AMDCC

THE ANIMAL MODELS OF DIABETIC
COMPLICATIONS CONSORTIUM

1) Web portal overview

2) Website Enhancements and New Features

3) Future Work and Enhancements

Web Portal Overview

AMDCC STATS	
Experiments	
In Progress	38
Public	4
Total	42
Microarrays	
Total	0
Models	
In Progress	70
Public	2
Total	72
Protocols	
Total	41
Publications	
In Press/Published	18
Strains	
Breeding complete	2
Breeding ongoing	19
Characterizing multiple lines	3
Embryonic rederivation	1
Not specified/Other	1
Phenotyping complete	3
Phenotyping final	1
Phenotyping ongoing	19
Total	49

Previous Steering Committee meeting

Experiments: 16 (4295 measurements)
Models: 14
Strains: 4
Publications: 6

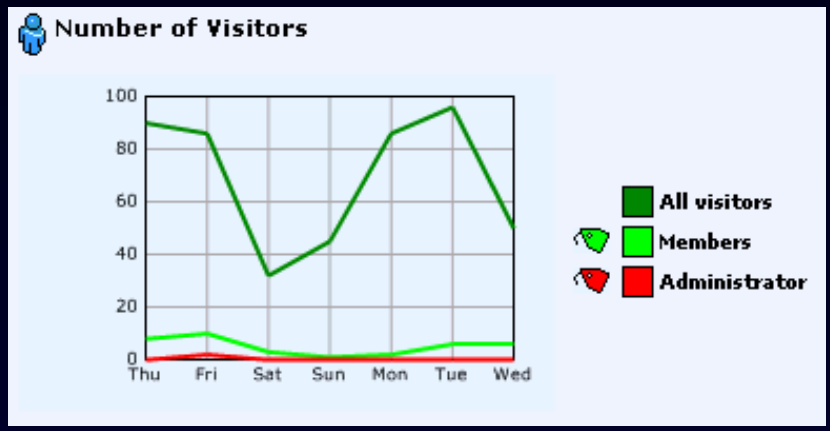
Since last Steering Committee meeting

Experiments: 12 (14674 measurements) **342% Increase !**
Models: 1
Strains: 3
Publications: 2

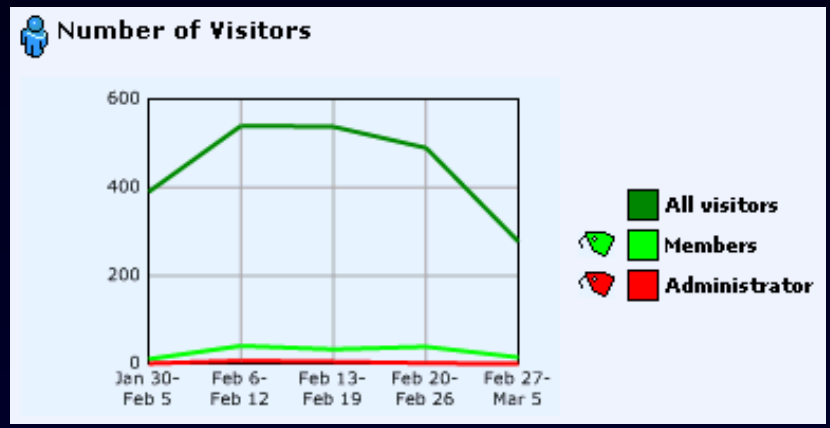
Average number of visitors per month: 2235 (**190% Increase**)

Average number of visitors per day: 75

Sample Week



Sample Month



All numbers reflect non-AMDCC members

Top Search Engine Referrers

Google	51.8%
Yahoo!	7.5%
MSN	3.9%
www.niddk.nih.gov	1.1%
Netscape	0.5%
AOL	0.4%
www.cbqm.mcg.edu	0.3%
AltaVista	0.3%
dels.nas.edu	0.3%
grants.nih.gov	0.2%
Other	3.0%
None	30.6%

American Society of Nephrology

American Diabetes Association

UT Southwestern

University of Michigan

University of North Carolina

University of Florida

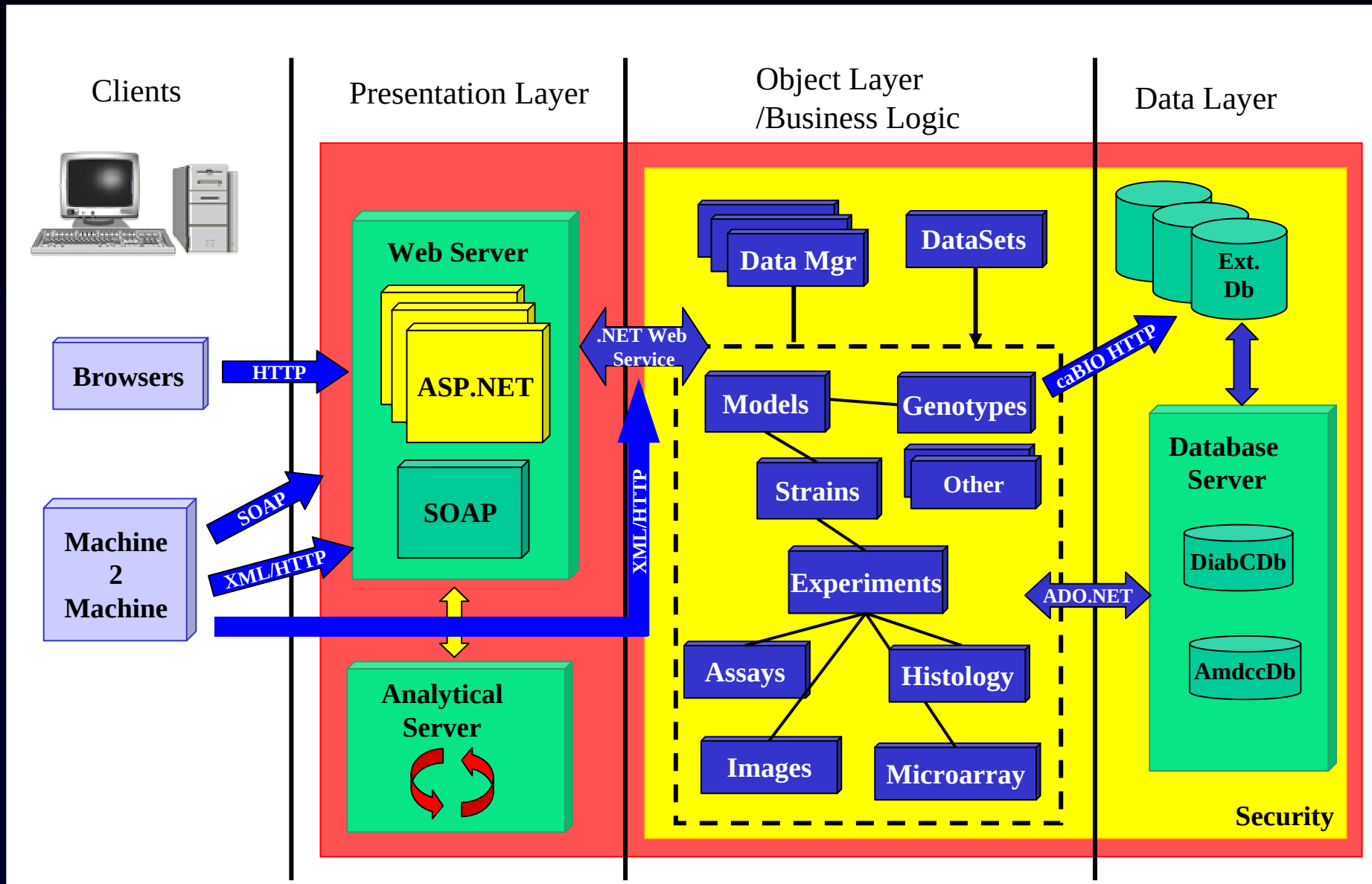
Washington University, St. Louis

Juvenile Diabetes Research Foundation

Top Search Terms

tbars	1.7%
mouse dissection	1.6%
glomerular filtration rate	1.1%
amdcc	0.9%
diabets	0.8%
tbars assay	0.7%
thiobarbituric acid	0.6%
catalase assay	0.6%
exocell	0.6%
ipgtt	0.4%
fplc	0.4%
thiobarbituric acid reactive substances	0.4%
diabetic complications	0.4%
streptozotocin	0.3%
glucose clamp	0.3%
animal models	0.3%
trap assay	0.3%
animal models of diabetic complications consortium	0.3%
glomerular filtration	0.3%
ripa buffer	0.2%
tbars protocol	0.2%
animal models of diabetes	0.2%
langendorff	0.2%
amdcc protocols	0.2%
thiobarbituric acid assay	0.2%
aortic sinus	0.2%

