




H2020 MSCA - ITN - 2017 - 766030

CONTRA

Computational Oncology Training Alliance

ESR 15 - Reconciling tumour trees and multiple tumour progression models

Research project	This project aims at producing progression models from single-cell data for tumour collections. Producing tumour progression models have earlier been attempted based on bulk data for tumour collections. As the attention of the research community has turned from bulk data to single cell data, the methodological focus has turned from progression models for tumour collections to phylogenies for single tumour. As single cell data become increasingly cost efficient, the attention will return to progression models. As a first step towards progression models for single cell data we consider how progression models and tumour trees can be reconciled. The next step consists of inference of progression models from collections of tumour trees. Finally, integrated models that can be used for simultaneous inference of tumour trees and progression models will be considered.
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Host institution	Royal Institute of Technology, Sweden School of Electrical Engineering and Computer Science
	
PhD program	Computer Science
Expected results	Models, algorithms and software for : 1) reconciling tumour trees and progression models 2) inference of progression models from tumour trees 3) simultaneous inference of tumour trees and progression models from single cell data
Planned secondments	1) KLC-Crick Institute and Ciccarelli to participate in a "more applied project" (1 month) 2) Ardigen and Radkowski to learn software development (2 months) 3) UCAM and Markowitz to get a broadened view on progression models and cancer research (2 months) 4) BCCRC and Shah to a transatlantic perspective on computational cancer research (1 month)
Required profile	Computer Science, Machine Learning, Statistics, Mathematics, Computational Biology