

Use Case 20: Exploring the role of epigenetics in myeloid cancer using reference epigenomes from the Human Epigenome Atlas

American Society of Human Genetics
Boston, MA

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Presented by the
Bioinformatics Research Laboratory

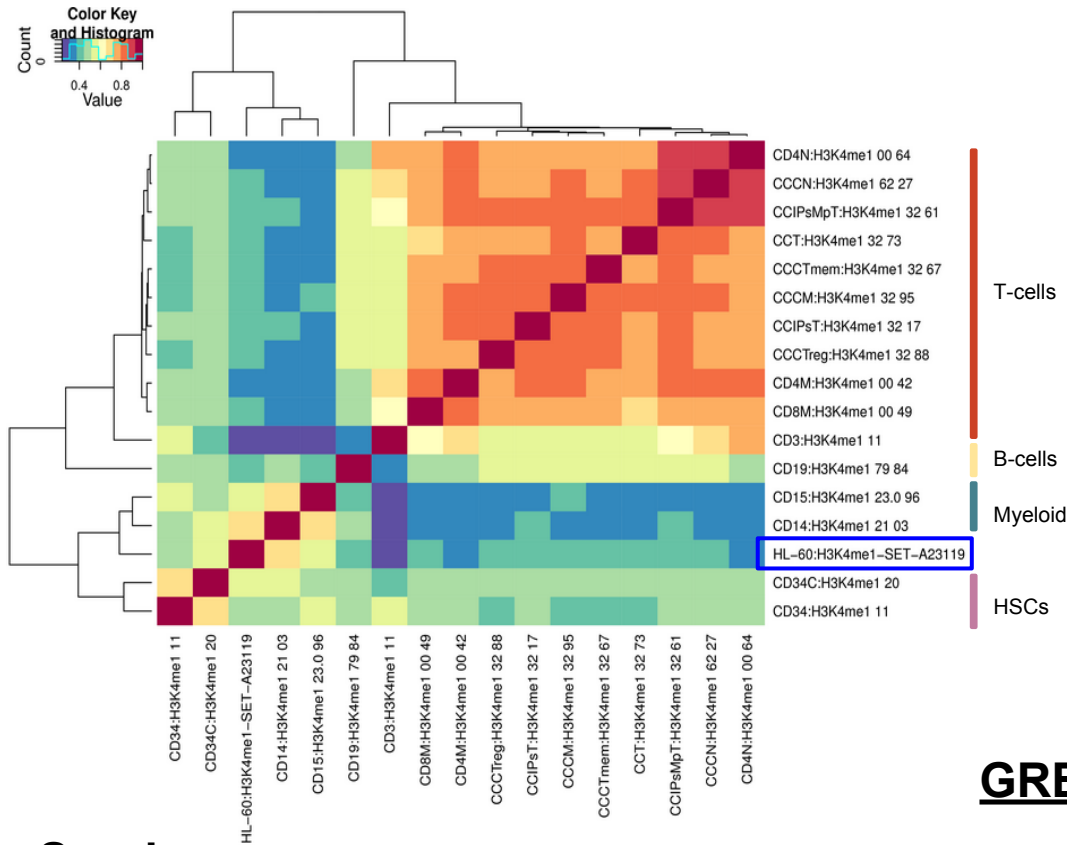
Baylor
College of
Medicine

Summary of Use Case 20

Background: Studying regions of epigenomic changes in normal versus disease state can help determine pathways that are involved in disease progression. In cancer, genomic locus are altered with copy number changes. Such changes can result in gain or loss of driver or suppressor genes. These changes not only alters the genome but also the epigenome. Studying changes in the epigenomic landscape of a tumor vs normal reference epigenomes can be used as marker to help determine pathways that are activated in disease progression. As a proof of principle, we sought to examine the functional significance of epigenomic changes in the human myeloid leukemia cell line HL60, by comparing it to reference epigenomes.

