CRUK Cambridge Centre MRes rotation project

Rotation Project Title	Characterization of the mutational progression in gastrointestinal adenocarcinomas
Head of Laboratory (PI) Name	Rebecca Fitzgerald, MRC Cancer Unit
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Programme	Early Detection
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Laboratory Location	EMBL-EBI

Project Outline	**Aims and objectives** GI adenocarcinomas may share a similar cell of origin despite affecting different organs. However, mutational signatures and structural alterations vary across the various GI cancers. Comparing the genomic landscapes of oesophageal, gastric, and colon adenocarcinomas may help to identify early genomic lesions, common molecular properties of their origins and indicators of disease progression.
Experimental plan	Using genomic and transcriptomic data available in the TCGA and ICGC datasets the successful student will early molecular lesions, analyze their evolutionary relationships and develop rational approaches for measuring and predicting disease progression.
Main Techniques	• Statistics/machine learning, particularly neural networks/deep learning • R (or Matlab), Python, Linux • Experience with HPC clusters • A general understanding of bioinformatics/genomic data would be helpful
Key References	Secrier M et al. Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. Nat Genet. 2016; 48(10):1131-41. Martincorena I et al. Universal Patterns of Selection in Cancer and Somatic Tissues. Cell. 2017; 171(5):1029-1041. Gerstung M et al. Precision oncology for acute myeloid leukemia using a knowledge bank approach. Nat Genet. 2017; 49(3):332-340. Abelson S et al. Prediction of acute myeloid leukaemia risk in healthy individuals. Nature 2018. doi: 10.1038/s41586-018-0317-6. [Epub ahead of print]