H2020 MSCA - ITN - 2017 - 766030

CONTRA

Computational Oncology Training Alliance

ESR 12 - Mutational patterns and models within tumours

Research project	Cancer data shows distinct genomic mutation rates that often are context-dependent and can be specific of distinct cancer types (i.e., mutational signatures). In this project we will try to understand in more detail how and which point mutations accumulate in cancer genomes within single patients, and using both single-cell and bulk Next-Generation Sequencing (NGS) tumour data. In this context, we will explore different models and their fit (statistical model selection), homogeneity of the mutational signatures in time and space, and relationship to cancer subtypes and progression, in bulk and single-cell NGS data. These models will be fitted to individual patients to evaluate their potential utility in precision medicine.
Supervisor	name David Posada e-mail dposada@uvigo.es website http://darwin.uvigo.es
Host institution	University of Vigo, Spain Biomedical Research Center (CINBIO) (http://cinbio.es)
PhD program	Methodology and Applications in Life Sciences (http://cvida.uvigo.es; in Spanish)
Expected results	1) New methods for assessing mutational signatures in time and space 2) Software for mutational model selection in time and space 3) Potential NGS biomarkers for precision medicine
Planned secondments	1) IRB-Lopez-Bigas to learn cancer genomics (2 months) 2) ETH-Beerenwinkel to learn mutational modelling (2 months) 3) KTH-Lagergren to learn modelling and computation (2 months) 4) Gradiant to learn statistical methods and software development (2 months)
Required profile	The candidate should possess excellent statistical and computational abilities. Knowledge about evolution, genomics and/or cancer is not necessary, as this will be acquired during the PhD.

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