The dynamic development of modern medicine and molecular biology is based on complex measurement techniques such as sequencing, microarrays, and flow cytometry. They make it possible to learn about the molecular mechanisms occurring in the cell, the molecules involved in them, and to characterize the genetic sequences encoding these molecules. The human genome, in addition to coding sequences, contains information about the interrelationship, i.e. the complex regulation pattern of genes, which depends directly on the chromatin organization. The families of transcription factors are responsible for tissue-specific regulation both during the organism development and in disease-related processes.

The availability of the sequenced genomes of many organisms allows us to understand the molecular evolution of the regulatory process itself. It turns out that some features arise as a result of the so-called *phylogenetic exaptation* where a certain previous evolutionary adaptation begins to play a new function. As an example, consider the regulatory region for the FOXF1 and TBX4 genes, that in all species are associated with lung development, and their disturbances in humans lead to fatal developmental disorders in newborns. It contains a highly conserved *non-coding region* that evolutionarily first appeared in the genomes of *coelacanthiformes* and *lungfish.* The role of this regulation in evolutionary adaptation at the exit of aquatic animals to land is very interesting. We postulate that these enhancers predate animals emerging from water and terrestrial adaptation. Through exaptation, they may have been co-opted in fish to permit the critical steps of lung formation that were needed for this evolutionary leap forward 390-360 MYA.

The enormous selection pressure associated with such a leap means that evolutionary benefits may be associated with genome instability. Events that drastically accelerate evolution are the burst of transposons activities line in the genomes of lungfish fish. The challenge we undertake in the project is to model the evolution of genetic regulation encoded by chromatin interaction and studied by HiC technology, in response to structural variations in the genome. We want to use the previously developed tool for the analysis of regulation disorders (https://tadeus2.mimuw.edu.pl/) and create a HiC experiments database for genomes altered by structural variants, which will be used as a training set for the model. The deep learning-based model will make it possible to predict changes in chromatin organization induced by structural variants of the genome and to understand the process of phylogenetic exaptation of tissue-specific non-coding regulatory regions.

Inference from gigabytes of data describing genomic architecture, dynamics and evolution of regulation requires the use of mathematical models and computational methods. Our previous experience in the analysis of the proliferation of transposon sequences, the stability of the human genome and the dynamics of regulation in disease processes will allow us to propose new algorithms that will be helpful in biomedical analyzes while being a non-trivial contribution to the development of machine learning methods.