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 highdimensional 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.

View this CV online with links at https://grantn5.github.io/cv/

CONTACT

grant.neilson5@gmail.com

GitHub

in LinkedIn

LANGUAGES

QR

PVthon

</>
Bash

Nextflow

TECHNOLOGIES

GitLab/GitHub

Docker

aws aws

Azure

INDUSTRY EXPERIENCE

Senior Computational Biologist

CoSyne Therapeutics

O London UK

- · Led the WGS analysis of 80 primary glioblastoma cell lines, and characterised these lines based on their SNV, SV and CNV profiles.
- WGS Analysis: 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.
- Conducted CNV calling on WGS data, this included writing an internal python package for custom analysis.
- · CRISPRi Pipeline Integration and Target Identification: Contributed to incorporating CNV calls into the CRISPRi drop-out analysis pipeline, to identify potential target biomarker pairs.
- 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 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

- · Directed projects focusing on high-dimensional omics data types (WES, WGS, scRNA-seg, proteomics), delivering comprehensive analyses and reports for
- · 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.

Made with the R package pagedown.

The source code is available on github.com/nstrayer/cv.

Last updated on 2025-07-04.

2023

2025

2023

2020

2020 2019

Computational Biologist

Complex Diseases Epigenetics group, Exeter Medical School

Exeter, UK

- · Developed novel bioinformatics pipelines for Epigenome/Genome wide association studies, mQTL analysis and quality control of Illumina EPIC array
- 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

2019 2015

MSCi Biology

University of Southampton

Southampton, UK

- · 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).

2015 2013

School

Merchiston Castle Shool

• Edinburgh, UK

· A Levels: Biology, Chemistry, Maths



SELECTED PUBLICATIONS

2025

Multi modal single cell foundation models via dynamic token adaptation

BioRxiv

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

2025

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

BioRxiv

- · Wenmin Zhao, AnaSolaguren-Beascoa, Grant Neilson, Regina Reynolds, Louwai Muhammed, Liisi Laaniste, Sera Aylin Cakiroglu
- · Role: Data Preprocessing
- 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