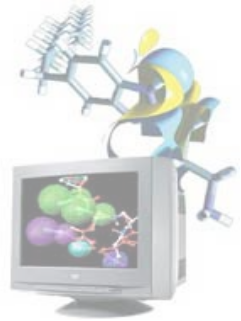
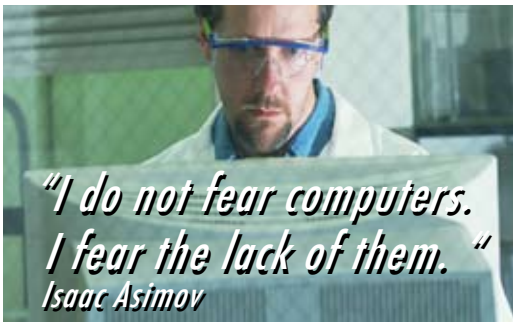
Bioinformatics Shared Resource

Connect to your data

We provide effective solutions to your data analysis and data management needs. Modern research efforts increasingly rely on computational power and domain expertise to extract meaningful results from gene expression and proteomics data, to sift through public databases, and to perform detailed sequence and structural analyses of interesting gene families.



- Informatics Guidance
- Systems Biology Support
- Gene Family Analysis/Annotation
- Human Genome Analysis
- Structural Modeling
- Virtual Screening for drug leads
- Website & Database Development
- Microarray Data Analysis
- Proteomics Data Analysis
- Grant Preparation Assistance



Notably, we have recently changed our name from Information and Data Management (IDM) to The Bioinformatics Shared Resource (BSR). Our informatics services are open to all at the Burnham Institute for Medical Research.

Advantages

- Focus on your core strengths while we manage your data.
- Boost your efficiency and become more competitive.
- Spread the cost: a shared resource is a cost effective resource.
- Maintain continuity in your informatics records.
- Gain access to 80 years worth of informatics expertise.

For latest information and resources see website

Bioinformatics Shared Resource

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858 646 3100 x3915
idmweb.burnham.org
email: idm_help@burnham.org

Services We Provide

1. **Informatics guidance.** We can help you determine where the application of informatics might be most beneficial to your biological problem, and what techniques and approaches might best fit your specific set of questions. Additionally we can provide extensive advice on automation, from picking PCR and sequencing primers to setting up entire automated analysis pipelines. Finally, we can use our extensive experience to advise you on how to proceed with developing new software for an application or customizing pre-existing applications.

2. **Systems Biology Support.** We have experience with state-of-the-art software for dealing with the analytical problems that microarray and proteomics technologies can throw up. We can help you integrate your sequence, expression and proteomics data into one cross-experiment platform. We have experience with the free and open source software packages available from the Institute for Systems Biology and other Genomics Institutes and can deploy them as required. See our list of recommended software on the web site.

3. **Custom analysis and annotation of genomic data.** This includes focused gene sets, ESTs, SNPs and splice variants. Sequence data can be analyzed for gene family members and tailored for specific emphasis as required. We are involved in the development of high-level annotation tools including the new team-oriented annotation tool called SEED. This allows teams of experts to collaborate and pool detailed annotation data.

4. **Structural modeling and Virtual screening.** Structural information is used to examine the potential for interaction between proteins and small molecules. After the SARS pilot study we are excited to offer virtual screening as a new service for the detection of potential drug leads. This technology builds on a wealth of protein structure modeling and docking expertise to be found within The Bioinformatics Shared Resource.

5. **Website development.** We supply free, up-to-date, and user-friendly tools that put you in control of your web site and its content. Additionally, we can create databases and web user interfaces to fit your specifications. Examples include the Stem Cell Community web site at http://www.stemcellcommunity.org and The Center for Proteolytics Pathways homepage at http://cpp.burnham.org. The stemcellcommunity.org web site receives many thousands of hits per month and is an evolving repository where genome-wide data sets are made available to the public.

6. **Grant assistance.**

Team Personnel

Andrei Osterman (Director): supervising Systems biology, comparative and functional genomics, pathways.

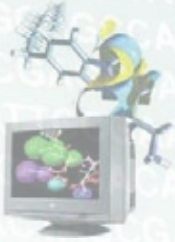
Adam Godzik (Co-Director): supervising Structural Biology, 3-D Modeling and Docking

Recent Projects

Dr. A. Eroshkin provided ongoing support for The Bioinformatics Shared Resource (BSR) collaboration with the Center on Proteolytic Pathways (PI: Dr. J. Smith), spearheading efforts to launch the CPP's main project website. BSR screened SARS genes against a library of 50,000 compounds in an effort to identify potential drug leads (PI: Dr. A. Godzik). Among other significant projects undertaken by BSR: Identification of pig EST genes (PI: Dr. E. Ruoslahti), E3 ubiquitin ligase gene family analysis (PI: Dr. K. Vuori), Antigen site prediction tools (PI: Dr. S. Krajewski), Illumina microarray analysis (PI: Dr. J. Smith), 3D protein interaction visualization (PI: Dr. J. Millan), Protein tyrosine phosphatase gene family analysis (PI: Dr. T. Mustelin), Mascot proteomics data parsing (PI: Dr. G. Salvesen), Microarray chip design (PI: Dr. S. Malkhosyan).

Our Rates Schedule:

Consultation and Small Projects (1-2 hours): Free. Medium Projects (2-5 hours): Free for Cancer Center projects, otherwise $63 per hour. Large Projects (5 hours+): Cancer Center projects $50 per hour, others $63 per hour.



Gerry Deckert (x3081; gdeckert): My background is automated sequence analysis and genome annotation, and my strengths are in project planning, Perl programming, database design, and website integration. As Manager of the BSR you can ask me about new projects, resource availability, data management, and high performance computing.

Alexey Eroshkin (x3923; eroshkin): Developing protease specificity models and identification of substrates, protein functional annotation, analysis of protein structure-activity relationships, genome mining for new genes, multiple alignments and phylogenetic analysis, drug target selection and prioritization, database development. I also do virtual ligand screening, protein structure modeling and molecular graphics.

Kutbuddin Doctor (x3488; ksdoctor): Analysis of protein structure and function, esp. enzymes, apoptosis signaling; finding functional annotations via homology or structure; creating review articles based on families of proteins; writing bioinformatics/informatics sections of grants which were funded (MLSCN, caBIG); writing technical documents for bioinformatics work (caBIG); project oriented bioinformatics systems (Apoptosis database, RIKEN mouse genome apoptosis functional annotation, Cancer Molecular Pages).

Ying Su (x3622; ysu): Cheminformatics and computational chemistry. Broad experience in the application of computer aided design/compound library analysis, diversity based or target based compound selection for HTS screening, hit SAR analysis and hit follow-up design, hit to lead optimization, virtual compound screening and pharmacophore modeling.

Roy Williams (x3915; royw): data analysis (microarray and proteomics) and genome annotation. You might want to ask me questions about methods for analyzing systems biology data and how to view it in a suitable biological context. I have worked with Affymetrix, GeneSpring, MatLab, Bioconductor and related software extensively over the last six years.