AMDCC IT Structure

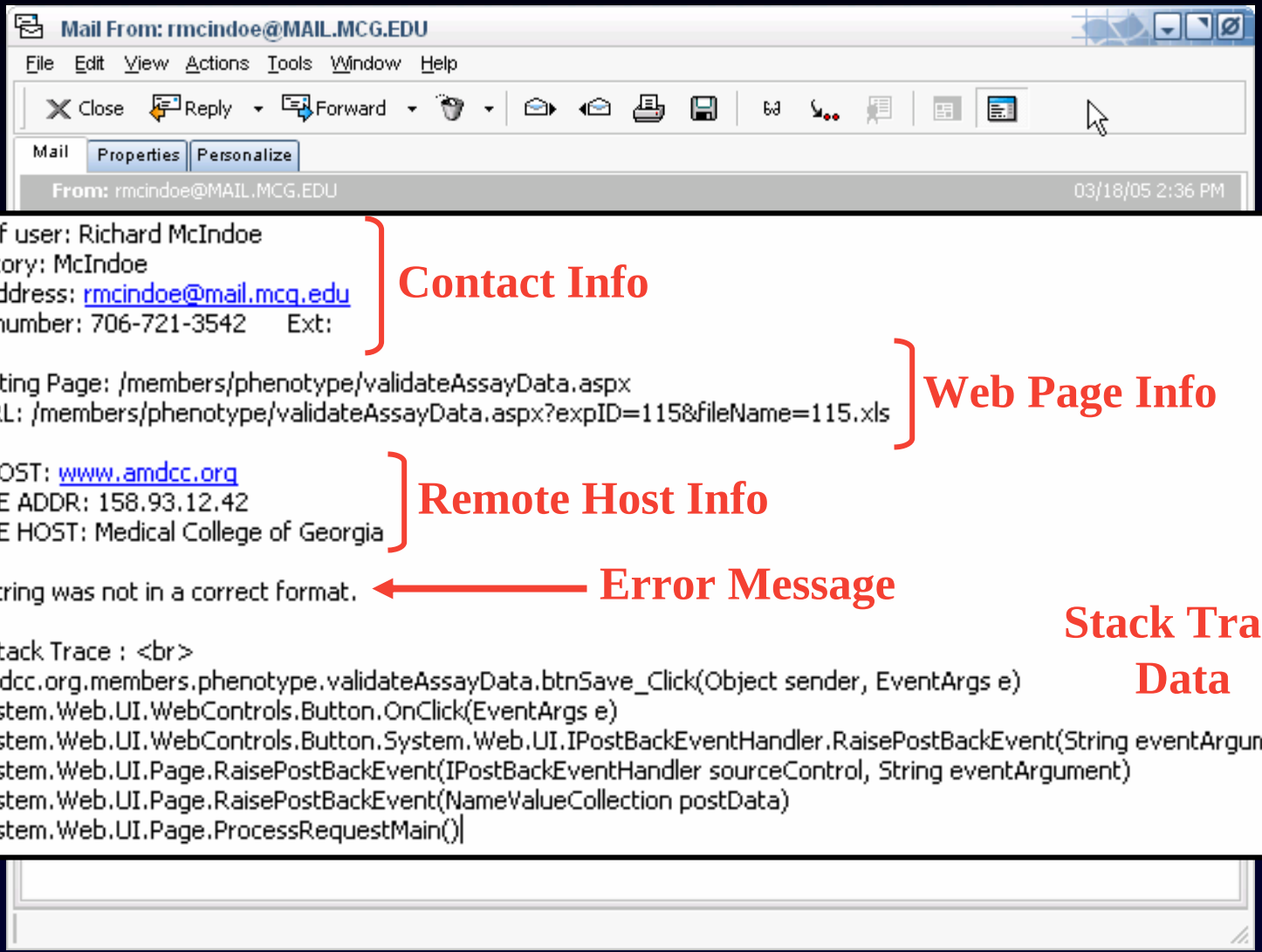


AMDCC Web portal Enhancements and New Features

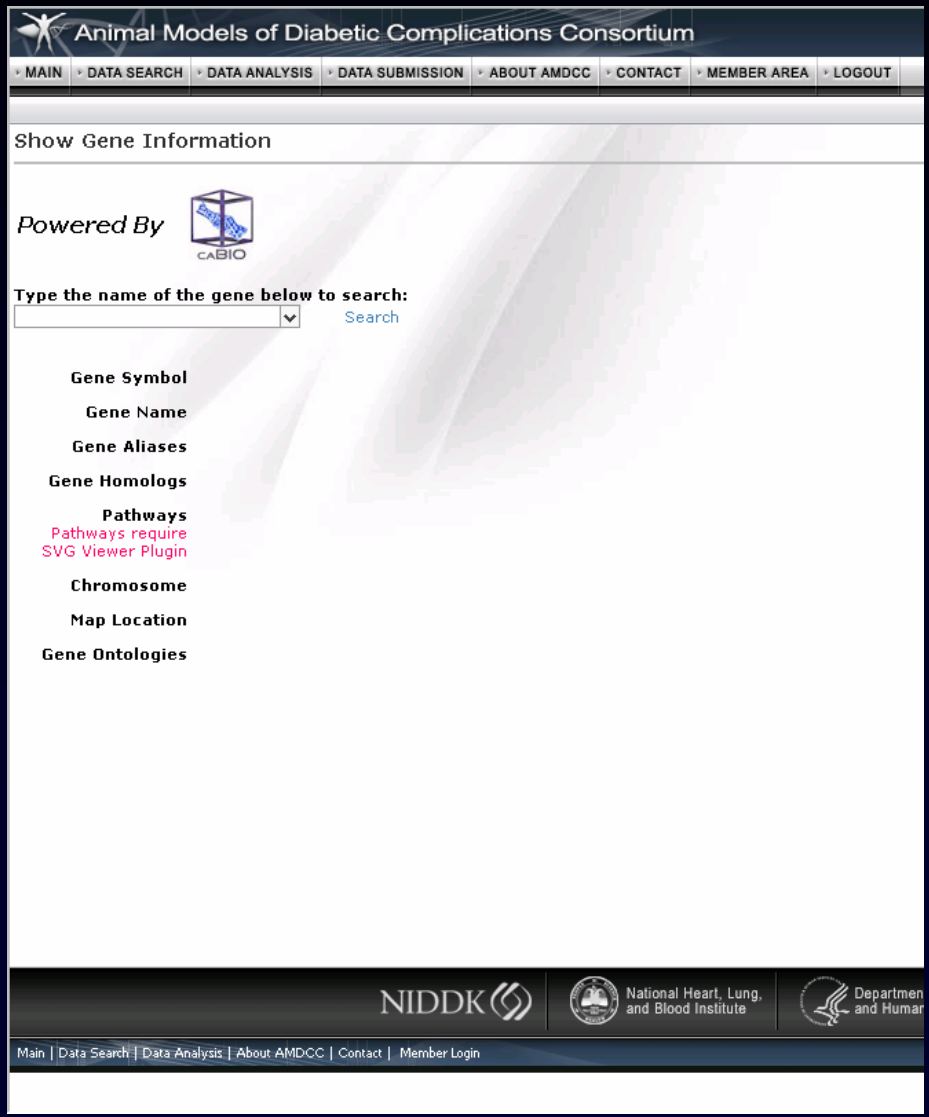
- Improved Error System: added IT notifications.
- Improved Data Retrieval for large data lists (eg. Gene lookups).
- Added Bioinformatics subsection (data/object models, software distribution, Webservice WSDL file)
- Added Annual Reports and SC Presentations subsection
- Strain Genotype data model/user interface completed
- Statistical Exploration: ANOVA analysis completed (1 and 2 way)
- Added Chart Exploration: Column, Line, XY charts
- Adhoc Datasets incorporated into Charting, Basic Statistics, ANOVA analysis
- AMDCC Webservice architecture started

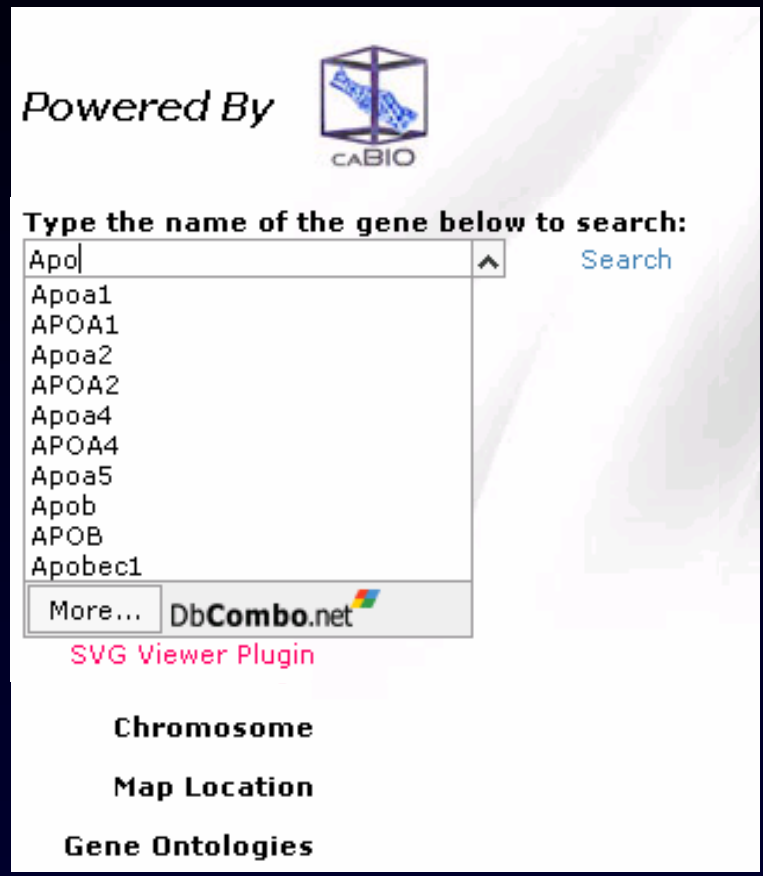
Improved Error Subsystem

Automated error notifications of unhandled exceptions to CBU in order to improve our response time to correct website errors.



Improved Data Retrieval for large data lists (eg. Gene lookups).





Added Bioinformatics subsection

Click the links below for more information.

Infrastructure Information

AMDCC IT Infrastructure

Our programming paradigm is to develop software systems based on an n-tier architecture, where we create the presentation layer, business logic and data layer into separate software systems. These systems have been developed to minimize maintenance, but provide a robust scalable model for future growth and interactions at the national level with other organism databases. These systems have been designed using the unified modeling language (UML) with the designs available to the general public. The two UML modeling tools we use are Rational Rose and Powerdesigner.

AMDCC Data Model

The core relational data model for the AMDCC was created using SQL Server 2000 and was based on a number of existing schemas containing our key subject areas: animal models, genotypes (including array experiment data), histopathology, and phenotype Assays. The Mouse Models of Human Cancer Consortium (MMHCC) and the Jackson Labs were particularly helpful, and shared several successful models. The current version of the database addresses several domains, including administration, models, strains, genotypes, publications, external database references, ontology management, experiments, phenotype assays, microarray data, histology, images and dataset persistence. This data model required 166 tables, 55 functions, 530 stored procedures, 141 data views and a total of 9344 lines of code.

AMDCC-OM

The AMDCC Object Model (AMDCC-OM) created for the consortium fully describes the activities of the AMDCC and provides an OOP API to access the data generated by the consortium. The AMDCC-OM was designed using Powerdesigner and UML, written in C# and compiled as a .NET DLL. The object model contains both administrative and domain specific classes. However, only the data centric classes are available to the public. The Domain classes provide both object specific classes (e.g. Model, Strain, Experiment, Protocol, etc.) as well as DataManager and SearchCriteria classes used to retrieve data from the system. These DataManager classes are specific for each of the datatypes maintained by AMDCC. For example, the StrainMgr class provides methods to retrieve strain specific data. The SearchCriteria classes are also datatype specific and are used by the DataManager classes to query the database using different type specific parameters. For example, the StrainSearchCriteria class provides queryable properties specifc for the Strain data in the system.
In order to provide the broadest access to the data, we are also creating a WebService that exposes specific portions fo the AMDCC-OM to the public. Specifically, the WebService will provide access to all the object specific classes as well as the DataManager and SearchCriteria classes. This provides a mechanisms for programmers to create local AMDCC-OM objects in other languages. The current version of the AMDCC-OM has 185 object classes.

Software Applications

caBIONet

The National Cancer Institute's Center for Bioinformatics (NCICB) has developed a java based data management and information system called caCORE. One component of this software suite is the object oriented API (caBIO) used to access the rich biological datasets collected at the NCI. caBIONet is a set of .NET wrapper classes (managers, genes, chromosomes, sequences, etc.) capable of serializing an XML data stream into local .NET objects. The software is able to search NCICB databases and provide local objects representing the data that can be manipulated and used by other .NET programs. The software was written in C# and compiled as a .NET DLL.

Agreement

Please enter your name and email address below.

Name (First and Last)

Email Address

All software provided by the AMDCC is under the following license agreement.

Agree

DO NOT agree

Please indicate that you have read and agree.

