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.

Publications

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

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

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

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

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

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

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

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

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

Teaching and mentoring experience

Mar 2023 - Introduction to multiomics data integration and visualisation | Instructor for data integration case study

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

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

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

Oct 2015 – Jan 2018 - <u>OWL - Open Wet Lab</u> | 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 - <u>Model European Parliament</u> | 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.