

When a strand of RNA folds onto itself, the resulting secondary structure gives information about the function of the molecule. We use combinatorial objects, such as non-crossing perfect matchings and plane trees, to model the possible secondary structures of a strand of RNA. Meanders are another combinatorial object of interest in comparing secondary structures as they are a pair of non-crossing perfect matchings which form a single closed curve when drawn on opposite sides of a single horizontal line. We discuss a number of interesting mathematical problems found at this interface of discrete mathematics and molecular biology.