Submit

THE OPEN SOFTWARE LICENSE V1.1

This Open Software License (the "License") applies to any original work of authorship (the "Original Work") whose owner (the "Licensor") has placed the following notice immediately following the copyright notice for the Original Work:

Licensed under the Open Software License version 1.1

1) **Grant of Copyright License.** Licensor hereby grants You a world-wide, royalty-free, non-exclusive, perpetual, non-sublicenseable license to do the following:

a) to reproduce the Original Work in copies;

b) to prepare derivative works ("Derivative Works") based upon the Original Work;

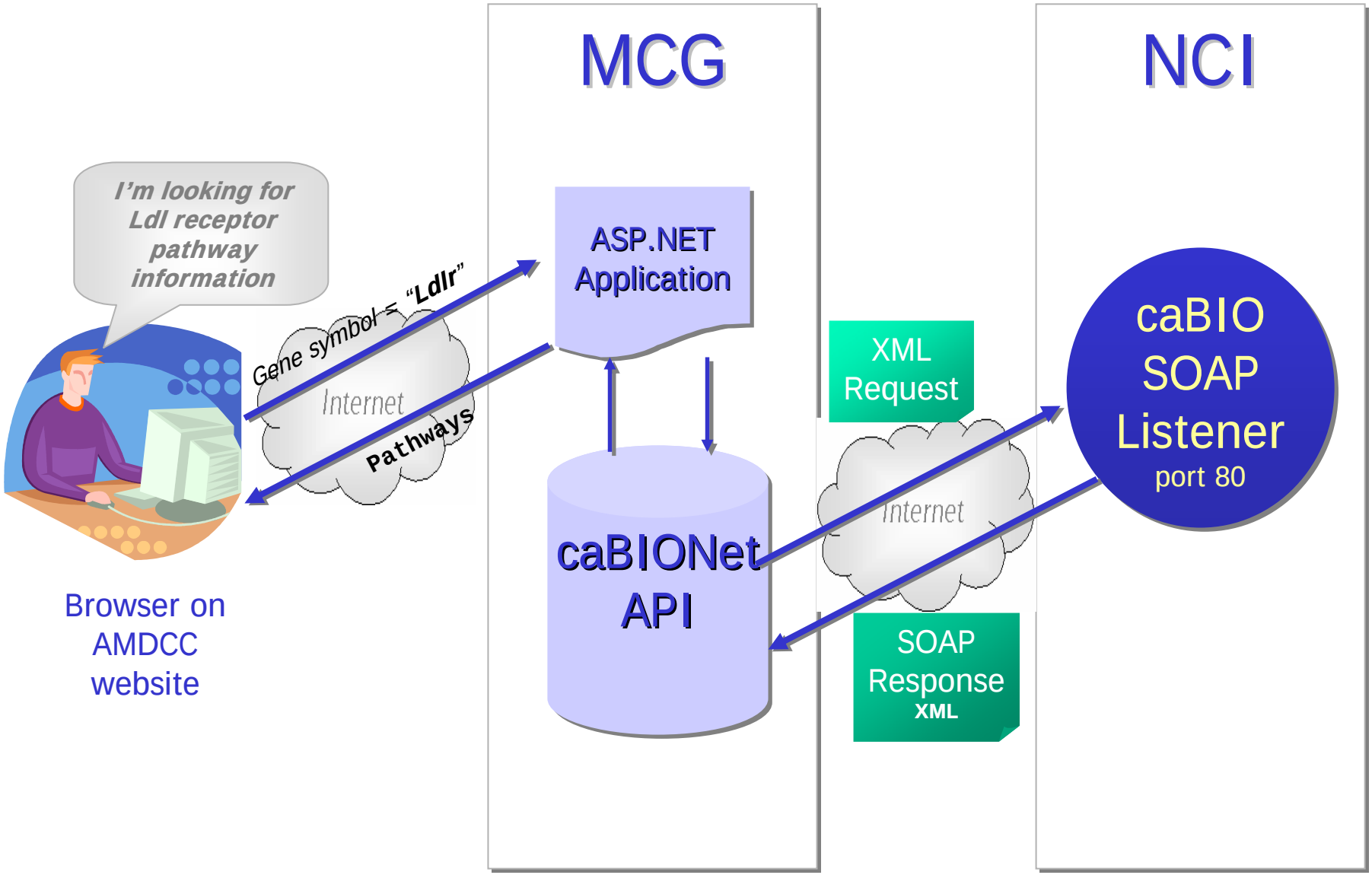
c) to distribute copies of the Original Work and Derivative Works to the public, with the proviso that copies of Original Work or Derivative Works that You distribute shall be licensed under the Open Software License ;

d) to perform the Original Work publicly; and

e) to display the Original Work publicly.

2) **Grant of Patent License.** Licensor hereby grants You a world-wide, royalty-free, non-exclusive, perpetual, non-sublicenseable license, under patent claims owned or controlled by the Licensor that are embodied in the Original Work as furnished by the Licensor ("Licensed Claims") to make, use, sell and offer for sale the Original Work. Licensor hereby grants You a world-wide, royalty-free, non-exclusive, perpetual, non-sublicenseable license under the Licensed Claims to make, use, sell and offer for sale Derivative Works.

3) **Grant of Source Code License.** The term "Source Code" means the preferred form of the Original Work for making modifications to it and all available documentation describing how to modify the Original Work. Licensor hereby agrees to provide a machine-readable copy of the Source Code of


MCG
NCI
I'm looking for Ldl receptor pathway information
Gene symbol = "Ldlr"
Internet
Pathways
ASP.NET Application
caBIONet API
XML Request
Internet
caBIO SOAP Listener
port 80
SOAP Response
XML
Browser on AMDCC website

Animal Models of Diabetic Complications Consortium

MAIN | DATA SEARCH | DATA ANALYSIS | ABOUT AMDCC | CONTACT | MEMBER AREA

Show Gene Information

Powered By caBIO

Gene Symbol	Ldlr
Gene Name	Low density lipoprotein receptor
Gene Aliases	Mm.ldlr Ldlr
Gene Homologs	LDLR
Pathways	m_fxrPathway m_s1pPathway
Chromosome	
Map Location	
Gene Ontologies	receptor activity low-density lipoprotein receptor activity lipid transporter activity calcium ion binding protein binding endosome coated pit lipid transport endocytosis cholesterol metabolism membrane integral to membrane cholesterol homeostasis

NIDDK | National Heart, Lung, and Blood Institute

Main | Data Search | Data Analysis | About AMDCC | Contact | Member Login

Animal Models of Diabetic Complications Consortium

MAIN | DATA SEARCH | DATA ANALYSIS | ABOUT AMDCC | CONTACT | MEMBER AREA

Show Gene Information

Powered By caBIO

Type the name of the gene below to search:

☑ Gene starts with:

Icam1 Search

Gene Symbol	Icam1
Gene Name	Intercellular adhesion molecule
Gene Aliases	Mm.cd54 Icam1
Gene Homologs	ICAM1
Pathways	m_blymphocytePathway m_ctlPathway m_lymphocytePathway m_monocytePathway m_neutrophilPathway m_tcytotoxicPathway m_thelperPathway
Chromosome	
Map Location	
Gene Ontologies	protein binding cell adhesion membrane integral to membrane cell-cell adhesion

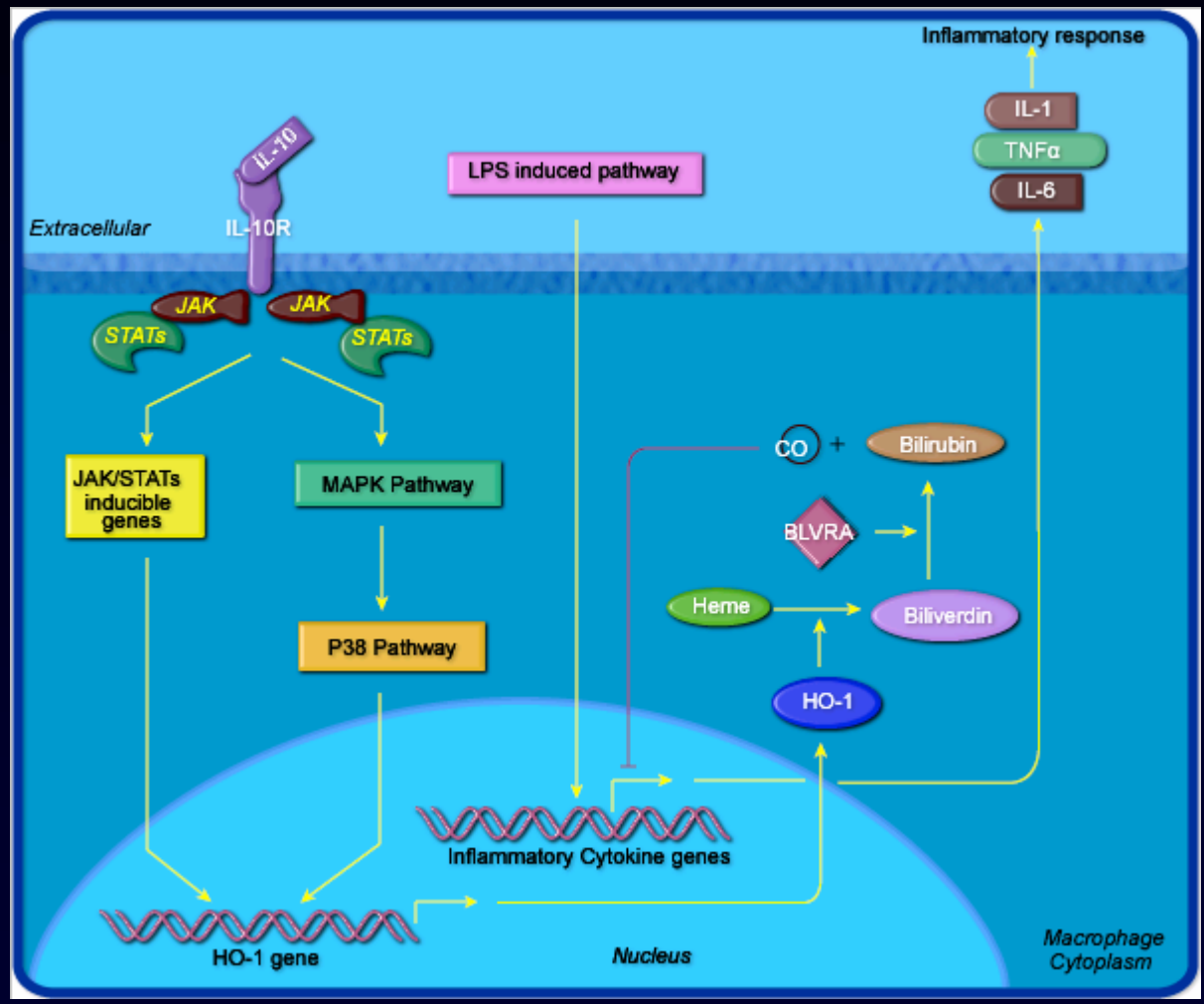
NIDDK | National Heart, Lung, and Blood Institute

Main | Data Search | Data Analysis | About AMDCC | Contact | Member Login

AMDCC

Retrieve BIOCARTA pathways via caBIONet

* requires and SVG Viewer plugin



Added Annual Reports and SC Presentations subsection

Click the links below for more information.

