ApiDB: User Studies and Impact on Development

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ApiDB Bioinformatics Resource Center

ApiDB.org

- ApiDB: A Bioinformatics Resource Center for Biodefense and Emerging/Re-emerging Infectious Diseases.
- ApiDB.org -- umbrella /integrated site for apicomplexan parasites
 - CryptoDB.org ---
 - Cryptosporidium; causes cryptosporidiosis
 - PlasmoDB.org
 - Plasmodium species; causes malaria
 - ToxoDB.org
 - Toxoplasma; causes toxoplasmosis

Outline

- About the workshop
- Surveys
- Interviews
- Video capture of lab exercise sessions
- Card-sorting analysis of query categories
- Tour
- Conclusions

About the workshop

- June 26th 29th, 2006 at UGA
- approx. 30 participants from global audience
 - selected on the basis of their need to become an expert user of one or more of the ApiDB database resources (CryptoDB, ToxoDB, PlasmoDB).
- introduction to apicomplexan database resources that are part of the <u>ApiDB.org</u> Bioinformatics Resource Center (<u>PlasmoDB</u>, <u>ToxoDB</u>, <u>CryptoDB</u> and <u>ApiDots</u>).
- "tours" of databases and tools, hands-on exercise sessions
- User surveys, studies, exercises

Pre-workshop survey

- Online, anonymous survey at start of first session.
- What do users know? What kinds of adaptations do we need to make?
- Participants presented with a list of 147 terms related to biological databases and the analysis of biological data.
- For each term, the participants asked to rank their familiarity as:
 - not at all familiar
 - heard of it
 - slightly familiar
 - very familiar

Pre-workshop survey – Results

- For only 21 of the 147 terms(14.3%) were 50% or more of the participants able to claim that they were "very familiar".
- Terms:
 - AA sequence
 - Annotated
 - BLAST
 - cDNA
 - Chromosome
 - Coil
 - Contig
 - Daltons,

- GC number
- Gametocyte
- GenBank
- gene
- Helix
- Locus
- Mitochondrion
- NCBI
- Oligo
- Promoter
- sequence similarity
- Strand
- translation

Pre-workshop survey – Results

- For 31 of the 147 terms (21%) 50% or more of the participants responded that they were "not at all familiar". These terms were:
 - Affymetrix Genotyped SNP probes
 - annotation density
 - ApiDoTS alignments
 - Boolean intersect
 - Boolean join
 - Boolean subtract

- CryptoCycMetabolic Pathway
- Eimeria Gene Models
- e-PCR data
- expression timing
- FullPhat
- Genes by Volatility (Mutability)
- GenPept protein
- GLEAN gene
- GO component
- GO process
- MR4 reagents

