

Emma Dann

📍 Wellcome Sanger Institute, Cambridge (UK) | ✉ emma.dann@sanger.ac.uk
🌐 emdann.github.io | 🔄 [emdann](https://github.com/emdann) | 🐦 [@emmamarydann](https://twitter.com/emmamarydann)

Education

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

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](#) – Statistical methods for comparative meta-analysis of single-cell datasets and exploitation of reference cell 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

SingleCellOpenProblems | [singlecellopenproblems/SingleCellOpenProblems](#) | contributor

Publications

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 [doi:10.1038/s41586-021-03852-1](https://doi.org/10.1038/s41586-021-03852-1)

Jardine L., Webb S., ... , **Dann E.**, ... , Göttgens B., Roberts I., Teichmann S. and Haniffa M. (2021) Intrinsic and extrinsic regulation of human fetal bone marrow haematopoiesis and perturbations in Down syndrome, bioRxiv [doi:10.1101/2021.06.25.449771](https://doi.org/10.1101/2021.06.25.449771)

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 [doi:10.1038/s41591-021-01329-2](https://doi.org/10.1038/s41591-021-01329-2)

Dann E., Henderson N.C., Teichmann S.A., Morgan M.D., Marioni J.C. (2020) Milo: differential abundance testing on single-cell data using k-NN graphs, bioRxiv [doi:10.1101/2020.11.23.393769](https://doi.org/10.1101/2020.11.23.393769)

Kleshchevnikov V., Shmatko A., **Dann E.**, ... , Stegle O., Bayraktar O.A. (2020) Comprehensive mapping of tissue cell architecture via integrated single cell and spatial transcriptomics, bioRxiv, [doi:10.1101/2020.11.15.378125](https://doi.org/10.1101/2020.11.15.378125)

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, [doi:10.1172/JCI131041](https://doi.org/10.1172/JCI131041)

Talks / presentations

Chan Zuckerberg Initiative Single Cell Biology Meeting (Oct 2021)

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

Next Generation Genomics Meeting (Sept 2021)

Differential abundance testing on single-cell data using KNN graphs (selected talk)

Human Cell Atlas General Meeting (Jun 2021)

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

Cambridge Center for Physical Biology Single Cell Symposium (Mar 2021)

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

Chan Zuckerberg Initiative Seed Networks Computational biology meeting (Mar 2021)

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

Other projects

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 / 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)