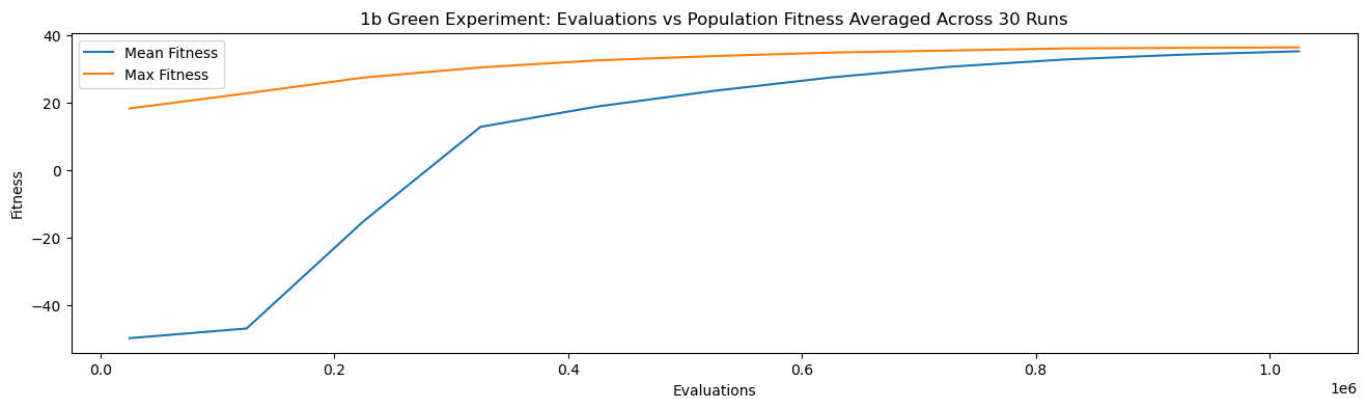
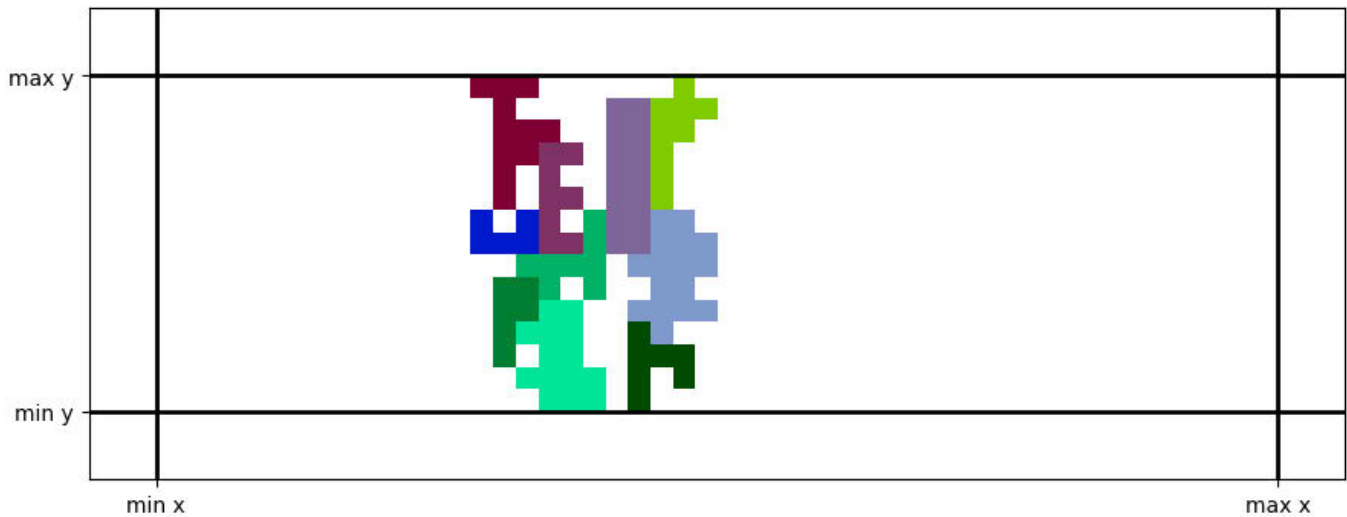


mu	num_children	mutation_rate
	25,000	100,000
		0.075

parent_selection	parent_selection_kwargs	recombination_kwargs
k_tournament_with_replacement	k = 16	method = one-point

survival_selection	survival_selection_kwargs	mutation_kwargs
k_tournament_without_replacement	k= 16	bonus= False



1b data mean: 36.3

1b data stdv: 1.2635472781569872

1a data mean: 25.033333333333335

1a data stdv: 1.5643293888377885

p-value: 1.618304511960623e-36

Because our p-value is so close to zero this is strong evidence to suggest that the two algorithms are unlikely to be similar. More plainly, the p-value shows strong support that the differences between the two algorithms are statistically significant