Investigator Reports 2004

Erwin Bottinger
Jan Breslow
Mathew Breyer
Frank "Chip" Brosius
Dave Clemmons/Tim Nichols
Tom Coffman
Firuoz Daneshgari
Eva Feldman
Willa Hsueh
Timothy Kern
Don McClain
Richard McIndoe

Investigator Reports 2005

Erwin Bottinger
Jan Breslow
Mathew Breyer
Frank "Chip" Brosius
Dave Clemmons/Tim Nichols
Tom Coffman
Firuoz Daneshgari
Eva Feldman
Willa Hsueh
Timothy Kern
Don McClain
Richard McIndoe

Please note: These are Adobe PDF versions of the Powerpoint slides. This will require the Adobe Reader to view. Click the links below for more information.

Steering Committee Meeting 10/19/2004

All Presenations (Zip file)

Erwin Bottinger
Jan Breslow
Mathew Breyer
Frank "Chip" Brosius
Dave Clemmons/Tim Nichols
Tom Coffman
Firuoz Daneshgari
Eva Feldman
Willa Hsueh
Timothy Kern
Don McClain/Dale Abel
Richard McIndoe

Strain Genotype data model/user interface completed

Show AMDCC Strain

B6.Cg-Ldlr^{tm1Her} Ipf1 $^{+/-}$

ADD TO FAVORITES

Investigators	Breslow , Jan
Species	M. musculus
Official Name	B6.Cg-Ldlr^{tm1Her} Ipf1 $^{+/-}$
Common Name	C57BL6/J-Ldlr$^{-/-}$ Pdx1 $^{+/-}$
Development Status	Breeding ongoing
Creation Method	congenic

Genomic Information

Genomic Modification | Transgene | Genomic Segments

Gene	Allele 1	Allele 2	Protocol
Ldlr	knockout	knockout	
Ipf1	wild	knockout	

Treatment Protocol	Not Specified
Background	C57BL/6J
Maternal / Paternal Strain	B6.129S7-Ldlr^{tm1Her} /J/C57BL/6-Ipf1 $^{+/-}$
Child Strains	No child strains found
Breeding Type (Generations)	Not Specified
Breeding Protocol	Not Specified
Phenotype Description	Not Specified
Models	No Models found
Experiments	Breslow: Effect of Hyperglycemia on Atherosclerosis

External References

Reference	Link to Reference
Mouse Phenome Database: Strains	*not available*

Provides a very flexible way to define the modifications.

Genomic Modification | Transgene | Genomic Segments

Gene	Allele 1	Allele 2	Protocol
Ldlr	knockout	knockout	
Pparg	knockin[loxP]	knockin[loxP]	

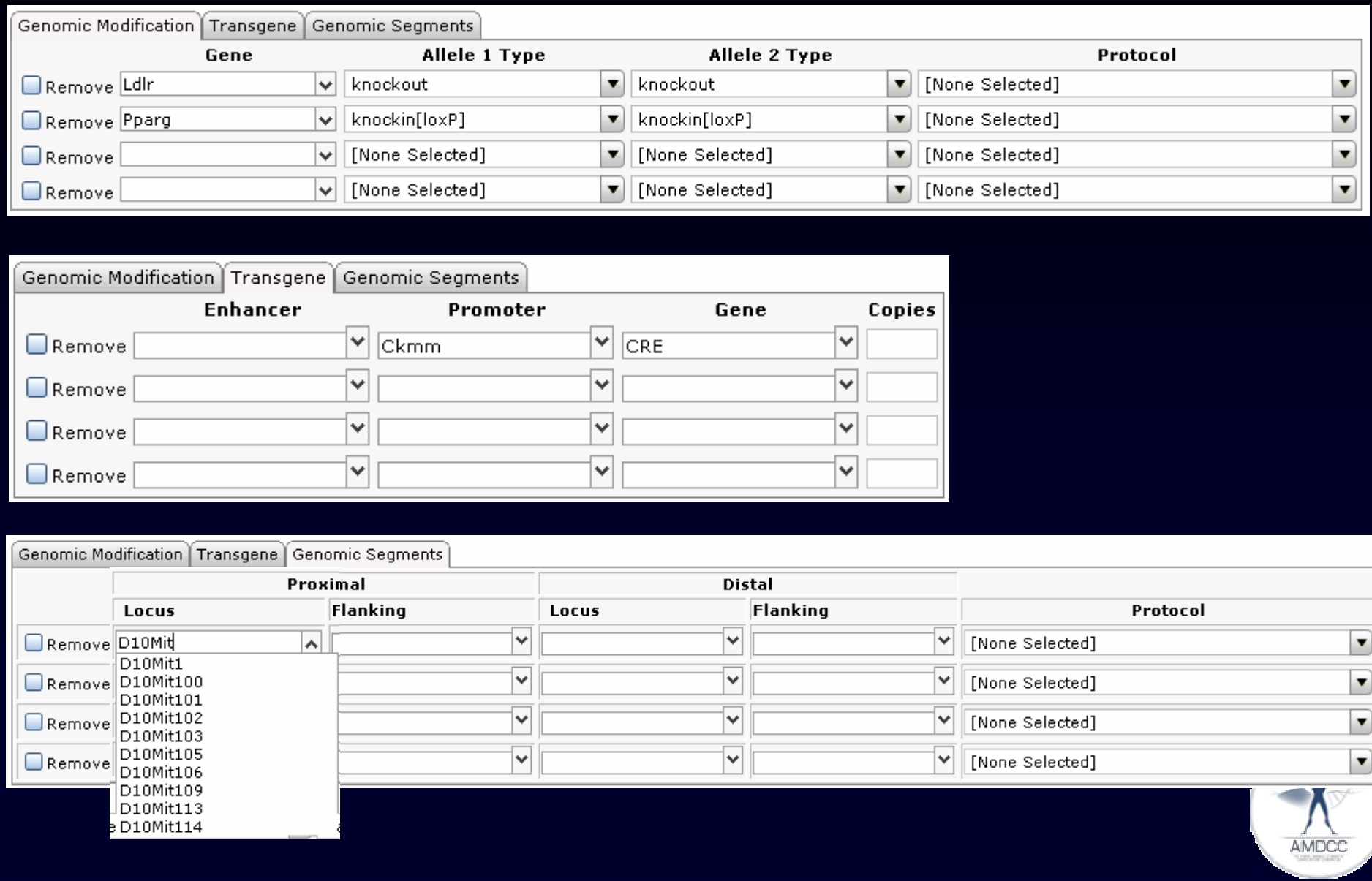
Genomic Modification | Transgene | Genomic Segments

Regulatory Element	Gene	Copies
Ckmm promoter	CRE	

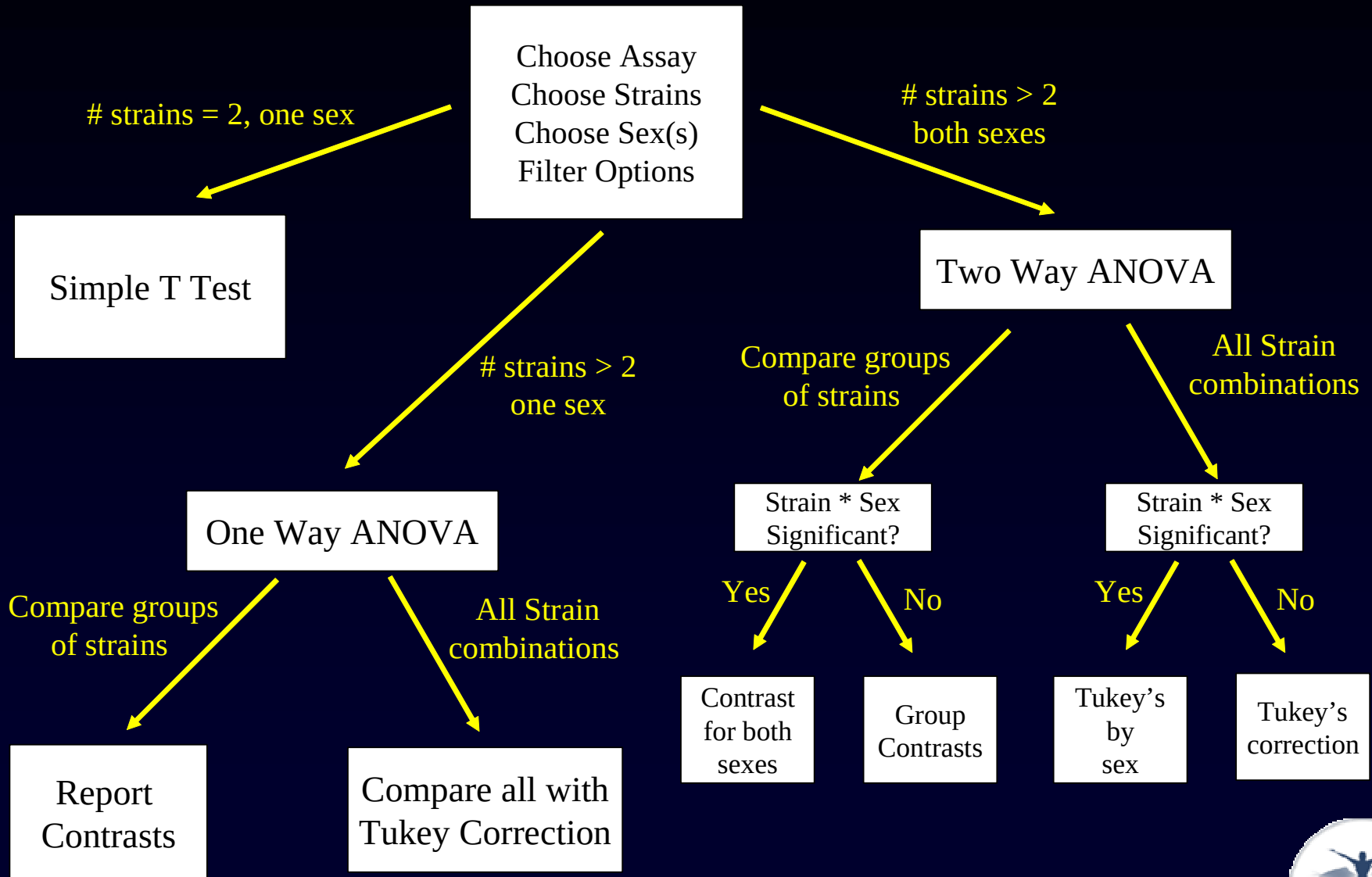
Genomic Modification | Transgene | Genomic Segments

Proximal		Distal		
Locus	Flanking	Locus	Flanking	Protocol
D10Mit68	D10Mit203	D10Mit103		

