

**Barthélémy Meynard**

LCQB, Sorbonne Université — Politecnico di Torino, Bocconi University

**Title:**

Generating Interacting Protein Sequences using Domain-to-Domain Translation and modeling the TCR-peptide binding.

**Abstract:**

Being able to artificially design novel proteins of desired function is pivotal in many biological and biomedical applications. Generative statistical modeling has recently emerged as a new paradigm for designing amino acid sequences, including in particular models and embedding methods borrowed from Natural Language Processing (NLP). However, most approaches target single proteins or protein domains, and do not take into account any functional specificity or interaction with the context. To extend beyond current computational strategies, we develop a method for generating protein domain sequences intended to interact with another protein domain. Using data from natural multi-domain proteins, we cast the problem as a translation problem from a given interactor domain to the new domain to be generated, i.e. we generate artificial partner sequences conditional on an input sequence. In the second part of the talk, we will extend the architecture to several interacting sequences and presents recent results on modeling the TCR-pMHC complex.