

Research Role Profile

Job Title:	Research Assistant in Multiomic Data Analysis
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Responsible to:	Head of research group, or principal investigator
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Responsible for:	There is no direct supervisory responsibility
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Job Summary and Purpose:
To support research activity in accordance with specified research project(s) under the supervision of the principal investigator

Main Responsibilities/Activities
<p>To support a research team by contributing to the planning of research projects and undertaking prescribed research tasks in accordance with specified research project(s), making use of standard research techniques and methods. These may include fieldwork, interviews, laboratory experimentation, computer-based data analysis or library research as directed by the research award holder and will entail co-ordinating own work with that of others to avoid conflict or duplication of effort. Analysing and interpreting results of own research, under the guidance of research award holder or supervisor. Write up results and contribute to the preparation of papers for submission to appropriate journals and conferences, and other outputs as required and/or appropriate. Attend appropriate conferences for the purpose of disseminating research results of personal development.</p> <p>Continually update knowledge and develop skills</p> <p>To carry out routine administrative tasks associated with a specified research project, for example risk assessment of research tasks, organisation of project meetings and documentation. This will entail planning own day-to-day research activity within the framework of the agreed programme, dealing with problems that may affect the achievement of research objectives and deadlines and implementing procedures required to ensure accurate and timely formal reporting and financial control</p> <p>Demonstrating, or occasionally assisting with undergraduate supervision within the post holder's area of expertise and under the direct guidance of a member of the Faculty academic staff.</p>

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Person Specification

The post holder must have:

A first degree or a professional qualification or equivalent in a relevant subject.

At least part-completed a relevant doctoral degree or have relevant experience in a given field.

Whilst there is no requirement for previous work experience, the post holder will be expected to be able to support research activities by performing experiments and/or undertaking studies and analysing/ interpreting results.

Relationships and Contacts

Direct responsibility to the principal investigator or academic supervisor.

Special Requirements

To be available to participate in fieldwork as required by the specified research project.

All staff are expected to:

- Positively support equality of opportunity and equity of treatment to colleagues and students in accordance with the University of Surrey Equal Opportunities policy.
- Help maintain a safe working environment by:
 - Attending training in Health and Safety requirements as necessary, both on appointment and as changes in duties and techniques demand
 - Following local codes of safe working practices and the University of Surrey Health and Safety Policy
- Undertake such other duties within the scope of the post as may be requested by your Manager.

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Addendum

This document provides additional information relating to both specific aspects of the post/faculty and any post specific person specification criteria. The information contained within this document should always be read in conjunction with the accompanying generic Job Purpose.

Job Title:

Research Assistant in Multiomic Data Analysis

Background Information/Relationships

As part of the British Heart Foundation project focussed on omics approaches to identify regulators of vascular remodelling in pulmonary hypertension, we offer an exciting postdoctoral position at the Faculty of Health and Medical Sciences, University of Surrey, to work within the group of Prof Inga Prokopenko, PhD and within the Section of Statistical MultiOmics as well as within the People-Centred AI institute. This role will focus on large-scale multiomic data analyses available for the large UK-based study for pulmonary hypertension with major focus on epigenome-wide association study (EWAS) analyses and combining of such information with proteomic data, clinical characteristics and other layers of data.

We are seeking candidates with expertise in an area pertinent to the project and experience in advanced statistics, machine learning, data integration, software development, sensor/wearable/mobile data, programming using C++/Python, and/or biomedical informatics. The successful candidate is expected to be able to organise his/her work with minimal supervision and prioritise work to meet deadlines of the project. Due to active collaborative interaction within this project, advanced oral and writing English knowledge are required.

Pulmonary arterial hypertension (PAH) is a rare condition characterised by pulmonary vascular remodelling leading to premature death from right heart failure. We performed a pilot study of blood DNA methylation analysis of PAH patients from a UK PAH Cohort. We gained access to available data from further controls from two distinct studies using the same Illumina IScan-EPIC 800k array chip, with analyses indicating baseline associations between methylation status and PAH diagnosis. One of the lead candidates is a CpG near the CTSZ gene, encoding a lysosomal cysteine proteinase cathepsin Z expressed ubiquitously in cancer cell lines and multiple tumours, which can interact with integrin- β 3 activating FAK/Src signalling. How DNA methylation patterns alter over time in response to therapy and in other forms of PH has yet to be established.

The data from serially sampled PAH patients will allow analyses of the relationship between dynamic changes in DNA methylation status and clinical phenotypes as detailed above. We will further expand the DNA methylation analyses to other forms of PH (e.g. secondary to lung disease, heart failure or thromboembolism) using 100 disease controls and 300 PH patients of mixed aetiologies using the established pipelines (The CPACOR pipeline - published by Lehne et al. was used

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for the processing on genome build GRCh37/hg19, quality control (QC) and normalization of the raw methylation data). Such an expanded EWAS analysis would allow the determination of the specificity of identified changes to PAH and further the definition of methylation patterns identifying and co-occurring in other presentations of PH.

A Research Fellow is required to work alongside the Surrey's Project Lead (Prof Inga Prokopenko), other research fellows and academic staff already engaged with the project, and a unique blend of researchers who are developing analytical algorithms and tools for predictive modelling of individual-specific health and disease with the potential to transform health and healthcare, and those with a deep understanding of healthcare systems and of the methodological steps needed to evaluate digital health interventions at every stage of the implementation cycle.

Person Specification

This section describes the sum total of knowledge, experience & competence required by the post holder that is necessary for standard acceptable performance in carrying out this role. This is in addition to the criteria contained within the accompanying generic Job Purpose.

Qualifications and Professional Memberships	Essential/ Desirable
A higher research degree (PhD) (or near completion) in a relevant subject	Desirable
Technical Competencies (Experience and Knowledge) This section contains the level of competency required to carry out the role (please refer to the competency framework for clarification where needed and the Job Families Booklet).	Essential/ Desirable
Experience of genome-wide genetic data analysis	Essential
Experience and proficiency in standard data modelling packages	Essential
Proficiency in working in UNIX, and R environment	Essential
PhD in genetics, statistics or a closely related discipline, or equivalent research, industrial or commercial experience	Desirable
Experience of methylation data analysis approaches	Desirable
Experience of proteomic data analyses	Desirable
Experience of whole-genome sequencing data quality-control and analysis	Desirable
Experience of working with large-scale epidemiological datasets	Desirable

Key Responsibilities

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This document is not designed to be a list of all tasks undertaken but an outline record of any faculty/post specific responsibilities. This should be read in conjunction with those contained within the accompanying generic Job Purpose.

1. Perform standard analyses of large-scale epigenomic and multiomic datasets by developing analytical procedures using standard programming languages, including R, C++, Java, Python
2. Implement and test analytical pipelines for high-dimensional omic datasets
3. Analyse and validate results from epigenomic and multiomic datasets
4. Contribute to the writing and submission of high-quality scientific papers and write reports for submission to research sponsors
5. Deliver scientific presentations to the research section and externally at national and international scientific conferences
6. Help with day-to-day technical supervision and pastoral care of junior students and researchers and take responsibility for own research
7. Contribute intellectually and analytically to the research project
8. Develop a personal programme of research, developing research proposals and funding bid and being successfully awarded them.

N.B. The above list is not exhaustive.