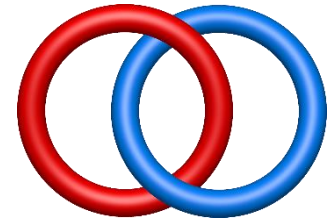


Proteins are the group of natural compounds with exceptionally wide range of activities. The function and properties of a protein (e.g. its thermal resistance) are strictly connected with its structure – spatial arrangement of the main chain. The main chain can arrange linearly, or can be entangled forming knots. Moreover, it can be stiffened with additional covalent bonds, forming closed loops. Such loops can thread one another forming a structure called a link (Fig. 1). Links are present in nucleic acids (RNA or DNA) and were synthesized by organic chemists, but they were unnoticed among proteins. However, my preliminary results show, that the links are present as well in proteins and they can be very important for protein function.



*Fig. 1 The simplest non-trivial link - the Hopf link.*

The first aim of my project will be to search through all known 3-dimensional structures of proteins and extract those, whose main chain forms a link. To this end I need an automatic method for structure analysis, using mathematical tools from knot theory, Gaussian Linking Number and so called minimal surfaces, which provide a mathematical description of soap bubbles. All the structures found will be made public as a web database and the optimized method will be used to make a server with which everyone will be able to detect links in any structure of interest.

The nascent protein chains do not possess their natural structure. In order to fulfill their biological function, they first have to fold. In case of proteins with complex spatial structure, the folding can be problematic, as it could require e.g. threading of one tail through the covalent loop. Therefore, the next goal of my project is to analyze the folding pathway of proteins with link structures and their properties in terms of their thermodynamics. To that end I will design appropriate model which will enable me to conduct fast and reliable simulations of protein dynamics in different conditions. Using this model I will characterize the folding process and behavior of proteins possessing links.

The model, as well as the database created earlier will be used to detect the influence of links on the proteins' properties and function. My preliminary studies show, that in spite of the potential difficulties in folding process, the link structure is present in animal, plant and fungal proteins, and therefore it seems to be especially important. My last goal is hence to show why it is so precious.

The results of this project will serve the scientists from different areas. The biophysicists will get the model useful for broad range of proteins, as well as new ways of describing protein dynamics. The biologists will get another piece of information about possible protein structures and folding processes. Especially important seems to be explaining the relationship between structure, function and properties of a protein. This information can be then used by biotechnologists, to consciously modify or design proteins with e.g. exceptional stability induced by the protein structure. Finally, the mathematicians will get an impulse to develop new techniques, e.g. from knot theory and all the internet users will get an access to an easy and intuitive browser of proteins with link structure, and will be able to analyze their own structures.