The Computational Molecular Biomedicine group is pursuing N major research topics as well as collaborative projects in diverse biomedical research areas. Most projects combine broad knowledge of molecular biology with state-of-the-art mathematical modeling and machine learning techniques.

1. Proteomics data analysis method and software development

The goal of this project is to develop high-performance, high-throughput analysis methods and software tools for proteomics datasets. In particular, we are interested in peptide identification and quantification from mass spectrometry data.

1. Integrative analysis of high-throughput biomedical datasets
2. Mathematical modeling and simulation of chromatin folding process