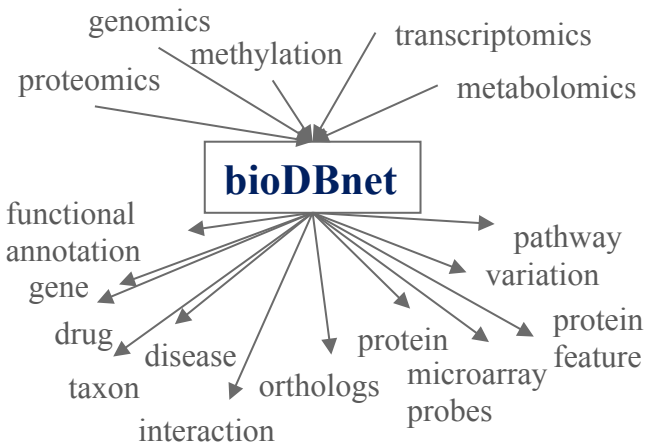
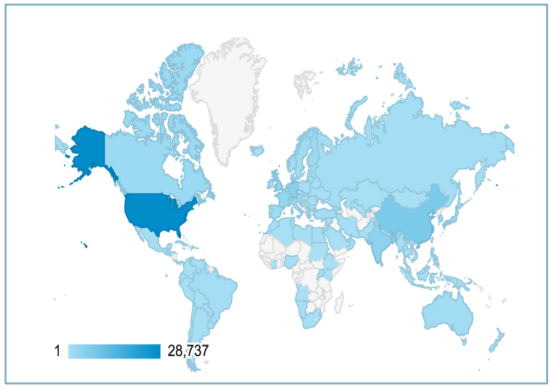
bioDBnet



- Convert across biological identifiers – 200 biological identifiers across 50 databases including EntrezGene, UniProt, RefSeq, Ensembl, DrugBank, OMIM, HMDB, Affy, dbSNP…
- Functional annotations – GO annotations, KEGG, Reactome, Biocarta
- Conversions across species – mouse affy probe id to human pathways
- 1000's of users across the world
- Integrated into EBI's BioServices

Mudunuri et. al., Bioinformatics 2009 (PMID: 19129209)

http://biodbnet.abcc.ncifcrf.gov



Core Infrastructure and Systems Biology

Advanced Biomedical Computing Center

Information Systems Program

Frederick National Laboratory
for Cancer Research

uma.mudunuri@fnlcr.nih.gov
301-846-6774

http://ncifrederick.cancer.gov/isp/abcc

ABCC

Core Infrastructure and Systems Biology

ISP, FNLCR

Data Mining

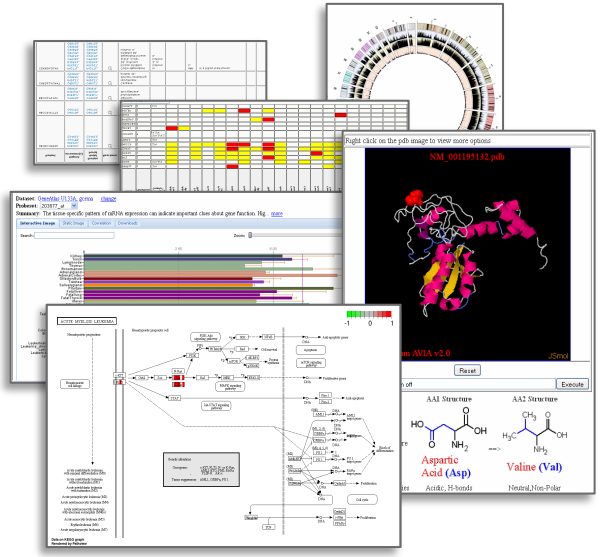
- Mine from multiple formats
- Species agnostic conversions
- Biological data warehouse
- Variant Impact Analysis
- Species agnostic conversions
- Large scale data integration
- SQL and NoSQL
- Literature Mining

Systems Biology

- Disease agnostic queries
- Clinical and genomic integration
- Multi-omics data integration
- Analysis on longitudinal data
- Secure role based access
- Data sharing across collaborators

AVIA

- Impact assessment
- Clustering and Functional Annotations
- Genomic and Protein positions as input
- Visualize tissue expression levels, pathways, 3D structures, Circos plots
- Prioritize and Summarize Variants and Genes

