

Emma Dann

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Education

PhD in Biological Sciences (Computational Biology) – University of Cambridge, UK (2019-present)

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

M.Sc. in Cancer, Stem Cells and Developmental Biology (Bioinformatics profile) –

Utrecht University, NL (2017-2019)

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

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

Final grade: 110 *cum laude*/110

Professional experience

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

[Teichmann lab](#) / [Marioni group](#) – Computational methods for comparative single-cell analysis of developmental atlases

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

[Huber group](#) – Integrative analysis of multi-omic profiles of perturbations for functional characterization of drug treatments and target discovery.

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

[Van Oudenaarden lab](#) – 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 (2017)

[Demichelis lab](#) – 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 (2016)

Lab equipment maintenance and general support for benchwork.

Software

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

milopy | [emdann/milopy](https://github.com/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

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

SingleCellOpenProblems | [singlecellopenproblems/SingleCellOpenProblems](#) | contributor | A python framework to formalize and benchmark open problems in single-cell genomics data analysis.

Publications

Dann E., Teichmann S.A., Marioni J.C. (2022) Precise identification of cell states altered in disease with healthy single-cell references, *bioRxiv* | [Full text](#) | [code](#) | [python package](#)

Lalchand V.*, Ravuri A.*, **Dann E.***, ... , Teichmann S.A., Lawrence N.D., Modelling Technical and Biological Effects in scRNA-seq data with Scalable GPLVMs. *arXiv* | [Full text](#)

*Equal Contribution

Botting R.A., Goh I., ... , **Dann E.**, ... , Teichmann S.A. , Haniffa M., Multi-organ functions of yolk sac during human early development. *bioRxiv* | [Full text](#)

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

*Equal Contribution

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](#)

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, *bioRxiv* | [Full text](#)

Dann E., Henderson N.C., Teichmann S.A., Morgan M.D., Marioni J.C. (2021) 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 presentations

Single Cell Genomics | Utrecht (NL) | October 2022

Precise disease-state identification with healthy single-cell references (poster presentation)

UK Conference of Bioinformatics and Computational Biology | virtual | September 2022

Mapping the developing immune system across organs (invited talk)

Single Cell Biology | Wellcome Genome Campus, Hinxton (UK) | June 2022

Mapping the developing immune system across organs (selected talk)

The Biology of Genomes | Cold Spring Harbor Laboratory (US) | May 2022

Mapping the developing immune system across organs (selected talk)

Maxwell Society Annual Conference | King's College London (UK) | Apr 2022

Best practices and open challenges in single-cell genomics data analysis (invited talk)

Chan Zuckerberg Initiative Single Cell Biology Meeting | virtual | Oct 2021

Milo: differential abundance testing on single-cell data using KNN graphs (selected talk)

Next Generation Genomics Meeting | virtual | Sept 2021

Differential abundance testing on single-cell data using KNN graphs (selected talk) ([video](#))

Human Cell Atlas General Meeting | virtual | Jun 2021

Mapping human immune system development across fetal organs (poster presentation)

Cambridge Center for Physical Biology Single Cell Symposium | virtual | Mar 2021

Milo: differential abundance testing on single-cell data using KNN graphs (invited talk)

Chan Zuckerberg Initiative Seed Networks Computational biology meeting | virtual | Mar 2021

Milo: differential abundance testing on single-cell data using KNN graphs (short talk)

Other projects

[Multimodal single-cell best practices](#) (2022) | Chapter contributor (compositional analysis)

[Systems biology: From large datasets to biological insight - EMBL-EBI Training](#) (2022) | Instructor for single-cell multi-omics module

[Advanced topics in Single Cell Genomics - SIB course](#) (2022) | Trainer for multi-omics module

[Advanced topics in Single Cell Genomics - Joint SciLifeLab-SIB Summer School](#) (2021) | Trainer for multi-omics project

[Open Problems in Single-Cell Analysis - Spring Jamboree](#) (2021) | Co-organizer and hacker.

EBI-Sanger-Cambridge PhD Symposium (2020) | Member of the organizing committee.

OWL - Open Wet Lab (2015 – 2018) | OWL is the first biohacking organization in Italy. I served as board member and directed the publication of OWL's blog and scientific outreach articles for local newspapers.

Model European Parliament (2012 – 2015) | International simulation of the working of the European Parliament for high school students. I was delegate, committee president and president of the general assembly at many local and international MEP sessions.

Fellowships and awards

4-year Wellcome Sanger Institute PhD studentship (2019-2023)

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

Merit Award - University of Trento (2017)