (2023), pp. 1076–1076.

[20] A. A. Hippen, N. R. Davidson, M. E. Barnard, L. M. Weber, J. Gertz, J. A. Doherty, S. C. Hicks, and C. S. Greene. "Deconvolution reveals compositional differences in high-grade serous ovarian cancer subtypes". In: *bioRxiv* (2023), pp. 2023–06.

[21] K. A. Lawson-Michod, D. Nix, L. Collin, N. Davidson, A. Hippen, C. Huff, A. Atkinson, L. A. Salas, L. Peres, C. Greene, et al. "High-grade serous ovarian cancer somatic mutational signatures in Black and White individuals". In: *Cancer Research* 83.7_Supplement (2023), pp. 3506–3506.

[22] A. A. Hippen, N. R. Davidson, and C. S. Greene. "Computational audits combat disparities in recognition". In: *Nature Human Behaviour* 6.4 (2022), pp. 473–474.

[23] D. Salloum, K. Singh, N. R. Davidson, L. Cao, D. Kuo, V. R. Sanghvi, M. Jiang, M. T. Lafoz, A. Viale, G. Ratsch, et al. "A rapid translational immune response program in CD8 memory T lymphocytes". In: *The Journal of Immunology* 209.6 (2022), pp. 1189–1199.

[24] P. Simmler, C. Cortijo, L. M. Koch, P. Galliker, S. Angori, H. A. Bolck, C. Mueller, A. Vukolic, P. Mirtschink, Y. Christinat, et al. "SF3B1 facilitates HIF1-signaling and promotes malignancy in pancreatic cancer". In: *Cell Reports* 40.8 (2022).

[25] D. Danko, D. Bezdan, E. E. Afshin, S. Ahsanuddin, C. Bhattacharya, D. J. Butler, K. R. Chng, D. Donnellan, J. Hecht, K. Jackson, et al. "A global metagenomic map of urban microbiomes and antimicrobial resistance". In: *Cell* 184.13 (2021), pp. 3376–3393.

[26] A. Irmisch, X. Bonilla, S. Chevrier, K.-V. Lehmann, F. Singer, N. C. Toussaint, C. Esposito, J. Mena, E. S. Milani, R. Casanova, et al. "The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support". In: *Cancer cell* 39.3 (2021), pp. 288–293.

[27] P. Markolin, N. Davidson, C. K. Hirt, C. D. Chabbert, N. Zamboni, G. Schwank, W. Krek, and G. Rätsch. "Identification of HIF-dependent alternative splicing in gastrointestinal cancers and characterization of a long, coding isoform of SLC35A3". In: *Genomics* 113.2 (2021), pp. 515–529.

[28] S. G. Stark, G. Gut, G. Rätsch, and N. R. Davidson. "PmVAE: Learning Interpretable Single-Cell Representations with Pathway Modules". In: *ICML Workshop on Computational Biology*. Paper presentation. Co-corresponding author. 2021. URL: https://icml-compbio.github.io/icml-website-2021/2021/papers/WCBICML2021_paper_24.pdf.

[29] C. Calabrese, N. Davidson, D. Demircioğlu, N. Fonseca, Y. He, A. Kahles, K. Lehmann, F. Liu, Y. Shiraishi, C. Soulette, et al. "PCAWG Transcriptome Core Group; PCAWG Transcriptome Working Group; PCAWG Consortium". In: *Genomic basis for RNA alterations in cancer. Nature* 578 (2020), pp. 129–136.

[30] C. Calabrese, N. R. Davidson, D. Demircioğlu, N. A. Fonseca, Y. He, A. Kahles, K.-V. Lehmann, F. Liu, Y. Shiraishi, C. M. Soulette, L. Urban, et al. "Genomic basis for RNA alterations in cancer". In: *Nature* 578.7793 (2020), pp. 129–136.

[31] "Pan-cancer analysis of whole genomes". In: *Nature* 578.7793 (2020), pp. 82–93.

[32] E. Segal, F. Zhang, X. Lin, G. King, O. Shalem, S. Shilo, W. E. Allen, F. Alquaddoomi, H. Altae-Tran, S. Anders, et al. "Building an international consortium for tracking coronavirus health status". In: *Nature Medicine* 26.8 (2020), pp. 1161–1165.

[33] P. T. Simmler, C. Cortijo, L. M. Koch, P. Galliker, M. Schäfer, S. Angori, H. A. Bolck, C. Mueller, A. Vukolic, P. Mirtschink, et al. "SF3B1 promotes tumor malignancy through splicing-independent activation of HIF1α". In: *bioRxiv* (2020), pp. 2020–11.

[34] G. P. Krishnamoorthy, N. R. Davidson, S. D. Leach, Z. Zhao, S. W. Lowe, G. Lee, I. Landa, J. Nagarajah, M. Saqcena, K. Singh, et al. "EIF1AX and RAS mutations cooperate to drive thyroid tumorigenesis through ATF4 and c-MYC". In: *Cancer Discovery* 9.2 (2019), pp. 264–281.

[35] N. R. Davidson, K. R. Godfrey, F. Alquaddoomi, D. Nola, and J. J. DiStefano III. "Disting: A web application for fast algorithmic computation of alternative indistinguishable linear compartmental models". In: *Computer Methods and Programs in Biomedicine* 143 (2017), pp. 129–135.

[36] Y. Y. Waldman, A. Biddanda, N. R. Davidson, P. Billing-Ross, M. Dubrovsky, C. L. Campbell, C. Oddoux, E. Friedman, G. Atzmon, E. Halperin, et al. "The genetics of Bene Israel from India reveals both substantial Jewish and Indian ancestry". In: *PLoS One* 11.3 (2016), e0152056.

[37] N. Davidson, K.-V. Lehmann, A. Kahles, A. Perez, and G. Rätsch. "Integrative analysis of transcriptome variation in uterine carcinosarcoma and comparison to sarcoma and endometrial carcinoma". In: *bioRxiv* (2014), p. 012708.