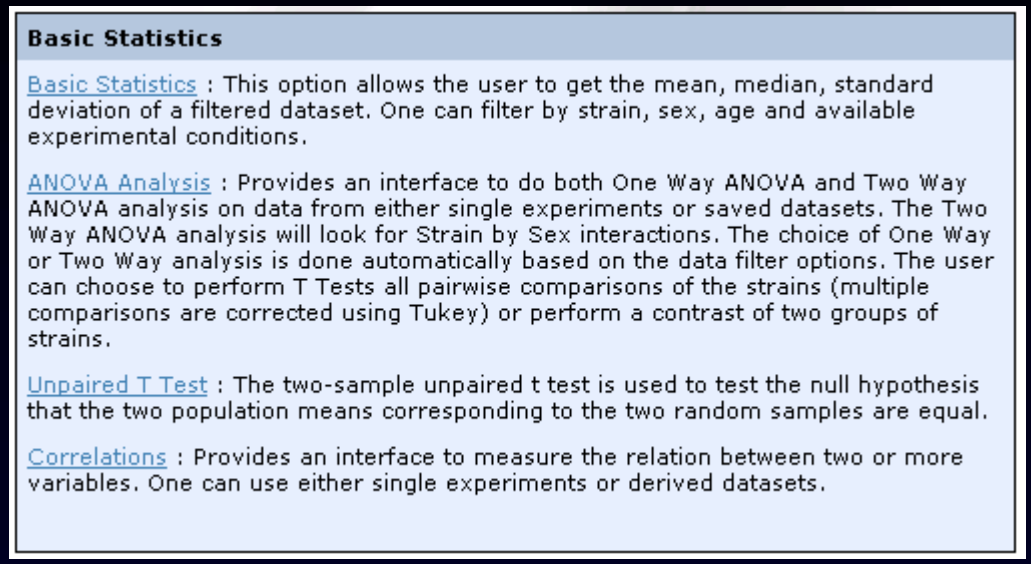
Strain Genotype data model/user interface completed



Statistical Exploration: ANOVA analysis completed (1 and 2 way)



Statistical Exploration: ANOVA analysis completed (1 and 2 way)



Basic Statistics

Basic Statistics : This option allows the user to get the mean, median, standard deviation of a filtered dataset. One can filter by strain, sex, age and available experimental conditions.

ANOVA Analysis : Provides an interface to do both One Way ANOVA and Two Way ANOVA analysis on data from either single experiments or saved datasets. The Two Way ANOVA analysis will look for Strain by Sex interactions. The choice of One Way or Two Way analysis is done automatically based on the data filter options. The user can choose to perform T Tests all pairwise comparisons of the strains (multiple comparisons are corrected using Tukey) or perform a contrast of two groups of strains.

Unpaired T Test : The two-sample unpaired t test is used to test the null hypothesis that the two population means corresponding to the two random samples are equal.

Correlations : Provides an interface to measure the relation between two or more variables. One can use either single experiments or derived datasets.

ANOVA Analysis : Provides an interface to do both One Way ANOVA and Two Way ANOVA analysis on data from either single experiments or saved datasets. The Two Way ANOVA analysis will look for Strain by Sex interactions. The choice of One Way or Two Way analysis is done automatically based on the data filter options. The user can choose to perform T Tests all pairwise comparisons of the strains (multiple comparisons are corrected using Tukey) or perform a contrast of two groups of strains.

AMDCC

ANOVA Analysis

This page will allow the user to analyze a single experiment or AMDCC dataset. The user will select the filter criteria for the data he/she wants for the analysis and click the 'Get Stats' button. An ANOVA analysis (One way or Two way) will be performed on the data based on the filter criteria.

Select a saved DataSet: [No selection] *New* **OR**

Select an Experiment: Coffman: Evaluation of STZ-induced DM in common laboratory strains

Get Stats

There are a total of 1986 measurements in this experiment

Select the Assay to Analyze and any filter criteria

Strains

- 129S6/SvEv
- BALB/cJ
- C57BL/6J
- DBA/2J
- MRL/MpJ

Sex

Both

Age @ Sample Date

Leave blank for all

from **to**

Experimental Conditions

time since Type 1 Diabetes onset (week)

-3 -1
0 2
3 6
7 8
9 12
13 15
16 17
19 20
23

IP STZ dosage plan

stz1 control

ANOVA Results - Microsoft Internet Explorer

AMDCC ANOVA Analysis

Based on the filter options either a One way ANOVA or Two way ANOVA is performed.
If the number of Strains > 2 and all animals of one sex, then a One way ANOVA is performed.
If the number of Strains > 2 and data has both males and females, then a Two way ANOVA is performed to determine if there are Sex by Strain interactions.

For each ANOVA, the user can decide whether to compare two groups of strains (contrasts) or output all possible pairwise comparisons for the strains selected.
The Two way ANOVA can handle data from an unbalanced design.

blood glucose

ANOVA Options

- ○ Analyze groups of strains
- ◉ All pairwise strain comparisons

Perform ANOVA

Average

Strain	F	M	Overall
129S6/SvEv	154.6071	197.4643	176.0357
BALB/cJ	116.9143	235.7429	176.3286
C57BL/6J	211.8750	311.8750	261.8750
DBA/2J	275.2895	478.7500	368.3000
MRL/MpJ	155.6061	267.8214	207.1148
Overall	184.1899	299.8912	239.9541

Count

Strain	F	M	Overall
129S6/SvEv	28	28	56
BALB/cJ	35	35	70
C57BL/6J	24	24	48
DBA/2J	38	32	70
MRL/MpJ	33	28	61
Overall	158	147	305

Two Way ANOVA Results: ***Strain by Sex Interaction is significant***

Source	Degrees of Freedom	Sum of Squares	Mean Square	F statistic	P value
Strain	4	1886703.720	471675.930	46.301	**0.00000000**
Sex	1	993616.937	993616.937	97.536	**0.00000000**
Interaction	4	210058.734	52514.683	5.155	**0.00049979**
Error	295	3005216.123	10187.173		
Total	304	6061989.357			

Requested Details for: ***All Pairwise Comparisons (Tukey Correction) - Males***

Strain 1	Strain 2	P value
129S6/SvEv	BALB/cJ	0.56603291
129S6/SvEv	C57BL/6J	**0.00056397**
129S6/SvEv	DBA/2J	**1.270×10^{-10}**
129S6/SvEv	MRL/MpJ	0.07143769

Done

Trusted sites

AMDCC

AMDCC ANOVA Analysis

Based on the filter options either a One way ANOVA or Two way ANOVA is performed.
If the number of Strains > 2 and all animals of one sex, then a One way ANOVA is performed.
If the number of Strains > 2 and data has both males and females, then a Two way ANOVA is performed to determine if there are Sex by Strain interactions.

For each ANOVA, the user can decide whether to compare two groups of strains (contrasts) or output all possible pairwise comparisons for the strains selected.
The Two way ANOVA can handle data from an unbalanced design.

blood glucose

ANOVA Options

- ○ Analyze groups of strains
- ◉ All pairwise strain comparisons

Perform ANOVA

Average

Strain	F	M	Overall
129S6/SvEv	154.6071	197.4643	176.0357
BALB/cJ	116.9143	235.7429	176.3286
C57BL/6J	211.8750	311.8750	261.8750
DBA/2J	275.2895	478.7500	368.3000
MRL/MpJ	155.6061	267.8214	207.1148

Count

Strain	F	M	Overall
129S6/SvEv	28	28	56
BALB/cJ	35	35	70
C57BL/6J	24	24	48
DBA/2J	38	32	70
MRL/MpJ	33	28	61

Average

Strain	F	M	Overall
129S6/SvEv	154.6071	197.4643	176.0357
BALB/cJ	116.9143	235.7429	176.3286
C57BL/6J	211.8750	311.8750	261.8750
DBA/2J	275.2895	478.7500	368.3000
MRL/MpJ	155.6061	267.8214	207.1148
Overall	184.1899	299.8912	239.9541

Count

Strain	F	M	Overall
129S6/SvEv	28	28	56
BALB/cJ	35	35	70
C57BL/6J	24	24	48
DBA/2J	38	32	70
MRL/MpJ	33	28	61
Overall	158	147	305

Two Way ANOVA Results: *Strain by Sex Interaction is significant*

Strain	4	1886703.720	471675.930	46.301	**0.00000000**
Sex	1	993616.937	993616.937	97.536	**0.00000000**
Interaction	4	210058.734	52514.683	5.155	**0.00049979**
Error	295	3005216.123	10187.173		
Total	304	6961080.357			

Requested Details for: *All Pairwise Comparisons (Tukey Correction) - Males*

129S6/SvEv	C57BL/6J	**0.00056397**
129S6/SvEv	DBA/2J	**1.270×10^{-10}**
129S6/SvEv	MRL/MpJ	0.07143769
BALB/cJ	C57BL/6J	**0.03784622**
BALB/cJ	DBA/2J	**1.270×10^{-10}**
BALB/cJ	MRL/MpJ	0.71981882
C57BL/6J	DBA/2J	**2.933×10^{-8}**
C57BL/6J	MRL/MpJ	0.51848391

Requested Details for: *All Pairwise Comparisons (Tukey Correction) - Females*

129S6/SvEv	C57BL/6J	0.24972093
129S6/SvEv	DBA/2J	**0.00002472**
129S6/SvEv	MRL/MpJ	0.99999950
BALB/cJ	C57BL/6J	**0.00406784**
BALB/cJ	DBA/2J	**1.196×10^{-9}**
BALB/cJ	MRL/MpJ	0.51148730
C57BL/6J	DBA/2J	0.11555296
C57BL/6J	MRL/MpJ	0.23234223
DBA/2J	MRL/MpJ	**0.00001052**

