REGINA H REYNOLDS

Molecular biologist turned bioinformatician, with experience translating large-scale omics data into actionable insights for drug discovery. I've led cross-functional analyses across transcriptomics, genomics, and functional screens, collaborating closely across teams to build reproducible pipelines that support impactful R&D decisions. I'm driven by a commitment to scientific rigour, integrity, and transparency — and by a broader desire to make a meaningful contribution to the world through thoughtful, data-driven science.

View this CV online with links at https://rhreynolds.github.io/cv

CONTACT

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

PROGRAMMING LANGUAGES

- R
- Git/GitHub
- Nextflow
- Bash
- docker
- Python

WORK EXPERIENCE

Present | 2022

Lead Bioinformatician

CoSyne Therapeutics — London, UK

- Provide scientific and strategic leadership as co-lead of a 5-person computational biology team, setting research priorities in collaboration with team members, experimental and AI teams, and senior leadership.
- Drive company-wide 'omics initiatives spanning whole-genome sequencing, transcriptomics and CRISPRi screens to support target discovery in glioblastoma multiforme.
- Establish scalable, robust, and reproducible computational workflows through adoption of tools such as Nextflow and Seqera Cloud for workflow orchestration, Docker for containerisation, R targets for reproducible exploratory data analysis, and Cruft templates for project scaffolding.
- Contribute to shaping company culture through active involvement in recruitment and development of CoSyne's personal development framework.

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 performed 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].

Made with the R packages datadrivencv and pagedown.

The source code is available GitHub.

Last updated on 2025-06-15.

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 GWAS summary statistics with bulk/single-cell transcriptomic, eQTL, and chromatin accessibility data to identify cell-type-specific regulatory mechanisms in Parkinson's disease. Methods used included partitioned heritability, COLOC, and MAGMA.
- Applied transcriptomic methods, including cell-type deconvolution, differential splicing analysis, and RNA-binding protein motif analysis, to investigate splicing alterations and their relevance to Lewy body diseases.
- 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.

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%)

TEACHING EXPERIENCE

2025 | 2021

Subsidiary PhD Supervisor

University College London — London, UK

- Secondary supervisor to Dr. Aaron Wagen. Provided support around transcriptomic analyses, bioinformatics workflows and statistical genetics.

2022 | 2019

R fundamentals with Clinician Coders[4]

University College London — London, UK

- Developed materials[5] and led workshops teaching basic R and tidy data principles to clinical academics.

2019 | 2017

Omics Techniques

King's College London — London, UK

- Lectured graduate level students on the principles of genome-wide association studies and led a workshop on how/why to use the Genotype-Tissue Expression portal.

VOLUNTARY WORK

Present | 2018

Peer Reviewer

London, UK

- Reviewer[6] for several scientific journals.

2022 | 2017

Mentor

Social Mobility Foundation

London, UK

- Mentored 4 A-level students looking to work in the field of biomedical research.

KEY PUBLICATIONS

2023

Local genetic correlations exist among neurodegenerative and neuropsychiatric diseases[7]

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[8] of local genetic correlations between neurodegenerative and neuropsychiatric disorders, with the aim of identifying genomic regions and genes that may drive pleiotropy.

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

2021

Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy body disorders[9]

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[10] of cell-type-specific changes in the Lewy body diseases.

2019

Informing disease modelling with brain-relevant functional genomic annotations[11]

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[12]

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.

CONFERENCES

2022 **AD/PD, Alzheimer's & Parkinson's Diseases Conference**
Hybrid event

- Talk: Identifying genetic correlations among neurodegenerative and neuropsychiatric diseases

2021 **Genomics of Brain Disorders**
Virtual event

- Talk: Dysregulation of splicing in human brain from individuals with Lewy body disease informs disease mechanisms

2019 **International Parkinson's Disease Genomics Consortium**
London, UK

- Talk: Pairing bulk and single-nuclear RNA-seq to identify dementia-related pathways in PD

2019 **AD/PD, Alzheimer's & Parkinson's Diseases Conference**
Lisbon, Portugal

- Talk: Mapping Parkinson's disease heritability to specific brain cell types
- Received mention in a blog post on Alzforum[13].

2018 **International Parkinson's Disease Genomics Consortium**
Reykjavik, Iceland

- Talk: Moving beyond neurons: exploring the importance of cell type-specific gene expression in Parkinson's disease

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://www.ucl.ac.uk/school-life-medical-sciences/about-slms/office-vice-provost-health/academic-careers-office/career-schemes/clinician-coders
5: https://github.com/ClinicianCoders/ClinicianCoders
6: https://publons.com/researcher/3017104/regina-hertfelder-reynolds/peer-review/
7: https://pubmed.ncbi.nlm.nih.gov/37117178/
8: https://rhreynolds.github.io/neurodegen-psych-local-corr/
9: https://pubmed.ncbi.nlm.nih.gov/34309761/
10: https://rhreynolds.github.io/LBD-seq-bulk-analyses/
11: https://pubmed.ncbi.nlm.nih.gov/31603214/
12: https://pubmed.ncbi.nlm.nih.gov/31016231/
13: https://www.alzforum.org/news/conference-coverage/expression-expression-expression-time-get-board-eqtls