

# GRANT NEILSON

Bioinformatician with six years of industry experience analyzing NGS datatypes with a specialism in WGS. An expert in programming with R and Python, have extensively used both languages for analysis of high dimensional omics data as well as developing packages for both languages. A named contributor on the NF- Core Sarek pipeline. Experience working with AWS services such as EC2, S3 and ECR. Have extensively used version control software (GitHub/Lab) and Docker to containerize analysis. An articulate and reliable individual with strong communication skills. This is demonstrated by my achievements and accomplishments to date.

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

## CONTACT

✉ [grant.neilson5@gmail.com](mailto:grant.neilson5@gmail.com)

🐙 [github](#)

in [LinkedIn](#)

## INDUSTRY EXPERIENCE

2025  
|  
2023

### • Senior Computational Biologist

[CoSyne Therapeutics](#)

📍 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.

2023  
|  
2020

### • Computational Biologist

[Fios Genomics](#)

📍 Edinburgh, UK

- 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.

## LANGUAGES

📊 R  
🐍 Python  
📄 Bash  
🔧 Nextflow

## TECHNOLOGIES

📁 Git/GitHub  
🐳 Docker  
📦 aws  
☁️ Azure

Made with the R package [pagedown](#).

The source code is available on  
[github.com/nstrayer/cv](https://github.com/nstrayer/cv).

Last updated on 2025-06-23.

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 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 invited to go on secondment to New York during the summer and work at the prestigious 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 School

📍 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