

Institute of Cell Biology and Neuroscience

Professor Dr. Ingo Ebersberger

Department:
Applied Bioinformatics



Brief Biography

How can evolutionary relationships between genes or species be reconstructed on the basis of molecular data? Which information on biological functions can this data provide? How did protein complexes evolve? Questions like these are at the focus of Professor Ingo Ebersberger's research. Existing species whose genomes have been decoded completely or partially are the starting point of his research. He analyses this data with regard to the differences in their DNA and protein sequences. In this context, his objective is to identify so-called orthologous genes, i.e. related sequences in different species, whose evolutionary lineages have split in the course of the speciation processes. In 2006, based on the comparison of such data, Ebersberger was able to show, for example, that the chimpanzee is not our closest relative with regard to approximately one quarter of the human genome.

Ebersberger also investigates protein complexes with specific functions. In the process, he considers the question of how the functional equivalence of protein sequences can be predicted with the aid of bioinformatic methods. In this context, among others yeast with its biosynthesis of ribosomes frequently serves him as a model organism. These results allow conclusions as to the point in the course of evolution at which the functional complexes under investigation probably developed.

For his analyses, Ebersberger develops algorithms as well as data comparison and simulation programs. "In order to find the most reliable hypothesis for our reconstructions, we test our results, if possible, on several meticulously selected and independent data sets and in comparison with previous research results. In case of doubt, a more sensitive analysis of the data is performed", reports Ebersberger.

In his work he cooperates with the Centre for Integrative Bioinformatics in Vienna, the Huazhong University in Wuhan, China, and the Carnegie Mellon University in Pittsburgh, Pennsylvania (USA). "Our objective is to combine the knowledge of different biological research facilities on evolution to an overall picture", explains Ebersberger.

In the "Bioinformatics" Bachelor's and Master's Curricula, Ebersberger not only desires to communicate the specific knowledge at the interface between biology, informatics and mathematics to the students, but also to stimulate them to critical and open-minded thinking.

Ingo Ebersberger studied biology at the University of Mainz. In 2003 he received his PhD from the University of Leipzig with a dissertation on a DNA-sequence comparison between humans and chimpanzees. As postdoctoral researcher and assistant professor, his research at the University of Düsseldorf was on the analysis of phylogenesis of animals and fungi based on gene fragments and on questions of the evolution of primates. In addition, Ebersberger taught bioinformatics in Düsseldorf. In 2006 he changed to the Centre for Integrative Bioinformatics at the University of Vienna. His research foci there were, e.g., work on the prediction of functional equivalence of proteins, the collection and interpretation of relevant data, and the phylogenesis of eukaryotes. In 2012 he was appointed professor of applied bioinformatics at the Goethe University in Frankfurt.

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