Genetic regulatory networks inference: modeling, parameters estimation & model validation
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Appendix B:
Details results of the different ES setting

The following tables [8.2 - 8.5] gives details on the different quality results of all the different settings. Different \((\mu, \lambda) - ES\) settings are used. In all cases, the number of selected individuals is \(\mu = \lambda/5\) but with population size \(\lambda = [200, 350, 500]\) and in the island-ES with 4 sub-populations, each sub-population is \(\lambda = 500/4 = 125\). In all setting, 20 simulations were run using the same initial seed. In total, 240 circuits were obtained and 91 were selected for analysis, based on the final root mean score.
Table 8.2: Results for the (200, 40) ES followed by DS. Twenty random seeds were generated and each of this configuration uses one of the initial seed. This results in 180 different simulations. In all simulation, $\gamma = 0.85$ and $\alpha = 0.2$. The table header $-2.5$, $-3.5$ gives the promoter threshold value in the 62-dimensional case. $F$ indicates a full search with 66 parameters to estimate. In each cell the first value stands for the RMS after ES and the second gives the RMS after DS.

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Table 8.3: Results for the (350,70) – $ES$ followed by $DS$. Twenty random seeds were generated and each of this configuration uses one of the initial seed. This results in 180 different simulations. In all simulation, $\gamma = 0.85$ and $\alpha = 0.2$. The table header $-2.5$, $-3.5$ gives the promoter threshold value in the 62-dimensional case. $F$ indicates a full search with 66 parameters to estimate. In each cell the first value stands for the RMS after ES and the second gives the RMS after DS.
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**Table 8.4:** Results for the (500, 100) – ES followed by DS. Twenty random seeds were generated and each of this configuration uses one of the initial seed. This results in 60 different simulations. In all simulation, $\gamma = 0.85$ and $\alpha = 0.2$. The table header $-2.5$, $-3.5$ gives the promoter threshold value in the 62-dimensional case. $F$ indicates a full search with 66 parameters to estimate. In each cell the first value stands for the RMS after ES and the second gives the RMS after DS.
Table 8.5: Results for the ES-island based with $P = 4$ sub-populations followed by DS. The same twenty random seed defined in the serial ES were used. This leads to 60 different simulations. In all simulations, $\mu = \lambda/\gamma = 0.85$ and $\alpha = 0.2$. The migration interval is after every 500 generations and only the best individual of each sub-population is migrated to another random sub-population. The header $-2.5$, $-3.5$ indicates the promoter threshold value in the 62-dimensional case. $F$ stands for full search with 66 parameters to estimates. In each cell the first value represents the RMS after island ES and the second gives the RMS after DS.

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