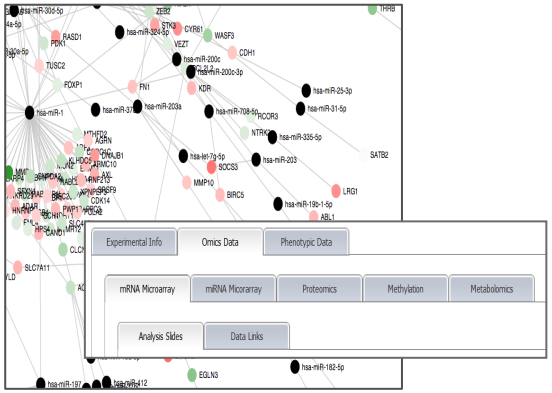


Vuong et. al., Bioinformatics 2014 (PMID: 24215028)

http://avia.abcc.ncifcrf.gov

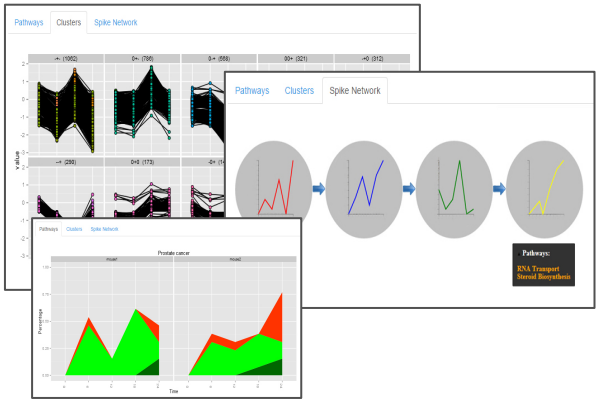
Systems Biology

- Role based secure data access
- Data type aware browsing
- Disease agnostic
- Integration of omics data
- Clinical and genomic data integration



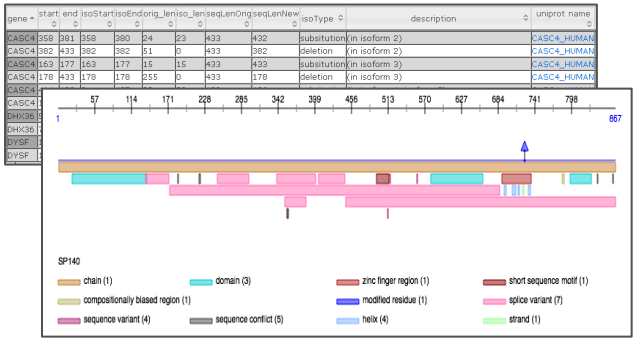
Omics Analysis

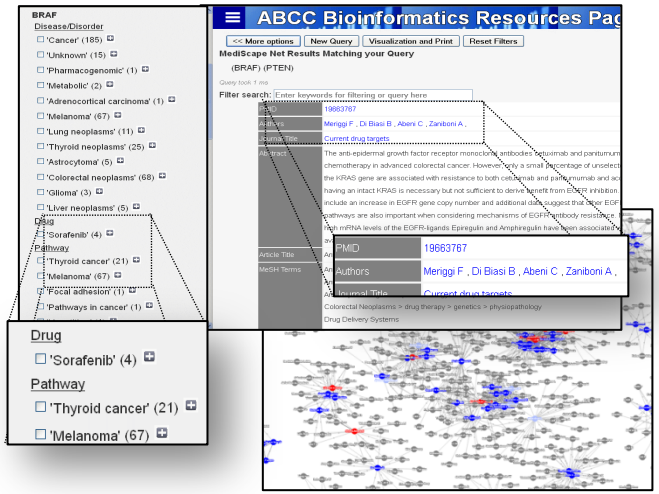
- Longitudinal analysis
- Dynamic pathway and functional analysis
- Applicable for multi-omics data sets



Protein Features

- Query based on protein names or amino acid positions
- All protein features from UniProt
- Visualization using BioJS
- Customizable user defined features
- Clinical and genomic data integration



Bioquery Medline

- Query using gene symbols
- Dynamic filtering options on known drug/disease/pathway associations
- Visualize co-author networks