



Candidate Information

Position:	Research Fellow (Colorectal Cancer Analytics Tool Development)
School/Department:	Centre for Cancer Research and Cell Biology
Reference:	20/108284
Closing Date:	Thursday 20 August 2020
Salary:	£33,797 per annum
Anticipated Interview Date:	Tuesday 1 September 2020
Duration:	Available until 31 July 2022

Job Purpose

Available from 1 January 2021 as part of a CRUK-Booby Moore Foundation funded Programme Grant "Impact of chemotherapy on anti-cancer immunity in molecular-stratified subgroups of colorectal cancer", working within the Functional Genomics and the Cell-Death groups, led by Dr Simon McDade and Prof Dan Longley as part of our internationally renowned colorectal cancer (CRC) research team based in the Patrick G Johnston Centre for Cancer Research at Queen's University Belfast .

Next Generation Sequencing technologies have driven a boom in Bioinformatics 'big data' over the last decade. Accessing much of the data requires significant computational skills, is time-consuming, hard to reproduce and share. To address this bottleneck we have developed suite suite of customisable applications using the R based wrapper, Shiny, built on a combination of novel and established analytics. These applications simplifies analysis and visualisation of genomics data to enable biologists, clinicians to rapidly iteratively interrogate genomics data and share analyses and insights in a robust supervised analysis framework.

The research fellow will develop a suite of bespoke CRC specific applications that will enable analysis of a broad range of in-house and publicly available CRC genomics and functional data to enable rapid interactive annotation, integration, visualisation, analysis and sharing. The wealth of data (including genomics, CRISPR screens, drug sensitivity and patient outcomes) incorporated into these resources, will in turn be leveraged by the research fellow to identify genetic or treatment induced targetable vulnerabilities (particularly those linked to p53/KRAS status, cell death and immunity) in molecularly defined sub-groups of CRC.

Applicants will therefore be expected to have significant experience working in the R/Shiny environment as well as using next-generation sequencing technologies (NGS). The successful candidate will also be expected to also provide organisational support to the programme, in terms of storage and analysis of data, and presentation of results. They will become an integral member of a dynamic, collaborative and well-equipped research group that puts a strong focus on interdisciplinary functional genomics driven research. The post holder will be expected to liaise strongly with the team leaders, learn and be familiar with appropriate techniques; as well as providing organisational support to the programme, in terms of storage and analysis of data, and presentation of results. Our group provides a stimulating research environment where collaboration and development of new ideas is strongly encouraged, alongside support for career development for emerging talents.

Main Activities and Responsibilities

1. Shiny application development and implementation on externally accessible servers
2. Development of bespoke workflows for downstream analysis of Genomics data
3. Pipelined genomics data analysis (RNA-seq, ChIp-seq, exomes, CRISPR-Screens etc.)
4. Lab support for Genomics within the programme (e.g. Library preparation and RNA seq/NGS analysis)
5. Development and support for data storage and archiving strategy and databases
6. Website development and management
7. Development of SOPs for data analysis workflows
8. Comply with health and safety procedures affecting self and others and ensure the work area is clean and safe at all times
9. Carry out all of the above according to the existing procedures and SOPs, including the laboratory rules related to laboratory accreditation, maintaining accurate records of results in a manner that will enable them to be accessed and interpreted

Planning and Organising

1. Ensure all genomics data and workflows are available so that work can proceed as scheduled.
2. Development implementation of new genomic workflows and Shiny applications.

3. Development and management of SOPs.

Resource Management Responsibilities

1. Responsibility for development and management of computational infrastructure.
2. Manage all shiny applications and underlying servers.
3. Website development and management.
4. To supervise students and staff and assist in their bioinformatics analyses and training.

Internal and External Relationships

1. Daily contact with supervisors, work colleagues and other members of staff.
2. Frequent contact with software and hardware sales representatives and maintenance engineers.
3. Attendance and involvement at seminars and research meetings as required.

Essential Criteria

1. Have or be in preparation for submission of a PhD in molecular cancer biology, computational biology, bioinformatics or related discipline.
2. 3 years relevant computational experience with genomic data analysis, to include NGS alignment pipeline development and implementation in high-performance computing cluster and downstream NGS analysis workflow development.
3. Significant experience in development of R/Shiny applications for genomics data analysis, integration and sharing.
4. Experience of working with Linux/UNIX and high performance computing environments.
5. Publication of peer-reviewed papers that include a component of bioinformatics analysis.
6. Relevant NGS laboratory experience (e.g. RNA-seq, ChIP-seq etc.)
7. Sufficient breadth or depth of specialist knowledge in the discipline and of research methods and techniques to work within colorectal cancer research.
8. Knowledge of relevant Health and Safety issues and of COSHH regulations.
9. Good communication and interpersonal skills.
10. Be capable of using own initiative.
11. Ability to work in a team and as an individual.
12. Ability to plan own work schedule responding to new pressures and adjusting priorities.

Desirable Criteria

1. Experience with high-throughput RNA-seq analysis methodologies.
2. Experience with single-cell genomic analyses.
3. Proficiency with perl, python, bash and/or equivalent languages.
4. Understanding of cancer datasets.