University of Nottingham
UK | CHINA | MALAYSIA

ROLE PROFILE

Job Title: Research Associate/Fellow (Bioinformatician)

School/Department: School of Life Sciences

Job Family and Level: Research and Teaching Level 4

Contract Status: Fixed to 31st December 2018

Hours of Work: Full time, 36.25

Location: Deep Seq Lab, D106, Medical School

Reporting to: Dr Matt Loose

Purpose of the Role:
The post holder will have responsibility for the analysis of Next Generation Sequencing data sets which have been primarily produced within the Deep Seq facility. This will include the use and creation of pipelines and tools to enable accurate and timely data analysis. The role holder will provide appropriate support and advice to facility customers to allow them to make full use of their data. Therefore the person appointed should be able to communicate effectively on both a biological and bioinformatics level. The role holder is expected to plan and conduct their own work using available software and tools, to modify methodologies and scripts and to create new pipelines and tools as required. The successful applicant will be responsible for writing up their work for the production of end user summaries or for their own publications. The facility currently houses Illumina MiSeq and NextSeq technologies and is an early access user of minION nanopore sequencing devices. The post holder should have broad knowledge of these technologies alongside previous generation sequencing methods such as 454 and SOLiD.

The person appointed will have the opportunity to develop their bioinformatics skills in a highly diverse and rapidly evolving setting as well as the ability to use their extensive scripting and coding skills to develop research tools and extend their bioinformatics portfolio.

	Main Responsibilities
1.	To manage and analyse data from in-house Next Generation sequencing machines and present the results in various formats according to the requirements of the end user and within a specified time-frame. The role holder will be able to lead on these analyses, using available softwares, or by creating novel pipelines and tools to enable efficient use of facility time and to produce accurate and comprehensive results.
2.	To providing appropriate support and advice to facility end users to allow them to make full use of their data, communicating on both a biological and informatics level.
3.	To read relevant scientific literature in order to plan and conduct analyses according to recognised approaches, methodologies and techniques.
4.	To work closely with facility staff to ensure the optimal experimental design and outcomes are obtained for facility customers.
5.	To prepare figures and data for manuscripts including publications.
6.	To write up research work for publication and/or present at national/international conferences.
7.	To provide support and guidance to staff and students within the school where appropriate in own

	area of expertise.
8.	To effectively plan and manage workloads.
9.	Any other duties appropriate to the grade and role

Knowledge, Skills, Qualifications & Experience

	Essential	**Desirable**
Qualifications/ Education	PhD (or close to completion) in a bioinformatics or relevant computational related field. OR an equivalent professional qualifications in a bioinformatics/ computational field. Or an MSc and high levels of experience of varied Next Generation Sequencing data analysis.	PhD in Bioinformatics or a relevant computational discipline with subsequent work experience of varied Next Generation Sequencing data analysis.
Skills/Training	Excellent knowledge of at least one scripting or coding language (e.g, Perl, Python, C++, Java) Excellent IT skills. Use of Linux operating systems. Excellent knowledge of NGS. Excellent oral and written communication skills, including the ability to communicate with clarity on complex information. Ability to analyse and illuminate data, interprets reports, evaluate and criticise texts and bring new insights to current methodologies. Ability to creatively apply relevant research approaches, models, techniques and methods. Good organisational skill.	Excellent knowledge of multiple scripting or coding languages. Knowledge of Linux System Admin. An excellent understanding of molecular biology. An excellent understanding of mathematics including statistics and algorithms and their role in relevant NGS analysis tools. Excellent understanding of version control and software repositories.
Experience	Experience with sequence search matching and alignment algorithms. Experience with database production of large datasets. Experience of genome annotation pipelines, strong knowledge of enseml, gbrowse etc. Experience of using NGS datasets. Evidence of working to strict deadlines and finishing projects as directed.	Experience of constructing pipelines for managing and analysing large amounts of NGS sequencing data. Experience of analysing and managing data from multiple sequencing platforms.

Statutory/Legal		

Additional Information

The role will be based in the University of Nottingham's Next Generation Sequencing Facility, Deep Seq, which is led by Dr Matt Loose. The person appointed will be part of a dedicated team which is in place to help staff and students with production of high quality NGS data sets and analysis. As part of the facility there will be ample opportunities to improve skills and learn new techniques, as well as to contribute to publishable research.

Athena SWAN Silver Award

The University of Nottingham strongly endorses Athena SWAN principles, with commitment from all levels of the organisation in furthering women's careers. It is our mission to ensure equal opportunity, best working practices and fair policies for all.