Reconstruction of Gene Regulatory Networks with Multi-objective Particle Swarm Optimisers

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Resumen(Abstract). The computational reconstruction of Gene Regulatory Networks (GRNs) from gene expression data has been modelled as a complex optimisation problem, which enables the use of sophisticated search methods to address it. Among these techniques, particle swarm optimisation based algorithms stand out as prominent techniques with fast convergence and accurate network inferences. A multi-objective approach for the inference of GRNs consists of optimising a given network's topology while tuning the kinetic order parameters in an S-System, thus preventing the use of unnecessary penalty weights and enables the adoption of Pareto optimality based algorithms. In this study, we empirically assess the behaviour of a set of multi-objective particle swarm optimisers based on different archiving and leader selection strategies in the scope of the inference of GRNs. The main goal is to provide system biologists with experimental evidence about which optimisation technique performs with higher success for the inference of consistent GRNs. The experiments conducted involve time-series datasets of gene expression taken from the DREAM3/4 standard benchmarks, as well as in vivo datasets from IRMA and Melanoma cancer samples. Our study shows that multi-objective particle swarm optimiser OMOPSO obtains the best overall performance. Inferred networks show biological consistency in accordance with in vivo studies in the literature.