Master project 2020-2021

Personal Information

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Project

Computational genomics

Project Title:

Functional genomics

Keywords:

genetics, genomics, statistics, bioconductor

Summary:

The research in the functional genomics group is geared towards the development of computational methods and pipelines to address questions of biological and clinical relevance. Depending on the profile of the candidate, different types of master projects are possible, ranging from software engineering and development in R/Bioconductor, development of new methods for the analysis of high-throughput genomics data, to the analysis of specific datasets to answer particular biological and clinical questions. Some of our contributions in all these aspects can be found in the list of references.

References:

1. Costa et al. Genome-wide postnatal changes in immunity following fetal inflammatory response. medRxiv, 19000109, 2020. 2. Roverato and Castelo. Path weights in concentration graphs. Biometrika, in press (arXiv:1907.05781) 3. Puigdevall et al. Genetic linkage analysis of a large family identifies FIGN as a candidate modulator of reduced penetrance in heritable pulmonary arterial hypertension. Journal of Medical Genetics, 56:481-490, 2019. 4. Puigdevall and Castelo. GenomicScores: seamless access to genomewide position-specific scores from R and Bioconductor. Bioinformatics, 18:3208-3210, 2018. 5. Roverato and Castelo. The networked partial correlation and its application to the analysis of genetic interactions. Journal of the Royal Statistical Society Series C -Applied Statistics, 66:647-665, 2017. 6. Costa and Castelo. Umbilical cord gene expression reveals the molecular architecture of the fetal inflammatory response in extremely preterm newborns. Pediatric Research, 79:473-481, 2016. 7. Baumstark et al. The propagation of perturbations in rewired bacterial gene networks. Nature Communications, 6:10105, 2015. 8. Tur et al. Mapping eQTL networks with mixed graphical Markov models. Genetics, 198(4):1377-1383, 2014. 9. Hänzelmann et al. GSVA: gene set variation analysis for microarray and RNA-Seq data. BMC Bioinformatics, 14:7, 2013.

Expected skills::

Programming, scripting, minimum understanding of statistics.

Possibility of funding::

No

Possible continuity with PhD: :

To be discussed