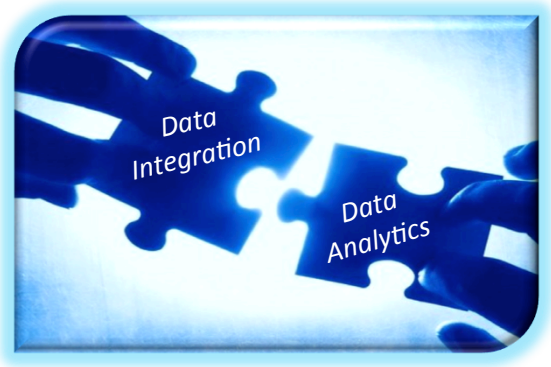
AMIA-010-T2013.
SysBioCube: A Data Warehouse and Integrative Data Analysis Platform Facilitating Systems Biology Studies of Disorders of Military Relevance.

AMIA TBI-CRI Joint Summits on Translation Science

March 18 - 22, 2013, San Francisco, CA



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Acknowledgment

USAMRMC

- Dr. Joseph Palma

USACEHR

- Dr. Marti Jett
- Dr. Rasha Hammamieh
- Dr. Nabarun Chakraborty
- Meskerem Jibitu
- Dr. Aarti Gautam
- Dr. Duncan Donohue
- Dr. Seid Yimer Muhie

ABCC/FNLCR

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ISB

- Dr. Inyoul Lee
- Dr. Lee Hood

UCSB

- Dr. Frank Doyle
- Dr. Bernie Daigle
- Dr. Linda Petzold

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ABCC/FNL Supportive Infrastructure

- Computational center dedicated to biology.
- Secure web hosting outside DOD.
- Database and IT admin support.
- Access to experts in the computational biology & modeling, next-generation sequencing and biological databases.
- Rich collection of open-source and commercial applications with grid computing environment.
- Connectivity to other FNCLR/NCI projects with mouse models and human clinical samples.
- Automated database update procedures in place for many publicly available data sources – rich, diverse annotations for many species

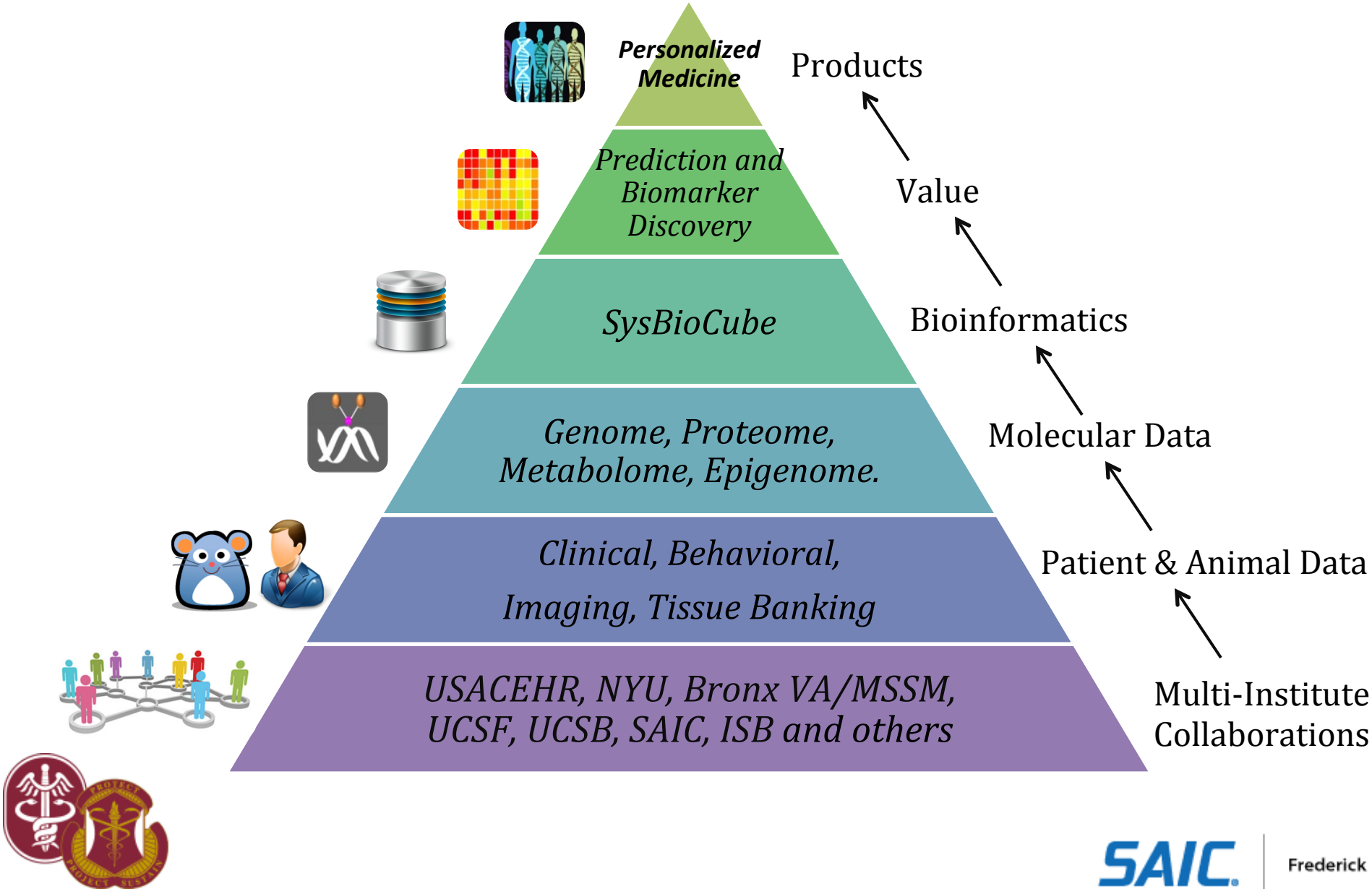
Outline

- Objective
- Vision and Architecture
- Features
  - Role based Secure data Upload and Download
  - Publications, Forums, FAQ's (SysBioCube Wiki)
  - Data exploration portal for PTSD Mouse and Plague data
  - Visual Data Mining Tools
  - Integrative Data Analysis/Associations
- Summary

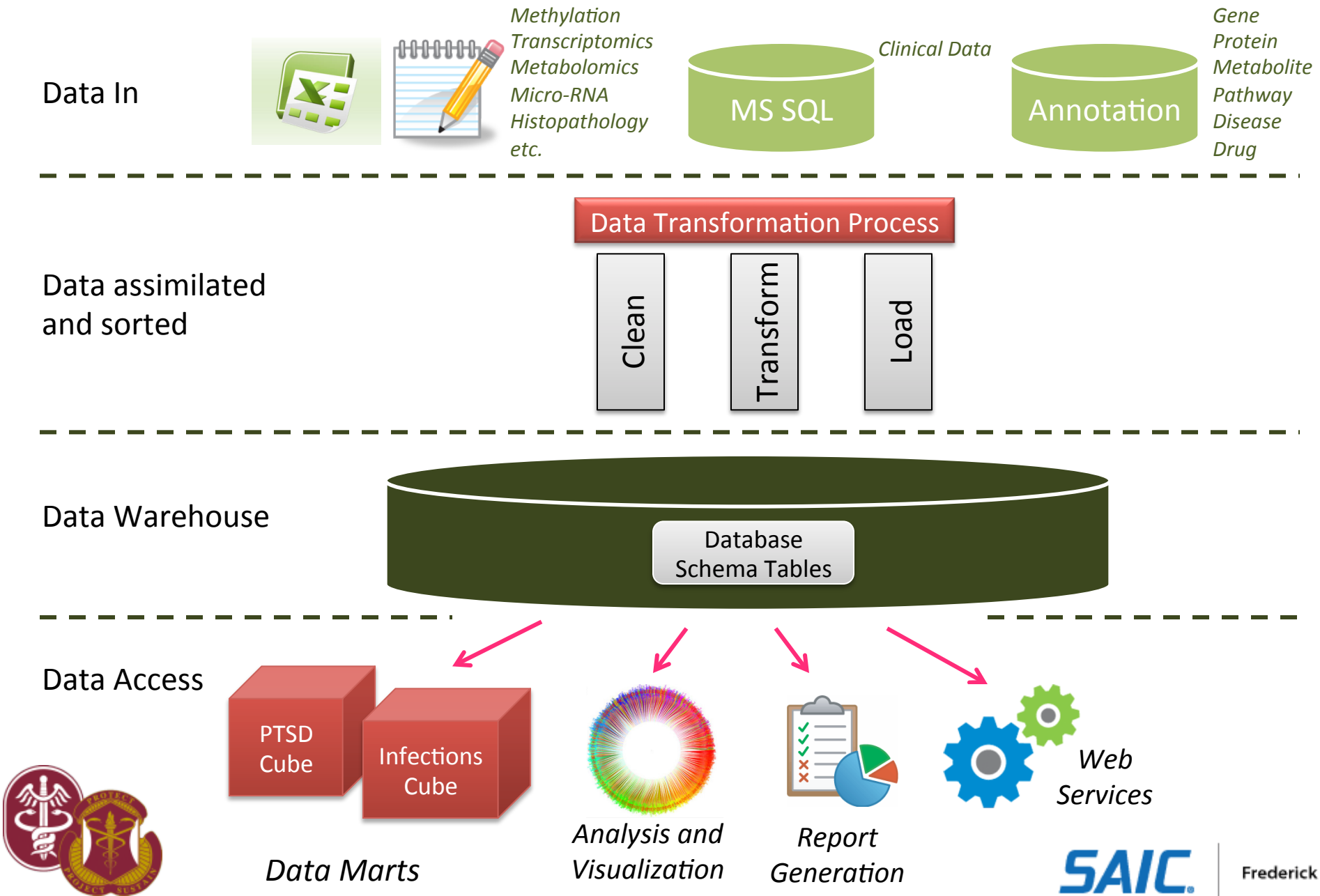
Objectives

- Storage and maintenance of diverse data types
  - Clinical, Animal/Human, Physiological and Pan-omics data
- Secure and common portal for depositing, retrieving, and analyzing molecular and animal/clinical data in a standard relational database model
- Sharing of data with Systems Biology Enterprise participants
- Facilitate integration and visualization of diverse data types using a user-friendly web interface
- Develop tools and algorithms to perform data mining and knowledge discovery

Vision for SysBioCube



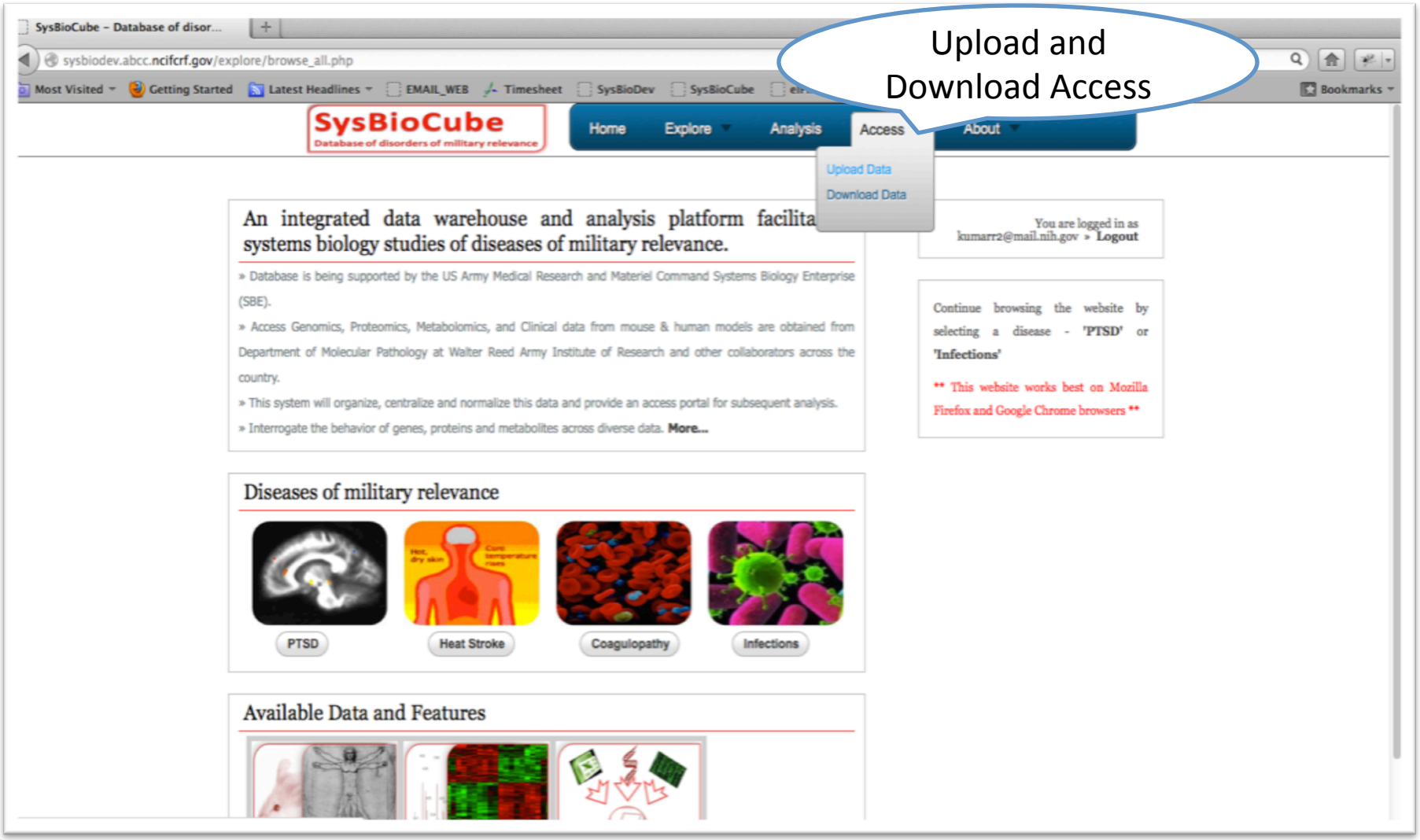
SysBioCube Software Application Architecture



