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## SÉMINAIRE

# Shape Abstraction in RNA Folding and Family Modelling

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When humans reason about functional structures of RNA, they speak of long hairpins with miRNA precursors, of clover leaf structures with tRNA, of neighbouring hairpins with attenuators, and so on. Most of the time, we do not care about individual base pairs or helix sizes, while the overall arrangement of helices and loops really matters. RNA folding programs, however, used to be ignorant of abstraction in RNA, deceiving us with a single, minimum free energy structure, or overwhelming us with a plethora of near-optimal structures, most of which are quite similar and therefore redundant. RNA shape abstraction alleviates this situation. RNA shapes are abstract structure images, retaining adjacency and nesting of structural features, but disregarding size information. Shape abstraction integrates well with dynamic programming algorithms, and hence it can be applied during structure prediction rather than afterwards. This avoids exponential explosion in the near-optimal folding space, and provides a non-heuristic and complete account of an RNA molecule's structural inclinations. Quite magically, some long-studied problems become easy. In the presentation, I will shortly review the notion of abstract shapes. I will then discuss several applications of this concept, including a highly effective filtering method when working with structural classes of RNA described by covariance models, such as provided by the Rfam data base.