C O N T R A

Computational Oncology Training Alliance

ESR 8 - Models and inference for Single-cell sequencing and tumour evolution

Research project	This ESR project is devoted to probabilistic models of all steps of single cell genomic sequencing and tumour evolution as well as inference methods for the tree reconstruction problem. Although, the sequencing technology and the important error prone amplification procedure are bound to change over time, the tree reconstruction problem is of fundamental importance and will require substantial research. By modeling both the uncertainty in the experimental procedure and that of the somatic evolution, an integrated analysis will be possible. By taking advantage of inference methodologies such as structural EM and particle Monte Carlo in combination with modern computational technologies for Big Data, the complex inference problem will be tractable also for large datasets. This research will then be continued in collaboration with ESR4 in order to develop a method for integrated SNV and CNA data.
Supervisor	name Jens Lagergren e-mail jens.lagergren@scilifelab.se website http://www.nada.kth.se/~jensl/
Host institution	Royal Institute of Technology, Sweden School of Electrical Engineering and Computer Science
PhD program	Computer Science
Expected results	1) A model for the amplification and sequencing steps in single cell genomic sequencing 2) software for reconstructing tumour trees based on point mutations 3) software for reconstructing tumour trees based in point mutations and copy-number data (in collaboration)
Planned secondments	1) IRB and Lopez-Bigas to learn about general cancer genomics (1 month) 2) Ardigen and Loska to learn software development 3) ETH and Beerenwinkel to get a broadened view on cancer phylogeny models and cancer research (3 months) 4) University of Vigo and Posada get a general understanding of evolution (1 month)
Required profile	Computer Science, Machine Learning, Statistics, Mathematics, Computational Biology