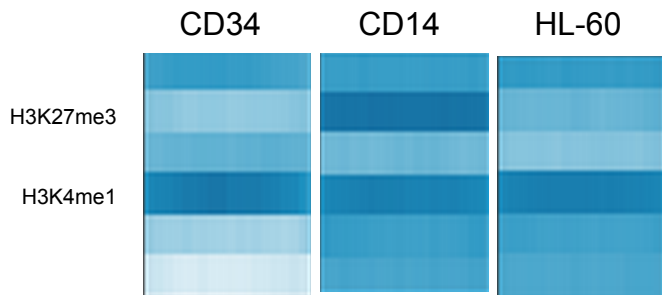
Results: Comparison of reference epigenomes with HL60 histone modifications correctly identify HL60 as being of myeloid origin, suggesting one may perform an initial epigenomic characterization of cell lines/tissues of unknown origin, or which have not been fully characterized, by virtual comparison to reference epigenomes. In addition, further computational approaches point to several pathways and transcriptional regulators previously shown to play a role in myeloid biology.

Summary of Results



Results: Comparison (heatmap) of reference epigenomes with HL60 histone modifications correctly identify HL60 as being of myeloid origin, suggesting one may perform an initial characterization of cell lines/tissues of unknown origin by virtual comparison to reference epigenomes. Spark tool was then used to identify 1025 enhancers that underwent epigenomic transition. GREAT tool was used to determine pathways cis-regulatory regions associated with these enhancers. C-MYB, previously known, transcriptional regulator was found to be significantly enriched.

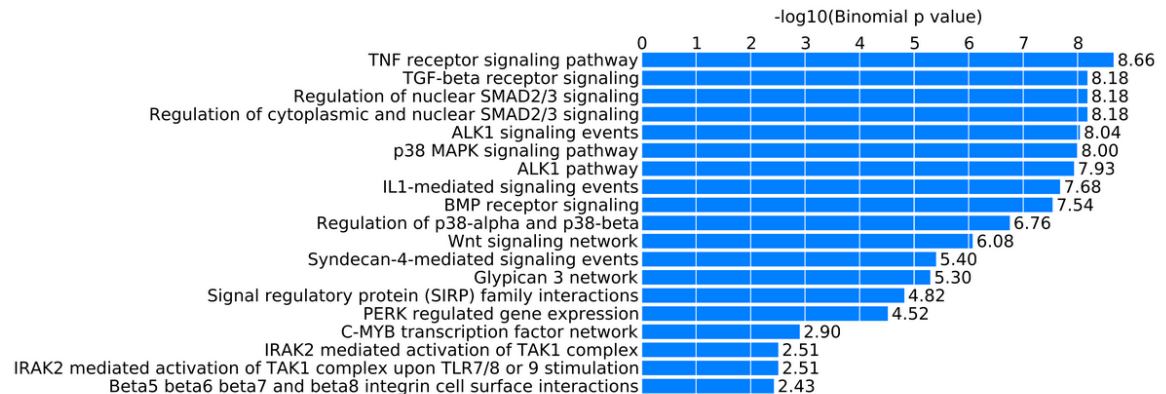
Spark



Epigenomic transitions of 1025 enhancers

GREAT

Pathway Commons



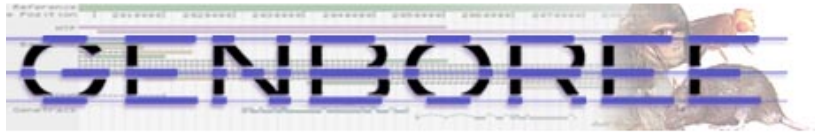
Use Case Overview

New Genboree Users - Slides 5-13 provide steps for new Genboree users on how to create a database, a project page, and view track grid of data generated in the NIH Roadmap Epigenome Project.

Existing Genboree Users - If you have attended past Genboree Workshops or are familiar with the Genboree Workbench then you may briefly review these slides and start on slide 14 for the actual use case

- Methodology
- Steps for reproducing the results

The Genboree Workbench: Web-based Data Management & Analysis



System/Network Data QC and Pre-processing Genome Transcriptome Cistrome Epigenome Metagenome Visualization Help

Welcome to the Genboree Workbench! [Getting Started]

Data Selector

Refresh Data Filter: Select a filter...

