



Postdoctoral Bioinformatician in Single Cell and Spatial Omics Data Analysis

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. In 2021, the SAGC was designated as a 10x Genomics Reference Site in spatial transcriptomics and is making significant new investments to develop and apply these technologies.

About the Role

An exciting opportunity now exists for an experienced (Level B) post-doctoral bioinformatician/computational biologist to join the SAGC bioinformatics platform. To flourish in this role, you will already have a deep understanding of single-cell transcriptomics data analysis and have at least a keen interest, if not existing experience, in the application of spatial transcriptomics and/or other spatial omics approaches to biomedical research questions.

As an experienced bioinformatician you will work with a relatively high degree of independence in the area of single cell and spatial omics data analysis. Single cell and spatial omics technologies available to us include the Chromium X, Visium, STomics, and NanoString technologies and we are actively collaborating with other researchers and facilities who are developing other spatial omics methods (e.g. spatial lipidomics and metabolomics).

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 single cell and spatial data analysis as well as the development of new methods, pipelines and data visualisation tools. Your career development will be supported and you will be encouraged to publish your research and to collaborate/lead major funding applications to NHMRC, ARC or MRFF.

This role requires the successful candidate to be a team player with excellent communication skills. You will also contribute to the SAGC's education and outreach activities by leading hands-on training workshops.



Key Responsibilities

- Provide end-to-end bioinformatics analysis support to our collaborators working in the single cell or spatial omics fields.
- Develop and publish new bioinformatics pipelines, software and resources that advance capabilities in single cell and spatial omics data analysis.
- Lead the writing 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.
- Ensure successful transfer of knowledge to other members of the SAGC bioinformatics team.

Essential Criteria

- PhD or equivalent experience, in either bioinformatics, computer science, physics, statistics or other relevant discipline
- Post-doctoral experience in a research, industry or bioinformatics role
- Have a deep understanding of single-cell transcriptomics data analysis
- Prior experience with, or a keen interest in, spatial transcriptomics data analysis - particularly the Visium, STomics and NanoString technologies
- Have a broad understanding of several of the following areas
 - **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 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
- To satisfy SAHMRI policies around vaccinations, particularly for COVID-19

Desirable Criteria

- Prior experience working in a biomedical context
- A strong publication track record in high impact journals, patents etc
- Prior experience developing and delivering hands-on bioinformatics training