(Future Research, Hiroe Oka):

For future research I will first proceed the theory of topological computation as described in the "Summary of Previous Research Results. We are considering three main subjects: (A) switching system, (B) time series arising from nonlinear phenomena and Reservoir Computing. (C) gene regulatory network as a coupled dynamical system.

(A) The term "switching network" refers to a network coupling dynamical system that appears in the life sciences, in which the smooth coupling function is replaced by a step function. This class was proposed by Leon Glass et al. For switching networks and their singularly perturbed network dynamical systems, we will consider a more efficient way to describe the global dynamics based on the special characteristics of them using the framework of topological computation theory by improving a simple calculation method for CM graphs that takes advantage of their features.

For the two elements, the general classification of CM graphs can be performed relatively easily by classifying the local structure near the discontinuity line of the step-type coupling function in the phase space. And it is successful in proving that the Morse decomposition persists for network coupled dynamical systems perturbed by a smooth function of the non-linearity from a step function. I will generalize these results to be applicable to higher dimensions. To do this, we need to identify general properties of the switching system that can be extended to higher dimensions than the simple two-element case. We first need to work on refining the ideas we have now.

(B) I attempt to apply the theory of topological computation to data such as time series arising from nonlinear phenomena, for which the equations are not given.

Time series analysis of dynamical systems refers to the retrieval of information on the original unknown dynamical system, using time series data obtained from experiments or observations of nonlinear phenomena that are presumed to be driven by an unknown dynamical system. Such time series analysis of dynamical systems started with Ruelle's idea in the 1970s and was improved by Takens ([T1981]) and Sauer ([SYC1991]). Unlike the conventional method of embedding attractors in time series data by Takens and others, I can obtain information on global structure including unstable dynamics from time series data, by the CM graph using the framework of topological computation theory, which may be important from an application viewpoint.

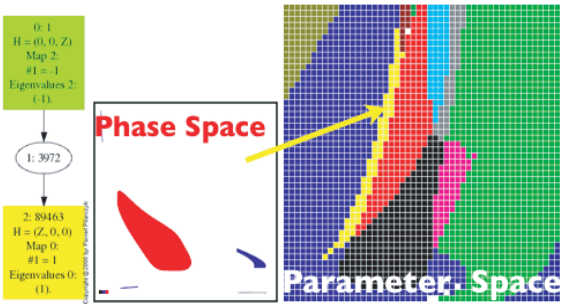

Figure 1: cmgraph の出力例

Based on these results, we will also consider a general and accurate formulation of time series analysis that can be applied to data obtained from experiments and other sources. We will present an efficient way to collect data and parameter dependencies of important invariant sets from time series data of images using persistent homology.

Apart from the framework of topological computation theory, we will also discuss reservoir computing, which has attracted much attention in recent years as a method for handling data such as time series. Reservoir computing is a type of machine learning method that uses regression neural networks to infer the underlying dynamical system from data such as time series, It is extremely fast and inexpensive to learn, and has made remarkable progress in technology and applications, However, research on the mechanism from the viewpoint of dynamical systems is still limited and only recently started. From the dynamical systems point of view, the branching reproduction of phenomena related to the surrounding parameters from the data of fixed parameters of logistic maps or Lorenz systems, which are often treated, is desirable to be clarified purely from a theoretical viewpoint. Moreover it is particularly interesting and practically significant to extend the framework formalized by Hara and Kokubu to cases where the dynamical system is not a diffeomorphism but a endomorphisms.

(C) Gene regulatory network as a coupled dynamical system that appear in life sciences are large-degree-of-freedom dynamical systems consisting of many elements with several conditions imposed on ordinary differential equations. I will refine their theory of gene regulatory networks to the case of a coupled system of gene regulatory networks of the same type and I further construct a symbolic model using the topological computational theory of dynamical systems.

References:

[T1981]Takens, Detecting strange attractors in turbulence, Lecture Notes Math., No. 898, 1981, pp. 366-381, Springer.

[SYC1991] T.Sauer, J.Yorke, M.Casdagli, Embedology, J. Stat. Phys. 65 (1991), 579-616.