

Description of Database Features

Step 1: “Annotation Data” – The annotation of Affymetrix probesets is derived from GeneChip® Mouse Genome 430 version 2.0 arrays.

Step 1: “Statistics” – Statistics for each of 531 ANOVA models to test for gene expression differences and for correlations between phenotype measurements and gene expression values are available for all 45,101 probesets on the array. ANOVA models were used to decompose gene expression estimates for each probeset (Y) into a sum of effects <model terms> and random error (ϵ). GROUP refers to STRAIN-SEX-DIET groups in OverallModel. STRAIN is treated as a random effect in Model 2. The subject headers include the following:

Gene Expression:

ANOVA Model Used

OverallModel: $Y = \mu + \text{GROUP} + \epsilon$

Model1: $Y = \mu + \text{SEX} + \text{DIET} + \text{STRAIN} + \epsilon$

Model2: $Y = \mu + \text{SEX} + \text{DIET} + \sim\text{STRAIN} + \epsilon$

Model3: $Y = \mu + \text{SEX} + \text{DIET} + \text{STRAIN} + \text{DIET}:\text{STRAIN} + \epsilon$

Model4: $Y = \mu + \text{SEX} + \text{DIET} + \text{STRAIN} + \text{DIET}:\text{STRAIN} + \text{SEX}:\text{DIET} + \text{SEX}:\text{STRAIN} + \text{SEX}:\text{DIET}:\text{STRAIN} + \epsilon$

Term tested

Group, Sex, Diet, Strain, StrainByDiet, StrainByDietBySex

Sex Used in Model

Female, Male

Diet Used in Model

LowFat, HighFat

Comparison Tested (for pairwise tests)

e.g., LowFat vs HighFat

“FoldChange” (for pairwise tests)

e.g., fold change in gene expression between LowFat and HighFat

“Fs_values”

Calculated values of modified F-statistic incorporating shrinkage variance components

“Ptab”

Tabulated permutation p-value (based on 1000 permutations of group labels)

“Qvalue”

Calculated false discovery rate (“q-value”) derived from Ptab distribution

Correlation:

cor_<phenotype>

Correlation between gene expression and phenotype

absolute_cor_<phenotype>

Absolute value of correlation between gene expression and phenotype

Step 1: “Data Columns” – Normalized microarray experiment data to be included in query results (Step 2) and plotted (Step 3).

Microarray Experiment Data:

Strain

Strain identifier (129, A, B6, BALB, C3H, CAST, DBA, I, MRL, NZB, PERA, SM)

Sex

Female or Male

Diet

LowFat or HighFat

Biological Replicate

Replicate1, Replicate2, Replicate3

Example Queries

EXAMPLE 1: Find the genes that are differentially expressed (false discovery rate < 0.05) between low-fat and high-fat diets for females in strain NZB.

Gene Expression Step 1:

1. Select “Gene Symbol” in “Annotation Data” tab

Step 1: Select Columns From Annotations, Statistics and Data

Select any Data, Annotations or Statistics that you would like to appear in your query results below. Use the Quick

Annotation Data

Statistics

Data Columns

Filter:

Select	Term Name
<input checked="" type="checkbox"/>	Affymetrix 430 2 NA28 Annotations: Gene Symbol

2. Enter search terms as “Model1 Diet Female NZB” (separate each term by a space) in “Statistics” tab and select all available statistics.

Step 1: Select Columns From Annotations, Statistics and Data

Select any Data, Annotations or Statistics that you would like to appear in your query results below. Use the Quick

Annotation Data

Statistics

Data Columns

Filter:

Select	Term Name
<input checked="" type="checkbox"/>	Model1 Diet Female NZB HighFat vs LowFat: FoldChange
<input checked="" type="checkbox"/>	Model1 Diet Female NZB HighFat vs LowFat: Fs_Values
<input checked="" type="checkbox"/>	Model1 Diet Female NZB HighFat vs LowFat: Ptab
<input checked="" type="checkbox"/>	Model1 Diet Female NZB HighFat vs LowFat: Qvalue

- Enter search terms as “Female NZB” in “Data Columns” tab and select all biological replicates.

