



ROLE PROFILE

Job Title: Research Associate/Fellow in advanced statistical modelling and machine learning applied to epidemiology of bacterial infection and antimicrobial resistance

School/Department: School of Veterinary Medicine and Science

Job Family and Level: Research & Teaching Level 4

Contract Status: Fixed-term until 31 December 2021

Hours of Work: Full-time: 36.25

Reporting to: Dr Tania Dottorini

Location: Sutton Bonington Campus

Project:

FARM WATCH: Fight AbR with Machine learning and a Wide Array of sensing TeCHnologies.

Main duties and responsibilities:

1	To conduct research at the highest level in accordance with the aims and objectives of the project and produce useful outputs of impact that lead to peer-reviewed publications of international quality.	80%
2	To contribute to research supervision and training of undergraduates and postgraduates, and to contribute to the development of the research group and the School.	5%
3	To operate as an effective team player within the group and to be accountable to the line manager on the progress and daily running of the project.	5%
4	To contribute to administrative work related to the research group.	5%
5	To update professional skills as appropriate and relevant in support of research excellence.	5%

Knowledge, Skills, Qualifications & Experience:

	Essential	Desirable
Qualifications/ Education	<p>PhD (or very close to completion). Preferably in epidemiology or data science.</p> <p>Alternatively, PhD (or very close to completion) in statistics, mathematics, machine learning, computational biology.</p>	<p>Covered post-doctoral position in epidemiology or data science</p> <p>Preferably with applications in microbiology or AMR</p>
Skills/Training	<p>In-depth expertise in the use of advanced statistical modelling and machine learning for data analysis in biological problems, preferably related to epidemiology of infectious diseases and antibacterial resistance including genome sequence data.</p> <p>Strong programming skills in a suitable language (e.g. Matlab, Python, R. etc)</p>	<p>Expertise in the use of deep learning</p> <p>Expertise in the development of diagnostics or forecasting tools</p> <p>Expertise in the development of surveillance/monitoring solutions for infectious diseases</p> <p>Expertise in the use of advanced statistical modelling and machine learning</p>

		for the analysis of bacterial whole genome sequencing data and metagenomic data
Experience	Evidence of publications in any of the essential or preferable listed subjects	<p>Post-doctoral research experience</p> <p>Experience of working in a multidisciplinary team</p> <p>Experience of collaboration within research projects dealing with antimicrobial resistance in humans and animals, epidemiology of zoonotic infections.</p>
Personal Attributes	<p>Commitment to delivering the aims of the project in the epidemiology of bacterial infections and antimicrobial resistance</p> <p>Ability to work to deadlines and prioritise tasks</p> <p>Highly motivated, able to work independently, as well as highly effectively in interdisciplinary teams.</p> <p>Excellent written and oral communication and presentation skills in English</p>	

Project Summary:

We are seeking an excellent research associate/fellow to join an exciting new awarded project dealing with antibacterial resistance (ABR) in humans and animals. The aim of this project is to understand the epidemiologic pathways underlying the insurgence and propagation of bacterial infection and antimicrobial resistance (AMR) in poultry (chicken) farming, with zoonotic transfer to the human population. We aim to improve diagnostic capabilities for the detection of infections and AMR to support treatment selection and to implement surveillance.

Overuse of antibiotics in intensive farming has been accompanied by increased appearance of antibiotic resistance (ABR) and zoonotic transfer to humans via direct contact, environmental contamination and food consumption. Understanding of the epidemiological pathways of infection, gained through the quantitative evidence on sources and transmission routes, is key for prevention and control. The project aims at large-scale collection of data and statistical modelling/data mining powered by machine learning and cloud computing. Such knowledge will be used for the development of effective and rapid diagnostic tools to predict and detect bacterial infection, insurgence of ABR, and zoonotic transfer to humans, by combining heterogeneous information collected from human, animals and environment.

The successful candidate will work closely with an interdisciplinary and international team of academics and industrial partners. The project offers a unique combination of expertise in machine learning, statistical and mathematical modelling, bioinformatics, sequencing, cloud computing, microbiology, infection control, food safety, surveillance, epidemiology.

The successful applicant will use advanced statistical modelling, data mining and machine learning to reconstruct the epidemiological pathways (sources and transmission routes) of infection and ABR, and will identify signature patterns for early detection of outbreaks in humans and animals. This will be done by applying and developing methods for analysing and correlating DNA sequencing data, such as whole genome and metagenomic data, with microbiological, environmental, clinical and data.

The applicant must have a PhD (or be very close to completion), preferably in epidemiology or data science. Alternatively, she/he must have a PhD (or very close to completion) in statistics, mathematics, machine learning, or computational biology. In-depth expertise in the use of advanced statistical modelling and machine learning for data analysis in biological problems, preferably related to epidemiology of infectious diseases and antibacterial resistance is essential. Strong proficiency in programming/software development is required. Experience/expertise in the following subjects would be desirable: use of deep learning for data analysis, use of advanced statistical modelling and machine

learning for the analysis of bacterial whole genome sequencing data and metagenomic data; development of diagnostics or forecasting tools; development of surveillance/monitoring solutions for infectious diseases.

Informal enquiries may be addressed to Dr. Tania Dottorini: tania.dottorini@nottingham.ac.uk. Please note that applications sent directly to this Email address will not be accepted.