

Jesús Fernández-Sánchez

Universitat Politècnica de Catalunya

The embedding problem for Markov matrices of evolutionary models

Continuous-time Markov processes are often used to model evolution on nucleotide sequences. The resulting models consider nucleotide substitution matrices that are the exponential of rate matrices and assume some extra restrictions in contrast to biological reality. A more general approach considers models where the parameters are given by the substitution probabilities between nucleotides. The understanding of the connection between these two approaches is fundamental for modelling evolution as it has practical and theoretical consequences, as the identifiability of rates from experimental biological data. In this talk, we will give a description of the embedding problem, and see some new results about embeddability when restricted to well-known evolutionary models.

This is a joint work with Marta Casanellas and Jordi Roca-Lacostena.