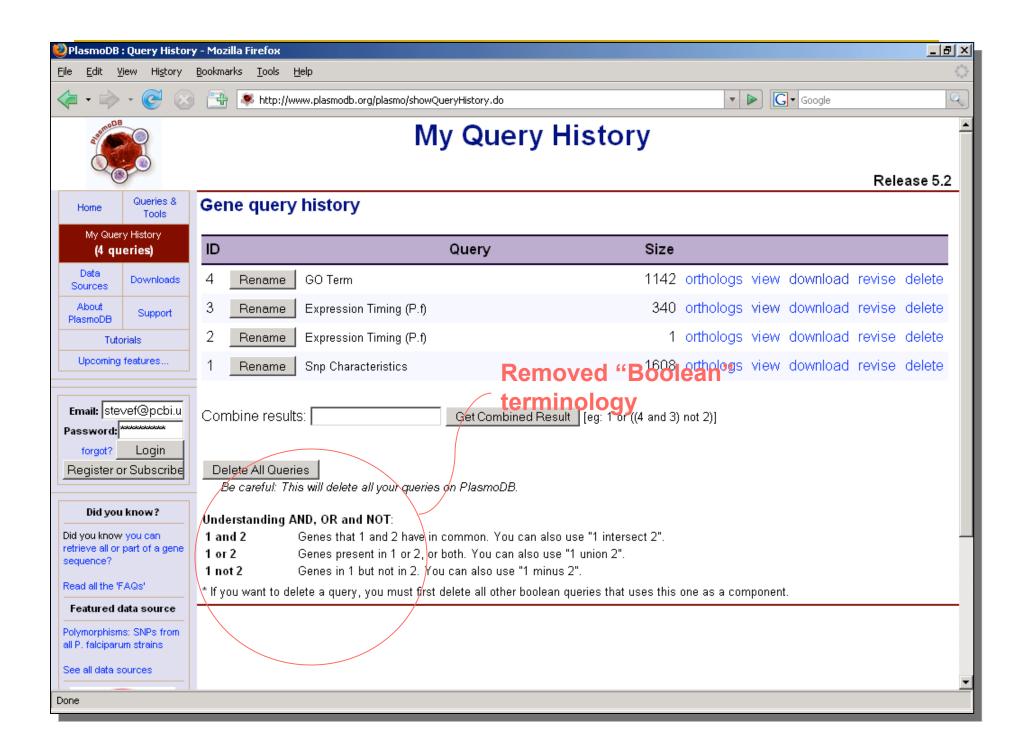
Unfamiliar terms, cont'd

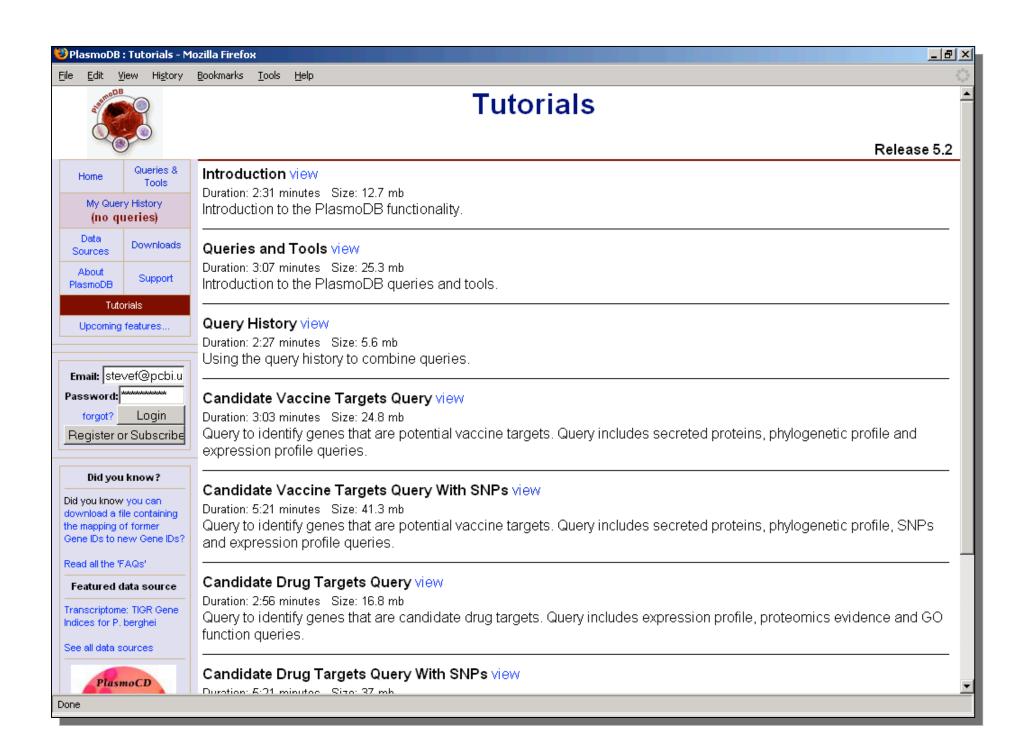
- ncRNA
- Optical maps
- Profile
- OrthoMCL
- PATS
- PlasMit
- PlasmoA
- ProDom

- Pubcrawler
- Refseq
- T. gondii UniGene EST alignments
- TigrScan Gene
- TwinScan Gene Models
- unigene

Pre-workshop survey – Impact

- Gave developers a clearer idea of the types of expertise possessed by users
 - Revisions to site/help text
 - Dropped "Boolean", annotation density terms
- Allowed workshop presenters to adjust details/level of aspects of workshop presentations





Individual interviews

- Conducted with six of the participants
 - Have you used these databases before?
 - Problems? Explain.
 - Feature requests?
 - Elicit "usage scenarios"
 - Anything else we should know?

