Welcome and Introduction

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SRI International Bioinformatics

Pathway Tools Workshop

Workshop format

- First three days formal presentations
- Last two days presentations and hackathon / working groups
- Let's accumulate suggestions for the working sessions

Hold workshops every 18 months



Workshop Goals

- Hear great science
- Present new developments in Pathway Tools
- Learn what new directions PTools should take
- See how other groups are making use of PTools
- Learn of PTools extensions being developed by other groups
- Work together on new directions
- Learn how to program PTools



Workshop Will be Available Live via Internet

Via WebEx plus Conference Call

WebEx shares the computer's desktop

Make your presentation from

- SRI laptop
- Your WebEx-enabled laptop

If you are willing, email your slides to <u>taltman@ai.sri.com</u> for posting on workshop Web site



SRI Campus is Secure



SRI International Bioinformatics

Pathway Tools Capabilities

- Create and maintain an organism database integrating genome, pathway, regulatory information
 - Computational inference tools
 - Interactive editing tools
- Query and visualize that database
- Use the database to interpret omics data
- Comparative analysis tools
- Systems biology analyses
- Model repository





Model Organism Databases / Organism Specific Databases

- DBs that describe the genome and other information about an organism
- Every sequenced organism with an active experimental community requires a MOD
 - Integrate genome data with information about the biochemical and genetic network of the organism
 - Integrate literature-based information with computational predictions

Curated by experts for that organism

- No one group can curate all the world's genomes
- Distribute workload across a community of experts to create a community resource



Rationale for MODs

• Each "complete" genome is incomplete in several respects:

- 40%-60% of genes have no assigned function
- Roughly 7% of those assigned functions are incorrect
- Many assigned functions are non-specific

 Need continuous updating of annotations with respect to new experimental data and computational predictions

• Gene positions, sequence, gene functions, regulatory sites, pathways

MODs are platforms for global analyses of an organism

- Interpret omics data in a pathway context
- *In silico* prediction of essential genes
- Characterize systems properties of metabolic and genetic networks



Pathway Tools Software: PathoLogic

 Computational creation of new Pathway/Genome Databases

 Transforms genome into Pathway Tools schema and layers inferred information above the genome

Predicts operons

- Predicts metabolic network
- Predicts which genes code for missing enzymes in metabolic pathways
- Infers transport reactions from transporter names



Pathway Tools Software: Pathway/Genome Editors

- Interactively update PGDBs with graphical editors
- Support geographically distributed teams of curators with object database system
- Gene and protein editor
- Reaction editor
- Compound editor
- Pathway editor
- Operon editor
- Publication editor





What is Curation?

- Ongoing updating and refinement of a PGDB
- Correcting false-positive and false-negative predictions
- Incorporating information from experimental literature
- Authoring of comments and citations
- Updating database fields
- Gene positions, names, synonyms
- Protein functions, activators, inhibitors
- Addition of new pathways, modification of existing pathways
- Defining TF binding sites, promoters, regulation of transcription initiation and other processes



Pathway Tools Software: Pathway/Genome Navigator

• Querying and visualization of:

- Pathways
- Reactions
- Metabolites
- Genes/Proteins/RNA
- Regulatory interactions
- Chromosomes

• Two modes of operation:

- Web mode
- Desktop mode
- Most functionality shared, but each has unique functionality









Obtaining a PGDB for Organism of Interest

Find existing PGDB

- In BioCyc
- From third party

Create your own



Pathway Tools Software: PGDBs Created Outside SRI

•2,580+ licensees: 205 groups applying software to 1,750 organisms

- Saccharomyces cerevisiae, SGD project, Stanford University
- 135 pathways / 565 publications
 FungiCyc, Broad Institute -- 23 fungi
 Candida albicans, CGD project, Stanford University
 dictyBase, Northwestern University
- Mouse, MGD, Jackson Laboratory
 Drosophila, FlyBase, Harvard University
 Under development:
 - *C. elegans,* WormBase
- Arabidopsis thaliana, TAIR, Carnegie Institution of Washington
 - 288 pathways / 2282 publications
- •ChlamyCyc, GoFORSYS
- PlantCyc, Carnegie Institution of Washington
- •Six Solanaceae species, Cornell University
- GrameneDB, Cold Spring Harbor Laboratory
- Medicago truncatula, Samuel Roberts Noble Foundation



Pathway Tools Software: PGDBs Created Outside SRI

- •E. Uberbacher, ORNL 33 Bioenergy-related organisms
- •G. Serres, MBL and ORNL: 18 Shewanella genomes
- •M. Bibb, John Innes Centre, Streptomyces coelicolor
- •TBDB Project, Mycobacterium tuberculosis
- F. Brinkman, Simon Fraser Univ, *Pseudomonas aeruginosa*Genoscope, *Acinetobacter*
- •R.J.S. Baerends, University of Groningen, *Lactococcus lactis* IL1403, *Lactococcus lactis* MG1363, *Streptococcus pneumoniae* TIGR4, *Bacillus subtilis* 168, *Bacillus cereus* ATCC14579
- •Matthew Berriman, Sanger Centre, *Trypanosoma brucei,* Leishmania major
- •Sergio Encarnacion, UNAM, Sinorhizobium meliloti
- •Mark van der Giezen, University of London, Entamoeba histolytica, Giardia intestinalis



Pathway Tools Software: PGDBs Created Outside SRI

• Large scale users:

- C. Medigue, Genoscope, 200+ PGDBs
- G. Sutton, J. Craig Venter Institute, 80+ PGDBs
- G. Burger, U Montreal, 60+ PGDBs
- Bart Weimer, UC Davis, *Lactococcus lactis, Brevibacterium linens, Lactobacillus acidophilus, Lactobacillus plantarum, Lactobacillus johnsonii, Listeria monocytogenes*

 Partial listing of outside PGDBs at <u>http://biocyc.org/otherpgdbs.shtml</u>



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Learn more from BioCyc webinars: biocyc.org/webinar.shtml



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BioCyc.org