

Emma Dann

📍 Wellcome Sanger Institute, Hinxton CB10 1RQ (UK)
✉ emma.dann@sanger.ac.uk | 🌐 [emdann.github.io](https://github.com/emdann) | 🐙 [emdann](https://github.com/emdann)

Education

PhD in Biological Sciences – University of Cambridge, UK (Oct 2019 – expected Oct 2023)

Advisors: Dr. Sarah A. Teichmann, Dr. John C. Marioni

Thesis title: *Discovering variation from cell atlases: comparative methods for single-cell genomics*

M.Sc. in Cancer, Stem Cells and Developmental Biology (Bioinformatics profile) – Utrecht University, NL (Sept 2017 – Aug 2019)

Final grade: *cum laude* (Honours, Avg. grade: 9.10/10)

B.Sc. in Biomolecular Sciences and Technology – University of Trento, IT (Sept 2014 – July 2017)

Final grade: 110 *cum laude*/110

Professional experience

Data science consultant – Ensocell Ltd (Oct 2023 – present)

Target discovery platform and analysis of single-cell data

Graduate researcher – Wellcome Sanger Institute, Cambridge, UK (Oct 2019 – present)

Supervised by Sarah Teichmann and John Marioni. Comparative analysis of single-cell omics data.

Research intern – European Molecular Biology Laboratory, Heidelberg, DE (Sept 2018 – Aug 2019)

Supervised by Wolfgang Huber. Integrative analysis of multi-omic profiles of perturbations for functional characterization of drug treatments and target discovery.

Research intern – KNAW Hubrecht Institute, Utrecht, NL (Sept 2017 – Aug 2018)

Supervised by Alexander Van Ourdenaarden. Biophysical modelling of whole-genome amplification via random priming, to predict and enhance coverage of single-cell bisulfite sequencing experiments.

Research intern – Center for Integrative Biology, University of Trento, IT (Feb 2017 – July 2017)

Supervised by Francesca Demichelis. Computational analysis of whole-methylome profiles of tumor samples from a large cohort of prostate cancer patients, for epigenetic biomarker discovery.

Research assistant – Center for Integrative Biology, University of Trento, IT (Feb 2016 – Feb 2017)

Lab equipment maintenance and general support for benchwork.

Publications

(*) denotes equal contribution as co-first author

Journal articles

Dann E., Teichmann S.A., Marioni J.C. (2023) Precise identification of cell states altered in disease with healthy single-cell references, *Nature Genetics* | [Full text](#) | [code](#) | [python package](#)

Botting R.A., Goh I., ... , **Dann E.**, ... , Teichmann S.A. , Haniiffa M. (2022) Yolk sac cell atlas reveals multiorgan functions during human early development. *Science* | [Full text](#)

Suo C., Polanski K., **Dann E.**, ... , Tuong Z.K., Clatworthy M., Teichmann S.A. (2022) Dandelion uses the single-cell adaptive immune receptor repertoire to explore lymphocyte developmental origins, *Nature Biotechnology* | [Full text](#) | [python package](#)

Heumos L., ... **Single-cell Best Practices Consortium**, ... , Theis F.J. (2023) Best practices for single-cell analysis across modalities. *Nature Review Genetics* | [Full text](#)

Suo C.*, **Dann E.***, ... , Haniffa M., Teichmann S.A. (2022) Mapping the developing human immune system across organs. *Science* | [Full text](#) | [code](#) | [data](#)

He P., Lim K., Sun D., ... , **Dann E.**, ... , Meyer K.B., Rawlins E.L. (2022) A human fetal lung cell atlas uncovers proximal-distal gradients of differentiation and key regulators of epithelial fates, *Cell* | [Full text](#)

Kleshchevnikov V., Shmatko A., **Dann E.**, ... , Stegle O., Bayraktar O.A. (2022) Cell2location maps fine-grained cell types in spatial transcriptomics. *Nature Biotechnology* | [Full text](#) | [python package](#)

Dann E., Henderson N.C., Teichmann S.A., Morgan M.D., Marioni J.C. (2022) Differential abundance testing on single-cell data using k-nearest neighbor graphs, *Nature Biotechnology* | [Full text](#) | [R package](#) | [python package](#)

