**Part I: Discrete models for  DNA recombination**

In this talk, we focus on DNA recombination processes that certain species of ciliates undergo during reproduction. We describe such processes using graph-theoretical models based on four-regular graphs as well as through word-based methods with double occurrence words and related operations. These techniques are applied to study recombination events in the model organism *Oxytricha trifallax*.

**Part II: Graph theory for DNA self-assembly**

In this talk, we look at self-assembling graph-like structures using branched junction DNA molecules which are star-shaped molecules that join together through adhesion sites on their arm ends. We introduce a combinatorial representation of these molecules and consider the problem of optimally building a target graph under different laboratory settings. We show how this question give rises to new graph invariants and how these invariants can be studied by means of graph-theoretical tools.

**Part III: Combinatorial methods for RNA secondary structure**

A central problem in molecular biology is understanding the shape into which an RNA molecule folds while it is being synthesized from DNA, as its shape encodes functional information. We analyze RNA secondary structure in this talk, that is the 2D arrangement of the final RNA configuration. For a given RNA sequence, we consider a representative set of secondary structures and discuss combinatorial methods to mine the structural information from the given ensemble.

**Part IV: Mathematical models for DNA-RNA complexes**

R-loops are three-stranded structures formed by a DNA-RNA complex and a single strand of DNA, often appearing during transcription. Despite an increasing interest in R-loops from experimentalists, there are few mathematical studies addressing R-loop structure and formation. In this talk, we introduce a model for R-loops based on formal grammars, that are systems to generate words widely applied in molecular biology.