AMDCC

Added Chart Exploration: Column, Line, XY charts

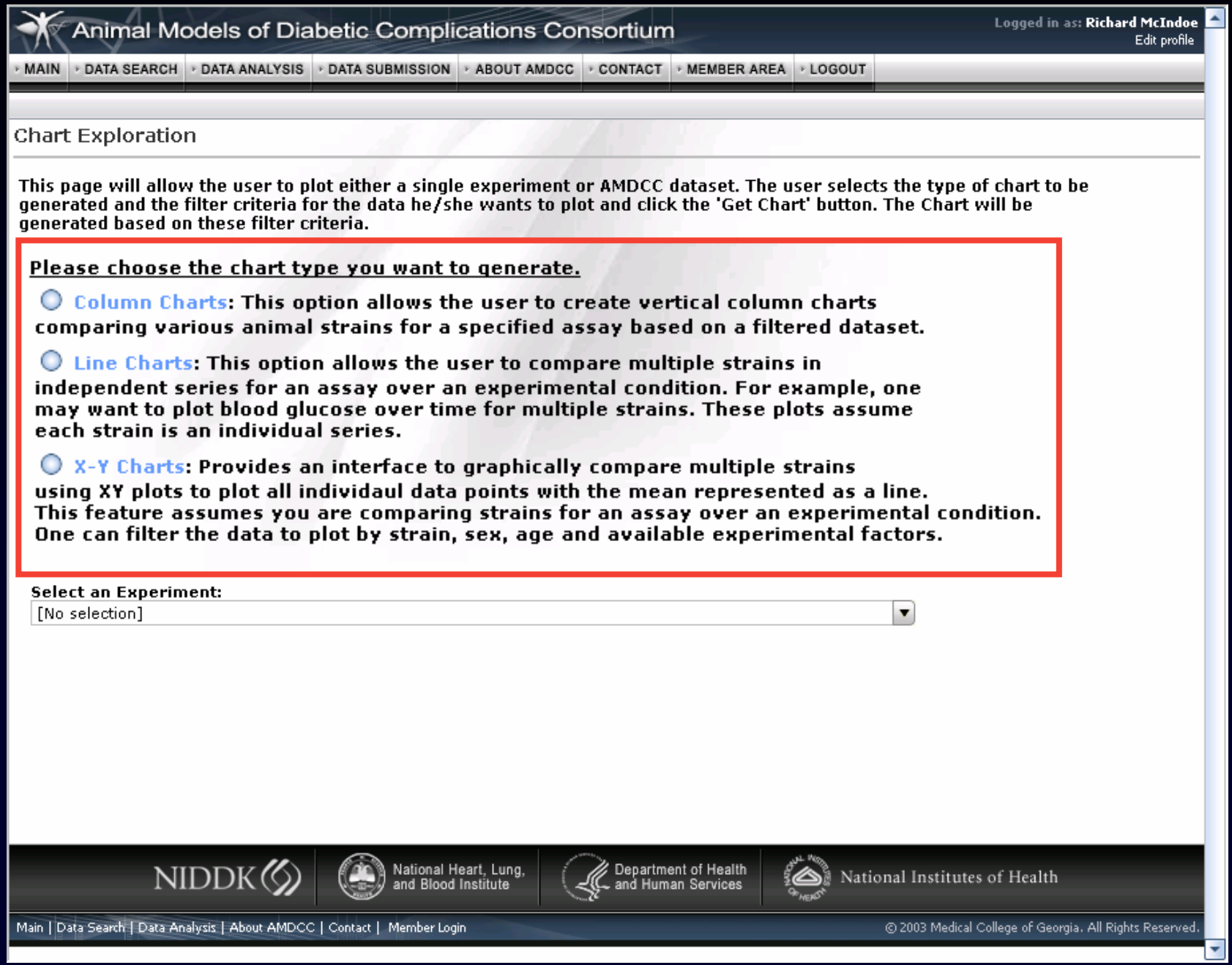


Chart Exploration

This page will allow the user to plot either a single experiment or AMDCC dataset. The user selects the type of chart to be generated and the filter criteria for the data he/she wants to plot and click the 'Get Chart' button. The Chart will be generated based on these filter criteria.

Please choose the chart type you want to generate.

- Column Charts: This option allows the user to create vertical column charts comparing various animal strains for a specified assay based on a filtered dataset.
- Line Charts: This option allows the user to compare multiple strains in independent series for an assay over an experimental condition. For example, one may want to plot blood glucose over time for multiple strains. These plots assume each strain is an individual series.
- X-Y Charts: Provides an interface to graphically compare multiple strains using XY plots to plot all individaul data points with the mean represented as a line. This feature assumes you are comparing strains for an assay over an experimental condition. One can filter the data to plot by strain, sex, age and available experimental factors.

Select a saved DataSet: [No selection] *New* OR

Select an Experiment:
Coffman: Evaluation of STZ-induced DM in common laboratory strains

Get Chart

Select the Assay, Strains and Experimental Factors to use in the plot and any filter criteria

Y Axis
[None Selected]

Strains
- 129S6/SvEv
- BALB/cJ
- C57BL/6J
- DBA/2J
- MRL/MpJ

Sex
Both

Age @ Sample Date
Leave blank for all
from to

Experimental Conditions

time since Type 1 Diabetes onset (week)
- -3, -1
- 0, 2
- 3, 6
- 7, 8
- 9, 12
- 13, 15
- 16, 17
- 19, 20
- 23

IP STZ dosage plan
- stz1, control

Select the Assay, Strains and Experimental Factors to use in the plot and any filter criteria

Y Axis
[None Selected]

Strains
- 129S6/SvEv
- BALB/cJ
- C57BL/6J
- DBA/2J
- MRL/MpJ

Sex
Both

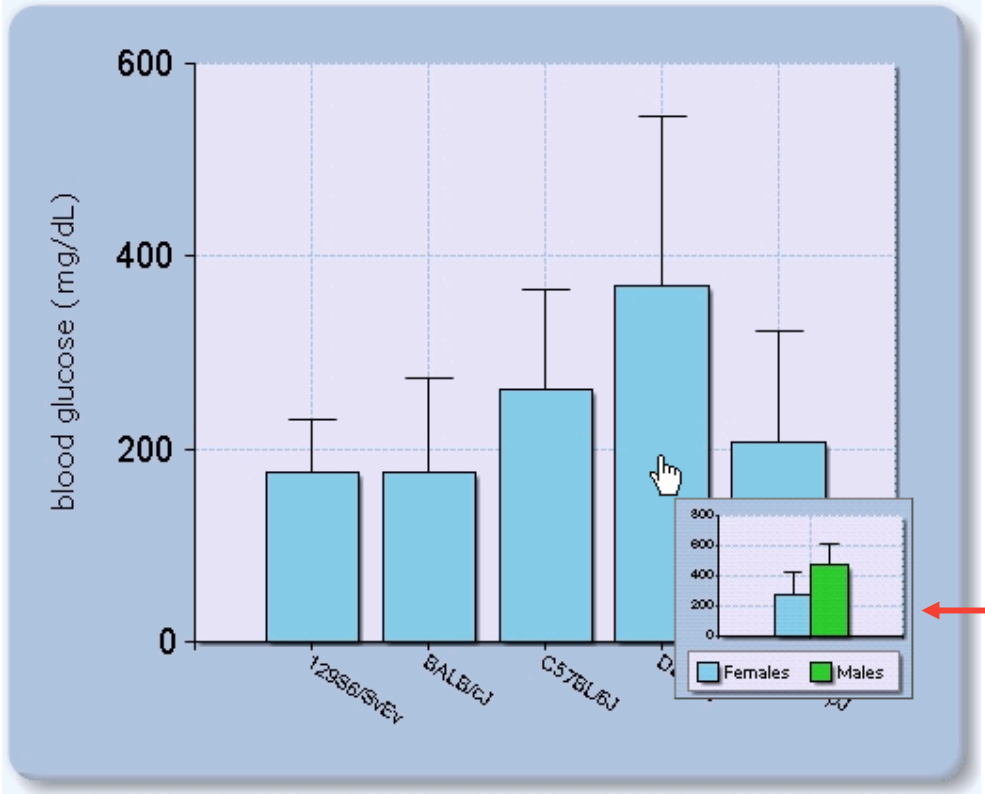
Age @ Sample Date
Leave blank for all
from to

Experimental Conditions

time since Type 1 Diabetes onset (week)
- -3, -1
- 0, 2
- 3, 6
- 7, 8
- 9, 12
- 13, 15
- 16, 17
- 19, 20
- 23

IP STZ dosage plan
- stz1, control

AMDCC::Phenotype Exploration::Charting Options::Column Charts - Microsoft Internet Explorer



Data Filter Criteria
Sex: Both
Age: no age filter given

Experimental Factors:
IP STZ dosage plan: stz1

The data is from the following experiments:
Evaluation of STZ-induced DM in common laboratory strains

Chart Title

Add Title

Y Axis Label
blood glucose (mg/dL)

Change Axis Title

Preview & Drill Down if data has both sexes

Y Axis blood glucose

Refresh

Change Assay to chart

To change the Y axis values, select from the appropriate dropdown control and click 'Refresh'

To change the Title and Y Axis Label, edit or fill in the appropriate text box to the right of the chart image.

The filter criteria used to select the data is given next to the upper right corner of the chart image. To change these criteria, return to the chart exploration page, select your criteria and click 'Get Chart' again

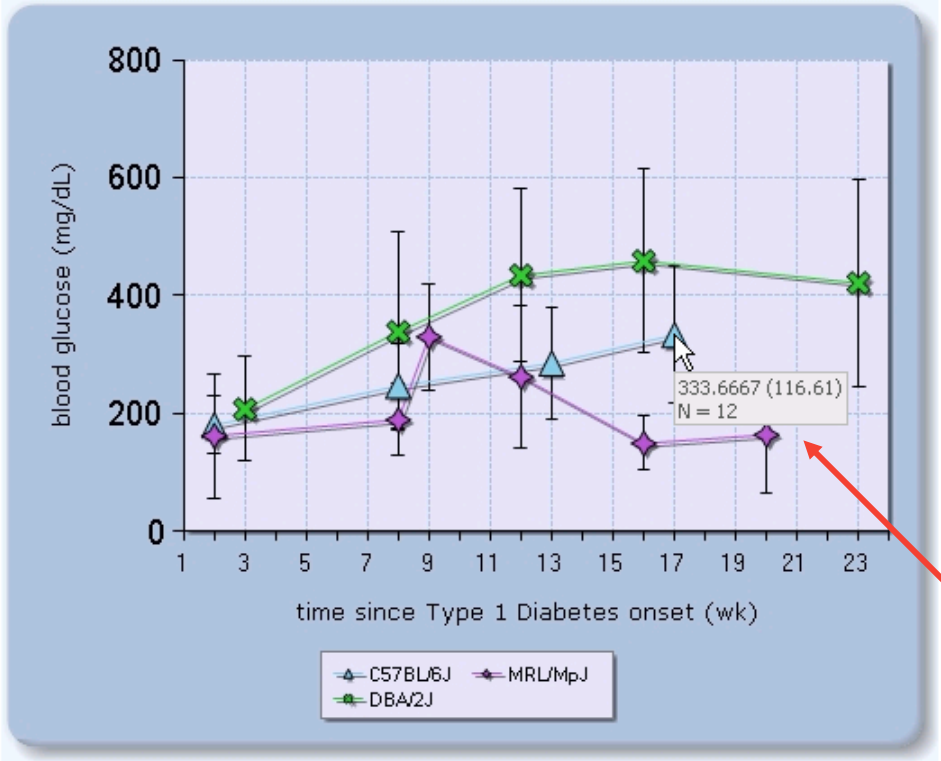
To see the value of each data point mouse OVER each data point and a tooltip will pop up with the value

https://www.amdcc.org/shared/colChartBySexDetail.aspx?strainID=1514

Trusted sites

AMDCC

AMDCC::Phenotype Exploration::Charting Options::Line Charts - Microsoft Internet Explorer



Data Filter Criteria
Sex: Both
Age: no age filter given

Experimental Factors:
IP STZ dosage plan: stz1

The data is from the following experiments:
Evaluation of STZ-induced DM in common laboratory strains

Chart Title

Add Title

Y Axis Label
blood glucose (mg/dL)

X Axis Label
time since Type 1 Diab

Change Axis Titles

Tooltips provide data

Y Axis blood glucose
X Axis time since Type 1 Diabetes onset
Refresh

Change X and Y axis data

To change the X and Y axis values, select from the appropriate dropdown control and click 'Refresh'

