GRANT NEILSON

Bioinformatician with six years of industry experience analyzing multiple NGS data types, with a specialism in whole genome sequencing (WGS). Highly proficient in R and Python, with a strong track record of developing analytical tools and packages for high-dimensional omics data. Passionate about building robust analytical workflows and contributing to open-source repositories to drive forward scientific research. An articulate and reliable individual with excellent communication skills and a strong track record of effective collaboration across multidisciplinary teams.

🖥 INDUSTRY EXPERIENCE

Senior Computational Biologist

CoSyne Therapeutics   📍 London, UK

2025 | 2023

- Led the end-to-end WGS analysis of 80 primary glioblastoma cell lines, from raw data alignment and QC to comprehensive genetic characterisation (SNVs, SVs, CNVs). Integrated these genomic profiles with CRISPRi screen data, applying advanced statistical models to identify novel genetic dependencies and potential biomarker-target pairs.
- Utilised the NF-Core Sarek pipeline; recognized as a named contributor in version 3.4.1. Optimised the running of the pipeline, achieving a 50% cost reduction and 30% decrease in computational time per sample.
- Executed single-cell CNV (sc-CNV) calling on proprietary perturb scRNA-seq data, identifying sub-clonal populations and contributing to the target identification platform.
- Collaborated with the AI team in aggregating and processing over 25 million cells from publicly available single-cell datasets for the sc-foundation model, led to co-authorship in 2 publications.
- Internal R&D: Responsible for developing an internal container system using Docker and ECR (later handed over to engineering). Author and Lead developer on several internal R and Python packages with responsibilities for maintenance. Established best practices for code development and review. Aided in the development of a project templating system using cruft.

Computational Biologist

Fios Genomics   📍 Edinburgh, UK

2023 | 2020

- Directed projects focusing on high-dimensional omics data types (WES, WGS, scRNA-seq, proteomics), delivering comprehensive analyses and reports for clients.
- Developed in-depth knowledge of statistical methodologies, mastering model selection and fitting techniques, including SVM, elastic net, random forest, and linear/logistic regression, while accounting for covariates.
- Conducted complex regression model analyses for biomarker discovery in bladder and lung cancer.
- Actively contributed to internal R&D by developing and maintaining specialized R packages, enhancing the team's analytical capabilities.
- Led client calls, effectively communicating complex analytical results, ensuring clarity and client understanding.

CONTACT

- ✉ grant.neilson5@gmail.com
- ⓖ GitHub
- in LinkedIn

LANGUAGES

- ® R
- 🐍 Python
- </> Bash
- ⌁ Nextflow

TECHNOLOGIES

- ⓖ GitLab/GitHub
- 🐳 Docker
- aws aws
- ⊞ Azure

Computational Biologist

Complex Diseases Epigenetics group, Exeter Medical School 📍 Exeter, UK

2020
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2019

- Developed novel bioinformatics pipelines for Epigenome/Genome wide association studies, mQTL analysis and quality control of Illumina EPIC array data.
- Took the lead on a project performing EWAS and GWAS analysis in ADHD patients. This involved fitting linear and logistic regression models while accounting for covariates.
- Was selected for a secondment to New York to work at the Mount Sinai medical school as a visiting bioinformatician. This was unfortunately cancelled due to COVID-19.

🎓 EDUCATION

MSCi Biology

University of Southampton 📍 Southampton, UK

2019
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2015

- Grade : First Class Honors
- Winner of the British Society for Immunology Graduate of the year award.
- Recipient of the summer studentship from the Genetics Society (2017).

School

Merchiston Castle Shool 📍 Edinburgh, UK

2015
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2013

- A Levels: Biology, Chemistry, Maths

📖 SELECTED PUBLICATIONS

Multi modal single cell foundation models via dynamic token adaptation

BioRxiv

2025

- Wenmin Zhao, AnaSolaguren-Beascoa, Grant Neilson, Regina Reynolds, Louwai Muhammed, Liisi Laaniste, Sera Aylin Cakiroglu
- Role: Data Preproccessing
- doi: https://doi.org/10.1101/2025.04.17.649387

Detecting cell level transcriptomic changes of Perturb seq using Contrastive Fine tuning of Single Cell Foundation Models

BioRxiv

2025

- Wenmin Zhao, AnaSolaguren-Beascoa, Grant Neilson, Regina Reynolds, Louwai Muhammed, Liisi Laaniste, Sera Aylin Cakiroglu
- Role: Data Preproccessing
- doi: https://doi.org/10.1101/2025.04.17.649395

2021

Novel epigenetic clock for fetal brain development predicts prenatal age for cellular stem cell models and derived neurons

Molecular Brain

- Leonard C. Steg, Gemma L. Shireby, Jennifer Imm, Jonathan P. Davies, Alice Franklin, Robert Flynn, Seema C. Namboori, Akshay Bhinge, Aaron R. Jeffries, Joe Burrage, Grant W. A. Neilson, Emma M. Walker, Leo W. Perfect, Jack Price, Grainne McAlonan, Deepak P. Srivastava, Nicholas J. Bray, Emma L. Cope, Kimberley M. Jones, Nicholas D. Allen, Ehsan Pishva, Emma L. Dempster, Katie Lunnon, Jonathan Mill & Eilis Hannon

2020

Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex

Brain

- Gemma L Shireby, Jonathan P Davies, Paul T Francis, Joe Burrage, Emma M Walker, Grant W A Neilson, Aisha Dahir, Alan J Thomas, Seth Love, Rebecca G Smith, Katie Lunnon, Meena Kumari, Leonard C Schalkwyk, Kevin Morgan, Keeley Brookes, Eilis Hannon, Jonathan Mill
- Role: Data Analysis and Alignment