Features

- Data Upload/Download
- Publications, Forum & Wiki
- Browse multiple data types
  - Experimental Metadata, Transcriptomics, Methylation, Metabolomics, Histopathology, Behavioral, Physiological
- Analysis options
- Visual data mining tools

SysBioCube Home Page



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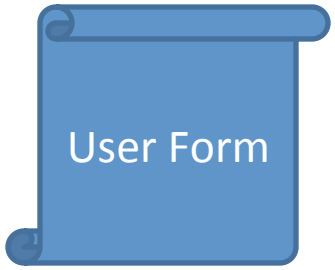
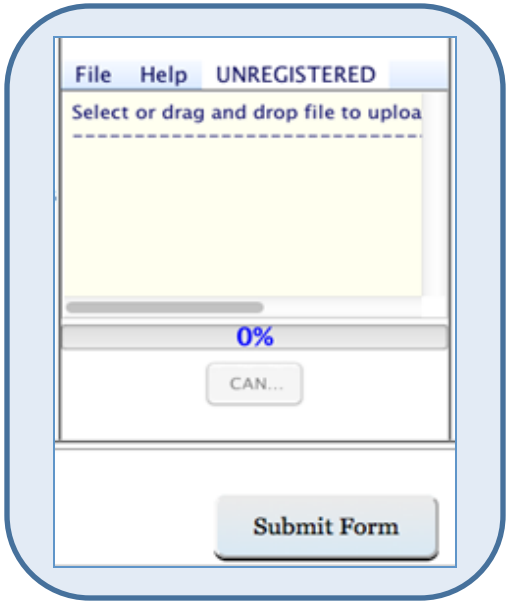
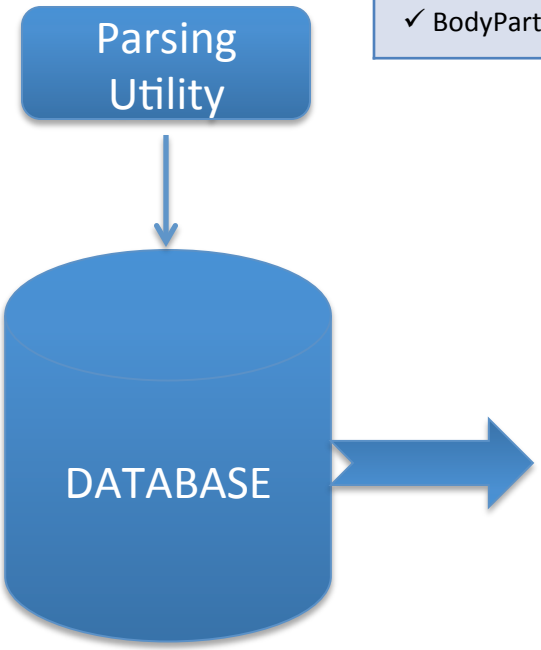
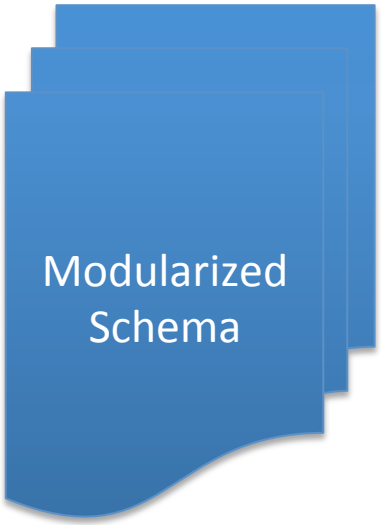
Data Upload

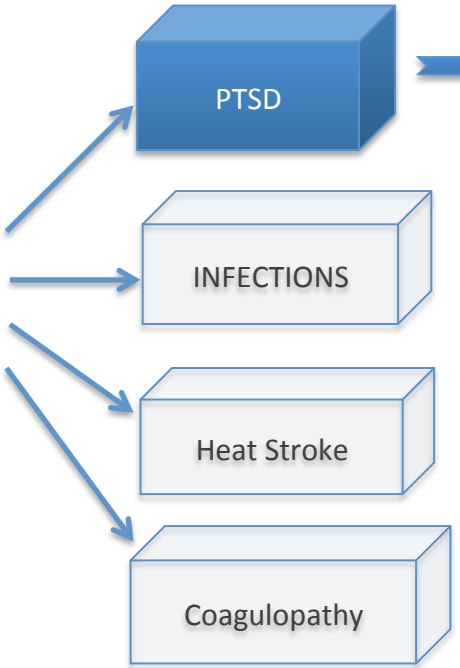


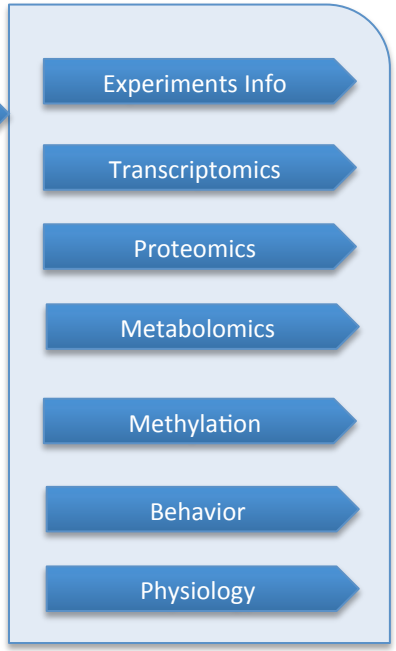
- ✓ Disease Type
- ✓ Experiment Type
- ✓ Analyzed/Raw Data
- ✓ Species Type
- ✓ Strain Type
- ✓ BodyPart/ Tissue Type











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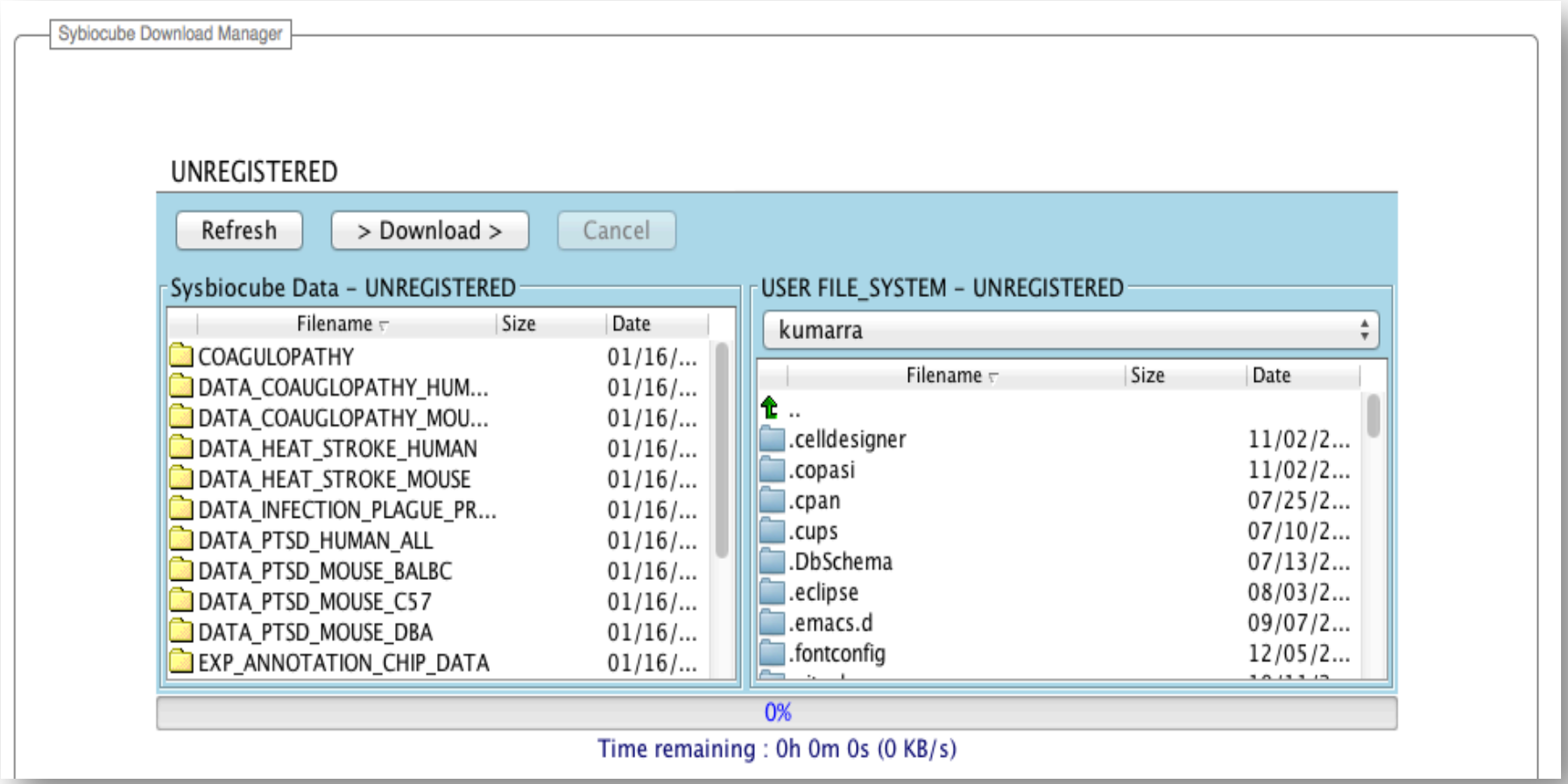
Secure Role Based Data Download



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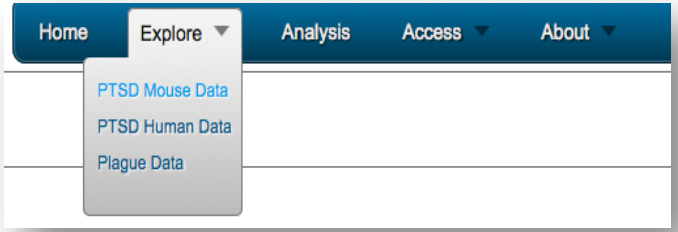
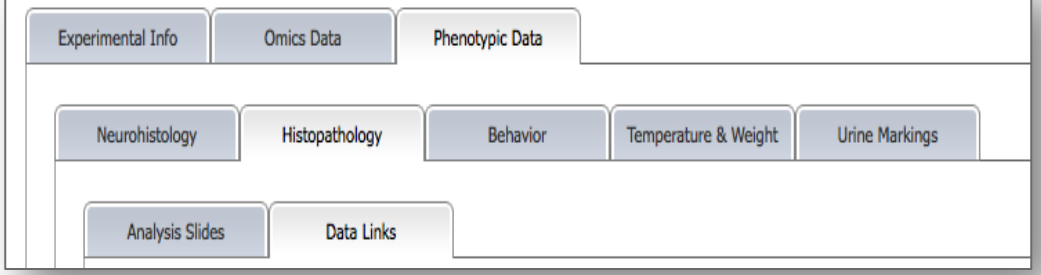
SysBioCube Data Explore



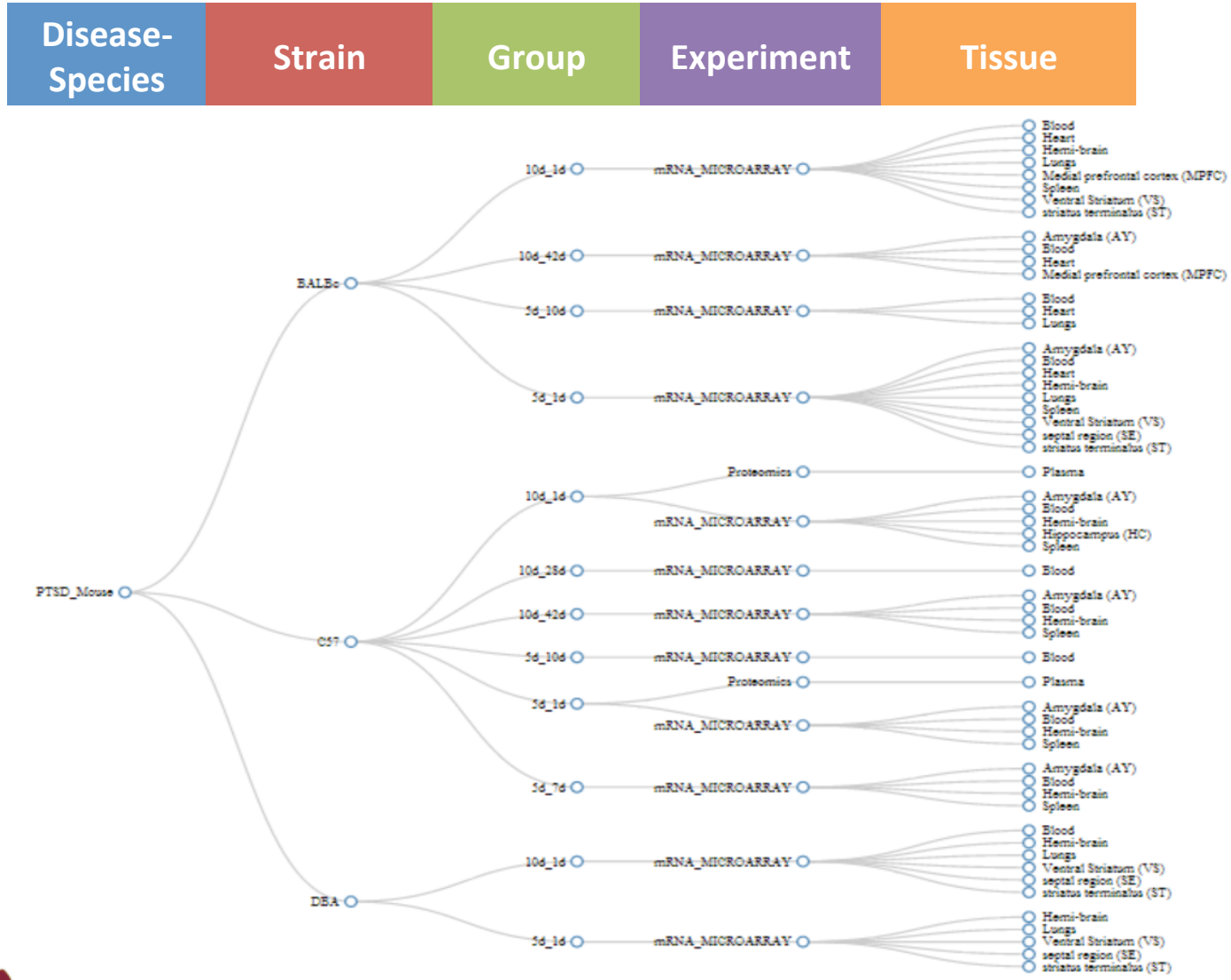
Explore Data with Hierarchical Tab Arrangement



