

Title: Exploring the RNA mutational landscape

Abstract:

Understanding the relationship between RNA sequences and structures is essential to decipher evolutionary processes, predict deleterious mutations and design synthetic molecules. In this talk, we introduce RNAmutants, the first algorithm for exploring RNA sequence-structures maps in polynomial time and space. Using statistical mechanics and weighted sampling techniques, we explore regions of the mutational landscape preserving the nucleotide composition and show how the GC-content influences the evolutionary accessible structural ensemble. Then, we illustrate the versatility of our techniques and apply them to (i) designing RNA sequences folding into target secondary structures, and (ii) to correcting sequencing errors in structured RNA sequences.

Joint work with Yann Ponty & Vladimir Reinharz.