



Martin Vingron has done his PhD in computational biology at EMBL in 1991. At the time and for a number of years of postdoctoral training his research has focused on the analysis of protein sequences, sequence analysis, sequence comparison, and molecular evolution. Methods of discrete optimization were used for the design of comparison algorithms and probability theory was applied to answer questions of significance of computational results. Later, as a department head at the German Cancer Research Center, his focus shifted towards the processing and mathematical analysis of DNA microarrays. Accordingly, the methods largely drew on statistical data analysis techniques. Recently his research has been focused on utilizing gene expression data as well as evolutionary data for the elucidation of gene regulatory mechanisms.