

# Emma Dann

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## Education

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**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

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**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.

## Publications

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### Key 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](#)

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

**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](#)

## Other

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](#)

Suo C., Polanski K., **Dann E.**, ... , Tuong Z.K., Clatworthy M., Teichmann S.A. (2022) Single cell antigen receptor analysis reveals lymphocyte developmental origins, *bioRxiv* | [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, *Cell* | [Full text](#)

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](#)  
\*Equal Contribution

Botting R.A., Goh I., ... , **Dann E.**, ... , Teichmann S.A. , Haniffa M. (2022) Multi-organ functions of yolk sac during human early development. *bioRxiv* | [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](#)

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](#)


## Software

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**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](https://github.com/MarioniLab/oor_benchmark) | primary developer | python framework to benchmark workflows for detection of out-of-reference cells in comparative single-cell analysis

**scverse-tutorials** |  [scverse/scverse-tutorials](https://github.com/scverse/scverse-tutorials) | contributor | tutorials for single-cell omics data analysis in python

**single-cell-best-practices** |  [theislab/single-cell-best-practices](https://github.com/theislab/single-cell-best-practices) | contributor | open source book on best practices for single-cell genomics data analysis

**cell2location** |  [BayraktarLab/cell2location](https://github.com/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](https://github.com/singlecellopenproblems/SingleCellOpenProblems) | contributor | A python framework to formalize and benchmark open problems in single-cell genomics data analysis.

## Presentations

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### 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

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

### Lab meetings

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

## Posters

October 2022 - Single Cell Genomics conference, Utrecht (NL)  
Jun 2021 - Human Cell Atlas General Meeting, virtual

## Teaching and mentoring experience

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

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

Sept 2021 – Dec 2021 - PhD rotation student recruitment and mentoring, Teichmann lab

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

## Professional service

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### Conference/workshop organization

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

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

### Peer review

Nature Biotechnology (2\* papers)

Cell (1\* paper)

OUP Bioinformatics (1 paper)

Bioinformatics Advances (1 paper)

\*Assisting a senior reviewer

## Fellowships & awards

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

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

Oct 2017 - Merit Award - University of Trento

## Leadership & Outreach

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

Nov 2012 – Apr 2015 - [Model European Parliament](#) | 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.