Individual Interviews - Results

- Output formatting:
 - Don't want all the columns that are returned
 - column configuration in progress
- More descriptions / better explanations
 - Tutorial movie clips
- Consistency with other sources:
 - data not synchronized with GeneDB and GenBank, leads to problems with analysis.
 - □ ?

Individual Interviews - Results

- Naming problems:
 - Gene synonymy; mapping of gene names & products to common names
- Frequent changes, occasional broken links frustrating.
- Want more explanation of how orthologs are determined and clearer descriptions of relationships between gene and orthologs

Individual Interviews: Desired Features

- Ability to save queries
 - In progress ...
- Support for local and high-throughput analysis: Web Services, XML format data format, etc.
 - Some elements available now/in progress
 - simpler-to-parse format coming; XML possibly on the horizon
- Ability to load a list of gene-ids, and then be able to just click "next" or choose from a list, right on the gene page.

Individual Interviews: Desired Features

- map view, as at NCBI.
- A codon usage table, as at kazusa.jp
 - Link added
- Better support for finding small pieces and identifying the location of hits.

Video capture of lab exercise sessions

- Video/audio capture during hands-on exercise sessions (with participant consent).
- Participants asked to work in pairs; person at keyboard used a microphone headset.
 - "SnapZPro" was used for video/audio capture.
 - (Camptazia Studio / Wink)
- Video segments were both burned to CD and placed on a secure web site, reviewed, text annotations added.

Video capture of lab exercise sessions -- Results

- Highlighted user difficulties in locating the appropriate queries to answer questions
 - Lack of familiarity with terminology used
 - Navigation problems
 - "Hidden" information

A nice-looking interface



PlasmoDB The Plasmodium Genome Resource

Release 5.2

Gene ID: PF11 0344

Text term: membrane

Gene type: protein coding

Sequence ID: MAL4

PlasmoDB.org hosts genomic and proteomic data (and more) for different species of the parasitic eukaryote Plasmodium, the cause of Malaria. It brings together data proviby numerous laboratories worldwide (see the Data Sources page), and adds its own data analysis. Publications relying on PlasmoDB should please acknowledge the datab developers and the scientists who have made their data available. PlasmoDB is part of an NIH/NIAID funded Bioinformatics Resource Center to provide Apicomplexan Database Resources.

Features not vet available in PlasmoDB 5.2 may still be accessed via PlasmoDB 4.4, and the results of PlasmoDB 4.4 queries may be exported to PlasmoDB 5.2 (see PlasmoDB 4.4 Query History).

As part of our ongoing education efforts, we are proud to announce the second of four annual apicomplexan database workshops. The registration deadline is January 19, 2007.

Queries & Tools

History

Downloads

Support

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Login

lubscribe

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 CryptoDB OrthoMCL-DB

ToxoDB

Related Sites:

ApiDB

Recent Plasmodium publications

News

- 05 December 2006 ApiDB Workshop, June 3-6, 2007
 - 17 November 2006 PlasmoDB 5.2 is released
- 16 August 2006 PlasmoDB 5.1 is released
- 25 May 2006 PlasmoDB 5.0 is fully released (PlasmoDB 4.4 still available)
- All PlasmoDB News

PlasmoDB Events | Release Notes

Quick Tools [Genome browser | BLAST | Sequence Retrieval | PlasmoCyc]

Search Genes

PlasmoDB Gene ID

Keyword (search product name, notes, etc.)

Gene Type

Search Genomic Sequences

Genomic Sequence ID

All available queries:

Search genes

All Categories

Chromosomal Location





now?

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a source





But can be difficult for novice to locate desired query ...





