





H2020 MSCA - ITN - 2017 - 766030

C O N T R A

Computational Oncology Training Alliance

ESR 6 - Identification and impact of clonal and subclonal driver alterations on cancer progression

| | |
|---------------------|--|
| Research project | Although several models of cancer progression have been proposed, the impact of driver mutations in directing/modifying cancer progression in time and space is still poorly understood. In this ESR project we will predict clonal and subclonal driver alterations starting from cancer genomic data of individual cancer samples. We will then develop and apply different models of cancer progression (linear, crisis-driven, big bang). This will allow a comparative assessment of models across patients and cancer types. |
| Supervisor | name Francesca Ciccarelli e-mail francesca.ciccarelli@kcl.ac.uk ; francesca.ciccarelli@crick.ac.uk https://www.crick.ac.uk/research/a-z-researchers/researchers-a-c/francesca-ciccarelli/ website ciccarelli/ |
| Host institution | King's College London and The Francis Crick Institute   The Ciccarelli lab is currently seconded to the Francis Crick Institute in London, where the student will be located. The group uses both computational and experimental approaches and has access to cutting edges experimental facilities. |
| PhD program | Faculty of Life Sciences & Medicine, School of Cancer and Pharmaceutical Sciences |
| Expected results | 1) New methods for comparing models of cancer progression based on cancer data 2) Methods to identify subclonal driver alterations 3) Predictive model of cancer prognosis based on clonal and subclonal alterations |
| Planned secondments | 1) IRB/Lopez-Bigas to identify driver alterations (3 months) 2) KTH/Lagergren to develop comparative assessment of cancer progression models (3 months) 3) UCAM/Markowitz to integrate models of spatial cancer progression (2 months) |
| Required profile | Solid background in statistics, computer programming, and cancer genetics. Previous experience with genomic data analysis would be favourable |