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An Approach for Reduction of False Predictions in Reverse Engineering of Gene Regulatory Networks

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Highlights

- In the present work, we have focussed on the reduction of false predictions in gene regulatory networks or **GRNs** reconstructed from time-series genetic expression datasets.
- For this, we have proposed a novel methodology to *reduce the number of false predictions by suitably combining several metaheuristic techniques*.
- We have employed *recurrent neural networks* (**RNN**) for modelling the dynamics of the temporal gene expression data.
- We have implemented *four* metaheuristic techniques for the training of the RNN model parameters, and they are: (i) *particle swarm optimisation* (**PSO**), (ii) *bat algorithm inspired particle swarm optimisation* (**BAPSO**), (iii) *grey wolf optimisation inspired particle swarm optimisation* (**GWPSO**), and (iv) *artificial bee colony* (**ABC**).
- We have constructed *four* GRNs using each of the above-mentioned formalisms and have then combined the results. Subsequently, we have constructed the final GRN using only those edges that are common to all the techniques.
- We have employed our proposed methodology on six different types of networks, some of which have been added on the advice of the respected reviewers. The different networks are:
 - The SOS DNA Repair network of *Escherichia coli* (an *in vivo* benchmark),
 - The IMRA network of *Saccharomyces cerevisiae* (an *in vivo* benchmark),
 - A DREAM3 Challenge network (an *in silico* gold standard),

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