

**Computational biology.**

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**ABSTRACT**

Computational biology is a multidisciplinary area that involves the development and applications of data analytical and theoretical methods, mathematical modelling and computation simulation techniques to the study of biological, behavioural, and social systems. Biomedical image analysis is a fast evolving field driven by the advancement of imaging modalities and high content screening techniques. Many clinical applications are also emerging that use biomedical image processing for decision support. Computational biology which covers the method development and applications, the latter notably in pharmaceuticals and medicine. On methodical side we perform research on the analysis of biological sequences(including recombination, viral evolution and computational epigenetic) analysis and prediction of protein structure and function, analysis of intermolecular interactions and interaction networks, gene and protein expression patterns, computational drug screening and drug design. On the application side, we focus on the diseases HIV/AIDS, where we analyze viral drug resistance patterns as well as variants of viral entry into the host cell, HCV/Hepatitis C, where we contribute to uncovering the molecular basis of host –pathogen interactions and neurodegenerative and auto immune disease, where we study underlying protein interaction networks.