- genboree.org
 - Atlas Tools Access
 - BRL AUTO TEST
 - EDACC
 - Epigenome Informatics Demo Output Data
 - Epigenome Informatics Workshop (May 2012)
 - Epigenome ToolSet Demo Input Data
 - Epigenome Informatics Workshop (May 2012)
 - ROI Repository
 - Targeted Atlases
- genboree.bcgsc.ca
- genboree.cbrc.jp
- www.brain-research-lab.org

Details

Attribute	Value
Name	GenboreeUser_group
Description	
Role	

Input Data

Tells the tool to use this input data/file

Output Targets

Tells the tool where to deposit results

Data Selector: Various Data Types (tracks, files, and ROIs (region of interests), etc)

Details: Specific information on files/samples selected in the "Data Selector"

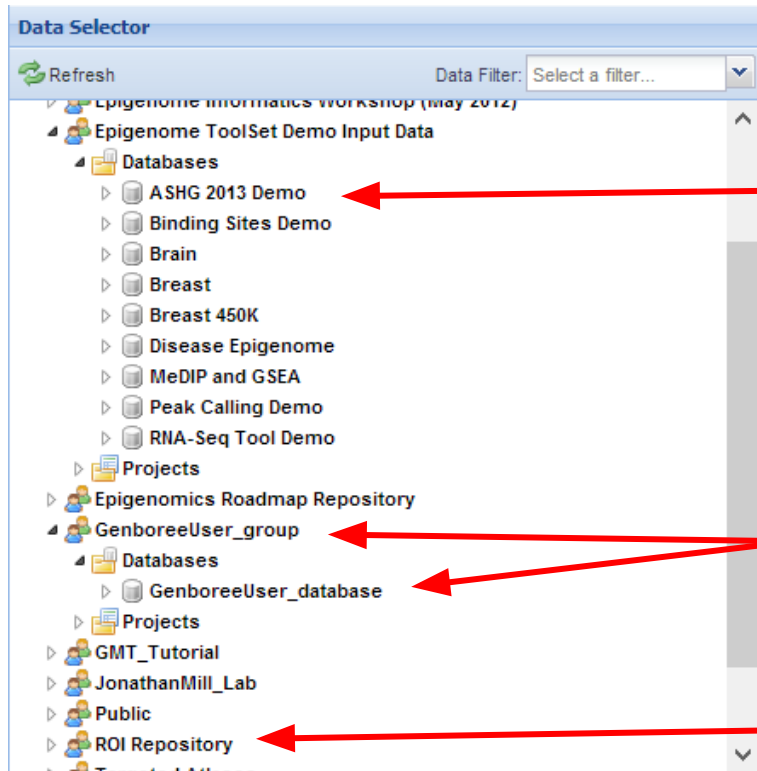
Input Data: Tells the tool to use this input data/file

Output Targets: Tells the tool where to deposit results

Important: Toolset Menu turns **GREEN** when "Input Data" and "Output Targets" are properly populated for a tool to run. Please note that "System/Network" and "Help" options are always green since "User Profile", "Jobs", and "Request Feature" are always available for use and do not need "Input Data" and "Output Targets" to be populated.

Preparation Prior to Starting the Use Case

- “**GenboreeUser_group**” is a name template for an automatically created Genboree user group **for you** where “**GenboreeUser**” is **your user name**.
- Similarly, “**GenboreeUser_database**” is a name template for your database.
- Of course, you may create many more databases and may create and be member of many other groups.



Under “Epigenome Toolset Demo Input Data” you will find “ASHG 2013 Demo” database, where we have provided you with sample data to try out the use cases

When making screenshots for providing instructions we have used “GenboreeUser_group” and “GenboreeUser_database” as output targets, however, you will use your own group and database. Following slides will show you how to create database and project

ROI Repository contains database of annotated regions (eg. Gencode and Refseq annotations)

Display Tool Setting “Help” dialogue box in the Workbench



The screenshot shows the GENBOREE Workbench interface. At the top, there are navigation tabs: System/Network, Data, QC and Pre-processing, Genome, Transcriptome, Cistrome, Epigenome, Metagenome, Visualization, and Help. The 'Data' tab is active, and a dropdown menu is open, showing options: Databases, Entity Lists, and Entrypoints. The 'Databases' option is highlighted, and a sub-menu is visible with options: Create Database, Rename Database, and Delete Database. A red box highlights the 'Create Database' option, with an arrow pointing to a larger dialog box.

