EuPathDB: Free, online genomics resources for eukaryotic pathogens and their hosts.

Abstract:
The Eukaryotic Pathogen Database Resources (EuPathDB, https://eupathdb.org) is a family of free, online resources that facilitate the discovery of meaningful biological and clinical relationships from large volumes of data. This platform supports hypothesis driven research and places the power of bioinformatics in the hands of the scientific community by combining pre-analyzed Omics data with advanced search capabilities, powerful data visualization and analysis tools. EuPathDB supports over 170 species within Amoebazoa, Apicomplexa, Chromerida, Diplomadida, Trichomonadida, Kinetoplastida, oomycetes and fungi. For these organisms, EuPathDB integrates a wide range of data including genome sequence and annotation, transcriptomics, proteomics, epigenomics, metabolomics, population resequencing of clinical and field isolates, and host-pathogen interactions. Data are analyzed using standard workflows and an in-house pipeline generates data including domain predictions, GO term associations, and orthology profiles across all genomes. These pre-analyzed data are easily accessed in a graphical interface that compiles data into record pages (genes, pathways, etc.) and provides tools to search and visualize the data. Our unique search strategies system offers over 100 preconfigured searches that query individual datasets. Searches can be combined into strategies that easily merge evidence from diverse data types and across organisms. Analysis tools enhance the search strategy system and include dynamic data visualization, comparative genome and population genetics tools, functional or pathway enrichment, and a Galaxy instance for the analysis of primary data. This platform has recently expanded to incorporate data from systems biology programs and clinical studies such as the International Centers of Excellence in Malaria Research. User support includes an email help desk (help@eupathdb.org), social media, YouTube tutorials, and a global program of workshops. Please stop by our poster for a demonstration.

Examples of recent additions and highlights:
-   Private Galaxy Workspace: Perform analysis of your own data and then easily port alignments to EuPathDB GBRowse to privately view against data already integrated into EuPathDB. Includes preloaded genomes and preconfigured RNA seq and variant calling workflows.
-   New Database: ClinEpiDB (https://clinepidb.org) hosts clinical and epidemiological data for the infectious disease research community.
-   Circadian Rhythm Analysis: *T. brucei* 927 Bloodstream and procyclic form transcriptomes during a 48-hour time-course of alternating temperatures or at constant temperature.
-   Improved Annotation: GO Slim data integrated for all genomes.
-   Knockout Phenotypes: PlasmoGEM knockout vectors were used to measure growth rate phenotypes in mice for 2,578 *P. berghei* genes. Gene record pages contain tabulated and graphical data.
-   Cellular localization of gene products: *T. brucei* 927 cellular localization images for 3180 genes from the TrypTag project. Search for genes based on GO annotation.
-   Translational Efficiency: *T. cruzi* transcriptome and translatome of epimastigotes and metacyclics.
-   Stage Specific Expression: *L. mexicana* transcriptomes of promastigote and amastigote stages.
-   Host-Pathogen Interactions: Paired host (mouse) and parasite (*T. gondii*) transcriptomes during infection of mouse neurons, astrocytes, fibroblasts and skeletal muscle cells. Interrogate parasite data in ToxoDB.org and mouse data in HostDB.org.