Emma Dann

Wellcome Sanger Institute, Cambridge (UK) | emma.dann@sanger.ac.uk
emdann.github.io | emdann | @emmamarydann

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

Research intern – European Molecular Biology Laboratory, Heidelberg, DE (2018 – 2019)
Huber group – Functional characterization of drug treatments and target discovery with multi-omic screens.

Research intern – KNAW Hubrecht Institute, Utrecht, NL (2017 – 2018)
Van Oudenaarden lab – Biophysical modelling of whole-genome amplification for single-cell bisulfite sequencing.

Research intern – Center for Integrative Biology, University of Trento, IT (2017)
Demichelis lab – Analysis of whole-methylome profiles of tumor samples 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 | primary developer | R/Bioconductor package for differential cell abundance analysis with KNN graphs for single-cell data

milopy | emdann/milopy | primary developer | python package for differential cell abundance analysis with 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

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

Fellowships & awards

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Oct 2019 – Oct 2023 - Wellcome Sanger Institute PhD studentship
Jan 2018 - U/Select honours programme and travel grant - Utrecht University
Oct 2017 - Merit Award - University of Trento

Professional service

Teaching and mentoring experience

Mar 2023 - Introduction to multiomics data integration and visualisation - EMBL-EBI Training (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)
Aug 2021 - Advanced topics in Single Cell Genomics - SciLifeLab-SIB Summer School (Trainer for multi-omics project)
Sept 2021 – Dec 2021 - PhD rotation student recruitment and mentoring, Teichmann lab

Conference/workshop organization

Apr 2021 - Open Problems in Single-Cell Analysis Jamboree | Co-organizer
Feb 2020 - EBI-Sanger-Cambridge PhD Symposium | Co-organizer

Outreach

Oct 2015 – Jan 2018 - OWL - Open Wet Lab | Board member and director of scientific outreach blog

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

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

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

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

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

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

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