SysBioCube 'Explore'

- **Experimental Info**
  1) Tree View
  2) Tabular View
  3) Formatted Files
- **Omics Data**
  1) Microarray
  2) Micro-RNA
  3) Proteomics
  4) Methylation
  5) Metabolomics
- **Phenotypic Data**
  1) Neurohistology
  2) Histopathology
  3) Behavior
  4) Temperature & Weight
  5) Urine Markings

Snapshot of PTSD Mouse Data as Tree View



SysBioCube Omics Data

SysBioCube
Database of disorders of military relevance

Home | Explore | Analysis | Access | About

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Experimental Info | Omics Data | Phenotypic Data

mRNA-Microarray | miRNA-Microarray | Proteomics | Methylation | Metabolomics

Analysis Slides | Data Links

Save | Show 10 entries | Search:

Strain	Data Type	Institute	Tissue	File Download
BALBC	raw_data	USACEHR	heart	
BALBC	raw_data	USACEHR	heart	
BALBC	raw_data	USACEHR	heart	
BALBC	raw_data	USACEHR	heart	
BALBC	raw_data	USACEHR	heart	
BALBC	raw_data	USACEHR	heart	
BALBC	raw_data	USACEHR	heart	
BALBC	raw_data	USACEHR	heart	
BALBC	raw_data	USACEHR	heart	
BALBC	raw_data	USACEHR	heart	
Strain	Data Type	Institute	Tissue	File Download

Showing 1 to 10 of 907 entries

First Previous 1 2 3 4 5 Next Last

Download Links

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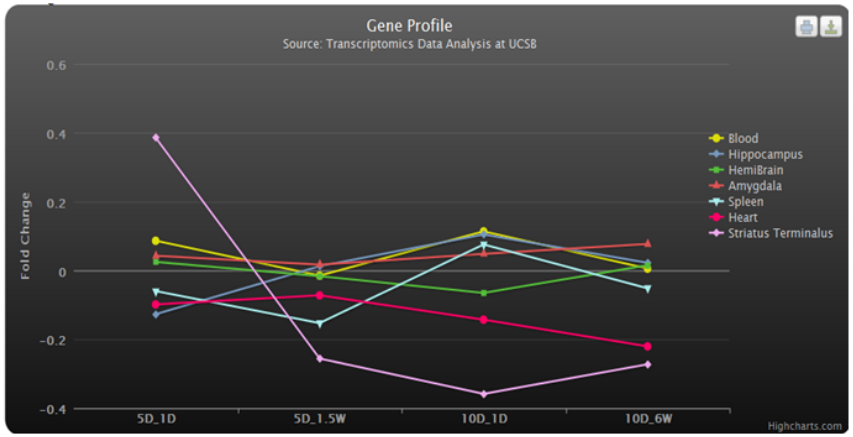
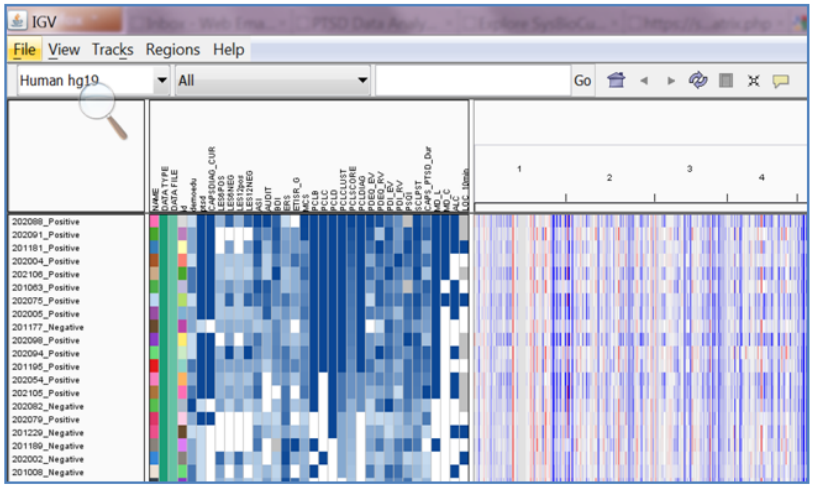
Forum, Publications and Wiki

Visual Data Mining Tools

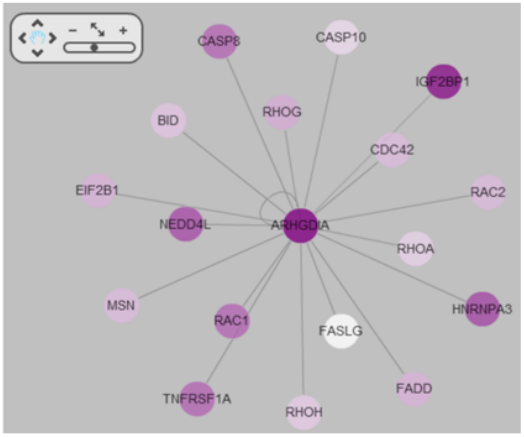
(A)



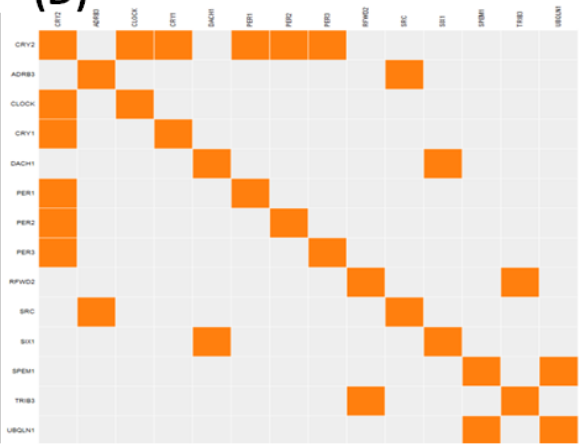
(B)



(C)

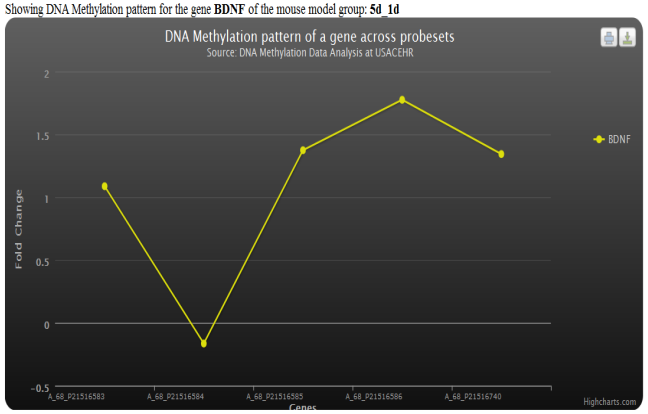


(D)



(E)

Showing DNA Methylation pattern for the gene **BDNF** of the mouse model group: **5d_1d**



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Exploratory and Integrative Data Analysis with SysBioCube

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Systems Biology Data Integrome

- Towards Global Data Exploration

- A prototype application to globally explore associations across different data types
- The goal is to visualize the correlations across multiple diseases, data-types, species, etc.
- Perform feature selection & predictive modeling and other data mining activities to derive biological hypothesis.

Explore Associations Across PTSD Data Types

Data Types

1. CLINICAL
   NYU, Bronx VA/MSSM
2. GENOMICS
   USACEHR, SAIC, UCSB
3. MICRO-RNA
   ISB

- Heat Map with Metdata Info
- Protein-Protein Interactions
- Transcriptomics to Epigenomics
- Transcriptomics to Micro-RNA
- Transcription Factor
- Genes to Disease
- Gene/Protein to Drug
- GO & Pathway Enrichment
- Genetic Variant to Disease
- Genome Browser

Coming Soon!

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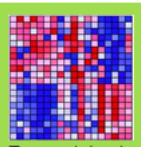
Query PTSD Human Data-Sets

Use the form below to select a single data type OR any two data types. Fill-up the parameters for each data type (*shown after each click*) and press 'Submit' to retrieve the database results matching your input parameters.

Select A Single Data Type OR Any Two Data Types



Transcriptomics

Cancel

Select Transcriptomics Data Parameters:

Data Set: PTSD Positive vs. Negative (47 samples)

Data analyzed by: SAIC

Select at least three metadata parameters

CAPSPART_CUR
CAPSTOT_CUR
CRAEDATEDAY
CRAEDATEMONTH

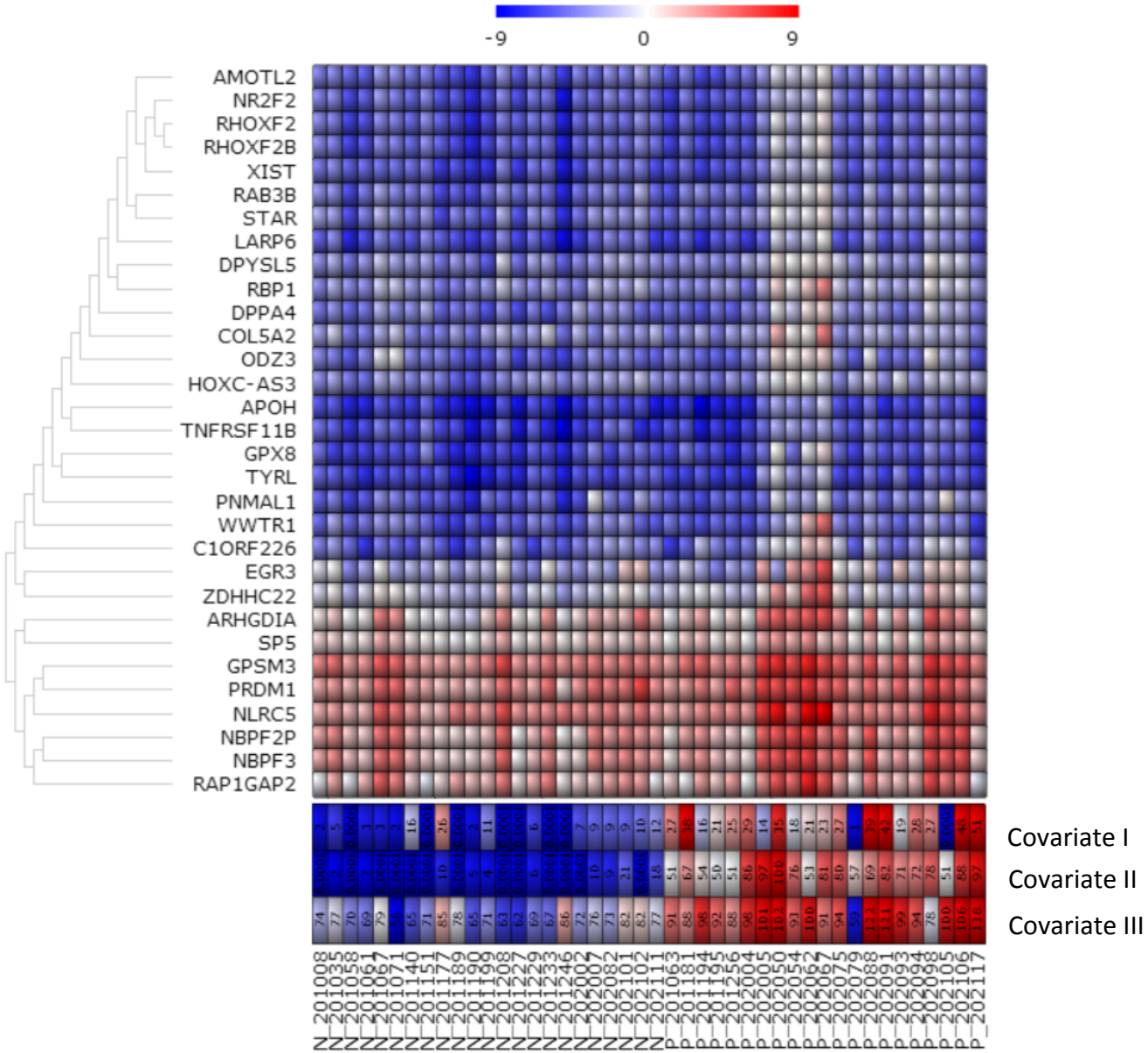
FILTER GENES BY:

