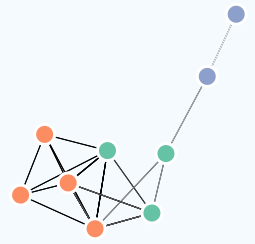


GRANT NEILSON

Bioinformatician with four 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 i.e., Gitlab and Docker to containerize analysis. An articulate and reliable individual with strong communication skills. This is demonstrated by my achievements and accomplishments to date.



INDUSTRY EXPERIENCE

2025
|
2023

Senior Computational Biologist

CoSyne Therapeutics

📍 London, UK

- Led WGS Analysis for GBM Cell Lines: Spearheaded the WGS analysis of 80 primary glioblastoma cell lines, and characterised these lines based on their SNV, SV and CNV profiles.
- NF-Core Sarek Pipeline Expertise: 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.
- CNV Analysis: 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, and identified potential targets.
- Single-Cell CNV Analysis and Sub-Clonal Identification: Executed single-cell CNV (sc-CNV) calling on proprietary perturb scRNA-seq data, identifying sub-clonal populations and contributing to the target identification platform.
- Collaboration with AI Team on Single-Cell Dataset Processing: Aided the AI team in aggregating and processing over 25 million cells from publicly available single-cell datasets for the sc-foundation model.

View this CV online with links at grantneilson.me/cv/

CONTACT

✉ grant.neilson5@gmail.com

🐙 [github](#)

in [LinkedIn](#)

LANGUAGES

📊 R

🐍 Python

📄 Bash

TECHNOLOGIES

🔧 nextflow

🔄 Git/GitHub

🐳 docker

🌐 aws

☁️ azure

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

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

Last updated on 2025-06-19.

2023
|
2020

Computational Biologist

Fios Genomics

📍 Edinburgh, UK

- Omics Data Analysis and Client Reporting: Directed projects focusing on high-dimensional omics data types (WES, WGS, scRNA-seq, proteomics), delivering comprehensive analyses and reports for clients such as Genentech, Zai Lab, and Syngenta.
- Advanced Statistical Analysis Proficiency: 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.
- Biomarker Discovery for Critical Health Indicators: Executed complex regression model analyses for biomarker discovery in bladder and lung diseases, contributing significantly to understanding these conditions.
- Client Communication and Results Presentation: Led client calls, effectively communicating complex analytical results, ensuring clarity and client understanding.
- Project Scoping and Strategy Advisory: Scoped projects and provided strategic advice to clients on leveraging public and private datasets, requiring extensive knowledge of statistical methods and quick, problem-solving capabilities.
- Contribution to Internal R&D and R Package Development: Actively contributed to internal R&D by developing and maintaining specialized R packages, enhancing the team's analytical capabilities.

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

Education

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 & Elis 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, Elis Hannon, Jonathan Mill
- Role: Data Analysis and Alignment