

# How closely should biology inspired algorithms match the biological process?

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## Introduction

Nature and biology have been an abundant source of inspiration for algorithm development. Algorithms have been developed to mimic the evolutionary process, the immune system and flocking behaviour of animals to name a few. How closely the developed algorithm matches the process being mimicked differs between algorithms. The question then becomes, does better matching the mimicked process produce better results as opposed to only partially matching the behaviour.

## Problem

When working with evolutionary algorithms the trade-off between exploration and exploitation has to be considered. Usually, during the initial generations of the algorithm, it will focus on exploration. This will allow the algorithm to identify portions of the search space that contain high quality solutions. The focus is then slowly shifted towards exploitation to find the best solutions in the identified areas. This process works fine when working with a static workspace, but is not ideal if changes occur in the search space. If a large enough change occurs, the algorithm will have to switch focus back to exploration to adapt to the change. The problem is that the algorithm requires population diversity to effectively switch focus to exploration and population diversity diminishes as the algorithm converges.

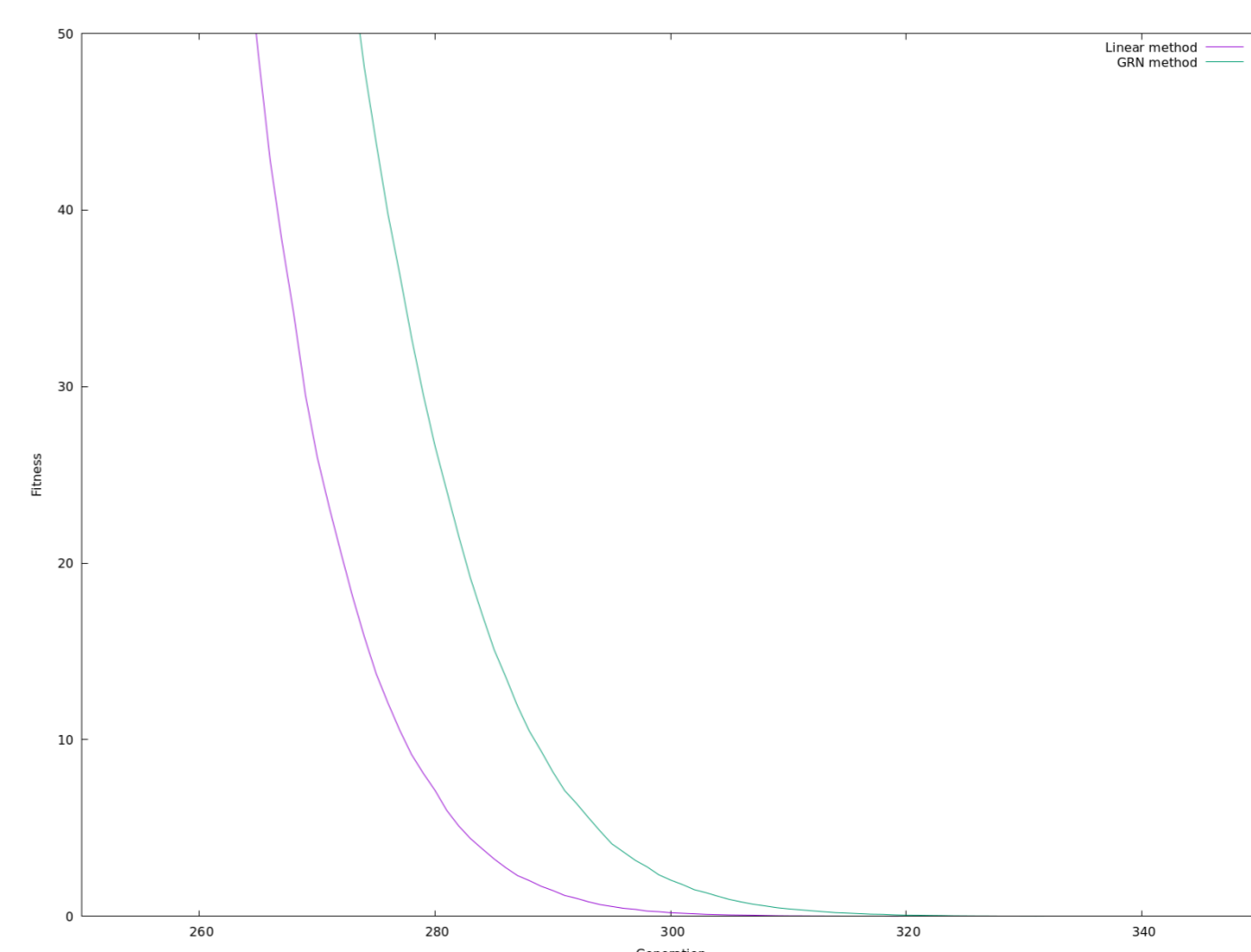
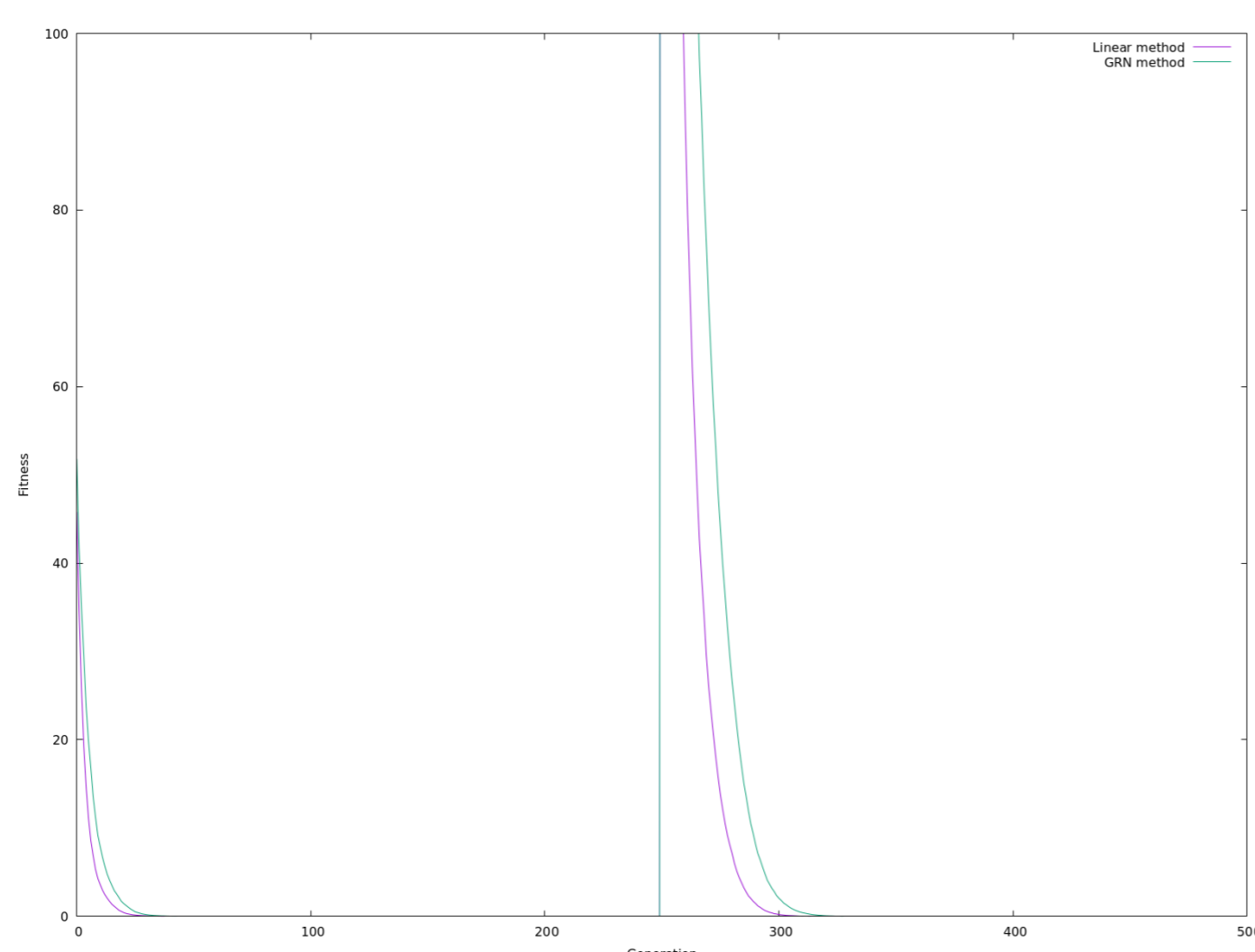
A group of algorithms was developed to maintain more diversity into the latter generations of the algorithm. This was achieved by drawing inspiration from biology and adding gene methylation to an evolutionary algorithm. This addition causes the solution to have coding and non-coding genes. The non-coding can then act as a reservoir of genetic diversity even after the coding portion converges and loses diversity.