Fold Change: greater than (>) 1.3

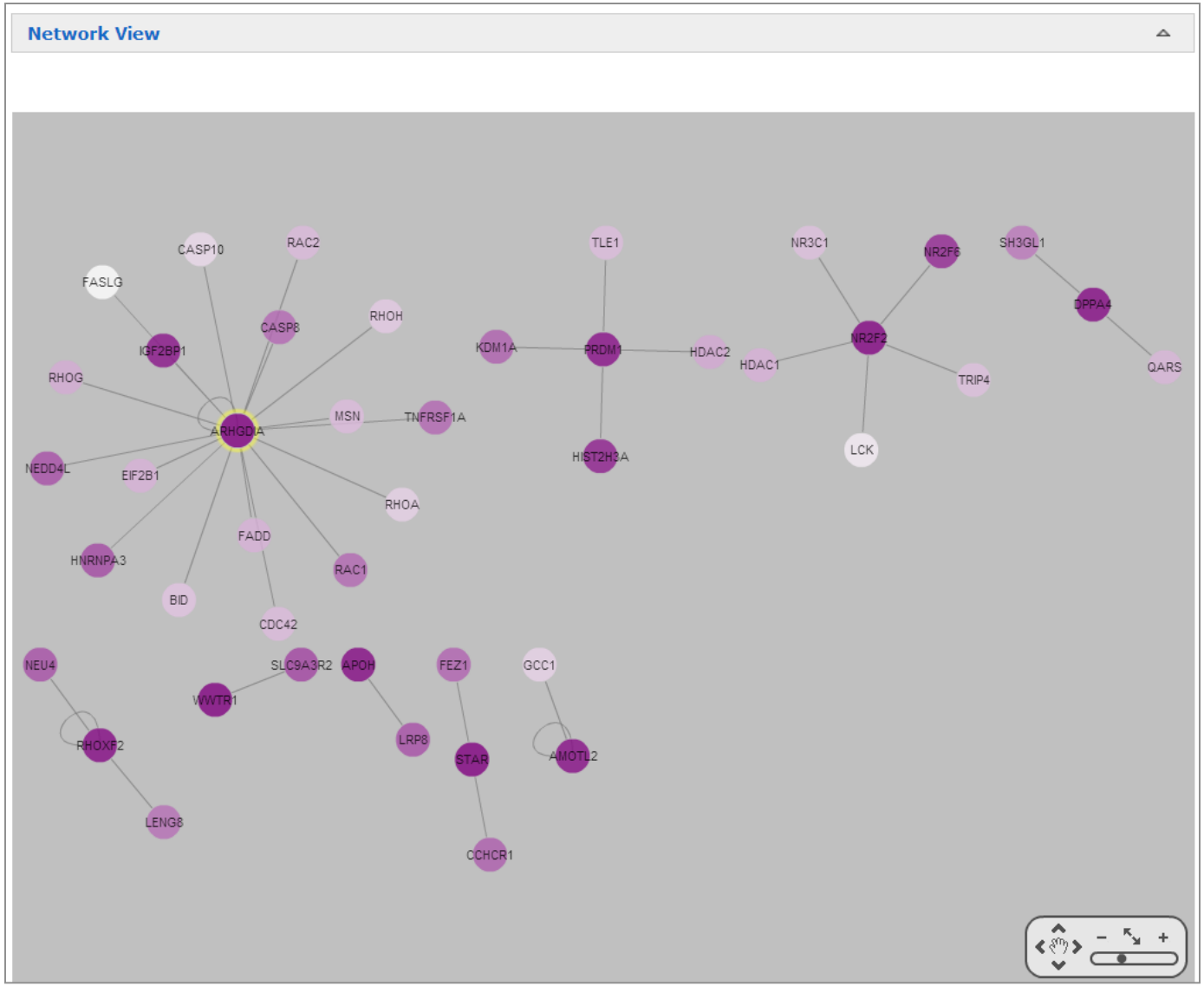
P-Value: 0.05

Send it

Heatmap + Metadata Annotation Visualization



What are the neighboring proteins and what is their expression?



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What is the methylation status of these genes?

GENE	GENE LOG-FC	METHYLATED GENE FC	X-FACTOR
SP5	1.4	.83	1.162
NR2F2	1.43	.83	1.1869
NR2F2	1.43	.86	1.2298
RAP1GAP2	1.33	1.19	1.5827
AMOTL2	1.33	1.2	1.596
SP5	1.4	1.25	1.75
AMOTL2	1.33	1.36	1.8088
SP5	1.4	1.31	1.834

What micro-RNAs target the genes and what is their expression?

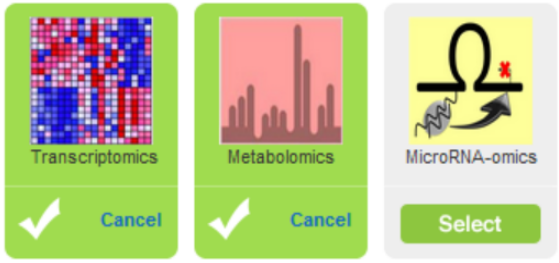
MICRO-RNA	MIRNA LOG-FC	GENE	GENE LOG-FC	X-FACTOR
hsa-miR-127-3p	-.25	PRDM1	1.31	-.3275
hsa-let-7f	.11	PRDM1	1.31	.1441
hsa-let-7a	.2	PRDM1	1.31	.262
hsa-let-7a	.2	EGR3	1.61	.322
hsa-let-7b	.35	PRDM1	1.31	.4585
hsa-miR-125b	.42	PRDM1	1.31	.5502
hsa-miR-151-5p	.47	ARHGDIA	1.48	.6956
hsa-miR-16	.48	ARHGDIA	1.48	.7104

Integration between Microarray and Metabolomics
(*Network View*)

Query PTSD Mouse Data-Sets

Use the form below to select a single data type OR any two data types. Fill-up the paramete
click) and press 'Submit' to retrieve the database results matching your input parameters.

Select A Single Data Type OR Any Two Data Types



Select Transcriptomics Data Parameters:

Strain: C57/BL6

Data analyzed by: USACEHR

Defeat-Recovery Group: 5d-1d

Tissue: Blood

Fold Change: greater than (>) 1

P-Value: 0.05

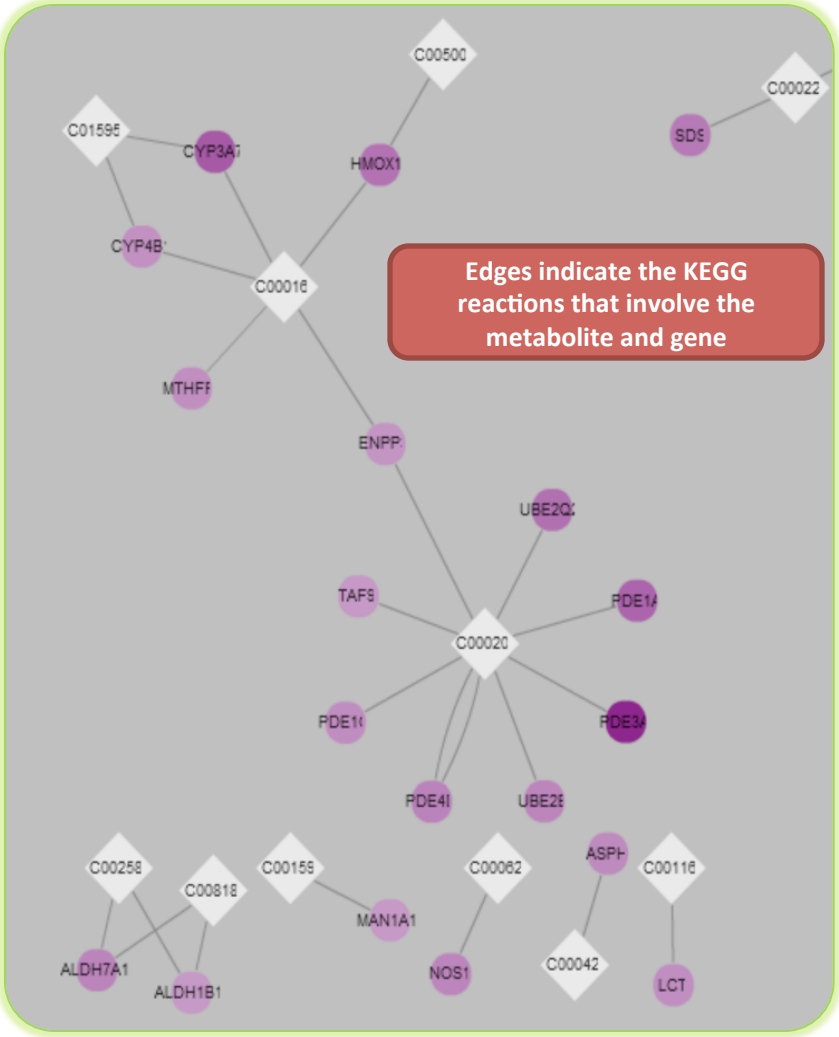
Select Metabolomics Data Parameters:

Selct the Experiment Group: 5D_1D

Tissue: Plasma

Fold Change: greater than (>) 1

P-Value: 0.05



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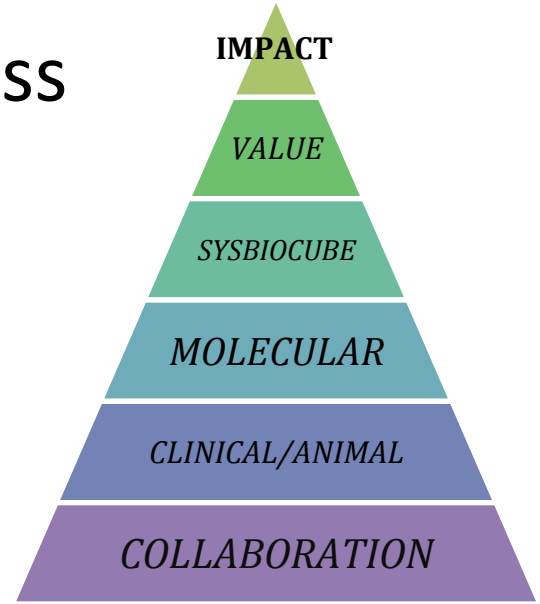
Summary

- Data is Secure
- User-specific Controlled Access
- Single integrated portal
  - Browse Multiple Data-types
  - Exploratory Analysis Tools
  - Visual Data Mining Tools



WE ♥ DATA

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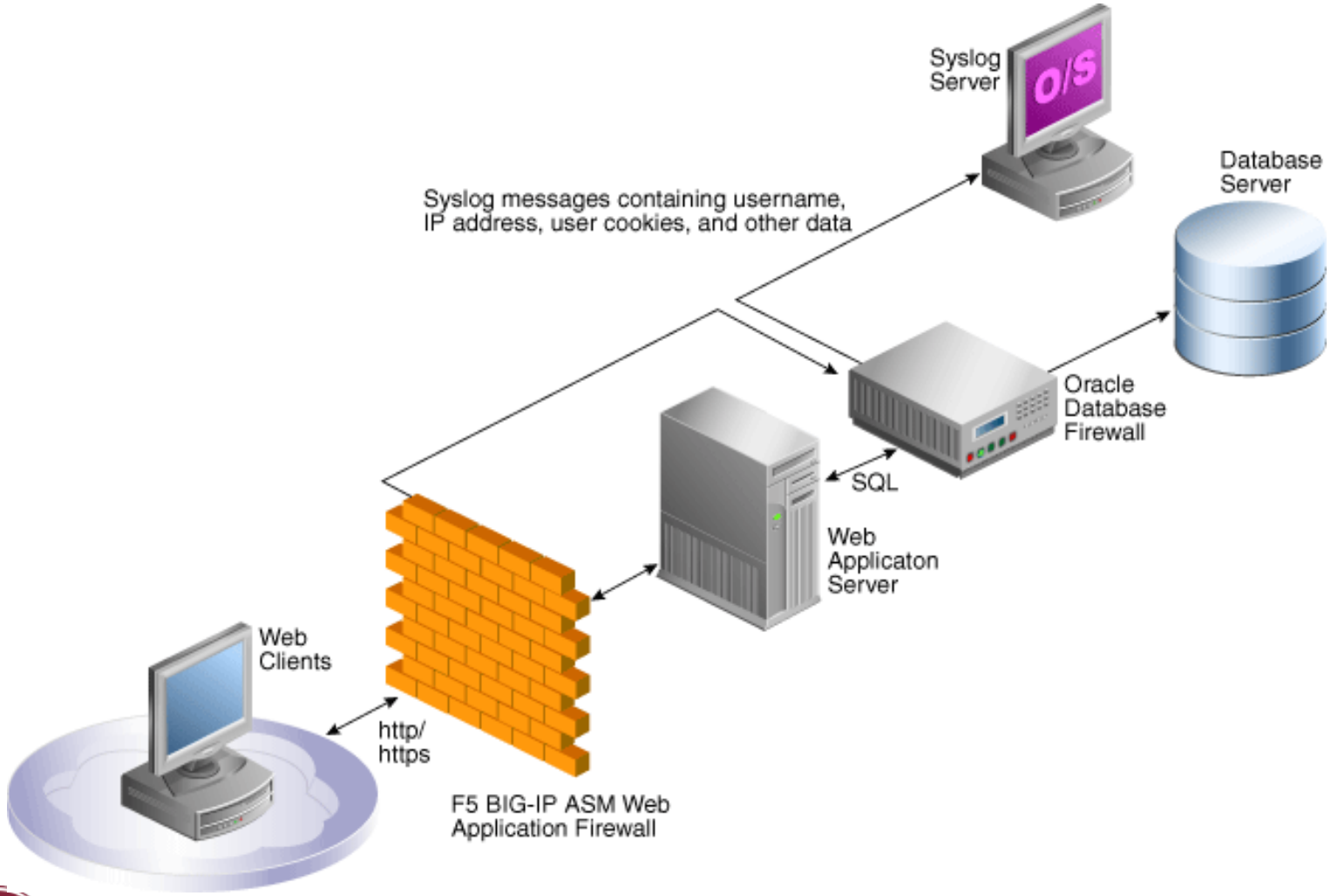
Thank You

Extras

Client – Server Architecture



Source: Oracle® Database Firewall Administration Guide, Release 5.0

Demo

https://sysbiocube.abcc.ncifcrf.gov/

Firefox

SysBioCube - Database of...

SysBioCube
Database of disorders of military relevance

Home | Browse | Analysis | Upload | File Manager

An integrated data warehouse and analysis platform facilitating systems biology studies of diseases of military relevance.

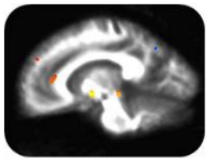
» Database is being supported by the US Army Medical Research and Materiel Command Systems Biology Enterprise (SBE).

» Access Genomics, Proteomics, Metabolomics, and Clinical data from mouse & human models are obtained from Department of Molecular Pathology at Walter Reed Army Institute of Research and other collaborators across the country.

» This system will organize, centralize and normalize this data and provide an access portal for subsequent analysis.