Help: Create Database

This tool is a recent addition. Please contact genboree_admin@genboree.org with questions or comments, or for help using it on your own data.

This tool will create/add a new database in the target Group. Note that the database to be created should NOT already exist in the group.

Output Targets

Instructions:

- Drag 1 destination group into "Output Targets". The new database will be created in this group.

Output type(s):

- Group
min: 1 ; max: 1

Can be empty? NO

Tool-Specific Settings

Settings:

- **Reference Sequence**
Select the genome assembly the database will use.
- **Database Name**
The name of the database to be created/added. [REQUIRED]
- **Description**
A line or two describing the database. [OPTIONAL]
- **Species**
Automatically selected based on Reference Sequence. [OPTIONAL]
- **Version**
Automatically selected based on Reference Sequence. [OPTIONAL]
- **Submit**
Once you've reviewed the name of the new database to be created.

Input Data

Output Targets

Bioinformatics Research Laboratory
of Medicine.

is available **free for academic use**.

HGSC
HUMAN GENOME SEQUENCING CENTER

A grey background (not green) means that the tool is not active. Clicking a non-active tool displays the help text that includes instruction for how to activate the tool.

To create a database, you need to drag a **Group** into "Output Targets".

Steps for Creating a Database

Step I - Drag **your** group from “Data Selector” into “Output Targets”. GenboreeUser_group and GenboreeUser_database is placeholder for your group and databases

Step II - Click “Data” => “Databases” => “Create Database”. “Create Database” tool **IS** active, since it requires a “Group” to be in “Output Targets”. Select “Create Database” for tool settings.

Step III - Select “Template: Human (hg19)”

Step IV - Type database name (i.e. “GenboreeUser_database” and click “Submit”



Steps for Creating a Project page

The screenshot shows the GENBOREE web interface. At the top, there is a navigation bar with tabs for 'System/Network', 'Data', 'QC and Pre-processing', 'Genome', and 'Transcript'. Below this is a 'Data Selector' panel on the left with a 'Refresh' button and a tree view of groups. The 'GenboreeUser_group' is selected. A 'Create Project' button is highlighted in the 'Data Selector' tree. A red box highlights the 'Create Project' button and the 'GenboreeUser_group' in the tree.



Step II - “Create Project” tool **IS** active, since it requires a “Group” to be in “Output Targets”. Select “Create Project” for tool settings.

The screenshot shows the 'Create Project' tool settings page. It has a 'Tool Overview' section with a 'Target Group' field set to 'GenboreeUser_group'. Below this is a 'Settings' section with fields for 'Project Name', 'Project Title' (containing 'ASHG workshop'), and 'Project Description' (containing 'Result output from ASHG Wks'). There is a 'Unique Name' checkbox which is checked. At the bottom are 'Submit' and 'Cancel' buttons.

Step I - Drag **your** group from “Data Selector” into “Output Targets”.

Step IV - Select “Refresh” in “Data Selector” to view your newly created database and project page in your group.

Step III - Type Project Name, Title, and Desc. and click “Submit”.