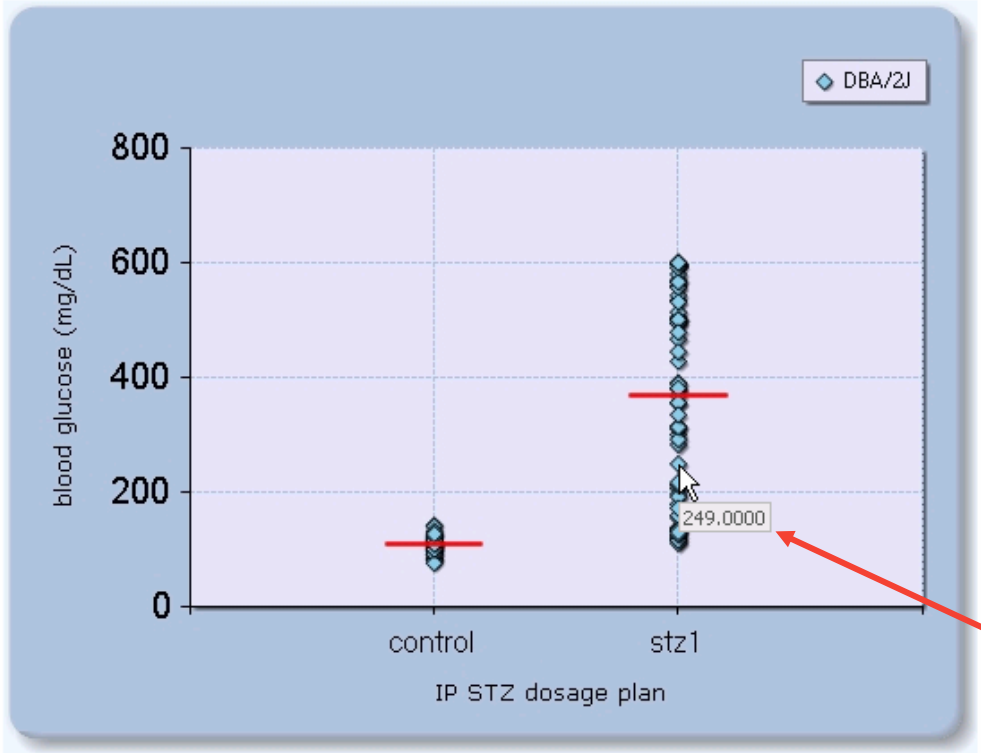
To change the Title, Y Axis Label and X Axis label, edit or fill in the appropriate text box to the right of the chart image.

The filter criteria used to select the data is given next to the upper right corner of the chart image. To change these criteria, return to the chart exploration page, select your criteria and click 'Get Chart' again

To see the value of each data point mouse OVER each data point and a tooltip will pop up with the value

Done
Trusted sites

AMDCC::Phenotype Exploration::Charting Options::Scatter Plots - Microsoft Internet Explorer



Data Filter Criteria
Sex: Both
Age: no age filter given

Experimental Factors: None selected.

The data is from the following experiments:
Evaluation of STZ-induced DM in common laboratory strains

Chart Title

Add Title

Y Axis Label
blood glucose (mg/dL)

Change Axis Titles

X Axis Label
IP STZ dosage plan

Tooltips provide data

Y Axis blood glucose
X Axis IP STZ dosage plan
Strain DBA/2J
Refresh

Change X and Y axis data

Change Strain

To change the X and Y axis values or Strain, select from the appropriate dropdown control and click 'Refresh'.

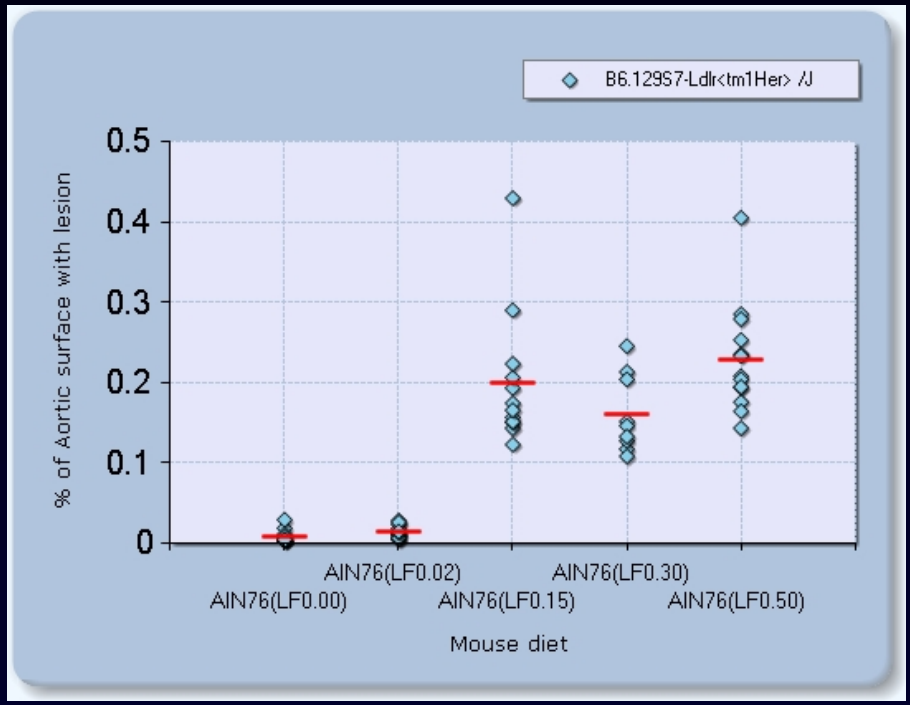
To change the Title, Y Axis Label and X Axis label, edit or fill in the appropriate text box to the right of the chart image and click 'Refresh'.

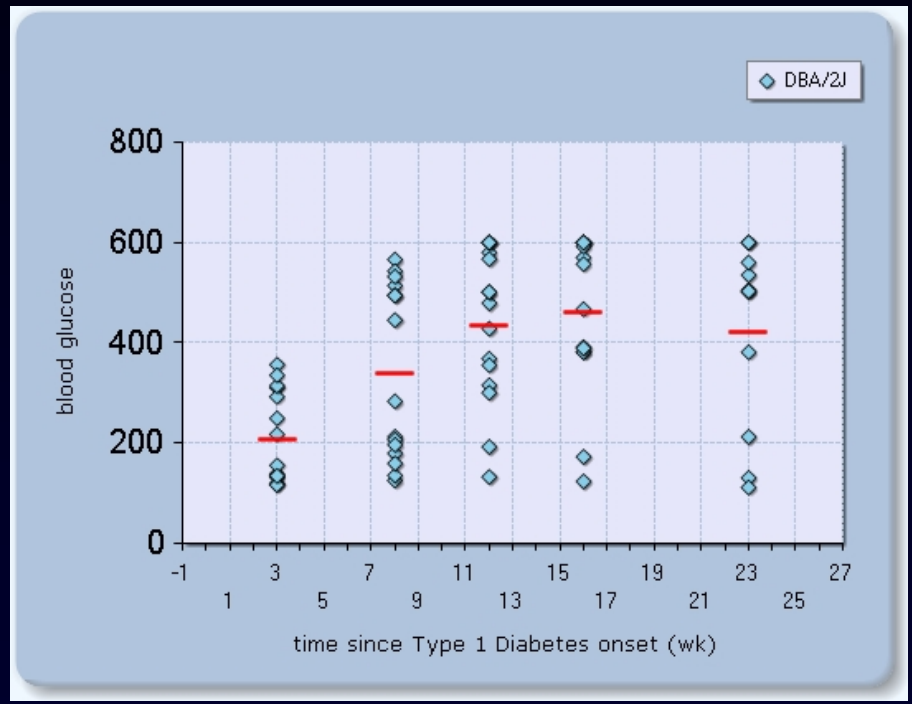
**The filter criteria used to select the data is given next to the upper right corner of the chart image.
To change these criteria, return to the chart exploration page, select your criteria and click
'Get Chart' again.**

To see the value of each data point mouse OVER each data point and a tooltip will pop up with the value.

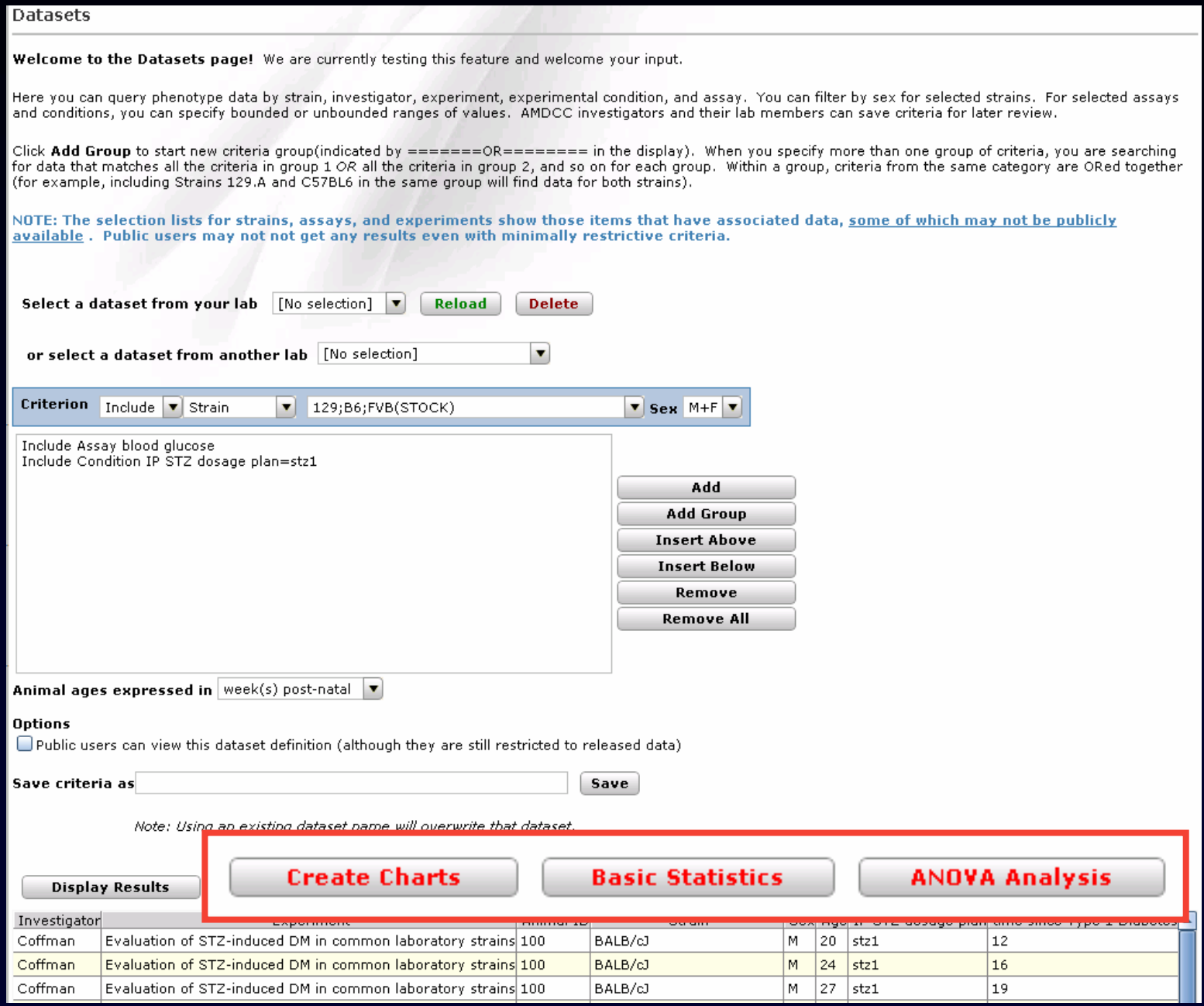
Done
Trusted sites

Can plot either categorical or numerical values for X axis.