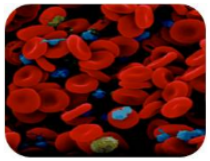
» Interrogate the behavior of genes, proteins and metabolites across diverse data. **More...**

Diseases of military relevance



PTSD

Heat Stroke

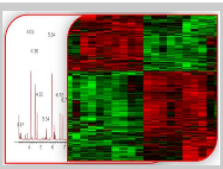


Coagulopathy

Infections

Available Data and Features

Mouse & Clinical data



Omics & Analysis

Integrated Search

Login

Email

sudhir.cr@gmail.com

Password

••••••••••••

Login

** This website works best on Mozilla Firefox and Google Chrome browsers **

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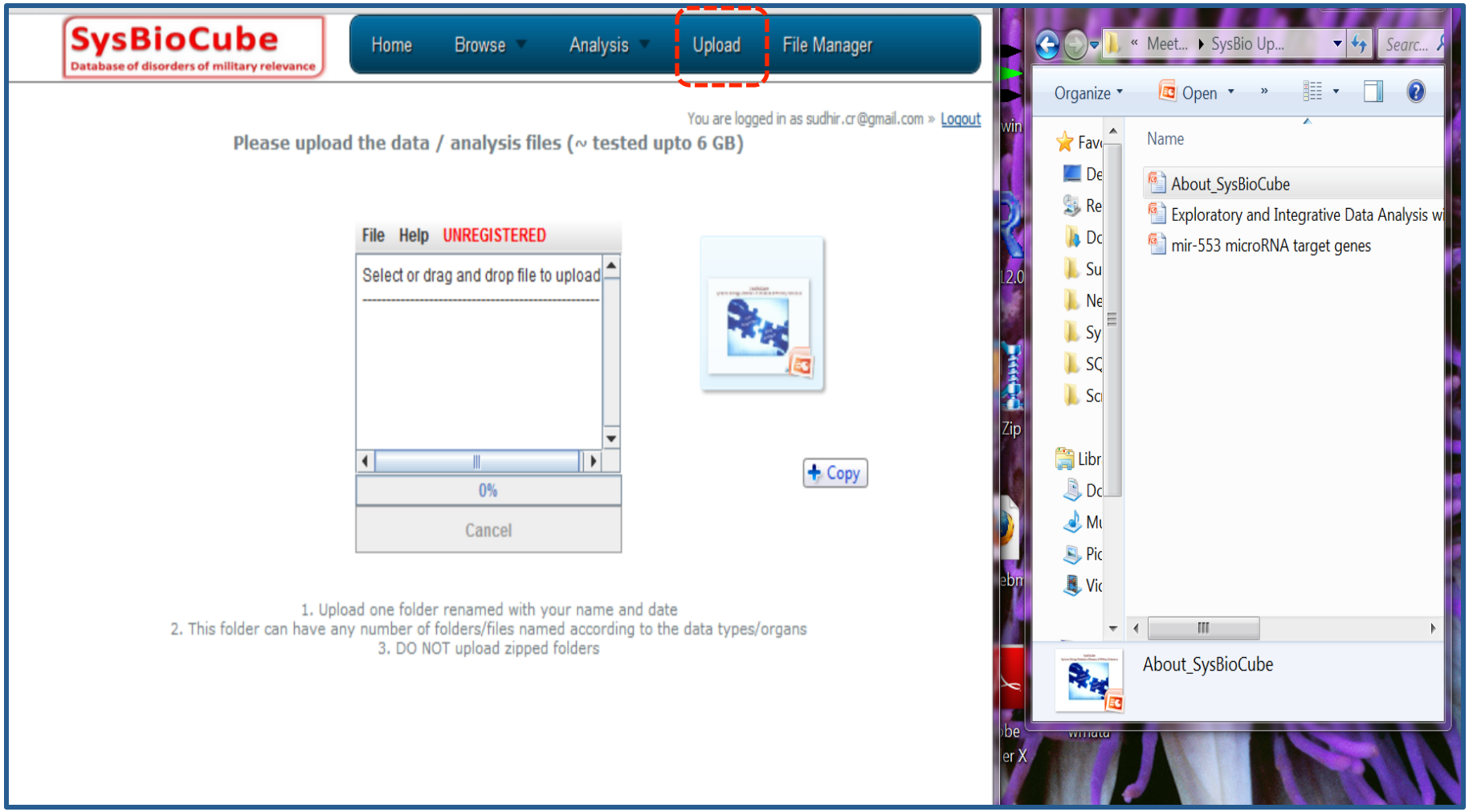
Data Upload



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About ▼

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Sysbiocube User Upload Form

Principal Investigator Info

Name: Dr. Robert Stephens

E-mail: stephensr@mail.nih.gov

Institute: ABCC Frederick, MD

Analyst Info

Name: Raina Kumar

E-mail: kumarr2@mail.nih.gov

Institute: ABCC Frederick, MD

Data Type

Raw Data:	Analyzed Data	Normalized Data

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Data Type

Raw Data:	Analyzed Data	Normalized Data

Study Type

PTSD:	Infections:	Coagulopathy:	Heat Stroke:

Experiment Type

mRNA Microarray:	microRNA Microarray:	Histopathology:	Metabolomics:
Methylation:	Physiology:	Behavior:	Proteomics:

Species Type

Mus musculus:	BALB:	C57:	DBA:
Homo sapiens	Macaca mulatta:	Rattus:	

Bodypart/SubPart

Brain Sections:

WholeBrain	Hemi-brain	Amygdala(AY)	Hippocampus(HC)	Cerebellum(CB)	Hindbrain(HB)
Medial prefrontal	cortex(MPFC)	Frontal Cortex(FCX)	septal region(SE)	hypothalamus(HY)	midbrain(MB)
Remainder of the cerebral cortex(ROC)	Posterior cingulate cortex(CNG)	ENTORHINAL CORTEX(ERC)	PIRIFORM CORTEX(PFM)	Olfactory bulb(OB)	Ventral Striatum(VS)
Striatus terminalus(ST)					

Blood:

Organ:

Spleen	Heart	Adrenal gland	Lungs
Stomach	Kidney	Deodenum	Ileum

Please upload the data / analysis files

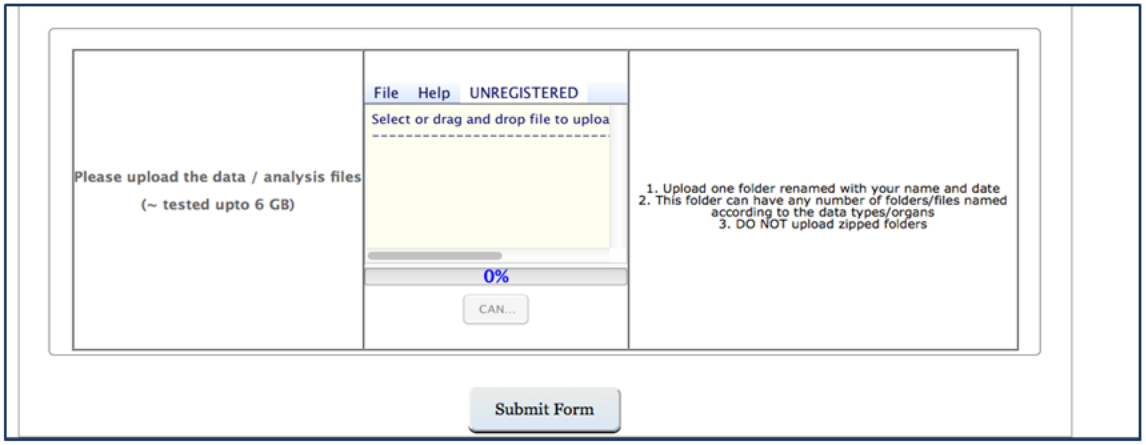
(~ tested upto 6 GB)

File Help UNREGISTERED

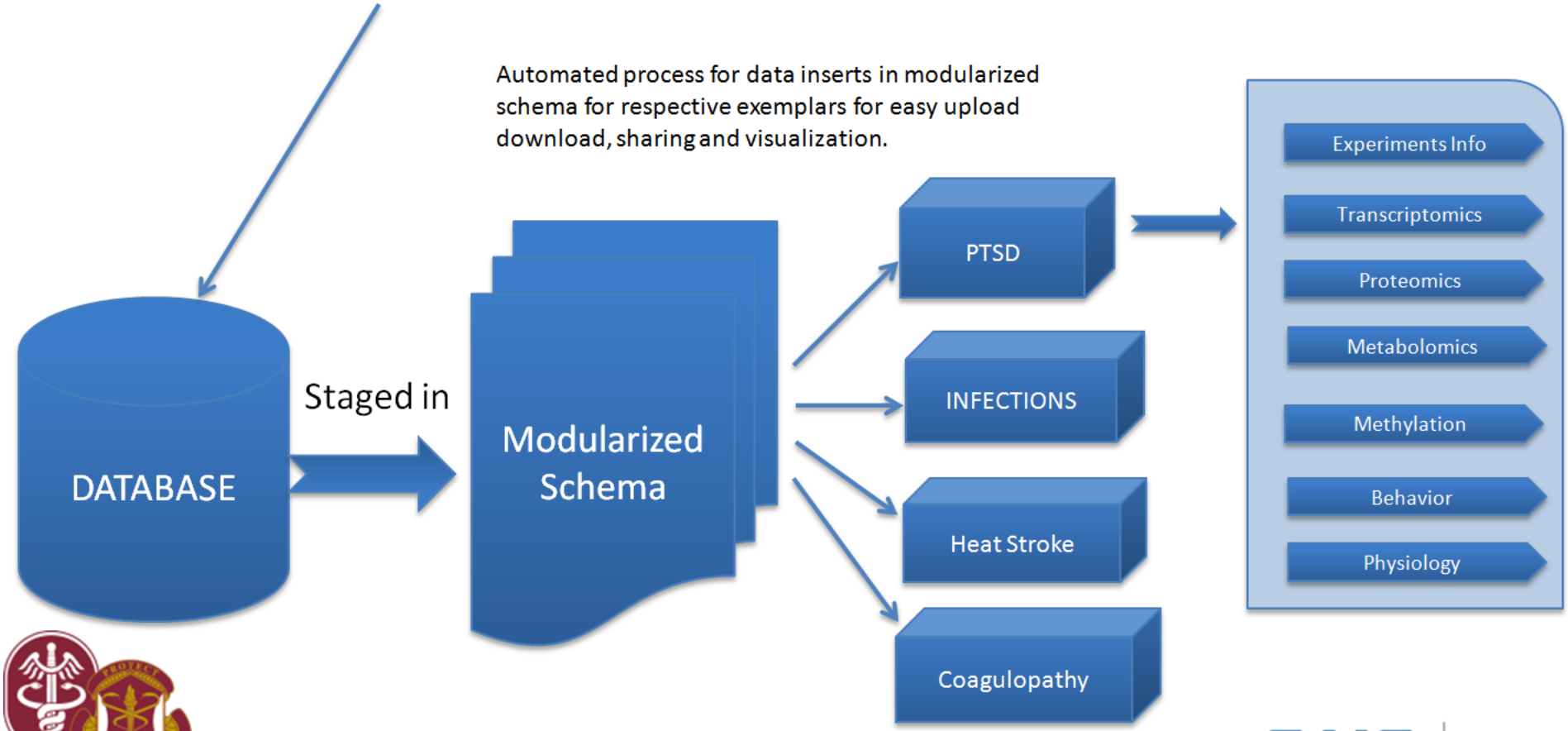
Select or drag and drop file to uploa

0%

1. Upload one folder renamed with your name and date
2. This folder can have any number of folders/files named according to the data types/organs
3. DO NOT upload zipped folders



Automated process for data inserts in modularized schema for respective exemplars for easy upload download, sharing and visualization.



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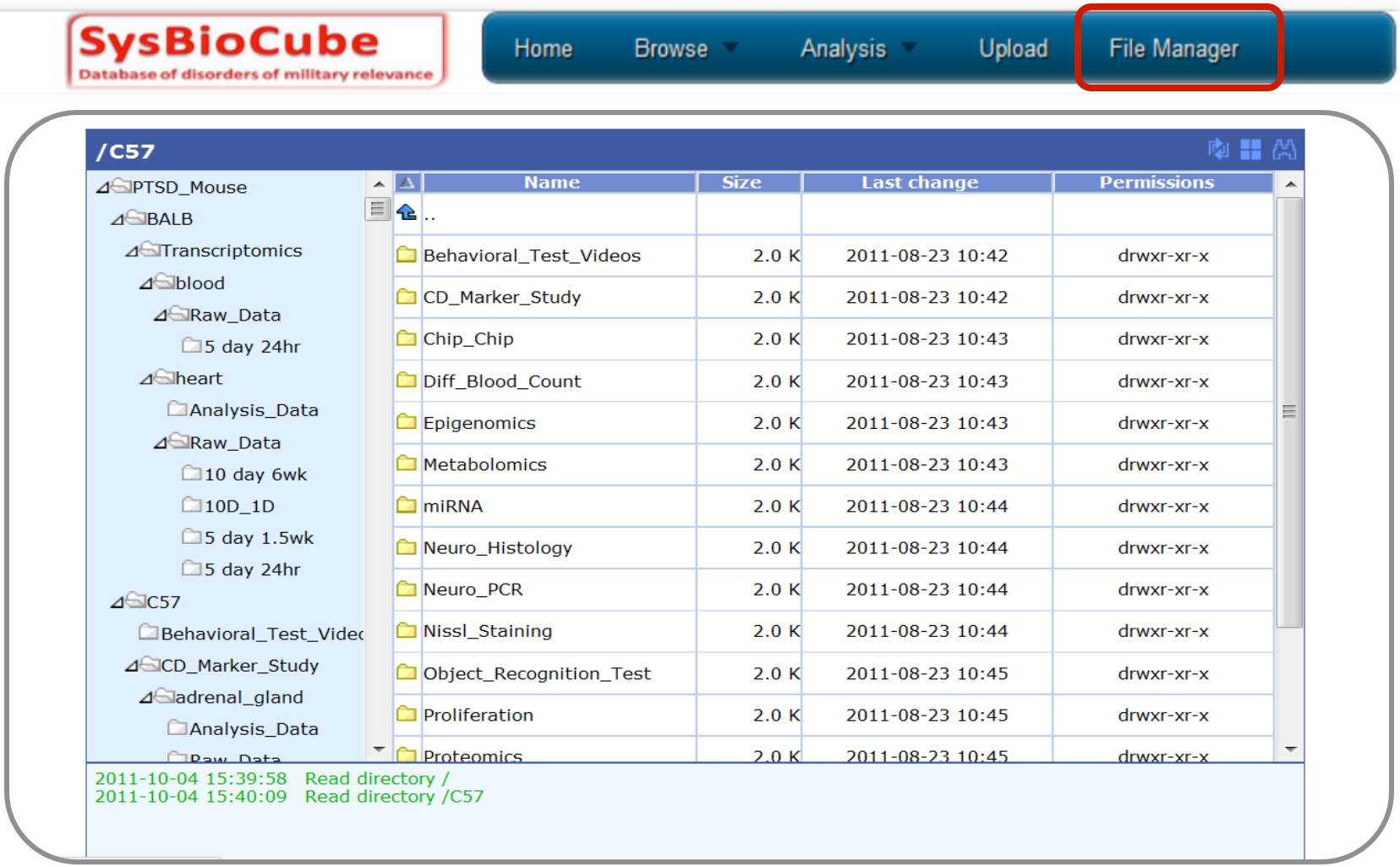
Download raw & analyzed data from “file manager”



