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Persistent Homology of Function Spaces

Jonathan Block, Fedon Manin, and Shmuel Weinberger

Persistent homology is a fundamental tool for measuring how topology changes for filtered spaces as one moves through a filtration. It was initially introduced as a tool for understanding the geometry of proteins, and it has become the most invariant used in topological data analysis.

If X and Y are finite complexes, the functions from X to Y are important objects of study. It is possible to model gene expression space as such a space where X is a circle and Y is a finite simplicial complex (whose vertices are proteins codded for by individual genes).

Various objects of biological interest are encoded in the local minima of a fitness function on this space. Tuca Auffinger has made the intriguing suggestion that critical points of higher index also are important in the non-edquilibrium dynamics of evolution. While the equilibrium measures of critical points are determined by "their fitness", the non-equilibrium dynamics, and the interchange between different critcial points, the "fitness barriers" are determined by the top endpoints of persistence intervals.

As pointed out by Pansu in a recent Bourbaki seminar, although there has been a lot of recent progress on 0 dimensional PH of function spaces, there has been essentially nothing proved about higher homology.

Our work, which has aspects of biomimicry, uses a mechanism similar to the action of enzymes in improving the rates of chemical reactions (to make them feasible) gives the first mathematical results on this problem:

Theorem (Block, Manin, Weinberger): If X is a finite complex and Y is one with finite homotopy groups (or whose rational homotopy type has positive weights) then in each dimension d, the persistence barcode of the function space with respect to Log(L), where L(f) is the Lipschitz constant of f consists of bars of infinite length (that are topologically invariant) or of uniformly bounded size C(d). This size depends only on the metric on Y.

This is completely false in general when Y is not simply connected (although it is true when Y has a nonpositively curved metric).

The techniques lead to the possibility of studying the geometry of function spaces which had heretofore only been considered as homotopy types. Whether it leads to biological insights is so far unclear. Further directions which suggest new mathematical problems include:

Studying random walks based on a mixture of a fitness function and a disorder "temperature" which might be constant or not (modelling a species choosing to allow more mutations in different settings), allowing more general types of genetic modification that point mutations, the implications of sex, and consideration of evolutions of measures on function spaces (i.e. the quasispecies model).

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