## Supplementary Information

In this supplement, we survey several models in the current literature of both Theory of Evolutionary Computation and Population Genetics and analyse how well our framework fares at being able to implement them.

It should be noted that the purpose of our model is to identify structural similarity between models in population genetics and evolutionary computation. The ultimate goal of this is to initiate a transfer of results, methods and tools between the two fields. As such, we limited the scope of our framework to discrete finite search spaces, since it seems that most theoretical results focus on these. Virtually all papers in the Theory track at GECCO (the major conference on Evolutionary Computation) can be represented in our framework. Here, we chose to look at papers from the Evolutionary Computation at large, namely several issues of both IEEE Transactions of Evolutionary Computation and Evolutionary Computation Journal. This literature includes many examples of algorithms that are used for practical purposes, which have very little theory behind them. Moreover, many models in this literature deal with continuous search spaces, which are not formally included in the current framework. The major difficulty in including these models is formal: the fact that property V1 and M2 do not carry immediately to continuous spaces. The spirit of these properties, that define variation operators in general, and mutation operators in particular, is easy to understand intuitively:

Property V1 states that variation operators should generate diversity isotropically or symmetrically. For continuous spaces this could be formalized by demanding that mutation operators generate symmetric distributions of genotypes.

Property M2 states that repeated applications of the mutation operator should be able to generate the whole of the search space. The equivalent for continuous spaces could be defined in terms of distributions: repeated applications of the mutation operator should have as a limiting distribution the uniform distribution over the whole search space.

As such, it seems feasible that analogous properties could be formally defined for continuous spaces but at the cost of significantly increasing the mathematical complexity of the framework. The same is true for papers focusing on genetic programming or other algorithms whose search space is tree-based: including them would significantly increase the mathematical complexity of the framework.

Many of the models in the PG literature deal with structured populations. Even though we do not define the necessary migration operators, the framework can represent these models since it represents populations as "sequences", which extend the notion of sets so that duplicate elements can co-exist and also that their order (position in the sequence) is important. As such, structured populations can be represented by a partition of the population sequence. Migration operators would be aware of this partition and their function is simply to move individuals between these partitions. Again, we chose not to include this extension here in order to avoid unnecessary mathematical complexity.

Below is a breakdown of the numbers of relevant papers, if they can be casted without modifications to the framework, or if they need the continuous extension.



## Papers in Population Genetics



"Shape matters: Lifecycle of cooperative patches promotes cooperation in bulky populations" by Misevic et al. [1]





# Papers in Evolutionary Computation

#### "On a vector space representation in genetic algorithms for sensor scheduling in wireless sensor networks" by Martins et al. [16]





Lässig and Sudholt [29]





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