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Publications

Firefox | Publications

sysbiodev.abcc.ncifcrf.gov/Sudhir/DataIntegrome/PUBLICATIONS/pubs.php

SysBioCube
Database of disorders of military relevance

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search

Types
- misc
- article
- all types

Years
- 2012
- 2011

Authors
- Oladimeji Abegunrin
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- Thereza Christina Monteiro De Lima
- Lucille Lumley
- James Meheroff
- Monique Melige
- James Meyerhoff
- Candace C. Moyler

Type:

[12] **SysBioCube: A data warehouse and integrative data analysis platform facilitating systems biology studies of disorders of military relevance (poster)** (Sudhir Chowbina, Rasha Hammamieh, Nabarun Chakraborty, Uma Mudunuri, Marti Jett, Joseph M. Palma, Robert Stephens), Presented at the Bio-IT World Conference, Boston, MA, 2012. [bibtex]

[11] **Histological markers of Cardiovascular Diseases in a mouse model of social stress simulating aspects of PTSD** (Umid Farach Urow, Monique Melige, Bintu Sowe, Nabarun Chakraborty, Erica Carroll, James Meheroff, Rasha Hammamieh, Marti Jett), *In faseb*, volume 26, 2012. [bibtex] [pdf]

[10] **Strain differences in response to stress: Territorial urine markings, body weight, and temperature** (William Jose Santos, Monique Melige, Nabarun Chakraborty, James Meyerhoff, Rasha Hammamieh, Marti Jett), *In faseb*, volume 26, 2012. [bibtex] [pdf]

[9] **MethCy: DNA Methylation Analysis Software** (Seid Muhie, Surajit Bhattacharya, Rasha Hammamieh, Nabarun Chakraborty, Marti Jett), *In faseb*, volume 26, 2012. [bibtex] [pdf]

[8] **The organosulfides diallyl sulfide, diallyl disulfide, and diallyl trisulfide accelerate benzo(a)pyrene metabolism in MCF-10A cells** (Candace C. Moyler, Yasmeen Nkrumah-Elie, William Dennis, Alicia Hudson3, Rasha Hammamieh, Selina Darling-Reed), *In faseb*, volume 26, 2012. [bibtex] [pdf]

[7] **Behavioral assessments of mouse Strain differences in response to social stress** (Meskerem Jibitu, James Meyerhoff, Nabarun Chakraborty, Thereza Christina Monteiro De Lima, Marti Jett, Rasha Hammamieh), *In faseb*, volume 26, 2012. () [bibtex] [pdf]

[6] **Screening of siRNA to identify the genes associated with vascular collapse when exposed to Yersinia pestis** (Allison Hoke, Aarti Gautam, Andrey Filippov, Kei Amemiya, Rasha Hammamieh, Marti Jett), *In faseb*, volume 26, 2012. () [bibtex] [pdf]

[5] **Murine model of repeated exposures to conspecific trained aggressors simulates features of post-traumatic stress disorder** (Rasha Hammamieh, Nabarun Chakraborty, Thereza C.M. De Lima, James Meyerhoff, Aarti Gautam, Seid Muhie, Peter D'Arpa, Lucille Lumley, Erica Carroll, Marti Jett), *In Behavioural Brain Research*, volume 235, 2012. () [bibtex] [pdf] [doi]

[4] **Integrated pathway-level analysis of transcriptome and metabolome data for mouse model of Social Stress** (Aarti Gautam, Seid Muhie, Nabarun Chakraborty, Allison Hoke, Rasha Hammamieh, Marti Jett), *In faseb*, volume 26, 2012. [bibtex] [pdf]

[3] **Identification of Host Factors to Block Vascular Leakage after Exposure to Staphylococcal enterotoxin B using the siRNA Approach** (Oladimeji Abegunrin, Allison Hoke, Aarti Gautam, Agnes Day, Rasha Hammamieh, Marti Jett), *In faseb*, volume 26, 2012. [bibtex] [pdf]

[2] **A data warehouse and integrative data analysis platform facilitating systems biology studies of disorders of military relevance. (poster)** (Sudhir Chowbina, Rasha Hammamieh, Nabarun Chakraborty, Uma Mudunuri, Marti Jett, David Jackson, Joseph M. Palma, Robert Stephens), Presented at the AACR-NCI Conference on Systems Biology: Confronting the Complexity of Cancer, San Diego, CA, 2011. [bibtex]

[1] **Pan-omic Approaches to Study the Effects of Microgravity on Host Responses to Toxins**, *In faseb*, volume 26. [bibtex]

Forum

SysBioCube
Database of disorders of military relevance

Index | News | User list | Search | Register | Login

You are not logged in. Please login or register. Active topics Unanswered topics

Test category

Forums	Topics	Posts	Last post
Test forum This is just a test forum	1	1	2012-09-27 20:26:31 by sudhir.chowbina

Total number of registered users: **1**
Newest registered user: **sudhir.chowbina**

Total number of topics: **1**
Total number of posts: **1**

Currently online: **1** guest, **0** registered users

Browse Multiple Data Types

Metadata

You are logged in as sudhir.cr@gr

Experimental Info | Transcriptomics | Histopathology | Metabolomics | Methylation | Behavioral Info

This section provides information about the kinds of data generated from the socially-stressed / recovery groups.

Checklist | Metadata

Experimental Meta-data

	Title	Experiment	Assays	Date	Platform	Metadat
1	PTSD Mouse Epigenetic profiling of Hemi Brain tissue from 10d SS+ 1d rest: C57B	DNA Methylation	5	05-NOV-10	Agilent	
2	PTSD Mouse Transcriptional profiling of Amygdala tissue from 10d SS+ 1d rest: C	RNA microarry	7	22-SEP-10	Agilent GPL4134	
3	PTSD Mouse Transcriptional profiling of Hippocampus tissue from 10d SS+ 1d res	RNA microarry	14	22-SEP-10	Agilent GPL4134	
4	PTSD Mouse Transcriptional profiling of Medial Prefrontal Cortex tissue from 10c	RNA microarry	14	20-DEC-10	Agilent GPL4134	
5	PTSD Mouse Transcriptional profiling of Spleen tissue from 10d SS+ 1d rest: C57	RNA microarry	14	23-SEP-10	Agilent GPL4134	
6	PTSD Mouse Transcriptional profiling of heart tissue from 10d SS+ 1d rest: C57B	RNA microarry	10	07-OCT-10	Agilent GPL4134	

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Transcriptomics – Tables

Experimental Info | Transcriptomics | Histopathology | Metabolomics | Methylation | Behavioral Info

Heatmaps | Gene Profile | Scatter Plots | Tables

5-Day / 1-Day 5-Day / 1.5-Weeks 10-Day / 1-Day 10-Day / 4-Weeks

Showing genes for a recovery group

	Gene	Description	Fold Chang	P-Value	FDR	TISSUE
1	0710001D07	RIKEN cDNA 0710001D07 gene	.2896	.03	.98	AY
2	Colec10	collectin sub-family member 10	.2293	.03	.98	AY
3	Oca2	oculocutaneous albinism II	.1992	.03	.98	AY
4	Lcorl	ligand dependent nuclear receptor corepressor-l	-.2184	.03	.98	AY
5	Alg14	asparagine-linked glycosylation 14 homolog (yea	.2094	.03	.98	AY
6	Aytl1b	acyltransferase like 1B	.2485	.03	.98	AY
7	Fcgr3	Fc receptor, IgG, low affinity III	.2836	.03	.98	AY
8	Arl6ip6	ADP-ribosylation factor-like 6 interacting protein	-.2521	.03	.98	AY
9	8430437O03	RIKEN cDNA 8430437O03 gene	-.3486	.03	.98	AY
10	Stard10	START domain containing 10	.5581	.03	.98	AY
11	Snrnp70	small nuclear ribonucleoprotein 70 (U1)	.6756	.03	.98	AY
12	Brdt	bromodomain, testis-specific	.3006	.03	.98	AY
13	Mei1	meiosis defective 1	.4146	.03	.98	AY
14	Vtn	vitronectin	3.498	.03	.98	AY
15	Repin1	replication initiator 1	.3512	.03	.98	AY

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Transcriptomics – Scatter Plots

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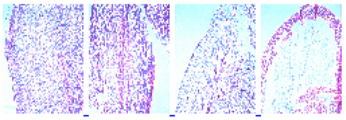
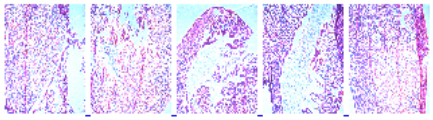
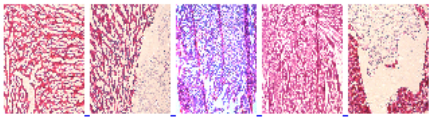
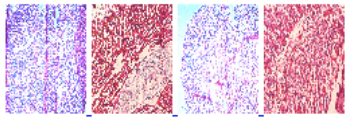
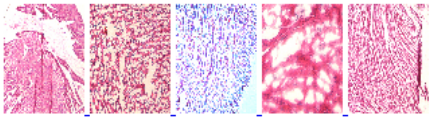
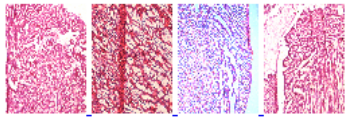
Histopathology - Images

You are l

Experimental Info | Transcriptomics | Histopathology | Metabolomics | Methylation | Behavioral Info

Images | Scoring

SS/REC Group	Group	Controls	Socially defeated
10 day / 1 day	2A		
10 day / 1 day	3A		
10 day / 1 day	1A		
10 day / 1 day	St-2		
10 day / 1 day	13		
10 day / 1 day	33		
10 day / 1 day	57-2		
10 day / 1 day	58-2		
10 day / 1 day	15		

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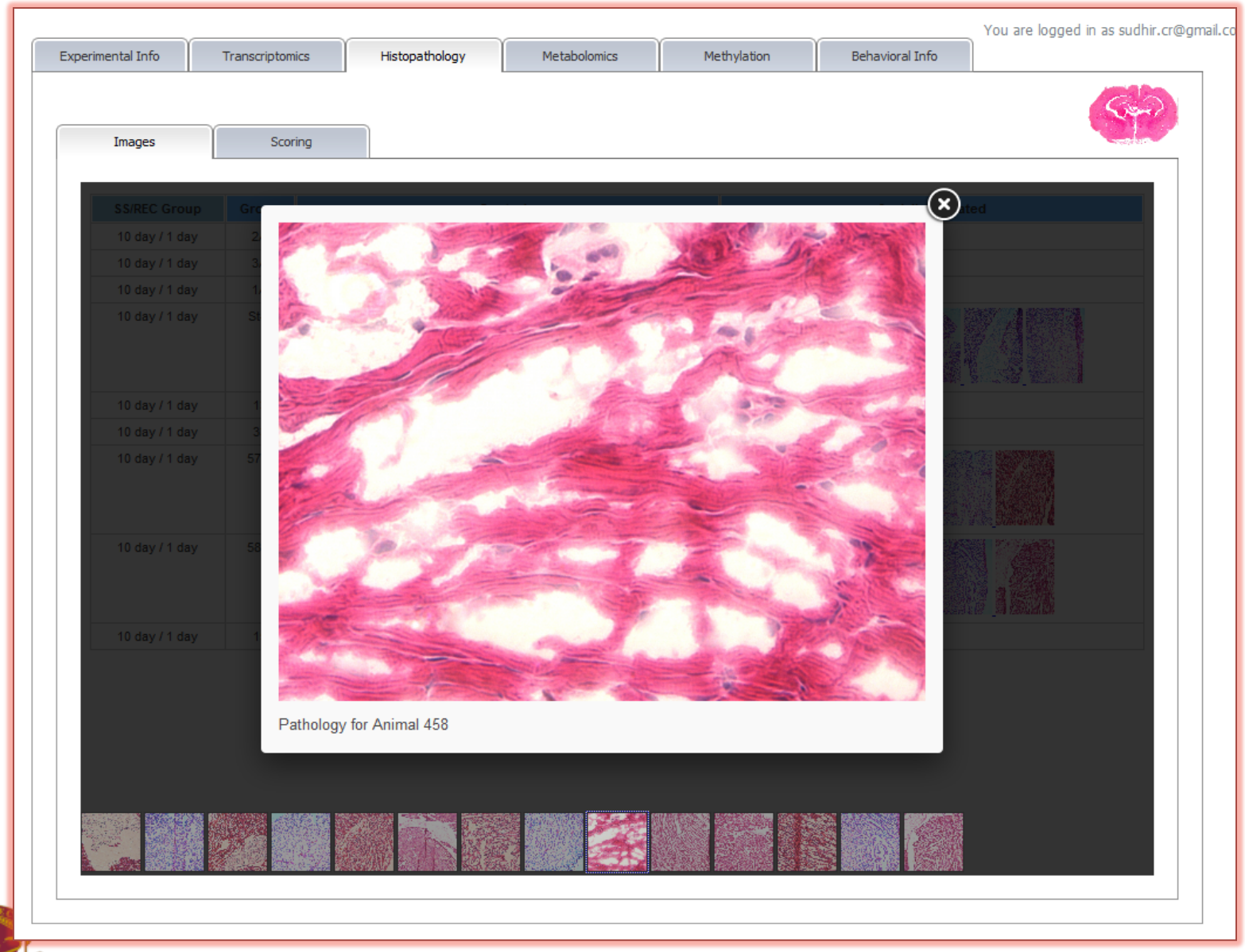
Histopathology - Images



