# Analysis of real world eco-evolutionary data using computational modelling and statistical inference

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#### **Abstract**

We present a quantitative method towards analyzing eco-evolutionary data where trait values *z* are recorded over a fixed time period. Statistical methods towards deriving confidence intervals towards parameter estimation are discussed and we see how we can arrive at a plausible estimate for environmental difficulty by means of the TEST (*Temporal Evolutionary Simulation Tool*) model. We briefly discuss the probabilistic inference regarding the mechanism of selection in light of the model.

#### Introduction

Under Charles Darwin's traditional theory of natural selection, a population of individuals in some locus is expected to develop towards increased fitness with respect to their environment as time passes. In his landmark publication, *On the Origin of Species*, Darwin informally defines natural selection by the following:

[...] If variations useful to any organic being ever occur, assuredly individuals thus characterized will have the best chance of being preserved in the struggle for life; and from the strong principle of inheritance, these will tend to produce offspring similarly characterized. This principle of preservation, or the

survival of the fittest, I have called natural selection.

Douglas Futuyama, a prominent figure in the field of evolutionary biology, defines adaption, a term closely linked with natural selection, as "a characteristic that enhances the survival or reproduction or organisms that bear it, relative to alternative character states". Fitness is an attribute which reflects the reproductive success or survivalistic ability of an individual. In this paper, we will denote fitness by  $\omega$ , where  $\omega_i$  represents the corresponding fitness of some individual with an index i in the population.

The term trait value is denoted by z and represents the quantitative measure of some biochemical, morphological, physiological or anatomical structure or construct which is subject to genetic variation. As we will see,