NOTE: Project name has to be unique for all Genboree users, so you could do something like ‘Use_case_18’ + your initials (i.e. “Use_case_18-abc”)

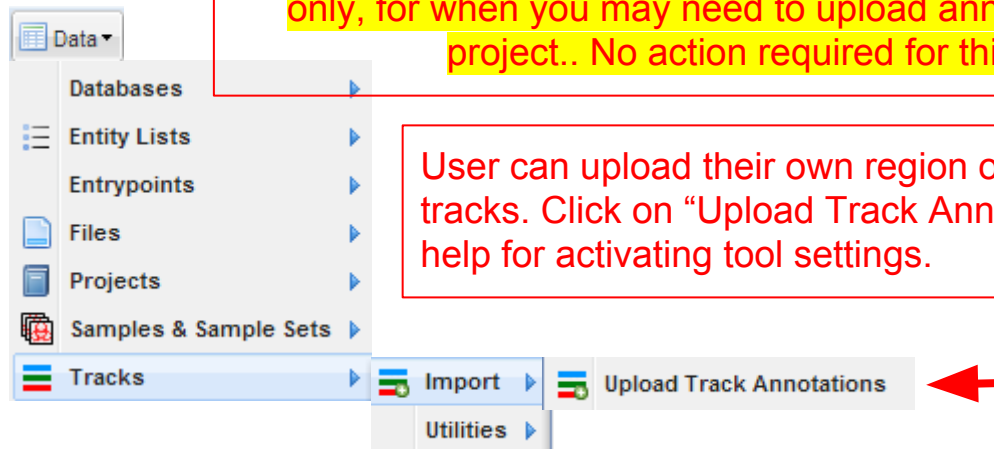
Description of Regions of Interest (ROIs) Tracks

Source of ROIs that will be used in this analysis:

- **Track “GeneProteinCoding_promoter”**: This track contains promoters of protein coding genes that were defined using Gencode V10 annotations (www.gencodegenes.org/), with transcription start sites (TSS) +/- 1500bp. The track contains 20,007 promoters from human genome build Hg19.
- **Track “GeneLincRNA_promoter”**: This track contains promoters of lincRNAs that were defined using Gencode V10 annotations, with transcription start site (TSS) +/- 1500bp. the track contains 5,484 promoters from human genome build Hg19.
- **Track “release9_H3K4me3”**: This track contains enhancers obtained from Manolis Kellis. Enhancers here are defined as H3K4me3 marks from the NIH Roadmap Consortium data (www.epigenomeatlas.org), wherein the coordinates were defined by ChromHMM.¹

Please note: Upload of annotations is provided for your information only, for when you may need to upload annotations for your own project.. No action required for this use case.

Upload your own
Track Annotations:



User can upload their own region of interests tracks. Click on “Upload Track Annotations” to see help for activating tool settings.

1. Ernst, J. & Kellis, M. “ChromHMM: automating chromatin-state discovery and characterization”. *Nat. Methods* **9**, 215–216 (2012).

System/Network Data QC and Pre-processing Genome Transcriptome Cistrome Epigenome Metagenome Visualization Help

Welcome to the Genboree Workbench! [Getting Started]

Step I - Drag "Release 9 Repository" database from "Epigenomics Roadmap Repository" to "Input Data"

Step II - Select "View Track Grid"

Attribute	Value
Group	Epigenomics Roadmap Repository
Role	public
Name	Release 9 Repository
Description	Release 9 Repository
Species	Homo sapiens

Input Data

- Release 9 Repository

Output Targets

View Track Grid
View Sample Grid
Tabular Annotation Viewer
Launch UCSC Genome Browser

Select how you want the tracks displayed in the “View Track Grid” tool.

The screenshot shows the 'View Track Grid' tool settings window. The 'Settings' section is expanded, showing the following fields:

- X-axis attribute:** eaAssayType (dropdown menu, highlighted with a red box and arrow pointing to the annotation 'Step III - Select “eaAssay Type”')
- Y-axis attribute:** eaSampleType (dropdown menu, highlighted with a red box and arrow pointing to the annotation 'Step IV - Select “eaSample Type”')
- Page Title:** Grid Viewer: Tracks from Relea
- Grid Title:** Tracks from Release 9 Reposit
- X Label:** eaAssayType
- Y Label:** eaSampleType

At the bottom of the window, the 'Submit' button is highlighted with a red box.

