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

WORK EXPERIENCE

Present | 2022

Lead Bioinformatician

CoSyne Therapeutics — London, UK

- Co-lead of a 4-member team overseeing company-wide bioinformatic analyses across several omics areas applied to drug discovery in glioblastoma multiforme. Influenced strategic decisions on transcriptomics, functional genomic screens and whole genome sequencing.
- Involved in establishing and maintaining robust bioinformatic infrastructure, end-to-end analysis pipelines and coding practices.
- Involved in recruitment efforts for roles in bioinformatics, machine learning, and software engineering.

2022 | 2021

Research Fellow

University College London — 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[1] initiative. This group aimed to maximize the value of data generated from finite post-mortem brain tissues through code alignment, which would enable eventual meta-analysis.
- Published 1 co-first author research article.

2016 | 2016

Research Assistant

University of Copenhagen — Copenhagen, Denmark

- Led project exploring the interactions between miR-34a, Sirt1 and p53 in a Huntington's disease mouse model, which culminated in a first author publication[2].

EDUCATION

2021 | 2016

PhD, Bioinformatics

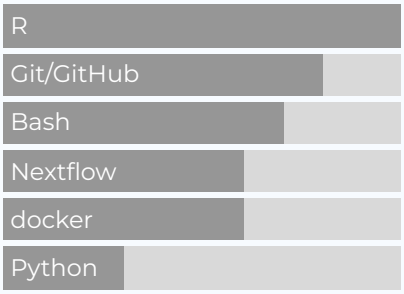
University College London — London, UK

- Thesis: Exploring the importance of cell-type-specific gene expression regulation and splicing in Parkinson's disease[3]
- Integrated bulk-tissue and single-cell 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.
- Successfully secured £10,000 from Signe og Peter Gregersens Mindefond to undertake transcriptional profiling of Parkinson's disease brain tissue.

CONTACT

- rhreynolds@hotmail.co.uk
- GitHub
- LinkedIn
- ResearchGate

PROGRAMMING LANGUAGES



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

Made with the R packages datadrivencv and pagedown.

The source code is available GitHub.

Last updated on 2023-09-09.

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%)

KEY PUBLICATIONS

2023

Local genetic correlations exist among neurodegenerative and neuropsychiatric diseases[4]

NPJ Parkinson's disease

- **Reynolds, RH**, Wagen, AZ, Lona-Durazo, F, Scholz, SW, Shoai, M, Hardy, J, Gagliano Taliun, SA, Ryten, M
- **Role**: Co-first author, lead analyst and corresponding author.
- Analysis[5] of local genetic correlations between neurodegenerative and neuropsychiatric disorders, with the aim of identifying genomic regions and genes that may drive pleiotropy.

2021

Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy body disorders[6]

Acta Neuropathologica

- Feleke, R, **Reynolds, RH**, Smith, A, Tilley, B, Gagliano Taliun, SA, Hardy, J, Matthews, PM, Gentleman, S, Owen , D, Johnson, MR, Srivastava, P, Ryten, M
- **Role**: Co-first author and analyst.
- Transcriptomic analysis[7] of cell-type-specific changes in the Lewy body diseases.

2019

Informing disease modelling with brain-relevant functional genomic annotations[8]

Brain

- **Reynolds, RH**, Hardy, J, Ryten, M, Gagliano Taliun, SA
- **Role**: First author.
- Review of conceptual advances in the generation of brain-relevant functional genomic annotations and among tools that allow integration of these annotations with genome-wide association summary statistics.

2019

Moving beyond neurons: the Role of cell type-specific gene regulation in Parkinson's disease heritability[9]

NPJ Parkinson's disease

- **Reynolds, RH**, Botía, JA, Nalls, MA, International Parkinson's Disease Genomic Consortium (IPDGC), System Genomics of Parkinson's Disease (SGPD), Hardy, J, Gagliano Taliun, SA, Ryten, M
- **Role**: First author and lead analyst.
- Analysis of Parkinson's disease common variation, with the aim of identifying cell types and pathways of importance to disease risk.

A full list of publications is available online at https://rhreynolds.github.io/cv

LINKS

1: https://parkinsonsroadmap.org/research-network/pd-functional-genomics/
2: https://pubmed.ncbi.nlm.nih.gov/29289683/
3: https://discovery.ucl.ac.uk/id/eprint/10119171/
4: https://pubmed.ncbi.nlm.nih.gov/37117178/
5: https://rhreynolds.github.io/neurodegen-psych-local-corr/
6: https://pubmed.ncbi.nlm.nih.gov/34309761/
7: https://rhreynolds.github.io/LBD-seq-bulk-analyses/
8: https://pubmed.ncbi.nlm.nih.gov/31603214/
9: https://pubmed.ncbi.nlm.nih.gov/31016231/