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 – 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 | 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

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

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

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* | <u>Full text</u>

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* | <u>Full text</u>

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) (<u>video</u>)

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

<u>Multimodal single-cell best practices</u> (2022) | Chapter contributor (compositional analysis)

<u>Systems biology: From large datasets to biological insight - EMBL-EBI Training</u> (2022) | Instructor for single-cell multi-omics module

<u>Advanced topics in Single Cell Genomics - SIB course</u> (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)