Step 1: Select Columns From Annotations, Statistics and Data

Select any Data, Annotations or Statistics that you would like to appear in your query results below. Use the Quick

Annotation Data
Statistics
Data Columns

Filter: Female NZB
Match All Terms
Run Filter
Toggle Select All

Select	Term Name
<input checked="" type="checkbox"/>	Microarray Experiment Data: NZB Female LowFat Replicate1
<input checked="" type="checkbox"/>	Microarray Experiment Data: NZB Female LowFat Replicate2
<input checked="" type="checkbox"/>	Microarray Experiment Data: NZB Female LowFat Replicate3
<input checked="" type="checkbox"/>	Microarray Experiment Data: NZB Female HighFat Replicate1
<input checked="" type="checkbox"/>	Microarray Experiment Data: NZB Female HighFat Replicate2
<input checked="" type="checkbox"/>	Microarray Experiment Data: NZB Female HighFat Replicate3

Gene Expression Step 2:

- Click the “Add a Filter” tab and find all “q-values” less than 0.05. Order the query results by “Fs_values” to find probesets with the largest F-statistics. All results may be downloaded to a CSV file by clicking the tab below the query output. Select a probeset to view the expression levels in a plot (Step 3).

Step 2: Run Probeset Query and Download Results as CSV

In this section you can filter probesets by clicking the add filter button and selecting the criteria that you want to filter probesets on. You can add up to 10 filters to your query. After running your query you will be able to download the results by clicking a link below the query results.