Histopathology - Scoring

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Experimental Info | Transcriptomics | Histopathology | Metabolomics | Methylation | Behavioral Info

Images | Scoring

Duodenum Ileum Spleen Adipose Tissue Liver Lung Adrenal Gland Diaphragm Pancreas Mediastinal Adipose Tissue Colon Kidney Esophagus Cecum Stomach Brain Heart

Tissue Histopathology Data

Observation	Scoring	SS-Harvest Group	Group ID	Animals
Spleen	N	10d_1d	21	T10-353
Spleen	N	5d_1d	24	T5-389
Spleen	N	5d_1d	24	C5-372
Spleen	N	5d_1.5w	29	C5-490
Spleen	N	5d_1.5w	29	C5-488
Spleen	N	10d_1d	33	T10-576
Spleen	N	10d_1d	33	T10-574
Spleen	N	10d_1d	33	T10-573
Spleen	N	10d_1d	21	C10-346
Spleen	*	5d_1d	24	C5-370
Spleen	*	5d_1d	24	C5-369
Spleen	N	10d_1d	25	C10-401
Spleen	N	5d_1.5w	29	T5-506
Spleen	N	5d_1.5w	29	C5-489
Spleen	N	10d_1d	33	C10-570

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KEYS: N=Normal; * = Unavailable; 1 = Minimal; 2 = Mild; 3=Moderate; 4=Marked; U=Unsuitable for evaluation; P=brown-black pigment;)=Focal; >=Multifocal;]=Diffuse; H=Hemosiderosis; I = Infiltrates, lymphoplasmacytic; ! = Aorta; He=Hemorrhage; C=Alveolar septal Congestion; F=fibrin; C5=C57BL

Metabolomics

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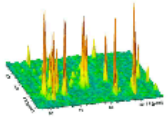
Experimental Info | Transcriptomics | Histopathology | Metabolomics | Methylation | Behavioral Info



5-Day / 1-Day 5-Day / 1.5-Weeks 10-Day / 1-Day 10-Day / 4-Weeks

Metabolomics Data

	Super-Pathway	Sub-Pathway	Metaboloite	Fold Change	P-Value	Q-Value
1	Lipid	Ketone bodies	1,2-propanediol	.94	.244	.825
2	Carbohydrate	Glycolysis, gluconeogenesis, pyruva	1,3-dihydroxyacetone	1.37	.544	.945
3	Carbohydrate	Glycolysis, gluconeogenesis, pyruva	1,5-anhydroglucitol (1,5-AG)	1.08	.41	.891
4	Lipid	Lysolipid	1-arachidonoylglycerophosphoethar	1.35	.581	.956
5	Lipid	Lysolipid	1-arachidonoylglycerophosphoinosit	1.28	.122	.702
6	Lipid	Lysolipid	1-arachidoylglycerophosphocholine	.97	.621	.972
7	Lipid	Lysolipid	1-docosahexaenoylglycerophosphoc	.89	.493	.929
8	Lipid	Lysolipid	1-docosapentaenoylglycerophospho	.93	.868	.993
9	Lipid	Lysolipid	1-eicosadienoylglycerophosphocholi	.95	.906	.993
10	Lipid	Lysolipid	1-eicosatrienoylglycerophosphochol	.98	.854	.993
11	Lipid	Lysolipid	1-heptadecanoylglycerophosphocho	1.03	.913	.993
12	Lipid	Monoacylglycerol	1-linoleoylglycerol (1-monolinolein)	2.01	.301	.829
13	Lipid	Lysolipid	1-linoleoylglycerophosphocholine	1.05	.484	.929
14	Lipid	Lysolipid	1-linoleoylglycerophosphoethanolan	1.21	.368	.875
15	Lipid	Lysolipid	1-myristoylglycerophosphocholine	.76	.112	.7

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Methylation Patterns

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Experimental Info | Transcriptomics | Histopathology | Metabolomics | Methylation | Behavioral Info

Methylation Pattern

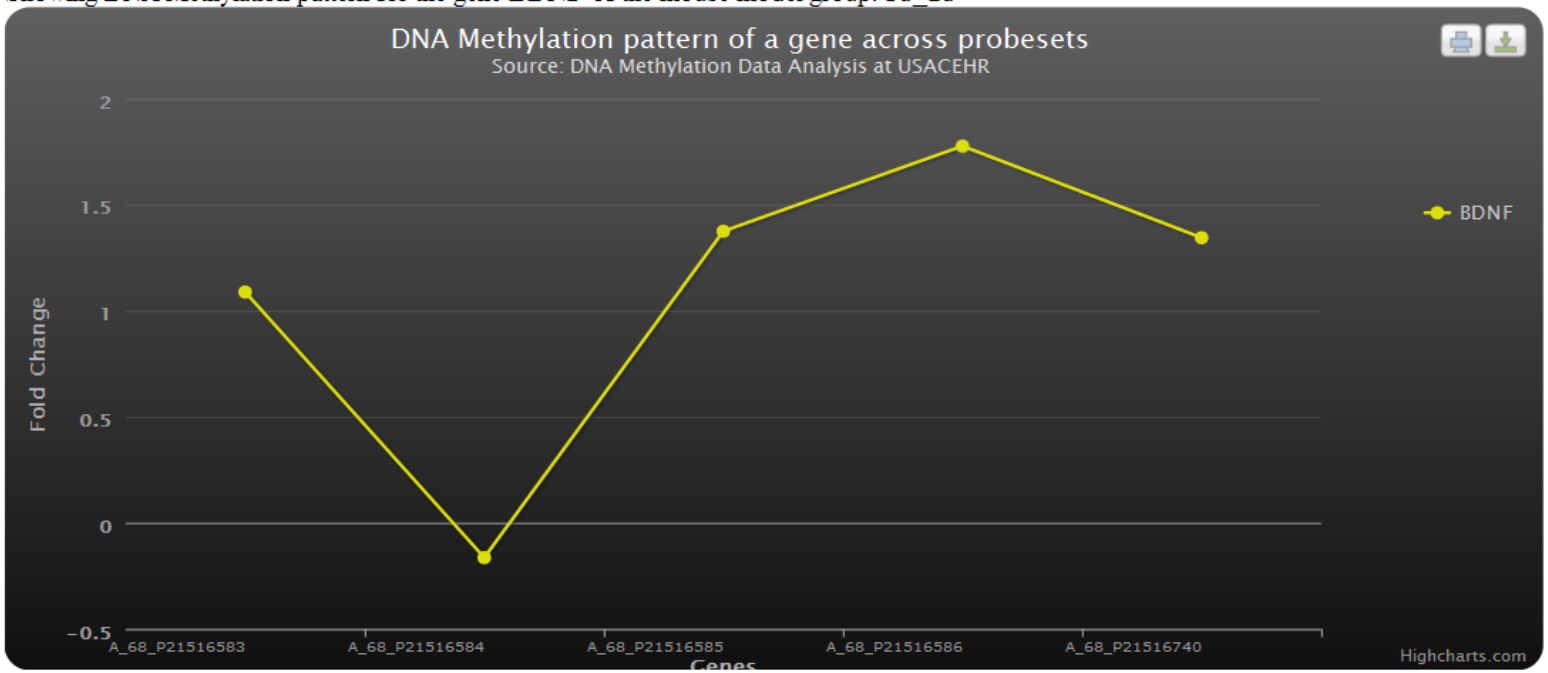
Enter one Gene Symbol: Bdnf *(start typing one letter at a time)*

Mouse model Group: 5-Day / 1-Day

Probes located in: Promoter of the gene

Show Pattern across probes

Showing DNA Methylation pattern for the gene **BDNF** of the mouse model group: **5d_1d**



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Behavior data

5-Day / 1-Day 5-Day / 1.5-Weeks 10-Day / 1-Day 10-Day / 4-Weeks

Behavior Data

	Animal	Activity	Locomotion	Avoidance	Velocity	Group
1	C10-144	2.637	.185	1.738	.725	10D_4W
2	C10-145	2.203	.218	4.471	.543	10D_4W
3	C10-146	1.401	.32	4.436	1.029	10D_4W
4	C10-147	2.1	.165	3.186	.501	10D_4W
5	C10-149	1.983	.116	4.24	.63	10D_4W
6	C10-150	2.697	.181	2.075	.467	10D_4W
7	C10-151	3.268	.114	1.993	.439	10D_4W
8	C10-152	3.036	.188	1.654	.632	10D_4W
9	C10-153	2.81	.09	1.028	.774	10D_4W
10	C10-154	2.132	.226	2.276	.647	10D_4W
11	T10-162	3.262	.142	3.109	.427	10D_4W
12	T10-163	2.896	.211	2.252	.586	10D_4W
13	T10-164	2.365	.142	2.558	.555	10D_4W
14	T10-165	2.007	.099	3.314	.5	10D_4W
15	T10-166	2.321	.176	2.949	.579	10D_4W

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Exploratory and Integrative Data Analysis with SysBioCube

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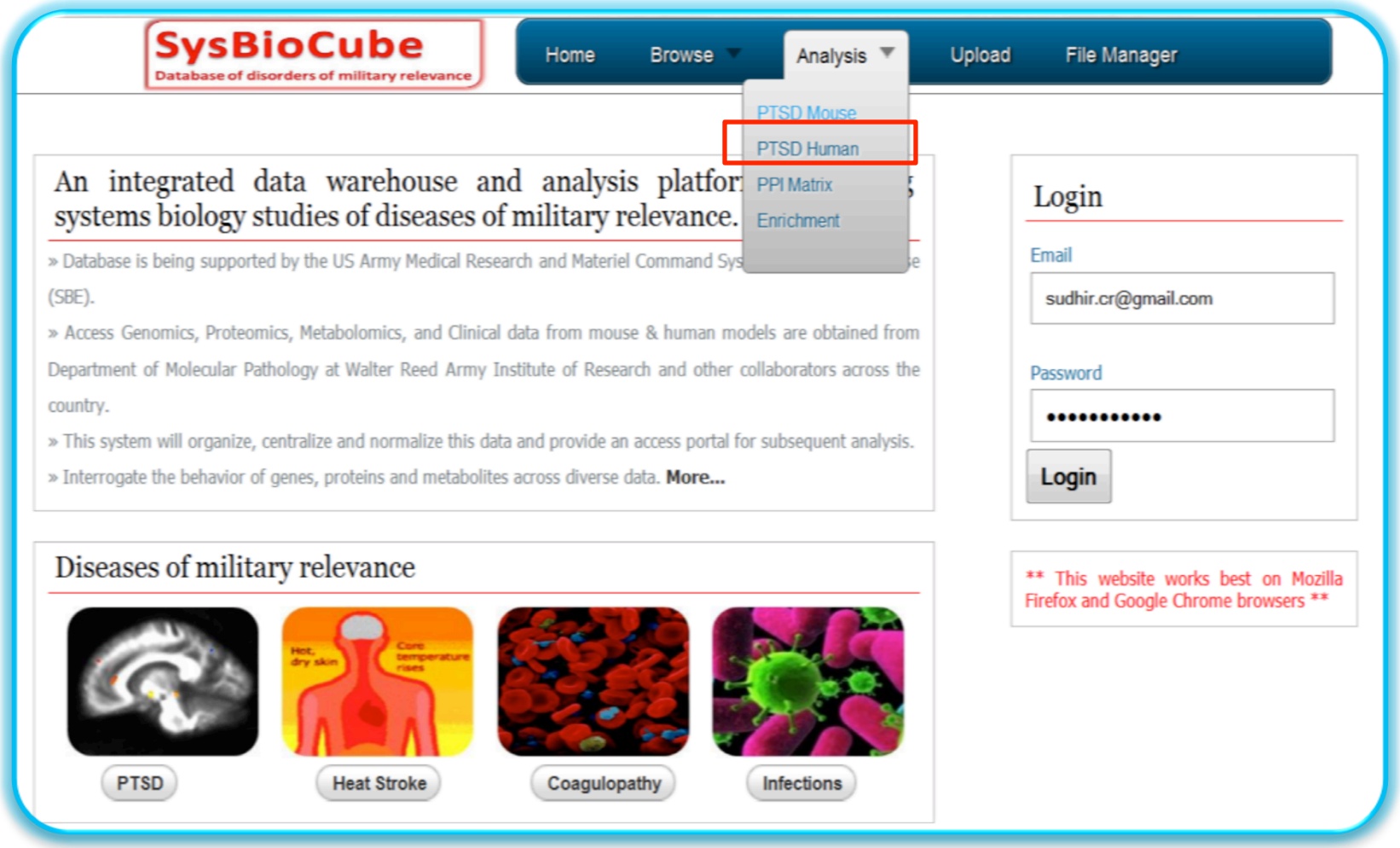
Query Across PTSD Human Gene Expression Data



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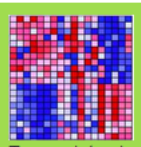
Query PTSD Human Data-Sets

Use the form below to select a single data type OR any two data types. Fill-up the parameters for each data type (*shown after each click*) and press 'Submit' to retrieve the database results matching your input parameters.