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- OrthoMCL-DB
- · Recent Plasmodium publications

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Search genes

Isoelectric Point Molecular Weight PDB 3D Structures Predicted 3D Structure (P.f.) Low Complexity Proteins (P.f.) ta provide e databas Protein Secondary Structure Similarity/Pattern ======== BLAST Protein Motif Pattern Interpro Domain Population Biology ========= Snp Characteristics Putative Function ========= EC Number (P.f.) GO Term Metabolic Pathway (P.f.) Y2H Protein Interaction (P.f.) Predicted Functional Interaction (P.f.) Transcript Expression ====== Expression Timing (P.f) Expression Profile Similarity (P.f.) Expression Percentile (P.f.) Gametocyte Expression (P.f.) Expression Percentile (P.b.) EST evidence Protein Expression ========= ⊬go! Protein Expression (P.f.) Protein Expression (P.b.) ≽go! Cellular Location ========= Subcellular Localization ⊧go! Transmembrane Domain Count Predicted Signal Peptide Exported Protein ⊦go! Homology Phylogenetic Profile (P.f.) Orthology Phylogenetic Profile

Chromosomal Location

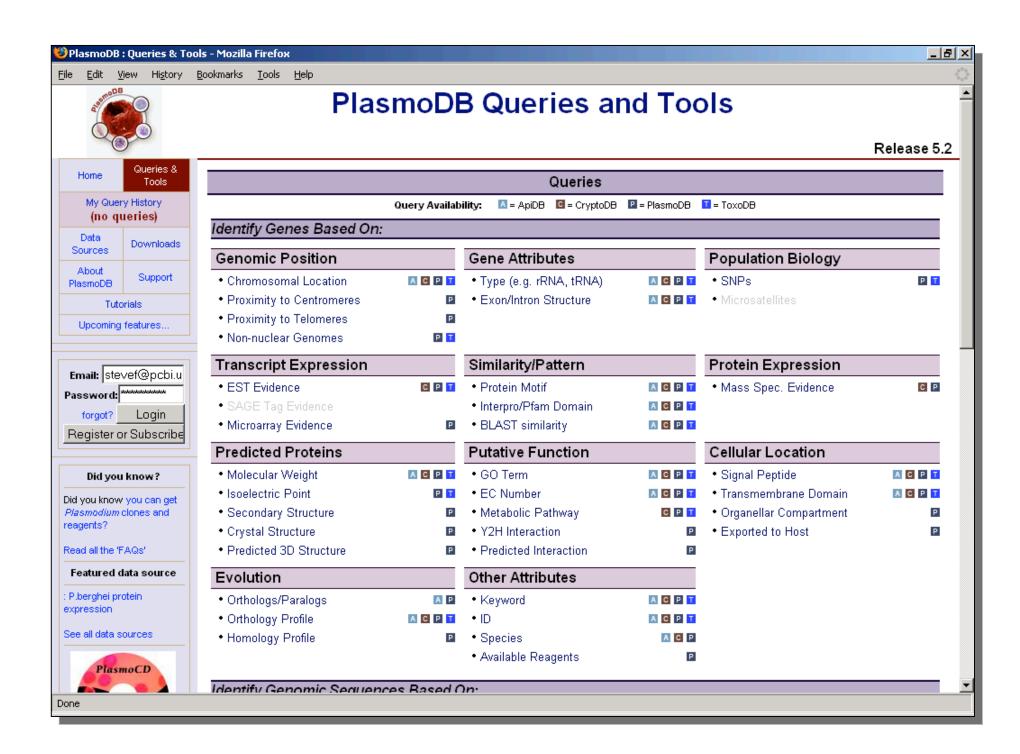
Gene Type

Exon Count

Predicted Proteins =========

Video capture of lab exercise sessions -- Impact

- Restructuring of query menus -> query grid
- Additional tutorials in form of movie clips
- Rethinking of some help text