Jardine L., Webb S., ... , **Dann E.**, ... , Göttgens B., Roberts I., Teichmann S. and Haniffa M. (2021) Blood and immune development in human fetal bone marrow and Down syndrome, *Nature* | [Full text](#)

Elmentaite R., Kumasaka N., Roberts K., Fleming A., **Dann E.**, ... , James K.R., Teichmann S.A. (2021), Cells of the human intestinal tract mapped across space and time, *Nature* | [Full text](#)

Stephenson E., Reynolds G., Botting R.A., Calero-Nieto F.J., Morgan M.D., Tuong Z.K., Bach K., Sungnak W., ... , **Dann E.**, ... , Duncan C.J.A, Smith K., Teichmann S.A., Clatworthy M.R., Marioni J.C., Gottgens B., Haniffa M. (2020) Single-cell multi-omics analysis of the immune response in COVID-19, *Nature Medicine* | [Full text](#)

Beltran H., Romanel A., ... , **Dann E.**, ... , Benelli M., and Demichelis F. (2020) Circulating Tumor DNA Profile Recognizes Transformation to Castration-Resistant Neuroendocrine Prostate Cancer, *Journal of Clinical Investigation* | [Full text](#)

Conference papers

Lalchand V.*, Ravuri A.*, **Dann E.***, ... , Teichmann S.A., Lawrence N.D. (2022) Modelling Technical and Biological Effects in scRNA-seq data with Scalable GPLVMs. *Proceedings of the 17th Machine Learning in Computational Biology meeting* | [Full text](#)

Pre-prints

Schuster V., **Dann E.**, Krogh A., Teichmann S.A. (2023) multiDGD: A versatile deep generative model for multi-omics data. *bioRxiv* | [Full text](#) | [python package](#)


Sumanaweera D., Suo C., Muraro D., **Dann E.**, ... , Teichmann S.A. (2023) Gene-level alignment of single cell trajectories informs the progression of in vitro T cell differentiation. *bioRxiv* | [Full text](#) | [python package](#)


Missarova A., **Dann E.**, ... , J.C. Marioni (2023) Sensitive cluster-free differential expression testing. *bioRxiv* | [Full text](#) | [R package](#)


Barnes J. L., He P., ... , **Dann E.**, ... , Teichmann S.A., Meyer K. B., Nikolic M. Z. (2022) Early human lung immune cell development and its role in epithelial cell fate. *bioRxiv* | [Full text](#)

Software

milor |  [MarioniLab/milor](#) | primary developer | R/Bioconductor package for the identification of differential cell abundance in KNN graphs for single-cell data


milopy |  [emdann/milopy](#) | primary developer | python package for the identification of differential cell abundance in KNN graphs for single-cell data

oor_benchmark |  [MarioniLab/oor_benchmark](#) | primary developer | python framework to benchmark workflows for detection of out-of-reference cells in comparative single-cell analysis

genomic-features |  [scverse/genomic-features](#) | primary developer | Genomic annotations using Bioconductor resources in Python.

scverse-tutorials |  [scverse/scverse-tutorials](#) | contributor | tutorials for single-cell omics data analysis in python

single-cell-best-practices |  [theislab/single-cell-best-practices](#) | contributor | open source book on best practices for single-cell genomics data analysis

cell2location |  [BayraktarLab/cell2location](#) | contributor | python package for mapping of tissue cell types via integration of single cell RNA-seq and spatial transcriptomics data

Presentations

Conference oral presentations

Nov 2022 - Machine Learning in Computational Biology conference, virtual
June 2022 - Single Cell Biology conference, Wellcome Genome Campus, Hinxton (UK)
May 2022 - The Biology of Genomes, Cold Spring Harbor Laboratory (US)
Oct 2021 - Chan Zuckerberg Initiative Single Cell Biology Meeting, virtual
Sept 2021 - Next Generation Genomics Meeting, virtual
Mar 2021 - CZI Seed Networks Computational biology meeting, virtual

