Biology Msc from 2018

Name of the specialisation:

Bioinformatics (BINF)

Bioinformatics is basically about the application of computer-based approaches in order to advance the scientific understanding of living systems. Practically, it helps to make sense of data that are generated by various high-throughput technologies at an exponentially growing rate and can lead to the generation of testable hypotheses directing biological research into new directions.

OVERVIEW OF THE FIELD

Biological sciences are being revolutionized by various high-throughput technologies producing massive amounts of data. This is a fantastic opportunity that enables researchers to gain a much deeper understanding of all aspects of life, including how species evolved, how certain mutations cause cancer, what types of cells make up the human body, how the brain functions and ages, how can we find better drugs and biomarkers for treatment and diagnosis of various diseases, how to design better crops and so on. In parallel, there is an increasing demand for bioinformaticians: experts who can solve problems arising from the management and analyses of biological data using various computational tools. This specialization complements the core biological knowledge with basic programming, algorithmic and data analytic skills and demonstrates how computational skills can be used to address various biological problems.

TEACHING CONTENT

Without assuming prior knowledge of programming, biology students will learn the basics of programming using the PYTHON language and data science skills based on R. The specialization also includes subjects on bioinformatics algorithms, molecular phylogenetics, structural bioinformatics, systems biology and the bioinformatics aspects of various types of omics data. In collaboration with the Physics Institute, there are specific subjects on the emerging field of data science. All courses have a very strong practical focus, encouraging thinking and problem solving instead of passive learning.

The core modules are:

PYTHON programming for biologists

During the course, students will learn how to navigate the linux operating system and become familiar with the basics of programming using PYTHON, one of the most commonly used programming language in bioinformatics. During this practice oriented course, they will write short scripts and encode simple algorithms that are relevant in biology and bioinformatics.

Computational Biology Algorithms

Students will become more familiar with the most fundamental bioinformatics algorithms by implementing them, and will get hands-on experience on how these algorithms can be used to solve biological problems. This course will also advance their programming skills and algorithmic thinking.

Analysis of Omics Data

During the course, students will learn the fundamentals of computational analysis of large biological datasets. They will learn about how to process, analyze and visualize data generated by various omics approaches, including genomics, transcriptomics, metabolomics, and proteomics. They will learn how to interpret the results in a biological context, and identify and apply follow-up analyses based on this.

Structural bioinformatics
Macromolecular structures are fundamental to our understanding of biochemical processes, as well as to our ability to manipulate them through various drug molecules. This course mostly focuses on proteins and covers structure determination methods, classification of protein structures, various structure prediction approaches and fundamental methods to characterize the dynamic properties of proteins.

Phylogenetics
This course gives a succinct introduction to modern phylogenetics methods with an emphasis on probabilistic methods. Starting with the conceptual foundations, the course proceeds by introducing substitution models in an accessible manner, starting with the simplest two state models, and proceeding to DNA models and arriving at state-of-the-art models of sequence evolution.

RESEARCH PERSPECTIVES
Bioinformatics is becoming part of research basically at every Department at the Biological Institute and also at some of Departments of the Physical Institute. Genomics, transcriptomics and proteomics data are used to understand basic biological processes underlying neurological development and diseases, the origin of immune response and antibiotic resistance or to explore the microbiome of water and soil. They develop novel computational tools to identify cancer mutations, understand the structural and functional properties of proteins and interpret the effect of mutations. Theoretical and bioinformatic studies carried out at the University help to understand basic evolutionary events. Bioinformatics is a key component of a project at our university that aims to find new biomarkers for various diseases, such as rheumatoid arthritis, cancer or neurodegenerative diseases.

TEACHERS AND RESEARCHERS

Eszter Ari
She studies evolution from a genomic and bioinformatics perspective. In collaboration with the Biological Research Centre of the Hungarian Academy of Sciences at Szeged, using a set of metagenomics tools she studies how antibiotic resistance appears and spreads in a bacterial population. She is also developing a functional enrichment analyser algorithm and R package.

Zsuzsanna Dosztányi
She performs studies on intrinsically disordered proteins and protein structures using mainly bioinformatic tools. Her current research is mainly focused on so-called linear binding motif-based protein-protein interactions. She developed various highly-cited bioinformatics tools and is the winner of the Momentum Grant.

Zoltán Gáspári
He studies the structural and dynamical properties of proteins with both experimental and computational methods. His current focus is on proteins involved in postsynaptic signal

transduction. He uses structure modelling and prediction tools as well as calculations that incorporate experimental parameters derived from NMR measurements.

Ádám Kun

He is a theoretical evolutionary biologist studying the origin of life and the origin and evolution of cooperation. He has a formal training in computer science and teaches computer programming for biologist since 1999. He has learnt bioinformatics from Pauline Hogeweg, the researcher coining the term.

Gergely Szöllősi

My research is best described as "model based evolutionary genomics" and is based on the recognition that our understanding of biological systems is often limited not by the lack of data, but by our ability to extract information from already available large scale datasets. My aim is to develop a coherent treatment of evolutionary process at different time scales, from the diversification of species over hundreds of millions of years, to the decade long development of tumours. Our research focuses on two topics that are currently the subject of intense international interest, each aiming to extract quantitative information on the underlying biological processes from large genomic datasets: 1.) reconstructing a dated tree of life from complete genomes using phylogenetic discord as molecular fossils and 2.) understanding cancer evolution in hierarchically differentiating tissue using tumour genomes.

More practically, my group develops bioinformatics methods (in particular phylogentics and phylogenomics software including ALE) and computational models (most recently stochastic simulations of somatic evolution) and uses these together with genome-scale datasets to address open biological questions.

CAREER OPPORTUNITIES

Bioinformaticians enjoy a wide selection of career paths with an overall positive job outlook. They can pursue academic careers: enrol to PhD programs and become part of research groups at prestigious universities and academic research centres in Hungary and abroad. They can go on and establish independent research groups by developing novel computational tools or addressing original research questions, taking advantage of publicly available datasets. Bioinformaticians can also hold positions at core facilities that assist other academic or clinical researchers. There is also a growing demand for bioinformaticians in the industry. Job opportunities are typically, but not exclusively, at companies doing large-scale analysis of genomic and/or transcriptomic data, mostly with the aim of supporting developments and therapies in personalized medicine.