ApiDB.org Queries and Tools

Login | Register



		Queries			
(Query Availabili	ty: A = ApiDB G = CryptoDB	P = PlasmoDB	3 ■ = ToxoDB	
Identify Genes Based O	n:				
Genomic Position		Gene Attributes		Population Biology	
Chromosomal Location	ACPT	• Type (e.g. rRNA, tRNA)	ACPT	• SNPs	PT
 Proximity to Centromeres 	P	 Exon/Intron Structure 	ACPT	 Microsatellites 	
 Proximity to Telomeres 	P				
Non-nuclear Genomes	PT				
Transcript Expression		Similarity/Pattern		Protein Expression	
EST Evidence	CPT	Protein Motif	ACPT	Mass Spec. Evidence	CP
 SAGE Tag Evidence 		 Interpro/Pfam Domain 	ACPT		
Microarray Evidence	P	 BLAST similarity 	ACPT		
Predicted Proteins		Putative Function		Cellular Location	
Molecular Weight	ACPT	GO Term	ACPT	Signal Peptide	A C P
Isoelectric Point	PT	 EC Number 	ACPT	 Transmembrane Domain 	A C P
 Secondary Structure 	P	 Metabolic Pathway 	C P T	 Organellar Compartment 	
 Crystal Structure 	P	 Y2H Interaction 	P	 Exported to Host 	F
Predicted 3D Structure	P	 Predicted Interaction 	P		
Evolution		Other Attributes			
Orthologs/Paralogs	A P	Keyword	ACPT		
 Orthology Profile 	ACPT	• ID	ACPT		
Homology Profile	P [*]	Species	A C P		

Card-sorting analysis of query categories

- Goals:
 - Determine the groups of the queries that users view as belonging together
 - Determine appropriate names for the groups that emerge.
 - Produce better menu structure

How The Exercise Was Conducted

- Users given 39 cards with titles and descriptions of queries available on PlasmoDB 4.4
- Sample card

Signal peptide

Search for genes whose protein products contain predicted signal peptides, as predicted by SignalP 3.0.

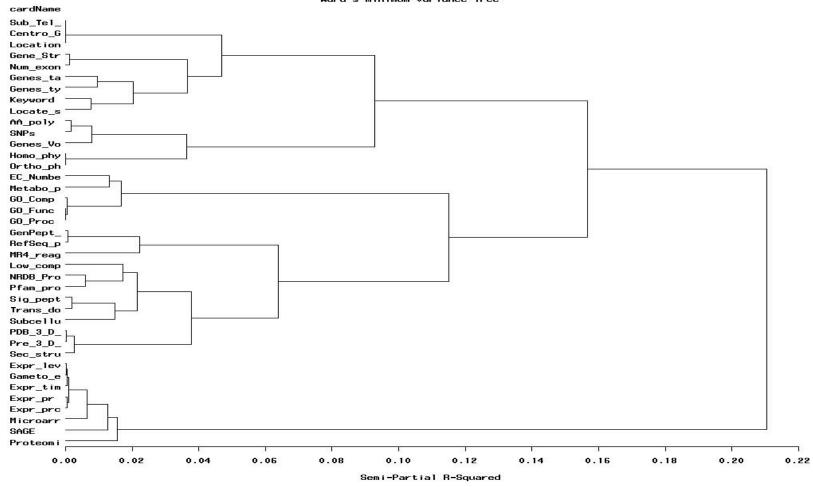
Card Sorting Analysis

- Users asked to place cards into meaningful groups, clip them together, and label the groups.
 - Hierarchies allowed -- rubber band together and label clipped stacks
- Cluster analysis and other analyses
 - □ 7 different methods; similar results across methods

Sample Cluster Output - Tree

Card Sort duster

Ward's minimum variance Tree



Site Tour

with Steve Fischer

Usability Guidelines

- A good place to start:
 - AskTog: First Principles of User Interaction
 Design
- Important Lessons:
 - Preference != performance
 - Clutter <-> visibility tradeoffs
 - Interaction behavior more important than appearance

Conclusions

- User studies can answer questions and guide development
 - Survey
 - provides info about user preferences (not performance!)
 - Easy to administer/analyze
 - Video capture
 - Provides info about user performance
 - Tedious to analyze
- Biggest impact:
 - Card-sorting exercise
 - Individual interviews
 - Both are easy to administer; straightforward to analyze