

Project ID: EUR25-01

EMBL Host group leader: Maria Bernabeu

Site: Barcelona, Spain

Host group webpage: <https://www.embl.org/groups/bernabeu/>

Project description:

The Bernabeu group uses bioengineered 3D blood-brain barrier to study cerebral malaria pathogenesis. The microfluidic 3D blood-brain barrier model is composed of human endothelial cells, astrocytes and pericytes. We work with both primary cells and differentiated cells from induced pluripotent stem cells. We challenge these models with *P. falciparum* infected red blood cells or to better understand mechanisms associated with vascular barrier disruption and inflammation. Although our models are highly complex. We offer training on basic lab techniques such as *P. falciparum* and human cell culture, as well as introduce the resident into complex bioengineering approaches including microfluidics or 3D culture on hydrogels.

You will obtain the following wet lab skills:

- *P. falciparum* culture
- *Human cell culture in two and three-dimensions*
- *Microfabrication*
- *Microfluidics*
- *Confocal imaging and analysis*
- *FACS (Fluorescence assisted cell sorting)*

You will obtain the following computational skills:

Not applicable

Project ID: EUR25-02

EMBL Host group leader: Wolfgang Huber

Site: Heidelberg, Germany

Host group webpage: www.embl.org/groups/huber

Project description:

In collaboration with the Ingham group at Heidelberg University Hospital (<http://tinyurl.com/3r4vkzas>), time course RNAseq is available for response to three bed nets: IG1, IG2 and chlorfenapyr only. Within this project, the RNAseq will be evaluated to identify candidates for CRISPR-cas in mosquito cells. The cells will be modified using this technique and changes to growth curves established. Any interesting candidates may be explored with RNAi in mosquitoes, depending upon time.

You will obtain the following wet lab skills:

- *Mosquito cell culture,*
- *CRISPR-cas*
- *FACS*
- *Growth assays*
- *Potential mosquito rearing*
- *RNAi*
- *qPCR and phenotyping*

You will obtain the following computational skills:

- R

Project ID: EUR25-03

EMBL Host group leader: John Lees

Site: Hinxton, Cambridgeshire, United Kingdom

Host group webpage: <https://www.ebi.ac.uk/research/lees/>; www.bacpop.org

Project description:

The Lees group develops bioinformatic methods and mathematical modelling approaches to analyse populations of pathogen genomes. We are particularly interested in understanding how to optimise genomic surveillance design, understand the evolution and transmission of pathogens, and developing fast and accessible methods to analyse pathogen data.

We welcome projects where the fellow has already collected genome data from a pathogen or microbiome, and we can provide help on formulating and carrying out a bioinformatic analysis plan. We also welcome applications from candidates with existing programming experience, who are interested in improving their skills to more of a method development focus. Please see our group website (www.bacpop.org) for details of software tools you may be interested in contributing to.

You will obtain the following wet lab skills:

Not applicable

You will obtain the following computational skills:

- Intermediate programming
- Microbial genomics

Project ID: EUR25-04

EMBL Host group leader: Nassos Typas

Site: Heidelberg, Germany

Host group webpage: www.embl.org/typas/

Project description:

The Typas group studies how pathogenic or commensal bacteria can colonize a community of gut bacteria from the human microbiome. In particular, we are interested in identifying the genes and mechanisms that enable or prevent a strain from colonizing a microbiome and how this differs among microbiomes from different individuals. In this project we will use transposon insertion libraries of a pathogenic and a commensal E. coli strain and introduce these in multiple bottom-up assembled microbiomes from diverse human donors. The project involves both wet-lab work: assembly of anaerobic bacterial communities, measuring growth dynamics and transposon library preparation for sequencing, and dry-lab work: running Barcode-sequencing pipelines, genome-wide mutant fitness analysis and advanced bioinformatics including metagenomics analysis for hypothesis generation.

