



**DOTTORATI DI RICERCA / PHD PROGRAMS IN
INFORMATION TECHNOLOGY AND ELECTRICAL ENGINEERING (ITEE)
INFORMATION AND COMMUNICATION TECHNOLOGIES FOR HEALTH (ICTH)
COMPUTATIONAL AND QUANTITATIVE BIOLOGY (CQB)**

Seminar announcement

Thursday 2 December 2021, Time: 10:30 - 12:30

“Aula L”, 2nd Floor, Piazzale Tecchio Building and on Teams, code qknzs5d

Dr. Raoul J.P. Bonnal

IFOM - the FIRC Institute of Molecular Oncology

Via Adamello 16, 20139 Milan, Italy

Single cell omics leverage Machine Learning to dissect tumor microenvironment and cancer immuno editing

Abstract: The development of a solid tumor is accompanied by the establishment of a peculiar environment which sustains the tumor grow, the so called “tumor micro-environment”. This environment is populated by many cell types such as cancer, immune, stromal and many other types which tightly communicate and interact. The single cell technologies offer unprecedented opportunities to extract omics and geographical information from the original tissue. Cutting edge bioinformatics tools embeds machine learning approaches to make it possible inferring relationships and discovering patterns from the ensembles of players represented in the tumor-microenvironment. Exploitation of this information can provide new insights on cancer progression and ultimately lead to the development of novel therapeutic opportunities.

The seminar will give an introduction on sequencing technologies, focusing on single-cell both at omics and spatial transcriptomic level. Will follow, a walk-through a recently published paper from our group, showing how we exploited and interpreted single cell data and the actual analysis pipeline. During the seminar many tools, relying on machine learning approaches, are discussed to understand when to use them and why. At the end, the seminar will present the spatial transcriptomics technology showing how to integrate this layer of information with “traditional” RNA-seq data and extract pattern and interpret the results.

The seminar is also an occasion to discuss about reproducibility and the challenges that arise when many people are collaborating to the the analytical process.

Raoul J.P. Bonnal, is a senior staff bioinformatician and head of data science in the laboratory of Prof. Massimiliano Pagani in IFOM. Computer scientist, since 2005 expert in NGS technologies and data analysis generated with different “omics” technologies: genomics, epigenomics and transcriptomics. In recent years he has focused on the analysis of single cell data and in the use and customization of IT tools aimed at improving their interpretation and communication. He has been involved in several international initiatives aimed at promoting Open Source practices such as eg. Google Summer of Code. Recently he participates as software engineer in the project “The explorer of cancer cells”, promoted by AIRC and Vodafone, hosted in the citizen-science platform DreamLab, recoding scientific algorithms so that they can work on Android and iOS mobile devices.

For information: Prof. Anna Corazza (DIETI, UniNA, tel. 081 679273 – anna.corazza@unina.it)