




H2020 MSCA - ITN - 2017 - 766030

# CONTRA

*Computational Oncology Training Alliance*

## **ESR 4 - Estimating tumour phylogenies from single-cell SNV and CNA data**

Research project	Cancer is an evolutionary process and the tumour phylogeny problem is to reconstruct the evolutionary history of a tumour from its genomic alterations. Single-cell data is much more informative about this process than bulk sequencing data. Most existing methods, however, focus on bulk data or they account only for single-nucleotide variants (SNVs). Since copy number alterations (CNAs) are common in most tumours, we will incorporate both pieces of information and develop novel computational methods to integrate SNV and CNA data obtained from individual cells. This task involves the primary analysis of the short-read data, including mutation and copy number calling, and their integration into a single evolutionary model. A major challenge is to account for spatial dependencies among CNAs, which requires dropping the infinite sites assumption, which is frequently made.
Supervisor	name      Niko Beerenwinkel e-mail <a href="mailto:niko.beerenwinkel@bsse.ethz.ch">niko.beerenwinkel@bsse.ethz.ch</a> website <a href="http://www.cbq.ethz.ch">www.cbq.ethz.ch</a>
Host institution	ETH Zurich Department of Biosystems Science and Engineering Basel, Switzerland
	
PhD program	Life Science Zurich Graduate School ( <a href="http://www.lifescience-graduateschool.uzh.ch/en.html">http://www.lifescience-graduateschool.uzh.ch/en.html</a> )
Expected results	1) Mathematical framework for integrating single-cell SNV and CNA data 2) Computational method for single-cell tumour phylogeny reconstruction avoiding the infinite sites assumption
Planned secondments	1) UCAM/Markowitz to work on CNA data (3 months) 2) KTH/Lagergren to work on tree inference (3 months)
Required profile	Strong background in mathematics, statistics, computer science, bioinformatics, or a related field; experience with phylogenetic model building is a plus