

# Anna Hutchinson

anna.hutchinson@mrc-bsu.cam.ac.uk; annahutchinson.com; github.com/annahutch

A final year biostatistics PhD student at the University of Cambridge interested in developing statistical methods to improve understanding of human diseases.

## Education

**PhD, MRC Biostatistics Unit, University of Cambridge and GlaxoSmithKline (iCASE Studentship)** (October 2018 – Present)  
“Statistical methods to better understand the genetic basis of complex human diseases”  
Supervised by Dr Chris Wallace and Dr David Willé

**BSc (Hons) in Mathematics and Biology with year abroad, Collingwood College, University of Durham.** (September 2014 - June 2018)  
1<sup>st</sup> Class honours degree in Mathematics and Biology with year abroad at the University of Calgary, Canada.

**A-Levels, Bishop Vesey's Grammar School** (September 2012 – June 2014)  
Mathematics (A\*), Further Mathematics (A\*), Biology (A)

## Research Experience

**“Ovarian-breast cancer causing mutations in white British and Punjabi women”** (July – August 2016)  
Professor Jean-Baptiste Cazier, Centre for Computational Biology, University of Birmingham. Bioinformatics research project to gather information on the frequency of mutations associating with breast and ovarian cancer in Caucasian and Indian populations.

**“Objectifying randomised clinical trials”** (January – May 2017)  
Dr Ying Yan, Department of Mathematics and Statistics, University of Calgary. Part-time research assistant project investigating methods to improve the objectivity of randomised clinical trials, with application to AIDS clinical trial data.

**“Visualising and analysing ‘big’ data”** (October 2017 – June 2018)  
Professor Steve Abel and Dr Sushma Grellscheid, University of Durham. Undergraduate research project examining dimensionality reduction techniques with application to RNA-seq data to study ageing in mice (1<sup>st</sup> class – 78%).

## Publications

Anna Hutchinson, Guillermo Reales, Thomas Willis and Chris Wallace (2021). **Leveraging auxiliary data from arbitrary distributions to boost GWAS discovery with Flexible cFDR.** <https://doi.org/10.1101/2020.12.04.411710> (under review at a peer-reviewed journal)

Anna Hutchinson, Jenn Asimit and Chris Wallace (2020). **Fine mapping genetic associations.** *Human Molecular Genetics*: <https://doi.org/10.1093/hmg/ddaa148>

Boris P.Hejblum, ..., Anna Hutchinson, ..., Annemarie H. Eckes-Shepard (2020). **Realistic and Robust Reproducible Research for Biostatistics.** *Preprint.org*: <https://doi.org/10.20944/preprints202006.0002.v1>

Anna Hutchinson, Hope Watson and Chris Wallace (2020). **Improving the coverage of credible sets in Bayesian genetic fine-mapping.** *PLOS Computational Biology*: <https://doi.org/10.1371/journal.pcbi.1007829>

Christophe Bourges, ..., Anna Hutchinson, ..., James C Lee (2020). **Resolving mechanisms of immune-mediated disease in primary CD4 T cells.** *EMBO Molecular Medicine*: <https://doi.org/10.15252/emmm.202012112>

## Teaching Experience, External Presentations and Awards

Lecturer - *MPhil in Computational Biology, University of Cambridge* (December 2021)  
Delivered lecture for the Genomics module

Supervisor - *Medicine, University of Cambridge* (October 2020 – April 2021)  
Supervised students on the Foundations of Evidence-Based Practice course, Faculty of Biology

“Not-so-credible credible sets” presentation (November 2019)  
*South of England Genetics and Epidemiology Group (SEGEG) Meeting*

“Not-so-credible credible sets” presentation (June 2019)  
*Quantitative Genomics Conference, awarded best long talk*

“Not-so-credible credible sets” presentation (April 2019)  
*Mathematical and Statistical Aspects of Molecular Biology (MASAMB) Conference, awarded best student talk*

## Courses

A variety of bioinformatics training courses offered by the University of Cambridge including: An introduction to solving biological problems with Python, ChIP-Seq and ATAC-seq analysis, Open Targets: Integrating genetics and genomics for disease biology and translational medicine, High Performance Computing: An Introduction, Snakemake workshop and Analysis of mapped NGS data with SeqMonk.

## Other Activities

Programming: Proficient in bash, R and LaTeX (familiar with python and C++)  
Journal peer-reviewer for *Nature*, *Cell Press* and *Genetic Epidemiology*  
PhD Student Representative at MRC Biostatistics Unit (2019-2021)  
Social Secretary at St Catharine's College, University of Cambridge (2019-2021)  
International travel; cooking; private tutoring; board games

## References

Available upon request.