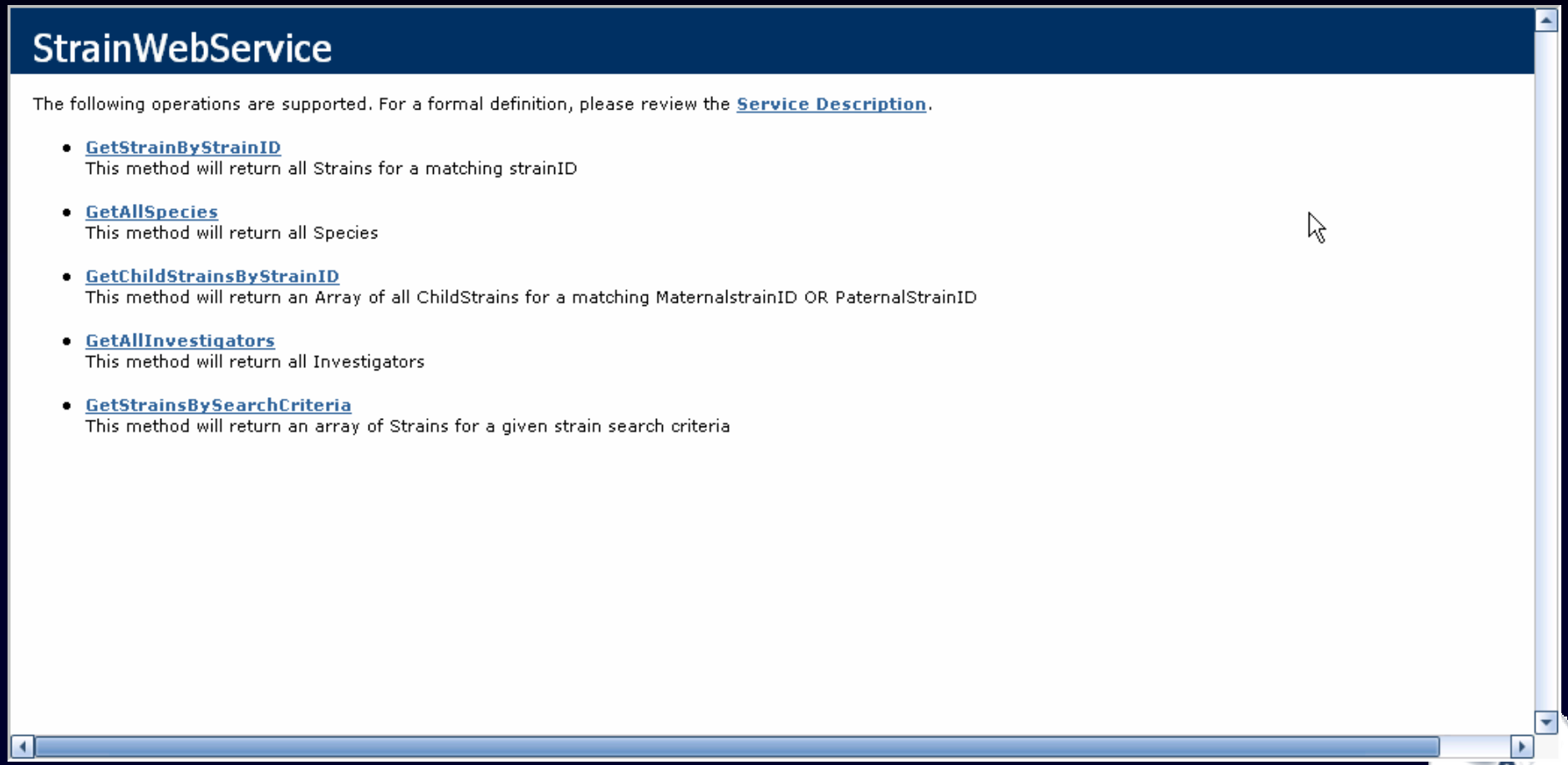
Adhoc Datasets incorporated into Charting, Basic Statistics, ANOVA analysis



AMDCC Webservice architecture started

Provide programmatic service for other platforms to access data using SOAP/HTTP

http://www.amdcc.org/Webservice/StrainWebService.asmx



StrainWebService

Click here for a complete list of operations.

GetStrainsBySearchCriteria

This method will return an array of Strains for a given strain search criteria

Test

The test form is only available for requests from the local machine.

SOAP

The following is a sample SOAP request and response. The **placeholders** shown need to be replaced with actual values.

```
POST /WebService/StrainWebService.asmx HTTP/1.1
Host: www.amdcc.org
Content-Type: text/xml; charset=utf-8
Content-Length: length
SOAPAction: "http://www.amdcc.org/WebService/GetStrainsBySearchCriteria"

<?xml version="1.0" encoding="utf-8"?>
<soap:Envelope xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns:xsd="http://www.w3.org/2001/XMLSchema" xmlns:soap="http://
  <soap:Body>
    <GetStrainsBySearchCriteria xmlns="http://www.amdcc.org/WebService/">
      <strainSearchCriteria>
        <SpeciesID>int</SpeciesID>
        <InvestigatorMemID>int</InvestigatorMemID>
        <CreationMethodID>int</CreationMethodID>
        <StrainDevelopmentStatusID>int</StrainDevelopmentStatusID>
        <StrainName>string</StrainName>
        <IsAMDCCStrain>boolean</IsAMDCCStrain>
        <StartWithFlag>boolean</StartWithFlag>
        <HasModels>boolean</HasModels>
        <HasPhenotypeData>boolean</HasPhenotypeData>
        <OrderBy>unsignedByte</OrderBy>
        <RowCount>int</RowCount>
      </strainSearchCriteria>
    </GetStrainsBySearchCriteria>
  </soap:Body>
</soap:Envelope>
```

ExperimentWebService

The following operations are supported. For a formal definition, please review the **Service Description**.

- **GetExperimentByExperimentID**
  This method will an Experiment for matching ExperimentID
- **GetExperimentsBySearchCriteria**
  This method will return all Experiments for a specified experiment search criteria
- **GetAllSpecies**
  This method will return all Species
- **GetAllInvestigators**
  This method will return all Investigators
- **GetAllExperimentStatus**
  This method will return all Experiment Status

GenomeWebService

The following operations are supported. For a formal definition, please review the **Service Description**.

- **GetAllTransgenesByStrainID**
  This method will return all Transgenes for a strainID
- **GetAllGenomicSegmentsByStrainID**
  This method will return all GenomicSegments for a strainID
- **GetAllRegulatoryElementsByTransgeneID**
  This method will return all RegulatoryElements for a transgeneID
- **GetAllGeneGenotypesByStrainID**
  This method will return all GeneGenotypes for a strainID

ProtocolWebService

The following operations are supported. For a formal definition, please review the **Service Description**.

- **GetProtocolsBySearchCriteria**
  This method will return an array of Protocols for a given protocol search criteria
- **GetProtocolByProtocolID**
  This method will return a Protocol for a matching protocolID
- **GetAllProtocolTypes**
  This method will return all Protocol Types

AMDCC

WSDL file will be available for each webservice.

```
<?xml version="1.0" encoding="utf-8" ?>
- <definitions xmlns:http="http://schemas.xmlsoap.org/wsdl/http/" xmlns:soap="http://schemas.xmlsoap.org/wsdl/soap/"
    xmlns:s="http://www.w3.org/2001/XMLSchema" xmlns:s0="http://www.amdcc.org/WebService/"
    xmlns:soapenc="http://schemas.xmlsoap.org/soap/encoding/" xmlns:tm="http://microsoft.com/wsdl/mime/textMatching/"
    xmlns:mime="http://schemas.xmlsoap.org/wsdl/mime/" targetNamespace="http://www.amdcc.org/WebService/"
    xmlns="http://schemas.xmlsoap.org/wsdl/">
  - <types>
    - <s:schema elementFormDefault="qualified" targetNamespace="http://www.amdcc.org/WebService/">
      - <s:element name="GetExperimentByExperimentID">
        - <s:complexType>
          - <s:sequence>
              <s:element minOccurs="1" maxOccurs="1" name="expID" type="s:int" />
            </s:sequence>
          </s:complexType>
        </s:element>
      - <s:element name="GetExperimentByExperimentIDResponse">
        - <s:complexType>
          - <s:sequence>
              <s:element minOccurs="0" maxOccurs="1" name="GetExperimentByExperimentIDResult" type="s0:Experiment" />
            </s:sequence>
          </s:complexType>
        </s:element>
      - <s:complexType name="Experiment">
        - <s:complexContent mixed="false">
          - <s:extension base="s0:AMDCCDomainObject">
            - <s:sequence>
                <s:element minOccurs="0" maxOccurs="1" name="Type" type="s0:Identifiable" />
                <s:element minOccurs="0" maxOccurs="1" name="Desc" type="s:string" />
                <s:element minOccurs="0" maxOccurs="1" name="Species" type="s0:Species" />
                <s:element minOccurs="1" maxOccurs="1" name="PublicReleaseDate" type="s:dateTime" />
                <s:element minOccurs="0" maxOccurs="1" name="Status" type="s0:Identifiable" />
                <s:element minOccurs="0" maxOccurs="1" name="AnimalAgeUnit" type="s0:Unit" />
              </s:sequence>
            </s:extension>
          </s:complexContent>
        </s:complexType>
      - <s:complexType name="AMDCCDomainObject">
        - <s:sequence>
```

Future Directions

1. Continue development of statistics modules to automate data analysis (current analysis does not take into consideration repeated measures)

2. Develop visualization and analysis modules for microarray data

3. Improve charting capabilities (eg. allow more flexibility for font, color, etc.)

4. Begin another round of training sessions for both data and analysis modules.

5. Organize cross consortium meta analysis of specific data.

The End

If you have any problems, questions or concerns don't hesitate to email us.
Use any of the following addresses:

General web:
amdcc_web-l@lists.amdcc.org (Listserv)

Data, assays, experiment help:
spatel@mail.mcg.edu (Sachen Patel)

Website
gmukherjee@mcg.edu (Gautam Mukherjee)