UNIVERSITY OF CAMBRIDGE
Department of Veterinary Medicine

## PhD Project: Pioneering advanced techniques to measure bacterial mutation rates

**Start Date: 1st October 2025**

**Supervisor:** Dr Lucy Weinert

Bacterial diseases have been a significant problem for most of human history but are largely controlled today thanks to vaccines and antibiotics. However, bacteria continue to pose risks due to their remarkable ability to adapt and evolve. A crucial aspect of this adaptation is their propensity to develop new mutations, which can vary significantly between bacterial strains and species. Measuring these mutation rates is challenging because such events are rare.

This PhD project aims to develop new, state-of-the-art tools for measuring bacterial mutation rates using microfluidic devices and high-fidelity sequencing techniques. The successful candidate will apply these tools to measure mutation rates in bacterial isolates from various sources, including the environment, carriers, and clinical cases. The goal is to understand how mutation rates influence bacterial disease phenotypes and their ability to develop antimicrobial resistance.

There are intriguing links between mutations, disease, and antimicrobial resistance. For instance, antimicrobial resistance in Mycobacterium tuberculosis is associated with specific types of mutations (Payne et al. 2019), and faster mutation rates have been linked to epidemics of Neisseria meningitidis (Richardson et al. 2002). Previous research conducted by the supervisor has demonstrated that clinical isolates of the porcine zoonotic bacterium Streptococcus suis exhibit faster mutation rates compared to carriage isolates (Murray et al. 2021). However, whether this change is a cause or consequence of disease remains unknown.

Accurate measurement of bacterial mutation rates is important for developing effective treatment strategies, designing robust surveillance systems, creating effective vaccines, and ultimately controlling the spread of bacterial diseases. This research will provide valuable insights into bacterial evolution and inform public health initiatives.

This project is a joint project with Dr Somenath Bakshi from Dept. of Engineering and Dr Alex Cagan from Dept. of Genetics. We invite candidates with a background in microbiology, bioinformatics, or related fields to apply for this exciting research opportunity. Skills will be developed in microbiology, nanotechnology and genome sequence analysis.

Murray, G. G., Balmer, A. J., Herbert, J., Hadjirin, N. F., Kemp, C. L., Matuszewska, M., ... & Weinert, L. A. (2021). Mutation rate dynamics reflect ecological change in an emerging zoonotic pathogen. PLoS Genetics, 17(11), e1009864.

Richardson, A. R., Yu, Z., Popovic, T., & Stojiljkovic, I. (2002). Mutator clones of Neisseria meningitidis in epidemic serogroup A disease. Proceedings of the National Academy of Sciences, 99(9), 6103-6107

Payne, J. L., Menardo, F., Trauner, A., Borrell, S., Gygli, S. M., Loiseau, C., ... & Hall, A. R. (2019). Transition bias influences the evolution of antibiotic resistance in Mycobacterium tuberculosis. PLoS biology, 17(5), e3000265.

**How to apply:** Contact the Supervisor to discuss the project before submitting an official application. More info on applying here: https://www.postgraduate.study.cam.ac.uk/courses/directory/cvvtmpvet