You will obtain the following wet lab skills:

- Microbial strain isolation
- Personalized microbial communities
- (drug) resistance evolution screens
- Genome-scale loss-of-function screens

You will obtain the following computational skills:

- intermediate programming in python/R
- Antibiotic resistance prediction
- Protein structure modelling
- Data analysis
- Machine learning

Project ID: EUR25-05

EMBL Host group leader: Evangelia Petsalaki

Site: Hinxton, Cambridgeshire, United Kingdom

Host group webpage: <https://www.ebi.ac.uk/people/person/evangelia-petsalaki/>

Project description:

The Petsalaki group develops network-based tools and approaches for extracting active signalling processes from multi-omics data. In this project we will curate omics data from infected individuals or cell lines and use multi omics data integration and network analysis to describe the mechanism of action of viral infections that will then be compared across different viruses. Previous experience programming in R or Python is required for this project.

You will obtain the following wet lab skills:

- Not applicable

You will obtain the following computational skills:

- Network analysis, data integration

Project ID: EUR25-06

EMBL Host group leader: Maria Zimmermann-Kogadeeva

Site: Heidelberg, Germany

Host group webpage: www.embl.org/zimmermann-kogadeeva/

Project description:

The Zimmermann-Kogadeeva group investigates bacterial metabolism and host-bacteria metabolic interactions with the focus on the human gut microbiota with computational and experimental approaches. We use genome-scale metabolic modelling to assess bacterial metabolism, predict bacterial metabolic phenotypes across conditions, and identify knowledge gaps in bacterial metabolism which we try to elucidate with computational and experimental approaches. We investigate bacterial growth and metabolism in the lab using phenotypic, transcriptomic and metabolomic assays, and use statistical, graph-based and machine learning methods to identify molecular features associated with observed phenotypes. We anticipate the successful candidate to work on an ongoing project in the lab focusing on investigating metabolic aspects of microbial physiology and/or host-microbe interactions using experimental and/or computational methods.

You will obtain the following wet lab skills:

- Bacterial culture including anaerobic (Escherichia coli, Bacteroidota spp)
- Metabolomics profiling
- Transcriptomics profiling

You will obtain the following computational skills:

- Intermediate programming in python and/or R
- Genome-scale metabolic modelling
- Multi-omics integration
- Machine learning

Project ID: EUR25-07

EMBL Host group leader: David Yuan

Site: Hinxton, Cambridgeshire, United Kingdom

Host group webpage: <https://www.ebi.ac.uk/people/person/david-yu-yuan/>

Project description:

The Pathogen Data Network is a global consortium aiming to provide infrastructure, tools, training, outreach and support to FAIR infectious-diseases data sharing and reuse. It will cover diverse biodata types, including host and pathogen genomics, transcriptomics, proteins, pathways and networks, imaging and cohorts.

The Pathogen Analysis System is a platform to process genomics data on Galaxy with full integration with ENA for pathogens. It is under development to expand the capabilities of the Pathogen Data Network from collecting and presenting pathogen data to analyse and annotate genomics data for pathogens. The design emphasizes the full integration of ENA, Galaxy computing environment and user-specific analysis pipelines, which would be particularly useful for researchers with limited computing resources and / or programming skills. The successful candidate will learn how to develop Galaxy tools to integrate with ENA, and will gain thorough understanding of the ENA programming model.

You will obtain the following wet lab skills:

- Not applicable

You will obtain the following computational skills:

- Python
- ENA programming APIs
- Galaxy Community Hub
- Git Hub
- Java
- Linux

Project ID: EUR25-08

EMBL Host group leader: Eva Kowalinski

Site: Grenoble, France

Host group webpage: www.embl.org/groups/kowalinski/

Project description:

The Kowalinski group studies RNA processing and modification in *Trypanosoma brucei*. A residency in the Kowalinski lab will offer training opportunities in cutting-edge structural biology, with a focus on RNA processing in the eukaryotic parasite *Trypanosoma brucei*. The Kowalinski lab applies advanced structural biology techniques, including X-ray crystallography and cryo-electron microscopy to characterize RNA processing enzymes and enzyme complexes complemented with biochemical and cellular assays. The prospective fellow will therefore participate in an ongoing project in the Kowalinski lab, depending on training needs.

You will obtain the following wet lab skills:

- Cloning
- Protein expression in bacterial, insect and mammalian expression systems
- Protein purification
- *Trypanosoma brucei* cell culture
- Genome editing
- Protein-protein interaction screening
- X-ray crystallography
- cryo-EM (electron microscopy)

You will obtain the following computational skills:

- Protein structure prediction, modelling and analysis