# REGINA H REYNOLDS

Molecular biologist turned bioinformatician, with a passion for systems-level biology, statistics and data visualisation and the application of these to answer biological questions. My current work explores the role of different cell types in neurodegeneration, making use of large-scale genomic and transcriptomic datasets.

View this resume online with links at \_https://rhreynolds .github.io/cv/\_

### **EDUCATION**

2021 2016

#### PhD, Bioinformatics

University College London

O London, UK

- Thesis: Exploring the importance of cell-type-specific gene expression regulation and splicing in Parkinson's disease<sup>1</sup>
- · Integrated transcriptomic data with summary-level genetic association data to investigate the role of cell-type-specific gene expression regulation and splicing in Parkinson's disease.
- Published 3 first/co-first author research articles and 1 first author review. Additionally, regularly collaborated with colleagues, resulting in several middle-author research articles.
- · Successfully secured £10,000 from Signe og Peter Gregersens Mindefond to undertake transcriptional profiling of Parkinson's disease brain tissue.

2016 2014

### MSc, Molecular Biomedicine

University of Copenhagen

• Copenhagen, Denmark

- · Thesis: Changes in the miR-34a-SIRT1 axis in Huntington's disease
- · Grade: A (92.5%)

2013 2010

#### BSc, Molecular Biomedicine

University of Copenhagen

• Copenhagen, Denmark

- Thesis: Pro-apoptotic factors in Huntington's disease: a study in the R6/2 transgenic mouse model
- · Grade: A (96.7%)

### **WORK EXPERIENCE**

Present 2021

#### Research Fellow

University College London

Q London, UK

- · Lead analyst involved in processing and analysing transcriptomic data generated with the aim of identifying molecular signatures of Parkinson's disease progression. Work done primarily using R, nextflow and docker.
- · Co-lead of Code and Pipeline Alignment Working Group in the Aligning Sciences Across Parkinson's initiative. This group aims to maximize the value of data generated from finite post-mortem brain tissues through code alignment, which will enable eventual meta-analysis.

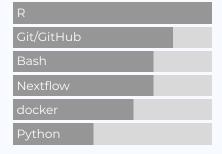
**CONTACT** 

**G** GitHub

in LinkedIn

ResearchGate

## PROGRAMMING LANGUAGES



The long-form version of my CV, with a list of publications, conferences attended and voluntary work is available here.

Made with the R packages datadrivency and pagedown.

The source code is available GitHub.

Last updated on 2022-02-20.

**Research Assistant** 2016 • Copenhagen, Denmark University of Copenhagen 2016 · Ran project exploring the interactions between miR-34a, Sirtl and p53 in a Huntington's disease mouse model, which culminated in a first author publication<sup>3</sup>. **Housing Assistant** 2015 **♥** Copenhagen, Denmark DIS, Study Abroad in Scandinavia, Denmark 2013 · Student assistant involved in general administrative tasks; organisation of bi-annual orientation meeting for hosts/students; and conflict mediation between hosts and students. **TEACHING EXPERIENCE** Subsidiary PhD Supervisor Present **Q** London, UK University College London 2021 · Involved in top-level project planning, providing a second opinion/additional areas of expertise where appropriate. R fundamentals Present **Q** London, UK Clinician Coders 2019 · Developed materials<sup>4</sup> and lead workshops teaching basic R and tidy data principles to clinical academics. **Omics Techniques** 2019 **Q** London, UK King's College London 2017

• Lectured graduate level students on the principles of genome-wide association studies and lead a workshop on how/why to use the

Genotype-Tissue Expression portal.