

# Emma Dann

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## Education

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**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

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**Graduate researcher – Wellcome Sanger Institute, Cambridge, UK** (2019 – present)  
[Teichmann lab](#) / [Marioni group](#) – Statistical methods for comparative meta-analysis of single-cell datasets

**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

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**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

**cell2location** | [BayraktarLab/cell2location](#) | contributor | python package for mapping of tissue cell types via integration of single cell RNA-seq and spatial transcriptomics data

## Publications

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**Dann E.**, Henderson N.C., Teichmann S.A., Morgan M.D., Marioni J.C. (2020) Differential abundance testing on single-cell data using k-nearest neighbor graphs, Nature Biotechnology [doi:10.1038/s41587-021-01033-z](https://doi.org/10.1038/s41587-021-01033-z)

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 [doi:10.1038/s41586-021-03929-x](https://doi.org/10.1038/s41586-021-03929-x)

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)

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)

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

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Chan Zuckerberg Initiative Single Cell Biology Meeting (Oct 2021)  
*Milo: differential abundance testing on single-cell data using KNN graphs* (selected 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

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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

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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)