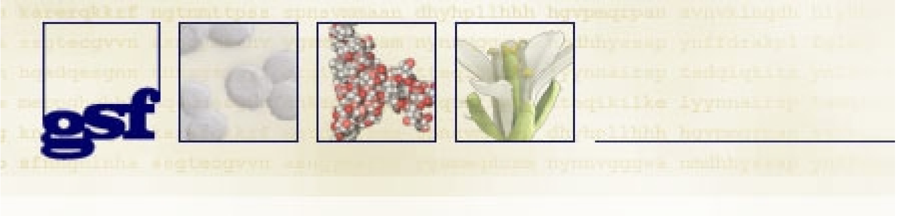

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GSF-Forschungszentrum f. Umwelt und Gesundheit

Job Opportunities in Bioinformatics

The Institute for Bioinformatics (IBI) of the GSF-Forschungszentrum invites applications for several positions in genome oriented bioinformatics. Applicants should have a sound background in computer science/bioinformatics and a strong interest in the exciting field of functional genome analysis.

GSF, the National Center for Envirionment and Health, is a life science research center of the Helmholtz-Association with strong emphasis on functional genome research. The research and development programme of the GSF is committed to the social tasks of environmental and health protection. The results of work performed at the GSF provide an important basis in the issuing of recommended limits in the area of environment and health and are taken up in the decisions of the legislator. The GSF performs studies to establish the scientific prerequisites for maintaining human health and conserving the natural elements necessary for human life. Supported by the Governments of the Federal Republic of Germany and the State of Bavaria, the GSF is a member of the Hermann von Helmholtz Association of National Research Centers.

An active network in functional genome analysis is formed by the mouse mutagenesis programme as well as other high throughput genome analysis techniques for positional cloning, mapping of single nucleotide polymorphisms (SNPs), proteomics and expression analysis. **The Institute for Bioinformatics (IBI/MIPS)** as part of the network is also part of several national and international genome analysis projects. We develop methods for the systematic analysis of genome function and provide the bioinformatics infrastructure for the these projects. In a collaborative effort with the Bioinformatics Chair of Bioinformatics at Technical University of Munich, the IBI also contributes to bioinformatics education.A full bioinformatics curriculum has been established since 2000 joining both Universities, the Max-Planck-Institute of Biochemistry, and the GSF (Bachelors, Masters and Diploma degrees). The Munich area is strongly fostering its bioinformatics research programme. Three full professorships and several associate professors will cover many aspects from theoretical to applied bioinformatics to analyse and explore functional and structural experimental data.

The **MIPS** group was established in 1988 at the Max-Planck-Institute f. Biochemistry. It has been responsible for major international networks in genome sequencing and functional analysis (*S. cervisiae* sequencing and Eurofan Functional Analysis project, *A. thaliana* and *N. crassa* sequencing and genome analysis, see also http://mips.gsf.de). In 1997 our first release of the PEDANT genome analysis suite was published. Currently close to 100 genomes are processed and systematically analyzed by PEDANT. Detailed results are accessible through our WWW-Server, descriptions of our major projects can also be viewed at our home-page. Please see the appendix for a list of recent MIPS publications.

The systematic analysis of genome data requires more than just the development of bioinformatics methods, it also needs the transformation of biological knowledge into computationaly accessible data structures. MIPS aims to bridge exprimental strategies and data interpretation into an integrated environment. Ongoing projects include the expression analysis in tissues of mouse mutants as well as proteome analysis of mammalian and bacterial samples. Several joint projects in functional genome analysis have been recently funded. We are looking for candidates that combine experience in computer science with a strong interest in the biosciences, in particular in the field of genome analysis. Young scientists eager to follow a carreer in the exciting and challenging field of bioinformatics will benefit from the experienced team at MIPS.

We search for candidates for the following projects:

BFAM (Bioinformatics for the Functional Analysis of Mammalian Genomes) is a regional project in Bavaria funded by the BMBF for a 5 years period. BFAM is part of the German Genome Analysis Network (NGFN). The BFAM consortium includes the Munich and Erlangen Universities, the GSF as well as several bioinformatics companies. BFAM comprises 5 areas of activities: applied bioinformatics with focus on the mouse genome and protein/protein interactions, computer science and mathematics, experiment related bioinformatics, bioinformatics infrastructure and teaching. Partners are research groups of the GSF, the Ludwig-Maximilians-University, the Technical University, the University of Erlangen, together with the companies Biomax, Genomatics, and Molecular Networks.

(1) Bioinformatician to build and structure a mouse genome database which will include functional classification of genes, analysis of expression and proteome data, protein/protein interactions, and gene modelling. Functional mouse genome analysis is a major research topic in the GSF (A. Hrabé de Angelis, see http://www.gsf.de/ieg/). The project will operate in close collaboration with our mouse expression (Mousexpress) and proteome analysis efforts. Candidates must have a background in sequence and genome analysis. Experience in database management required. The database will be supported by an experienced annotation group.

(2) Bioinformatician (employment at the Technical Univeristy, Life and Food Science Center Weihenstephan) to develop and apply computer linguistics methods for text retrieval for the mouse genome and protein interaction databases. Design of object oriented data structures in accordance to upcoming standards for data exchange (e.g. I3C). The candidates should have teaching skills to establish advanced courses and seminars of the bioinformatics curriculum.

(3) Biologist with strong bioinformatics interest to collaborate with the experimental groups and their bioinformaticians in mouse genome analysis. The project will include the incorporation of biological data into the mouse genome database. Programming and database skills required.

