

Preface

For the last three decades we have been witnesses of the exponential growth of biological data in repositories such as GenBank, Protein Data Bank, UniProt/SwissProt. The specificity of the data has inspired the scientific community to develop many algorithms that can be used to analyze the data and draw useful conclusions. A huge volume of the biological data caused many of the existing algorithms to become inefficient due to their computational complexity. Fortunately, the rapid development of computer science in the last decade has brought many technological innovations that can also be used in the field of bioinformatics and life sciences. The algorithms demonstrating a significant utility value, which have recently been perceived as too time-consuming, can now be efficiently used by applying the latest technological achievements like multithreading, Graphics Processing Units (GPUs), or cloud computing.

The book focuses on proteins and their structures, protein structure similarity searching carried out at main representation levels, and various techniques that can be used to accelerate similarity searches. The content of the book is divided into four parts. Part I provides a formal model of 3D protein structures for functional genomics, comparative bioinformatics, and molecular modeling. Part II focuses on the use of multithreading for efficient approximate searching on protein secondary structures. Parts III and IV concentrate on finding 3D protein structure similarities accelerated with the use of GPUs and cloud computing. Both parts describe the acceleration of different methods.

So, why proteins?, somebody can ask. I could answer the question by following Arthur M. Lesk in his book entitled *Introduction to Protein Science: Architecture, Function, and Genomics*. Because proteins are where the action is. But in fact, I have fallen in love with the beauty of protein structures at first sight inspired by the research conducted by R. I. P. Lech Znamirowski from the Silesian University of Technology in Gliwice, Poland. I decided to continue his research on proteins (Fig. 1).

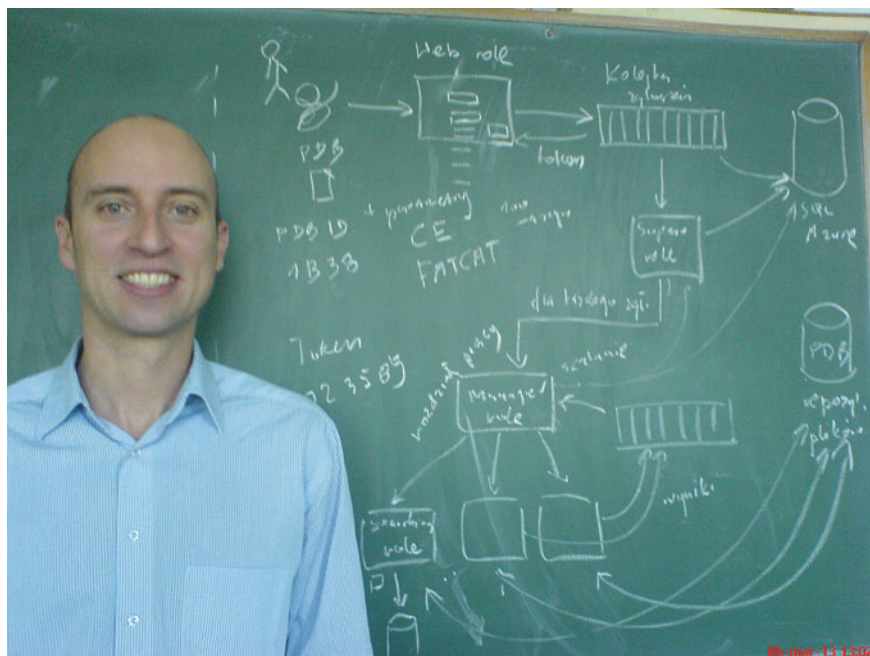


Fig. 1 Preliminary architecture of the cloud-based solution for protein structure similarity searching drawn by me during the meeting (March 6th, 2013) with Artur Kłapciński, my associate in this project. Institute of Informatics, Silesian University of Technology, Gliwice, Poland

I believe this book will be interesting for scientists, researchers, and software developers working in the field of structural bioinformatics and biomedical databases. I hope that readers of the book will find it interesting and helpful in their everyday work.

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