Invited seminars

Aug 2023 - University of Sri Jayewardenepura single-cell genomics seminar series, virtual
Jul 2023 - Sanofi Precision Medicine & Computational biology, Cambridge (US)
Jun 2023 - Chan Zuckerberg Initiative, Redwood City (US)
Apr 2023 - Cambridge AI club for biomedicine, Milner Institute, Cambridge (UK)
Dec 2022 - UMC Utrecht single-cell genomics meeting, virtual
Sept 2022 - UK Conference of Bioinformatics and Computational Biology, virtual
Jul 2022 - Computational Health Center seminar, Helmholtz Munich (DE)
Apr 2022 - Maxwell Society Annual Conference, King's College London (UK)
Apr 2022 - NYU Langone single cell journal club, virtual
Mar 2021 - Cambridge Center for Physical Biology Single Cell Symposium, virtual

Conference poster presentations

July 2023 - Human Cell Atlas General Meeting, Toronto (CA)
Oct 2022 - Single Cell Genomics conference, Utrecht (NL)
Jun 2021 - Human Cell Atlas General Meeting, virtual

Lab meetings

Aug 2023 - Marson lab @ Gladstone Institutes
Jun 2023 - Shalek lab @ Broad institute of MIT and Harvard
Jun 2023 - Ye lab @ UCSF
May 2023 - Pritchard lab @ Stanford Genetics
Jan 2023 - Theis lab @ ICB Helmholtz Munich
May 2022 - Pe'er lab @ Memorial Sloan Kettering Cancer Center
May 2022 - Satija lab @ New York Genome Center
Apr 2022 - Lawrence group @ Computer laboratory, University of Cambridge

Other meetings and events

Apr 2023 - Scverse community hackathon on software interoperability, Heidelberg (DE)
Dec 2022 - Scverse community hackathon on documentation, Innsbruck (AT)
Apr 2021 - [Open Problems in Single-Cell Analysis Jamboree](#), virtual

Teaching & mentoring experience

Mar 2023 - Introduction to multiomics data integration and visualisation (EMBL-EBI training course) – Instructor for data integration case study

Jul 2022 - Systems biology: From large datasets to biological insight (EMBL-EBI training course) – Instructor for single-cell multi-omics module

Apr 2022 - Advanced topics in Single Cell Genomics (Swiss Institute for Bioinformatics course) – Trainer for multi-omics module

Aug 2021 - Advanced topics in Single Cell Genomics (SciLifeLab / Swiss Institute for Bioinformatics Summer School) – Trainer for multi-omics project

Fall 2021 - PhD rotation student recruitment and mentoring, Teichmann lab

Fellowships & awards

Oct 2019 - Wellcome Sanger Institute PhD studentship (Wellcome Trust, UK)

Jan 2018 - U/Select honours programme and travel grant (Utrecht University, NL)

Oct 2017 - Merit Award for excellent graduates (University of Trento, IT)

Professional service

Conference/workshop organization

Nov 2023 - Scverse hackathon on multi-condition analysis tools, Cambridge (UK) - main organizer

Fall 2023 - [Open Problems Single-cell perturbations Kaggle competition](#) - member of judge panel

Apr 2021 - [Open Problems in Single-Cell Analysis Jamboree](#) - co-organizer

Feb 2020 - [EBI-Sanger-Cambridge PhD Symposium](#) - member of the organizing committee

Outreach

Sanger prize competition - member of the selection panel (Mar 2023)

The Sanger Prize competition funds research internships at Sanger for undergraduate students from LMI countries. I've volunteered as a member of the Grad Panel, evaluating essays from applicants.

Open Wet Lab (OWL) - board member (Oct 2015 – Jan 2018)

OWL is the first biohacking organization in Italy. I was in charge of the association's budget and directed the publication of OWL's blog and scientific outreach articles for local newspapers.

Peer review

Nature Biotechnology (2* papers)

Cell (1* paper)

OUP Bioinformatics (1 paper)

Bioinformatics Advances (1 paper)

Machine Learning in Computational Biology (MLCB)

*Assisting a senior reviewer