Annotations:

- Step III - Select “eaAssay Type”
- Step IV - Select “eaSample Type”

Track Grid view of the data from Roadmap Epigenome Project



Releases

Informatics

Publications

Forums

Contributors

- [Data Access Policy](#)
- Data embargo period: from 04/15/2013 - 01/15/2014 or earlier as specified [here](#)
- Select cells by clicking and dragging, then use "View Selections" in the Selections menu
- Use "Save Selections" in the Selections menu to save selected (highlighted) cells in a group
- To see data authors, other metadata, and to download data, click a sample name in the filter
- Expression Array data may be downloaded [here](#)
- Human Epigenome Atlas releases are intended to be cumulative: e.g. Release 3 includes data from all previous releases
- NOTE: Some pages may not be accessible over low bandwidth internet connections. This page is optimized for high bandwidth connections.

A Track/experiment or group of tracks (track-entity lists) can be selected and saved in your database by selecting "Selections" > "Save Selections". However, for this use case track-entity lists have already been generated for you.

Tracks from Release 9 Repository

Filter rows:

Selections

Choose Databases

eaSampleType	Bisulfite-Seq	MeDIP-Seq	MFE-Seq	FRBS	DNase Hypersensitivity	Digital Genomic Footprinting	miRNA-Seq	smRNA-Seq	ChIP-Seq Input	Histone H3K27me3	Histone H3K36me3	Histone H3K4me1	Histone H3K4me3	Histone H3K9ac	Histone H3K9me3	Histone H2AK5ac	Histone H2AK9ac	Histone H2A Z	Histone H2BK5ac	Histone H2BK12ac	Histone H2BK15ac	Histone H2BK20ac	Histone H2BK120ac	Histone H3K14ac	Histone H3K18ac	Histone H3K23ac	Histone H3K23me2	Histone H3K27ac	Histone H3K4ac	Histone H3K4me2	Histone H3K56ac	Histone H3K79me1	Histone H3K79me2	Histone H3K9me1		
Adipose Derived Mesenchymal Stem Cells									3	2	3	3	3	5	3																					
Adipose Nuclei									5	5	5	5	5	5	5												1									
Adipose Tissue	1						3		1																			1								
Adrenal Gland	1						2		2	4	2	2	1			1												2								
Adult Kidney				2					2	2	2	2	2	2	2	2												2								
Adult Liver	1						2		4	4	4	4	5	2	4													2								
Aorta	1						2		2	2	2	2	2		1													2								
Bladder							1		2		1	1																1								
Bone Marrow Derived Mesenchymal Stem Cell Cultured Cells				2						1	1	1	1	1	1													4								
Bone Marrow Derived Mesenchymal Stem Cells									4	3	3	3	3	3	3																					
Brain Angular Gyrus					1				2	1	2	2	2	1	2													2								
Brain Anterior Caudate					2				2	2	2	2	2	1	2													2								
Brain Cerebellum							1																													
Brain Cingulate Gyrus					1				2	1	2	2	2	1	2													2								
Brain Germinal Matrix	1	2					1	3	1	2	2	2	2		2																					
Brain Hippocampus Middle	2						2		3	3	3	3	3	1	3													3								

Methodology Overview

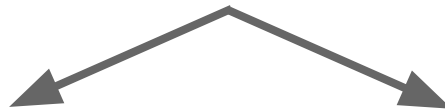
Clustering/Heatmap: select your experimental tracks (provided here as HL60) and epigenomes for comparison from the Human Epigenome Atlas to find closest reference epigenome



LIMMA: to find regions with differentially modified histone signals between two groups of data tracks.



Spark: visualizes epigenomic profiles on a genome-wide scale by clustering or collapsing regions with similar “epigenomic footprint”