Qvalue
<
0.05
Remove Filter

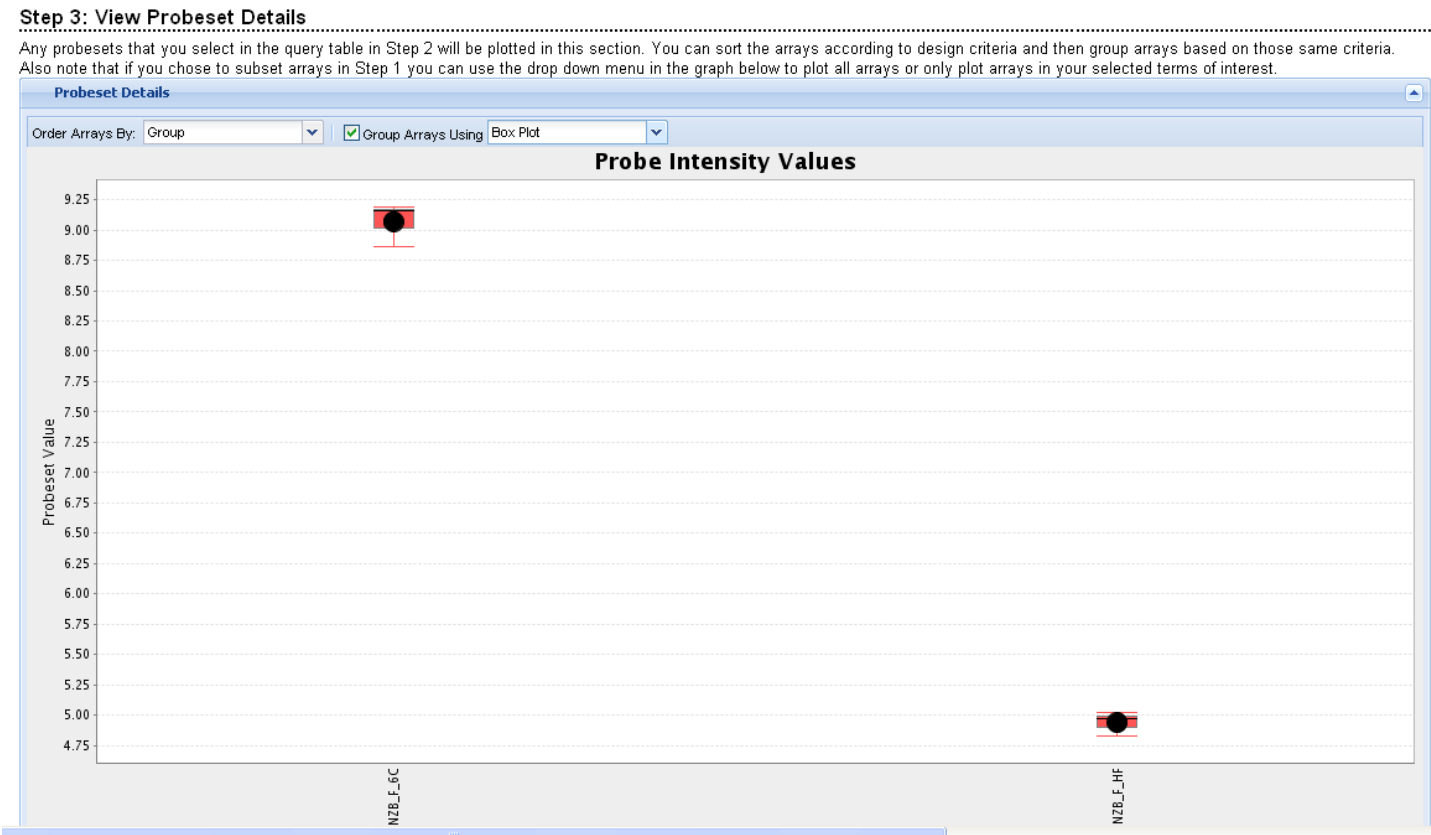
Add Filter

Run Query (1 Filter)
Order Query Results By: Fs_values
Descending

Query Results				
View Details	probeid	Gene Symbol	FoldChange	Fs_Values
<input type="checkbox"/>	1419144_at	Cd163	-27.0513808404709	2455.43111761486
<input checked="" type="checkbox"/>	1415993_at	Sqle	-17.5721928577118	1284.36066831114
<input type="checkbox"/>	1448303_at	Gpnmb	72.0411014198555	1254.40290390544
<input type="checkbox"/>	1450646_at	Cyp51	-15.1231384907477	999.329743893199
<input type="checkbox"/>	1449153_at	Mmp12	35.6304549591258	840.022060870621
<input type="checkbox"/>	1423804_a_at	Idi1	-35.8725732620965	786.076512779675

Gene Expression Step 3:

5. The probe set can be visualized in numerous formats. To view the boxplot format, order the arrays by Group. Click the “Group Arrays” button and group using Box Plot. The plot below shows that NZB mice (females) have a much higher expression for the selected probeset when fed the low-fat (6% chow) diet than the high-fat diet.



EXAMPLE 2: Find probesets for which gene expression and cholesterol correlation levels are correlated ($\text{cor} > 0.8$).

Correlation Step 1:

1. Select “Gene Symbol” and “Chromosomal Location” in “Annotation Data” tab

Step 1: Select Columns From Annotations, Statistics and Data

Select any Data, Annotations or Statistics that you would like to appear in your query results below. Use the Quick

Annotation Data | **Statistics** | **Data Columns**

Filter: Match All Terms

Select	Term Name
<input type="checkbox"/>	Affymetrix 430 2 NA28 Annotations: UniGene ID
<input type="checkbox"/>	Affymetrix 430 2 NA28 Annotations: Genome Version
<input type="checkbox"/>	Affymetrix 430 2 NA28 Annotations: Alignments
<input type="checkbox"/>	Affymetrix 430 2 NA28 Annotations: Gene Title
<input checked="" type="checkbox"/>	Affymetrix 430 2 NA28 Annotations: Gene Symbol
<input checked="" type="checkbox"/>	Affymetrix 430 2 NA28 Annotations: Chromosomal Location
<input type="checkbox"/>	Affymetrix 430 2 NA28 Annotations: Unigene Cluster Type
<input type="checkbox"/>	Affymetrix 430 2 NA28 Annotations: Ensembl

2. Enter search term as “cor_chol” in “Statistics” tab.

Step 1: Select Columns From Annotations, Statistics and Data

Select any Data, Annotations or Statistics that you would like to appear in your query results below. Use the Quick

Annotation Data | **Statistics** | **Data Columns**

Filter: Match All Terms

Select	Term Name
<input checked="" type="checkbox"/>	Gene Expression Phenotype Correlation: cor_CHOL

