

Dear all,

We would like to let you know that **Aurélien De Reyniès** will visit CNIO from **29 January to 2 February 2018** invited by Dr. Núria Malats (Genetic and Molecular Epidemiology Group) and Dr. Francisco X Real (Epithelial Carcinogenesis Group).

Aurélien De Reyniès is currently the **Scientific Director** of the Tumor Identity Card -CIT- research program at the French charity "Ligue Nationale Contre le Cancer", Paris. Before that he co-founded and headed the bioinformatics team of the CIT program. His work covers several aspects of translational research in oncology, with particular attention given to cancer molecular subtyping. He is involved in several international consortia for consensus on molecular subtyping, such as the colorectal and the bladder cancer subtyping consortium. He currently focuses on bioinformatics methods devoted to describe the cellular components of transcriptome signals, either tumor or non-tumor, including immune and stromal cells.

Next **Tuesday January 30th**, Aurélien will hold a **workshop on "Transcriptome analysis of tumours"**. The workshop will take place in the 3rd floor seminar room from 15h to 18:30h.

The event is addressed mainly to researchers with an interest in genomic analysis of tumors. The discussion will be relevant to both human and mouse tumors.

If you are interested in meeting him after the workshop or during the rest of the week, please let Gema Moreno know (gmoreno@srv.cnio.es)

We hope that you will enjoy these activities.

Thank you for your consideration of this event,

Workshop on “Transcriptome analysis of tumours”

Aurélien de Reyniès

CIT Program, Ligue Nationale Contre le Cancer, Paris, France

CNIO, 3rd floor seminar room (15h to 18:30h)

Tuesday, January 30, 2018

15-18:30 h

Oncology is facing two opposite problems: over-treatment (ex. prostate cancer) versus absence of therapeutic answer (ex. pancreatic cancer). Research in cancer genomics can help bringing answers to both problems, first by revisiting cancer (molecular) pathology, then by deriving biology-driven therapeutic strategies. We have to consider cancer as an adaptative ecosystem, with communicating cells, both tumoral and non-tumoral (microenvironment), characterized by genetic polyclonality and phenotypic diversity. In this mental frame, the first question is: 'what are the cell populations in this system and in which quantities?'. Answering this question is mandatory to answer key questions such as: 'what are cell-interactions in these systems? how do they relate to tumor metabolism / immune escape mechanisms / etc.?'.

In this workshop, I will propose some particular methods we developed to answer the first question, concerning both tumor and microenvironment cell populations. Firstly, I will discuss ways (i.e., algorithms) to reach a consensus from various views of the tumor cell populations that may exist (i.e., molecular subtyping systems). Then, I will present an original bioinformatics method allowing to analyze the intra-tumor heterogeneity (i.e., proportions of various tumor cell populations in a sample). I will also present the MCP-counter method, developed to analyze the microenvironment composition of a sample, either tumoral or not.

The specific topics I will cover during the event are:

1. Ways to consensus classification in molecular subtyping: which one to choose?
2. Transcriptome-based characterization of tumor's immune contexture: prognostic and therapeutic implications.
3. Weighted in Silico Pathology (WISP): bridging the gap between tumor molecular subtyping and pathology.