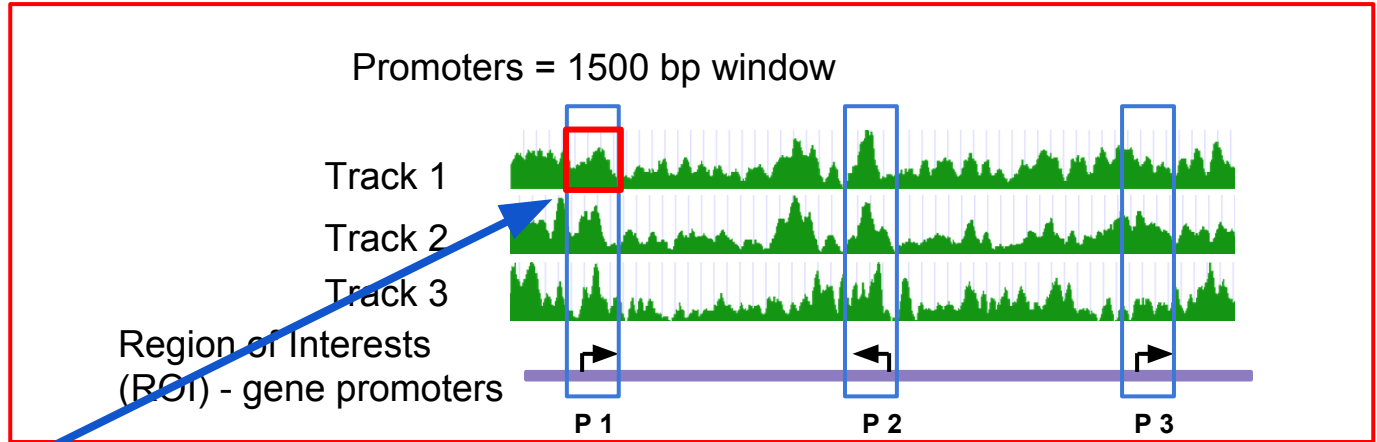


GREAT: assesses functional significance of cis-regulatory regions.

HOMER: de novo motif discovery.

Methodology: Clustering/Heatmap

I. Data Selection



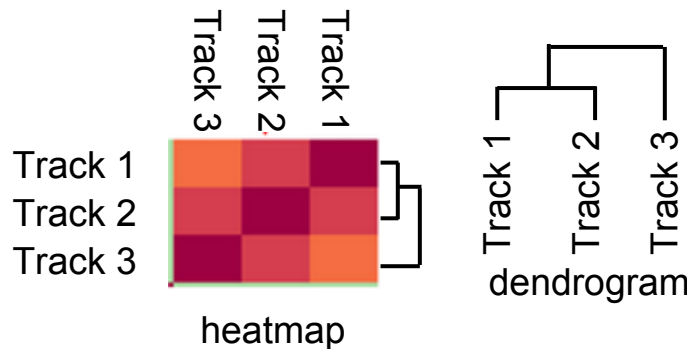
II. Signal processing-
Heatmap Tool calculates
average signal for each
track and ROI (promoter)
combination

	Track 1	Track 2	Track 3
P 1	0.8	0.7	0.3
P 2	0.7	0.6	0.7
P 3	0.6	0.8	0.2

Data matrix (3 x 3 shown here) with average signal is normalized and a correlation matrix generated. Correlation matrix is used to calculate distance measure and hierarchical clustering to group samples based on similarity to plot dendrogram

III. Visualization of results

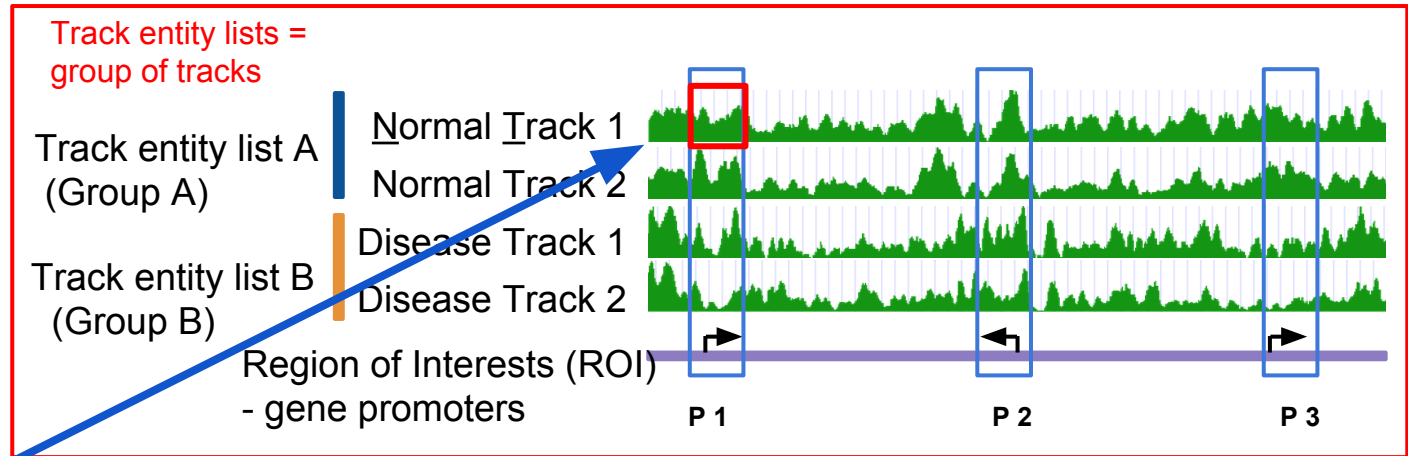
Correlation values are dynamically scaled and represented in heatmap.



