

# Novel Genetic Algorithm Crossover Approaches for Time-Series Problems

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## Abstract

Genetic Algorithms (GAs) are a commonly used stochastic search heuristic which have been applied to a plethora of problem domains. GAs work on a population of chromosomes (an encoding of a solution to the problem at hand) and breed solutions from fit parents to hopefully produce fitter children through a process of crossover and mutation. This work discusses two novel crossover approaches for GAs when applied to the optimisation of time-series problems, with particular application to bio-control schedules.

## 1 Introduction

In optimization of intervention schedules for models of dynamic systems, Genetic Algorithms (GAs) commonly use Uniform Crossover (UC) as a method of achieving recombination [8]. Recent work [4] has produced alternative crossover approaches which work on variable length chromosomes that have been shown to outperform UC when applied to dynamic problems, with specific application to the area of bio-control scheduling. Although alternative variable length crossover approaches such as Messy GAs (mGA) exist [6], these have considerable complexity and a two-phase evolutionary approach [1]. This work discusses a simplified approach, which is specifically designed for time-series problems.

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## 2 Problem Domain

This work focuses on the optimisation of intervention schedules and has been tested initially in scheduling bio-control agents to combat sciarid flies. In mushroom farming, the presence of sciarid flies can drastically affect the quality of crop produced. Sciarid fly larvae feed on the mycelium in the casing layer of mushrooms which cause degradation of the crop. The nematode worm *Steinernema feltiae* has proven effective as a bio-control agent to combat this pest. A set of differential equations which represents the life-cycle of the sciarid flies and potential infection from nematode worms has been produced [3]. These equations have been utilised as a fitness function for testing the novel crossover approaches developed in this work, described in [4] and [5].

## 3 Crossover Approaches

The novel crossover approaches detailed in [4] were designed to investigate if incorporating the number of interventions (application of bio-control agent) used by good solutions could be used to effectively drive the crossover process. These approaches, CalEB (Calculated Expanding Bin) and TInSSel (Targeted Intervention with Stochastic Selection) both provide mechanisms for crossover of variable and fixed length chromosomes, where each chromosome represents an intervention schedule. CalEB and TInSSel both use the number of interventions present in the parents to calculate the number required in the children, with CalEB utilising a “binning” approach to select the genetic material from the parents, whereas TInSSel contains an element of stochastic selection.

## 4 Experiments

Previous experiments reviewed CalEB, TInSSel and UC across varying initial intervention samples [4],[5]. These experiments were undertaken for initial population samples from min intervention to min intervention (i.e. 1 to 1, where each member of the initial population has 1 intervention) to min intervention to max intervention (i.e. 1 to 50, where each member of the initial population has between 1 and 50 interventions). These differing variances in possible initial interventions enabled evaluation of how initial spread affects each of the crossover approaches in finding a solution. In addition it demonstrates how the initial variance in population affects the

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Table 1: GA Run Parameters

Parameter	Value	Parameter	Value
Population size	50	Crossover probability	1
Number of parents	2	Mutation probability	0.05
Number of children	2	Days in nematode schedule	50
Fitness Evaluations	50 - 500	Nematodes / intervention	1000

robustness of each crossover approach. Current work reviews the quality of solutions produced when all experiments have min intervention to max intervention (1 to 50), which represents the decision maker being unsure of the sample population to use. The aim of this work is to evaluate the search ability of UC, CalEB and TInSSel across varying limits of fitness functions evaluations to ascertain if there is any difference in search ability between these crossover types. The run parameters used for both these and previous experiments are shown in Table 1. Each run was undertaken 500 times and averaged for each fitness function limit. Tournament selection was used to select parents for breeding as it has been shown to provide better or equivalent convergence and computational properties when compared to alternative approaches [2]. The average scores for these experiments along with the associated 95% confidence intervals are depicted in Figures 1 and 2. Figure 1 shows that regardless of the number of fitness functions available, UC solutions require more interventions than solutions returned by CalEB and TInSSel. Figure 2 shows a clear difference in fitness score between TinS-Sel, CalEB and UC for most experiments, with the exception being those experiments where the number of fitness functions are very large (as all approaches have sufficient time to find a solution). This experiment shows that both CalEB and TInSSel outperform UC in terms of intervention usage and quality of solution found over a varying number of fitness function limits. This was also true when experiments were undertaken over varying initial population intervention numbers [4].

## 5 Future Work

In order to better understand the dynamics of the novel approaches, application to varying problem domains is required. Future work will focus on deriving optimal treatment schedules for cancer chemotherapy [9], using the single drug model detailed in [7].

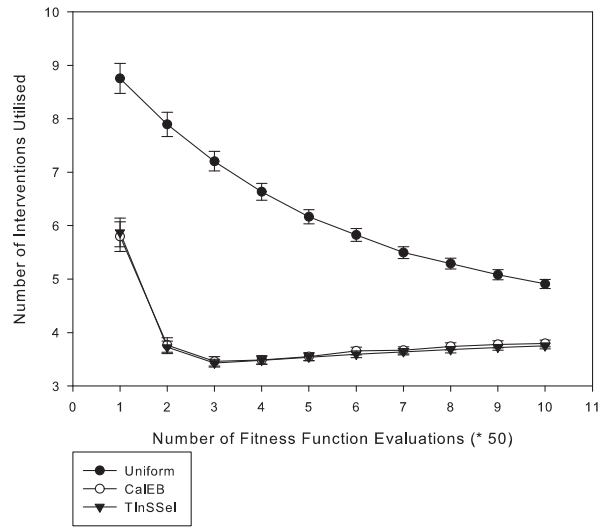


Figure 1: Intervention Utilisation for Solutions

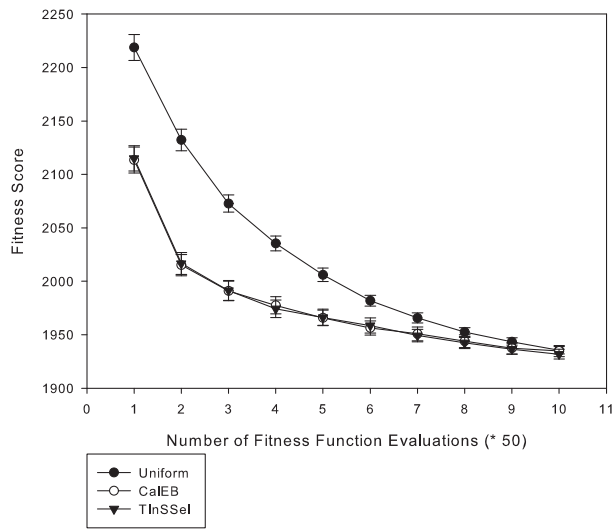


Figure 2: Fitness Scores for Solutions

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