



“Bioinformatics in cancer research”

Professor Peter van Loo

KU Leuven, Department of Human Genetics, Leuven, Belgium

January 29, 2014 (11:00)

Lunch meeting for Doctoral Schools students 12:00-14:00

Jozef Schell seminar room, Technologiepark 927 - 9052 Zwijnaarde

<http://www.nucleotides2networks.be/node/232>

<http://www.nucleotides2networks.be/events>

Abstract

Cancer evolves dynamically as clonal expansions supersede one another, driven by shifting selective pressures, mutational processes, and disrupted cancer genes. These processes mark the genome, such that a cancer's life history is encrypted in the somatic mutations present. We are developing algorithms to decipher this narrative from whole genome sequencing data and are applying them to several cancer types. We call such approaches “molecular archaeology of cancer”, as we are using genomics and bioinformatics algorithms to infer a tumour’s evolutionary history. I will discuss applications of our methods to breast cancer, allowing us to disentangle subclonal architecture from whole genome sequencing data, as well as time events such as chromosome duplications along a tumour’s lifetime. In addition, I will describe how extending these molecular archaeology approaches to multiple sampling studies allow enhanced and unique insights into cancer evolution, and I will illustrate that using genomics studies on prostate cancer metastases, where we are able to elucidate the patterns of metastatic spread in unprecedented detail.