

論文の内容の要旨

論文題目 A Study on Application of Persistent Homology to
Nonlinear Time Series Analysis
(非線形時系列解析に対するパーシステント・
ホモロジーの応用に関する研究)

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Persistent homology is a concept used in the field of topological data analysis. Homology groups represent the topological features of a shape: connected components, holes, voids, and so on. On computers, a shape is often given as a point cloud. A growing sequence of a shape, or a filtered simplicial complex is constructed from a point cloud. Persistent homology groups represent the appearance and the disappearance of the topological features of a filtered simplicial complex.

The nonlinear time series analysis provides a method to reconstruct an orbit in the phase space from an observed time series. The method is called attractor reconstruction. Attractor reconstruction is achieved with delay-coordinates. Delay-coordinates map observed values into a vector which consists of time delayed values.

The combination of persistent homology and attractor reconstruction enables us to compute the shape of an orbit. The topological features of reconstructed attractors are used to detect such dynamical properties as the periodicity of the observed signal or to classify the signals. It is needed to select the time delay of

delay-coordinates. The thesis investigated a criterion to select the delay and observed the behavior of the criterion applied to periodic signals and chaotic signals. The thesis proposed an index called the most significant death value (MSDV) and the criterion that the delay that maximizes an MSDV should be selected. The thesis observed that the criterion was effective for several non-chaotic signals with periodicity. However, the criterion was not effective for several chaotically periodic signals. The thesis compared the criterion with the mutual information, which is a method widely used to select the delay. The criterion produced the results better than the mutual information. Although the results did not give a complete solution, it may give us an insight to use the combination of persistent homology and attractor reconstruction.

The computation of the persistent homology of more than thousand points sometimes takes more than a day. It also takes more than hundred gigabytes of memory. The thesis proposed a method to make the computational time faster and the computational space smaller as long as the input is a continuous curve. The input time series was assumed to be continuous and the curve was assumed to be given as a set of sampled points. The proposed method obtained the line segments approximating to the given curve and computed the persistent homology of the line segments, instead of the points. The computational time of the proposed method was made ten times or more faster and its computational space was made ten times or more smaller. The proposed method also smoothed out the noise of data. It is obvious that these results are useful for the practical applications of the combination of persistent homology and attractor reconstruction.