Multiple variations were developed that differs in how closely they match the methylation process that is being mimicked. The variation that least closely matches biological process is referred to as the linear variation. It adds methylation to the genes, but the method used to manage the methylation does not match the biological process. Each gene is assigned an expression value, and the value alone determines if the gene is expressed or not. The gene regulatory network variation of the algorithm best matches the biological process. To determine if a specific gene is being expressed or not, the gene regulatory network has to be evaluated. This means that the expression of a gene is not just dependent on itself, but connected to the other genes making up the solution.

## Evaluation

To evaluate the algorithm variations, they were applied to the Rastrigin function. The algorithm was allowed to converge on a solution and for diversity to diminish. A change was then introduced into the search space. This was done by transposing the function to move the optimal point. The algorithms were thus forced to adapt to the change. At this point the algorithms should have some stored diversity and will have to access it to shift focus to exploration. The algorithm that performs this task better will be able to converge quicker. So to determine which of the variations were most effective the convergence rate after the change was introduced, was compared.

## Results



The graphs show the convergence rates of the developed algorithm variations. The first shows the convergence rate over the lifetime of the algorithm, while the second graph focusses on the generations following the change in the search space. From the graphs, it is clear that the linear variation was able to converge quicker than the gene regulatory network variation.

## Conclusion

Results showed that the linear variation was more effective than the gene regulatory network variation. This is probably due to the more complex methylation management mechanism, requiring more generations to reach a stable state. This does show that better matching a biological process will not necessarily produce better results. It is however possible that the effectiveness of the algorithms could change if a different metric was used to evaluate the algorithms.