The Bielefeld University Bioinformatics Server
Alexander Szybya, Jan Krüger, Henning Mersch and Robert Giegerich

Abstract
The Bielefeld University Bioinformatics Server (BiBiServ) supports Internet-based collaborative research and education in bioinformatics. Currently, 29 software tools and various educational media are available. These include tools from different areas such as Genome Comparison, Alignments, Primer Design, RNA Structures and Evolutionary Relationships. The BiBiServ resources are accessible at http://bibiserv.techfak.uni-bielefeld.de/

BiBiServ Tools
Here, we focus on the seven most prominent or recent tools on BiBiServ.

REPuter
Efficient detection of various types of repeats
REPuter [1] uses efficient algorithms and data structures to locate exact repeats in linear space and time. These exact repeats are used as seeds from which significant degenerate repeats are constructed allowing for mismatches, insertions and deletions. REPuter provides an evaluation of significance and interactive visualization (see figure 1). REPuter is available online on BiBiServ and as standalone application for most Unix based operating systems.

RNAhybrid
Finding the minimum free energy hybridization
RNAhybrid [6] is a tool for finding minimum free energy (mfe) hybridization of a long (target) and a short (query) RNA. The hybridization is performed in a kind of domain mode, i.e. the short sequence is hybridized to the best fitting parts of the long one. The tool is primarily meant as a means for microRNA target prediction. In addition to mfe, the program calculates p-values based on extreme value distributions of length normalized energies. RNAhybrid is available online as classical webinterface, as WebService and as download for various platforms.

RNAshapes
Folding of “relevant” RNA secondary structures
RNAshapes [8] is a tool for folding of “relevant” RNA secondary structures. In the analysis of RNA and especially when regarding the secondary structure it is often required to take also suboptimal structures into account. As the number of suboptimal structures is very large and even the number of near-optimal structures grows rapidly with sequence length, these kind of analyses are quite expensive. One property of suboptimal structures is that they often only differ in a few base pairs, while maintaining the same overall shape. These are less annoying because in most cases one is interested in those structures that are rather dissimilar, meaning those having a different shape. RNAshapes is an approach to the direct folding of only those structures having a different shape.

WebServices
A new technology for invoking programs on foreign computers are WebServices. Providing access using WebServices makes it possible to use the programs from local computers and compute results remotely without technical knowledge of the programs usage.

WebServices is described in a so called WSDL document, it includes all required information, like the location of the WebService and the interface. BiBiServ is part of the HOBIT project [9], which aims at providing and interconnecting bioinformatics tools as WebServices to offer easy and automated usage of these tools. WebService technology is also used, internally, the web servers offers user interfaces which can be accessed via a webbrowser. Internally the jobs are submitted to the WebServices server which processes the requests on a computing grid. This way, we can provide a high amount of distributed compute resources, which can be used through both interactive web and WebService interfaces. Currently BiBiServ offers four tools on bases of WebServices: E2G[2], REPuter[1], SplitsTree[10] and RNAhybrid[6]. We are currently working on integrating more tools, which will be finished shortly. An overview is also available [11].

Educational Media
The BiBiServ Media & Distance Education section supports teaching in bioinformatics with internet-based multimedia courses. Currently there are five online courses and tutorials available on BiBiServ. The recent ones are:

• The ADP pages: Interactive pages that allow to study and experiment with classical dynamic programming algorithms
• Sequencing and de novo assembly with Illumina Readmational Resources: A Web-based practical course on sequence analysis using resources from all over the world (see figure 5).

References
[9] B. Haus: SADR (Sequence Analysis with Distributed Resources) online course

Figure 1: REPuter: Comparison of mouse chromosome 11 assembled sequence (NCBI - Sep 02) (upper sequence) with small unordered draft contigs (bottom sequence). Matches between the sequences are indicated by connecting lines. The color code of the matches corresponds to the length of the match, red being the longest match of 48891 nt, short matches (about 1000 nt) are colored blue.

Figure 2: Graphical overview produced by E2G by mapping 16.5Kbp genomic sequence from M. musculus (Genbank GI: 28159921) to 4.1 Mill. mouse ESTs.

Figure 3: RNAshapes (Java version) running as applet in a browser, shown one structure of LepomisMcGulosa 5' End

Figure 4: RNAforester: Structure alignment of the human ferritin 5’UTR and the Drosophila melanogaster succinate dehydrogenase 5’UTR. Bases painted in black show structure elements that occur in both structures with the same sequence. Sequences variations are displayed by using red/letters. Bases or base pairs that can only be found in ferritin are printed in blue, while bases that only occur in succinate dehydrogenase are printed in green.

Figure 5: SADR (Sequence Analysis with Distributed Resources) online course