Select A Single Data Type OR Any Two Data Types



Transcriptomics

Cancel

Select Transcriptomics Data Parameters:

Data Set: PTSD Positive vs. Negative (47 samples)

Data analyzed by: SAIC

Select at least three metadata parameters

CAPSPART_CUR
CAPSTOT_CUR
CRAEDATEDAY
CRAEDATEMONTH

FILTER GENES BY:

Fold Change: greater than (>) 1.3

P-Value: 0.05

Send it

What transcription factors act on these genes? What is their expression?

GENE	LOG-FC	TRANSCRIPTION FACTOR	TF LOG-FC	PUBMED ID
C1orf226	1.95	GATA2	-.51	19941826
EGR3	1.61	MYC	-.76	12695333
EGR3	1.61	GATA3	.66	21878914
ZDHHC22	1.57	YBX1	-.06	19151767
NLRC5	1.56	GATA2	-.51	19941826
RAB3B	1.55	YBX1	-.06	19151767
RAB3B	1.55	GATA2	-.51	19941826
LARP6	1.5	GATA3	.66	21878914

Gene to Disease Association

« ‹ 1 2 3 › »

GENE	LOG-FC	NAME	DISEASE	ASSOCIATION	SOURCE	PUBMED
EGR3	1.61	early growth response 3	Hepatitis B	AlteredExpression	LHGDN	15173177
EGR3	1.61	early growth response 3	Schizophrenia	Marker	LHGDN	17360599
ARHGDIA	1.48	Rho GDP dissociation inhibitor (GDI) alpha	Colitis, Ulcerative	AlteredExpression	LHGDN	17330946
ARHGDIA	1.48	Rho GDP dissociation inhibitor (GDI) alpha	Colorectal Neoplasms	Marker	LHGDN	18651761
ARHGDIA	1.48	Rho GDP dissociation inhibitor (GDI) alpha	Crohn Disease	AlteredExpression	LHGDN	17330946
ARHGDIA	1.48	Rho GDP dissociation inhibitor (GDI) alpha	Neoplasm Metastasis	Marker	LHGDN	18651761
ARHGDIA	1.48	Rho GDP dissociation inhibitor (GDI) alpha	Oligodendroglioma	Marker	LHGDN	17653765
STAR	1.48	steroidogenic acute regulatory protein	Adrenocortical Adenoma	AlteredExpression	LHGDN	18505908

« ‹ 1 2 3 › »

Gene to Drug Association

GENE/PROTEIN	DRUG	DRUGBANK ID
APOH	Alpha-D-Mannose	DB02944
GPX8	Glutathione	DB00143
RBP1	Acitretin	DB00459
RBP1	Vitamin A	DB00162

Gene Ontology Enrichment

PAGE (Parametric Analysis of Gene Set Enrichment) using GO BP Terms

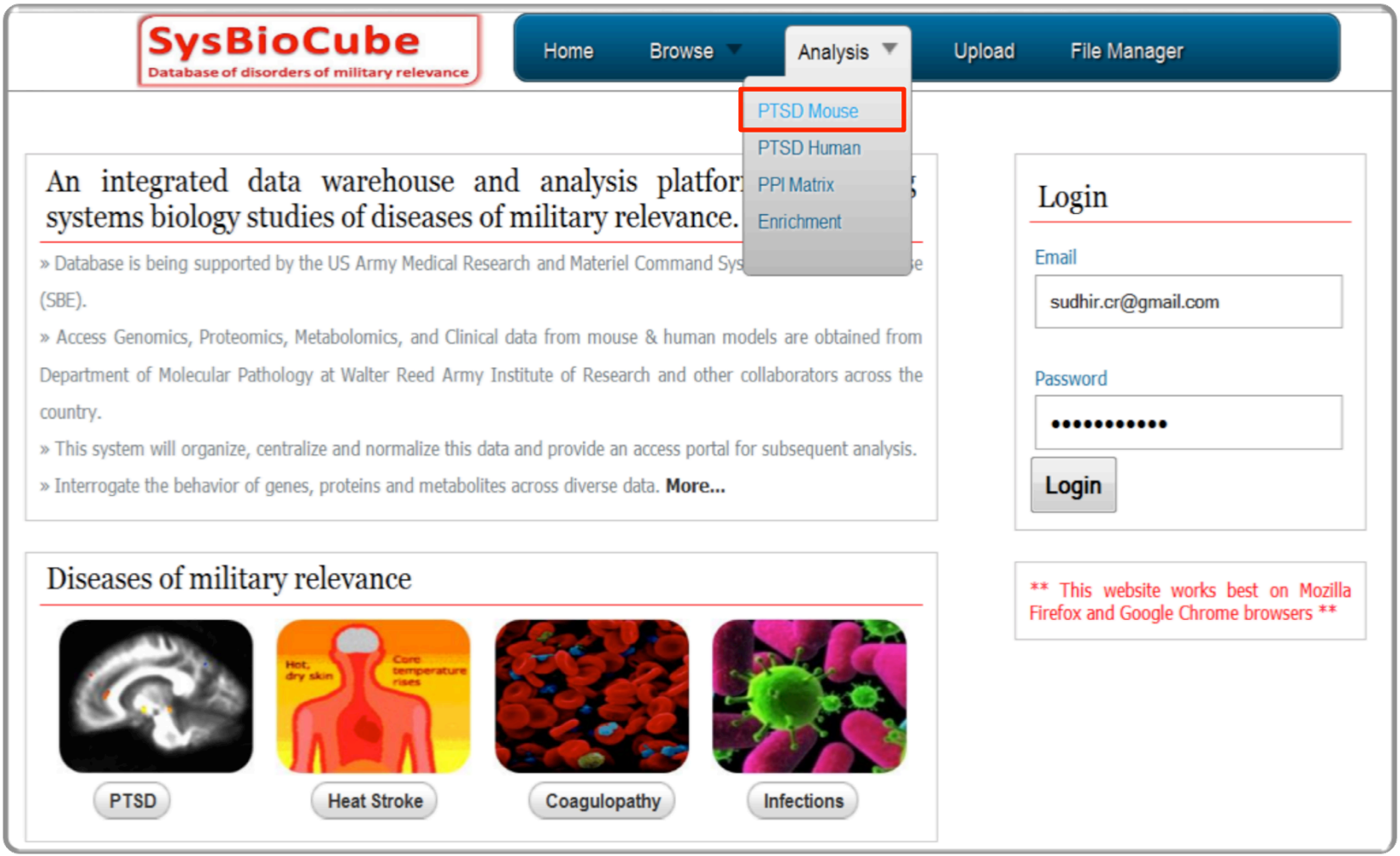
Gene Set	Z-score	Fold Change	No. of Genes
RHYTHMIC PROCESS	0.512198155298	0.0652	1
MUSCLE DEVELOPMENT	0.512198155298	0.0652	1
CIRCADIAN RHYTHM	0.512198155298	0.0652	1
SYSTEM DEVELOPMENT	-0.186644283862	-0.0168	2
ORGAN DEVELOPMENT	-0.186644283862	-0.0168	2
MULTICELLULAR ORGANISMAL DEVELOPMENT	-0.186644283862	-0.0168	2
ANATOMICAL STRUCTURE DEVELOPMENT	-0.186644283862	-0.0168	2
SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	-0.469776835687	-0.0598	1
RHO PROTEIN SIGNAL TRANSDUCTION	-0.469776835687	-0.0598	1
REGULATION OF PROGRAMMED CELL DEATH	-0.469776835687	-0.0598	1
REGULATION OF DEVELOPMENTAL PROCESS	-0.469776835687	-0.0598	1
REGULATION OF CELL ADHESION	-0.469776835687	-0.0598	1
REGULATION OF APOPTOSIS	-0.469776835687	-0.0598	1
RAS PROTEIN SIGNAL TRANSDUCTION	-0.469776835687	-0.0598	1
PROGRAMMED CELL DEATH	-0.469776835687	-0.0598	1
NEGATIVE REGULATION OF PROGRAMMED CELL DEATH	-0.469776835687	-0.0598	1
NEGATIVE REGULATION OF DEVELOPMENTAL PROCESS	-0.469776835687	-0.0598	1
NEGATIVE REGULATION OF CELLULAR PROCESS	-0.469776835687	-0.0598	1
NEGATIVE REGULATION OF CELL ADHESION	-0.469776835687	-0.0598	1
NEGATIVE REGULATION OF BIOLOGICAL PROCESS	-0.469776835687	-0.0598	1
NEGATIVE REGULATION OF APOPTOSIS	-0.469776835687	-0.0598	1
INTRACELLULAR SIGNALING CASCADE	-0.469776835687	-0.0598	1

Pathway Enrichment

PAGE (Parametric Analysis of Gene Set Enrichment) using Biocarta, KEGG and REACTOME pathways

Gene Set	Z-score	Fold Change	No. of Genes
ST DIFFERENTIATION PATHWAY IN PC12 CELLS	0.512198155298	0.0652	1
BIOCARTA VIP PATHWAY	0.512198155298	0.0652	1
KEGG TIGHT JUNCTION	0.0487059595529	0.0062	1
REACTOME SIGNALLING BY NGF	-0.469776835687	-0.0598	1
REACTOME RHO GTPASE CYCLE	-0.469776835687	-0.0598	1
REACTOME P75 NTR RECEPTOR MEDIATED SIGNALLING	-0.469776835687	-0.0598	1
KEGG VASOPRESSIN REGULATED WATER REABSORPTION	-0.469776835687	-0.0598	1
KEGG NEUROTROPHIN SIGNALING PATHWAY	-0.469776835687	-0.0598	1
REACTOME STEROID METABOLISM	-0.501200035399	-0.0638	1
REACTOME STEROID HORMONES	-0.501200035399	-0.0638	1
REACTOME STEROID HORMONE BIOSYNTHESIS	-0.501200035399	-0.0638	1
REACTOME METABOLISM OF LIPIDS AND LIPOPROTEINS	-0.501200035399	-0.0638	1
REACTOME HORMONE BIOSYNTHESIS	-0.501200035399	-0.0638	1
KEGG CYTOKINE CYTOKINE RECEPTOR INTERACTION	-0.776153032875	-0.0988	1

Query Across PTSD Mouse Data Types



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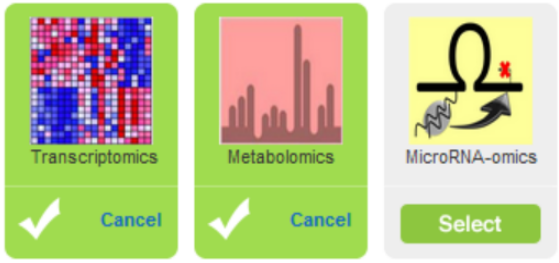
Integration between Microarray and Metabolomics
(*Network View*)

Query PTSD Mouse Data-Sets

Use the form below to select a single data type OR any two data types. Fill-up the paramete
click) and press 'Submit' to retrieve the database results matching your input parameters.

Select A Single Data Type OR Any Two Data Types



Select Transcriptomics Data Parameters:

Strain: C57/BL6

Data analyzed by: USACEHR

Defeat-Recovery Group: 5d-1d

Tissue: Blood

Fold Change: greater than (>) 1

P-Value: 0.05

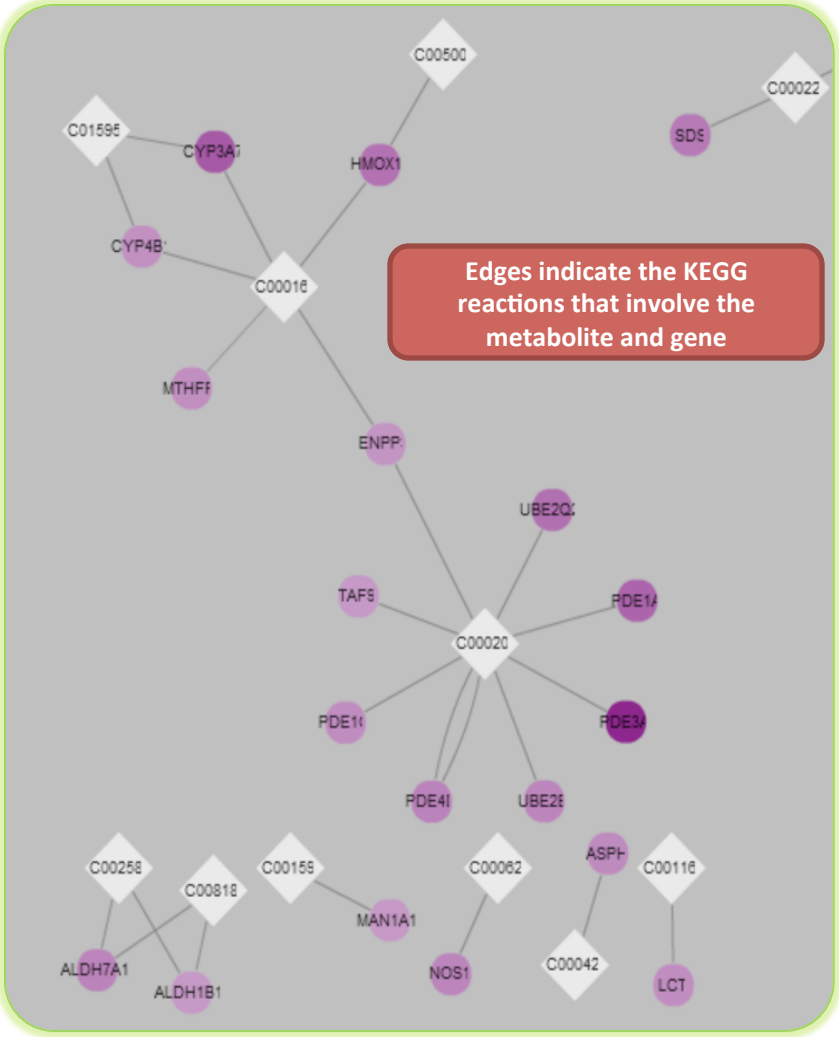
Select Metabolomics Data Parameters:

Selct the Experiment Group: 5D_1D

Tissue: Plasma

Fold Change: greater than (>) 1

P-Value: 0.05



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