3. Click “Toggle Select All” in “Data Columns” tab to select all biological replicates for each strain.

Step 1: Select Columns From Annotations, Statistics and Data

Select any Data, Annotations or Statistics that you would like to appear in your query results below. Use the Quick

Annotation Data	Statistics	Data Columns
Filter: Eg: term1 term2 ... Match All Terms <input type="button" value="Run Filter"/> <input type="button" value="Toggle Select All"/>		
Select	Term Name	
<input checked="" type="checkbox"/>	Microarray Experiment Data: 129 Female LowFat Replicate1	
<input checked="" type="checkbox"/>	Microarray Experiment Data: 129 Female LowFat Replicate2	
<input checked="" type="checkbox"/>	Microarray Experiment Data: 129 Female LowFat Replicate3	
<input checked="" type="checkbox"/>	Microarray Experiment Data: 129 Female HighFat Replicate1	
<input checked="" type="checkbox"/>	Microarray Experiment Data: 129 Female HighFat Replicate2	
<input checked="" type="checkbox"/>	Microarray Experiment Data: 129 Female HighFat Replicate3	
<input checked="" type="checkbox"/>	Microarray Experiment Data: 129 Male LowFat Replicate1	

Correlation Step 2:

- Click the “Add a Filter” tab and find all correlation coefficients greater than 0.8. Order the query results by correlation values. All results may be downloaded to a CSV file by clicking the tab below the query output. Select a probeset to view the expression levels in a plot (Step 3). The top two probesets correspond to the gene “Akr1b3”.

Step 2: Run Probeset Query and Download Results as CSV

In this section you can filter probesets by clicking the add filter button and selecting the criteria that you want to filter probesets on. If you don't add any filter can add up to 10 filters to your query. After running your query you will be able to download the results by clicking a link below the query table.

cor_CHOL	>	0.7	<input type="button" value="Remove Filter"/>		
<input type="button" value="Add Filter"/>					
Run Query (1 Filter)	Order Query Results By:	cor_CHOL	Descending		
Query Results					
View Details	probeid	Gene Symbol	Chromosomal Location	cor_CHOL	129 Female LowFat Replica
<input checked="" type="checkbox"/>	1437133_x_at	Akr1b3	chr6 B1j6 13.0 cM	0.880221911365725	7.39041966797003
<input checked="" type="checkbox"/>	1448319_at	Akr1b3	chr6 B1j6 13.0 cM	0.845201060747147	7.29126178481298
<input type="checkbox"/>	1434517_at	Wdfy2	chr14 D1	0.843350138122013	7.01512371435458
<input type="checkbox"/>	1456381_x_at	Mcl1	chr3 F2.1j3 43.6 cM	0.832332566963134	9.06597726266947
<input type="checkbox"/>	1438097_at	Rab20	chr8 A1.1j8 10.0 cM	0.820645934459376	6.17557865314232
<input type="checkbox"/>	1423570_at	Abcg1	---	0.818766515549173	6.57707534950526
<input type="checkbox"/>	1436970_a_at	Pdgfrb	chr18 E1j18 30.0 cM	0.818576826468292	6.27692629142764
<input type="checkbox"/>	1456590_x_at	Akr1b3	chr6 B1j6 13.0 cM	0.817702809524668	5.5422208506131
<input type="checkbox"/>	1425801_x_at	Cott1	chr8 E1	0.817198405123246	7.25169012477228
<input type="checkbox"/>	1420898_at	Snap23	chr2 E5j2 61.8 cM	0.812072863799766	5.24564958120651

Correlation Step 3:

5. To view the boxplots, order the arrays by Group. Click the “Group Arrays” button and group using Box Plot. The plot below shows the results for all 48 STRAIN-SEX-DIET groups.

Step 3: View Probeset Details

Any probesets that you select in the query table in Step 2 will be plotted in this section. You can sort the arrays according to design criteria and then group arrays based on those same criteria. Also note that if you chose to subset arrays in Step 1 you can use the drop down menu in the graph below to plot all arrays or only plot arrays in your selected terms of interest.