(4,5)2 Bioinformatics positions to study protein/protein interactions in the mouse genome. The successful candidates will participate in the design and implementation of the database of protein-protein interactions and algorithms for their prediction. Scientists with both biological and computer science background willing to learn bioinformatics skills are encouraged to apply. For computer-oriented applicants specific experience with any or all of the following will be extremely beneficial: Perl, C, SQL, HTML/CGI, Unix. For biologists, familarity with modern biology techniques is essential.

Analysis of human cDNAs. MIPS supports the analysis of complete human cDNAs , in close collaboration with sequencing groups and the co-ordinator (S. Wiemann, DKFZ). Tasks include the systematic analysis of human ESTs, the sequences of full-length cDNA clones as well as the maintenance of the the database of annotated cDNAs.

(6) Biologist/bioinformatician with sound knowledge in sequence data analysis and organisational skills to maintain the established pipeline of EST and cDNA sequence analysis and interpretation and to collaborate with the sequencing groups. Candidates should have a Ph.D. in molecular biology, alternatively a degree in computer science with basic experience in bioinformatics.

Helmholtz Netzwerk Bioinformatics (HNB). The Helmholtz Netzwerk is an association of bioinformatics groups throughout Germany to offer a comprehensive interface to bioinformatics tools in genome and sequence analysis for the academic community. Partners are the DKFZ, the GMD, the University of Cologne, the Max-Delbrück Center, and the Bork-Group at the EMBL.

(7) Bioinformatician with good knowledge of sequence data analysis. Together with two experienced fellows, this position has to implement interactive methods for genome comparison, protein family analysis and systematic functional classification (MIPS functional catalogue). Based on the systematic PEDANT analysis, we will develop methods to apply rule based functional classification. Programming skills required (PERL, C++).

Plant genome analysis (GABI, PlaNet). At the green side of life, MIPS supports the functional analysis of plant genomes. A broad spectrum of organisms is covered from model organisms such as Arabidopsis to agronomically interesting species like barley, rice, banana and others. We are serving as a bioinformatics resource within the german GABI project (Genomanalyse im Biologischen System Pflanze) and as coordinator of a Europe- wide association of plant databases (PlaNet) to setup a europwide plant genome database integrating both genome as well as experimental data.

(8) We are looking for a **biologist** experienced in plant genomics and sequence analysis to join the GABIinfo group. In the group, the successful applicant will collaborate with biologists and computer scientists and participate in the annotation and analysis of genome data, the integration and display of data supplied by collaborators in specialized databases, and the bioinformatics support of collaborating groups. Current projects involve the maintenance of the MIPS Arabidopsis thaliana database, analysis of expression analysis data, EST assembly and annotation, protein/protein interactions, comparative genomics as well as transcription factor binding site and promoter prediction.

Candidates should have a PhD in plant molecular biology, genetics or related science and broad experience in sequence analysis. Background in bioinformatics, basic programming skills (HTML, Perl) will be advantageous. You should be able to take over responsibility for an independent project while integrating your competence into a group effort.

(9) Bioinformatician/ computer scientist

We are looking for a computer scientist or bioinformatician experienced in database integration and software design to join the GABIinfo group. In the GABIinfo group, you will participate in the management and development of the MIPS *Arabidopsis thaliana* database, the PlaNet database and software tools for database integration and plant genome analysis.

You should have a degree in computer science or bioinformatics and experience in database and/or software design and development. Background in biology, sequence analysis and/or genomics will be advantageous. You are enthusiastic and willing to acquire new skills in an interdisciplinary team of computer scientists and biologists.

PROTEOMICSof pathogenic bacteria involves the development of bioinformatics methods for the systematic and exhaustive analysis of 2D-gel patterns based on known genome sequences. The analysis of the profiles recorded for a wide variety of conditions (e.g. knock-outs, pathogenic/non-pathogenic strains) will allow to gain insight into the molecular mechanisms of bacterial pathogenesis. Partners are the Max-Planck-Institute for Infection Biology (P. Jungbluth) and the Univerisity of Greifswald (Prof. M. Hecker).

(10) Computer scientist to build a relational database of protein profiles from 2D-gel experiments that is linked to the genome database and the functional and regulatory properties of pathogenic microorganisms. The project includes the development of methods for data integration as well as applications for the statistical evaluation of protein profiles.

(11) Biologist for the collaboration with the research groups in Berlin and Greifswald to develop, support and maintain the bioinformatics resources of the project. Strong communication and team skills are expected. Sound background in molecular biology of microorgansims (Ph.D.) and good computer handiness are prerequisites for candidates.

(12) For the Institute f. Bioinformatics, we look for a computer scientist with bioinformatics background for the further development of an object-orientated Genome Annotation Management System (GAMS). GAMS will serve as the global platform for functional and structural genome annotation in the future, and will allow for the comprehensive annotation of related genetic elements which are represented and implemented as different classes (e.g. proteins, regulatory sites, tRNAs etc.).

All positions are paid according to the BAT. Application screening will begin immediately upon receipt of curriculum vitae. Maximum consideration will be given to applications received by September 15th, 2001.

The GSF is located in close vicinity to thecity of Munich. The Bavarian lakes and alpes, lifestyle, sports and culture give ample opportunities to relax from science.

Candidates should contact Prof. Dr. H.W. Mewes and submit their written applications to the GSF-Forschungszentrum f. Umwelt und Gesundheit, Institut f. Bioinformatik, 85764 Neuherberg, Germany.