



Bioinformatician/Computational Biologist

About SAGC

The South Australian Genomics Centre (SAGC) is a multi-institutional, national genomics and bioinformatics facility that is supported by Bioplatforms Australia (BPA) through the Australian Government's National Collaborative Research Infrastructure Strategy (NCRIS). The SAGC has consolidated genomics and bioinformatics expertise in the state, with a group of ~10 genomics and bioinformatics staff working side-by-side to deliver innovative genomics and bioinformatics solutions across all areas of genomics research, including agriculture, healthcare and ecology.

About the Role

An exciting opportunity now exists for an experienced (Level B) post-doctoral bioinformatician/computational biologist to join the SAGC bioinformatics team. To flourish in this role, you will need to be able to thrive in a fast-paced environment, work across multiple different projects and to possess excellent organisational and time-management skills.

As an experienced bioinformatician you will have a deep understanding of at least one area of bioinformatics and have the ability to work independently and support junior members of the team to reach their full potential. You will have a sound understanding of software and workflow development best practices such as source control, test driven programming and continuous integration/deployment. Staff are expected to enable research by leading the development of reproducible, standardised pipelines for genomics data analysis and, where necessary, new methods and pipelines. Your career development will be supported and you will be encouraged to publish your research and to collaborate on major funding applications to NHMRC, ARC or MRFF.

The role requires a significant amount of face-to-face time with clients to scope out projects, communicate findings over the course of a project, and present a final report. In addition, you will lead hands-on training workshops, in your area of expertise, to teach attendees how to extract maximum value from their data.

Key Responsibilities

- Provide end-to-end bioinformatics analysis support to SAGC clients
- Develop and publish new bioinformatics software and resources that supports SAGC researchers
- Develop reproducible analytical workflows with a view to improve internal efficiencies as well as client experiences and to add new SAGC service offerings
- Contribute or lead the drafting of reports and publications relating to your work
- Contribute or lead the development of competitive funding applications to NHMRC, ARC, MRFF or other funding agencies
- Contribute to the development and organisation of hands-on training workshops



Essential Criteria

- PhD or equivalent experience, in either bioinformatics, computer science, physics, statistics or other relevant discipline
- Post-doctoral experience in research, industry or bioinformatics support role
- Have a broad understanding of several of the following areas and a deep understanding in at least one:
 - **Transcriptomics:** bulk RNAseq, scRNAseq, spatial transcriptomics
 - **Genomics:** variant, haplotype and diversity analysis, genome assembly, metagenomics, epigenetics
 - **DevOps:** version control, test driven development and continuous integration, containerisation using Docker/Singularity
 - **Systems biology:** multi-omics data integration, statistics
 - **Statistics:** linear models, ANOVA, hypothesis testing
 - **Visualisation:** data visualisation and User Interface/Experience design
 - **Workflow systems:** Snakemake and/or Nextflow
 - **Other omic's technology:** metabolomics, proteomics
- Prior experience working in biomedical, agricultural or environmental research
- Prior experience with at least two of the following scripting languages: bash, R, Python and Perl
- A highly collaborative person, a strong team player and an excellent communicator
- Ability to work in an organised, methodical way and to manage multiple ongoing projects
- Attention to detail and a desire to understand a project and the intricacies of the data analysis
- Prior experience working in a high-performance computing environment

Desirable Criteria

- Prior experience working in a client-oriented bioinformatics role
- A strong publication track record in high impact journals, patents etc
- Experience applying for and attracting funding
- Experience with programming languages such as C/C++, Go, Rust, Java
- Prior experience developing and delivering hands-on bioinformatics training
- Working in a cloud computing environment
- Linux systems administration