Title of PhD project / theme	**Genomic diversity of malaria parasites around Lake Victoria, Kenya**
Supervisory team	Professor Taane Clark (LSHTM) Dr. Susana Campino (LSHTM) Prof. Kiyoshi Kita (Nagasaki) Prof. Akira Kaneko (Nagasaki)
Brief description of project / theme	Malaria, a mosquito-borne disease caused by *Plasmodium* parasites, is an important public health problem causing an estimate of >200 million cases and >400,000 deaths annually. The majority of malaria cases and deaths occur in sub-Saharan Africa, including in Kenya. To assist the task of malaria elimination, it is crucial to improve our understanding of the biological features of malaria parasites. Knowledge of the complexity and variability of the *Plasmodium* genomes and their diversity, could provide insights into the biology underlying the disease; such insights could inform the process of drug discovery, inform the development of tools for rapid diagnosis, surveillance and evaluation of malaria control interventions. Advances in high throughput sequencing technology mean it is now possible to perform whole genome sequencing on a large scale, and feasible to conduct large genome diversity studies. In this project, we propose to collect and sequence malaria parasites close to Lake Victoria, Kenya, assess geographical and temporal differences in genomic diversity, infer anti-malarial drug resistance profiles, and establish any hotspots of transmission. The outputs of this work will inform disease control measures and policy.
Particular *prior* educational requirements for a student undertaking this project	A background in molecular biology, parasitology or another related area; an interest in genomics and sequence data analysis
Skills we expect a student to develop/acquire whilst pursuing this project	Bioinformatics, population genetics, whole genome sequencing, advanced molecular biology skills, and genomic epidemiology