Professional experience

After my apprenticeship at the Swiss Bank Corporation I worked for several years in profession-related fields. To improve my common knowledge I decided then to prepare for the “Matura”. During these studies I became fascinated from biology and decided to study microbiology and biochemistry at the University of Bern. During my thesis work and one year postdoc in Dr. W. Lesslauer’s lab in Bern I worked on the characterization of membrane receptors on human T-lymphocytes. These receptors play an important role during the process of immune responses and we were able to characterize some of their important features. Because the work in Dr. Lesslauer’s lab was focused on protein chemistry I decided to learn molecular biology. I spent three years with Prof. Kohli in Bern learning these techniques. During this postdoctoral period I designed new shuttle vectors for the transformation of the yeast Schizosaccharomyces pombe and the bacterium E.coli. With these vectors I was able to introduce foreign genes into the yeast and/or into the bacterium. This tool allowed me to analyze genomic elements which stabilize such vectors. I also investigated the function of promoters of higher eukaryotes in this yeast and I was able to introduce a gene for antibiotic resistance into the yeast.

In 1988 I entered Hoffmann-La Roche in Basle in the department of Infectious Diseases. I specialized in a DNA gyrase inhibitor program. DNA gyrase is an essential bacterial enzyme and therefore a good target for antibiotics. I isolated and purified this enzyme from E.coli and established assays for testing potential antibiotics deriving from a natural compound. This was detected during a screening program and a chemical program was started to synthesize derivatives of it. In order to improve our knowledge of the function and the structure of this enzyme in later collaborations we cloned, purified and crystallized many subdomains of the enzyme in the presence of an ATP analogue or in the presence of inhibitors. I also performed some studies to characterize the mechanism of the enzyme and the influence of DNA gyrase inhibitors on this mechanism and on the development of resistance.

Over the years I also started new projects with the goal to find inhibitors for other essential bacterial enzymes.

Because the methods for genetic analysis have been drastically improved over the last few years I wanted to learn these techniques. Since 1997 I have worked on the DNA microchip technology as a visiting scientist at Roche Bioscience in Palo Alto. This technology provides methods to determine simultaneously the relative abundance of thousands of genes expressed in different tissues. The results can be used to profile complex diseases and to discover novel disease related genes. I was able to establish one of the scientifically most accepted techniques in Renu Heller’s lab at Roche Bioscience. I could also use this technique to profile various human

diseases and to evaluate animal models of human diseases. I initiated in collaboration with a postdoc from the Stanford University a project to profile the changes in gene expression in a mouse model for multiple sclerosis.

After my sojourn in Palo Alto I have started implementing this new technique in our department for the analysis of the gene expression during bacterial infections. The aim of such studies is to find out which genes are important during a bacterial infection. In this context I have also established strong collaborations with our bioinformatic group in order to be able to analyze all the data by 'data mining' tools.

Because informatics and bio-informatics become more and more important and because I am highly interested in the possibilities and power of this technology, I decided to broaden and to deepen my knowledge about informatics. As a starting point I initiated a course of instruction with the goal to get the diploma as PC-Supporter. The aim of this course is to train people to such a level that they will be able to act as 'Power-PC-User', as PC-Supporter or as PC-Trainer. As mentioned before, this was only a starting point, but the next steps was to improve my knowledge in statistics and finally to step into the field of knowledge management and data mining.

After getting my diploma as PC-Supporter I started as data mining consultant at Predict AG, Reinach, in the Pharma Business Unit. There, the work was mainly centered on the areas of Data Mining, Data Warehousing, Knowledge Management, Statistical Modeling and Artificial Intelligence/Neural Networks. The large amount of data produced in each research project today does not allow a deductive investigation. New advances in inductive analysis methods use techniques, which are usually summarized in the literature as "Data Mining". These methods combine classical statistics (e.g. logistic regression, clustering), together with artificial intelligence methods (neural nets, decision trees, etc.) and enable the analyst to investigate large amounts of data.

Because Genedata is a leader in developing computational data analysis systems for the drug discovery process, an area where I could bring in my biological experiences much better, I joined this company with the task to support scientifically Genedata' customers and to communicate the customers need to the software developers. The company specializes in the computational analysis of genomes, transcriptomes, proteomes, metabolomes and high-throughput screening, and offers a network of communication software modules, each of which addresses a critical step in the product development cycle of life science companies. Genedata is a leading provider of high-volume data storage and high-throughput analysis software for functional

genomics research and Genedata’s solutions empower scientists to extract relevant information from large, complex biological data sets generated by current high-throughput technologies.