Nanopore RNA-Seq data analysis for characterising transcriptome malleability

This project is one of a number that are in competition for funding from the South West Biosciences Doctoral Training Partnership (SWBio DTP) which is a BBSRC-funded PhD training programme in the biosciences, delivered by a consortium comprising the Universities of Bath, Bristol, Cardiff and Exeter, along with the Rothamsted Research Institute. The partnership has a strong track record in advancing knowledge through high quality research and teaching, in collaboration with industry and government.

Studentships are available for entry in September/October 2019.

All SWBio DTP projects will be supervised by an interdisciplinary team of academic staff and follow a structured 4-year PhD model, combining traditional project-focussed studies with a taught first year which includes directed rotation projects.

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Co-supervisor: Prof Samuel Sheppard (University of Bath)

Collaborators: Prof Mark Robinson (University of Zurich), Dr Charlotte Soneson (University of Zurich)

Project description

The human transcriptome is highly malleable with alternative mRNA splicing for example playing a key role in regulating the vast complexity observed. However, while Illumina-sequencing can for example identify individual mRNA alternative splice sites comprehensively and accurately, reconstruction of this information into true mRNA transcript isoforms remains problematic. An additional important feature of biologically-important transcriptome malleability is covalent modification, such as methylation, that can be made to ribonucleotides within cellular RNAs. Surveys of the 'epitranscriptome' however currently rely on complex library preparation protocols and ultimately sequencing via a DNA intermediate, meaning that identification of RNA modification sites can currently be prone to error.

The aforementioned problems can potentially be solved by sequencing native RNA strands using Oxford Nanopore-based sensing. The method enables full-length RNAs to be sequenced in a single pass, meaning that reconstruction of short sequence reads is unnecessary, and thus quantification of alternative transcript isoforms may be achieved much more unequivocally. As Nanopore-sequencing works by making measurements that depend directly on the biophysical properties of each RNA ribonucleotide, the presence of covalent modifications can also be made directly thus potentially allowing for accurate and reliable mapping of the epitranscriptome.

The bioinformatics-based PhD project will focus on performing computational analysis of Nanopore native RNA sequencing data generated in our laboratory, in order to characterise various aspects of transcriptome malleability including mRNA splicing patterns and covalent modifications. A Master's degree or some equivalent (professional placement etc.) in bioinformatics analysis of RNA-Seq data is a prerequisite for this post.

Funding

Studentships provide funding for a stipend at the standard UKRI rate (currently £14,777 per annum, 2018/19 rate), research and training costs and UK/EU tuition fees for 4 years.

UK and EU applicants who have been residing in the UK since September 2016 will be eligible for a full award; a limited number of studentships may be available to EU applicants who do not meet the residency requirement. Applicants who are classed as Overseas for tuition fee purposes are not eligible for funding.

Applications

Applicants must have obtained, or be about to obtain, a First or Upper Second Class UK Honours degree, or the equivalent qualifications gained outside the UK, in an appropriate area of science or technology.

Applications should be submitted on the University of Bath's online application form for a PhD in Biosciences. Please ensure that you quote the supervisor's name and project title in the 'Your research interests' section. You may apply for more than one project if you wish but you should submit a separate personal statement relevant to each one.

The deadline for the receipt of applications is Monday 3 December 2018.