

Séminaire LAL

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Mardi 26 novembre 2019 à 11h00

ML for gene mutation research

Cancer is caused by genetic alterations that induce uncontrolled cell proliferation. Thanks to the current DNA sequencing technologies, these alterations can now be assessed efficiently, thereby paving the way for a wider application of precision medicine in clinical practice. DNA mutations are one crucial type of alteration that is commonly found in tumours. The statistical analysis of mutation profiles is however challenging. Within a given form of cancer, two patients usually do not share the same set of mutations and can even have none in common. This lack of similarity makes it difficult to compare tumour mutation profiles. To overcome this issue, methods have been proposed to identify shared disrupted biochemical pathways. In this talk, I will define a novel representation for tumour mutation profiles that exploits prior knowledge on protein-protein interaction networks. For certain cancers, this representation allows improving survival predictions from mutation data as well as stratifying patients into meaningful subgroups.

Salle 101 - Bât. 200, Orsay

Organisation :

Joao Coelho - Thibaud Louis - Aurélien Martens - Dimitris Varouchas (LAL) - seminaires@lal.in2p3.fr

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