

The foundations of evolution and population genetics respectively can be found in studies at the level of the organism. Such models will virtually always focus on intrinsically discrete features/characters such as nucleotides or the absence-presence of a character capturing a continuous feature. However, this precludes a large class of characters that are of major interest in biology and cannot be well reduced to discrete characters, namely shapes and patterns. This project will only focus on simple models of shape evolution and their application to leaf shapes.

Shape analysis is a well established, but difficult, topic that is approached through a variety of models. Shape/form/patterns are considerably more complicated than other biological because it cannot be constructed by a cartesian product [vector] of real numbers, integers, set or group and thus the standard concepts describing relationship between entries in a vector, such as correlation or dependence are insufficient as shape can be a highly structured object.

The specification of a shape might involve both discrete components [for instance a topological classification] and continuous parameters like sizes, lengths etc. The latter implies that there often is a transfinite number of shapes and it is rare to observe a transfinite number of variables. Often a shape is then estimated by observing/measuring landmarks on the shapes. This is sometimes seen as a necessity but can also be a source of error, since choosing these landmarks are not perfect. New methods attempt to avoid the specification of landmarks and, in principle, operate on functional data (Jones and Moriarty, 2011 Ramsay and Silverman 1998)