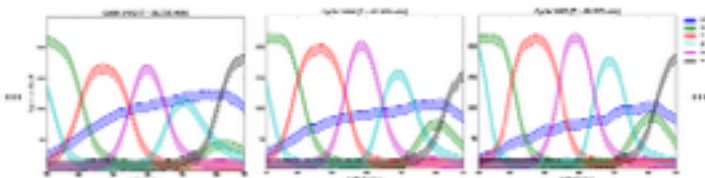
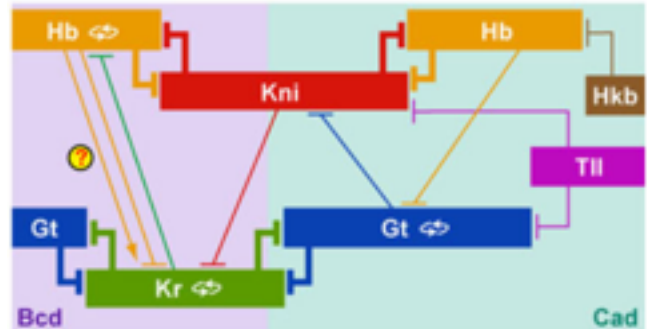


Inferring Drosophila Gene Regulatory Network using Multi-objective optimisation

Inferring Drosophila gene regulatory network became an ideal system for benchmarking the performance of network inference algorithms due to the enough accurate data available such as the gene expression levels for different genes during the embryonic development or quantitative mRNA expression. Methods like Simulated Annealing and Evolutionary Strategies have been used successfully to infer the network; However, they are not guarantee the robustness of the solutions. We have tried the multi-objective optimisation algorithm, namely, Non-dominated sorting algorithm, NSGA-II in order to measure the performance of this group of optimisation algorithm on a large search space.



The connectionist model of gap genes is used to model the Drosophila gene regulatory network. Then, the reverse-engineering problem has been solved using NSGA-II algorithm in order to find over 40 unknown parameters of the model. The objectives have formulated in such a way to consider the effects of

optimisation one gene on the other genes.

Although the results found by the NSGA-II are not precise enough, the main characteristic of the gene regulatory network as well as the gap genes pattern strips could be captured. Moreover, the results from the optimisation process could be used to find the possible conflicts between objectives or the deficiency in the model. Finally, the diverse set of solutions in the Pareto Front could be used as a set of good initial values for other optimisation algorithms like Scatter Search or Local search algorithms.