Note: Heatmap and dendrogram are shown as result. Genboree generates dendrogram separately, since if the output contains many tracks, row/column labels may be hard to visualize in heatmap.

Methodology: LIMMA (Linear Model for Microarray Analysis)

I. Data Selection



II. Signal processing- Tool calculates average signal for each ROI and each track

	Group A		Group B	
	NT1	NT 2	DT1	DT2
P 1	0.8	0.7	0.3	0.2
P 2	0.65	0.6	0.7	0.5
P 3	0.8	0.8	0.2	0.15

Data are normalized and LIMMA tool compares average signal for each ROI (row) between two groups. Note: for limma to work, need at least two tracks in each group.

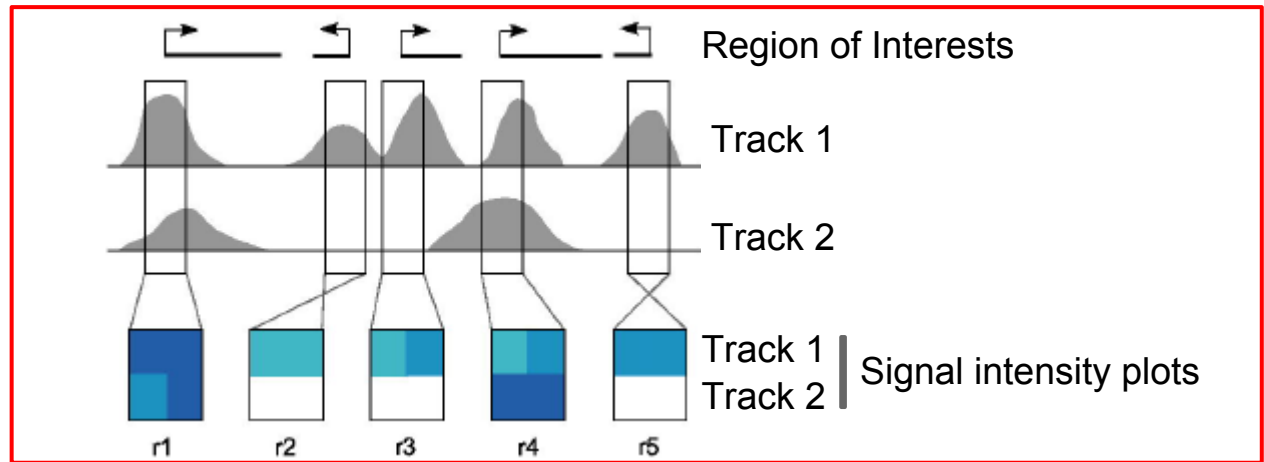
III. Results output

ROIs (i.e. promoter, enhancers, etc) that exhibit significantly different signal between the groups compared, are provided to users as a region track which can be downloaded or used for downstream analysis

Methodology: Spark

Spark allows user-guided k-means clustering to visualize epigenomic profiles on a genome-wide scale.

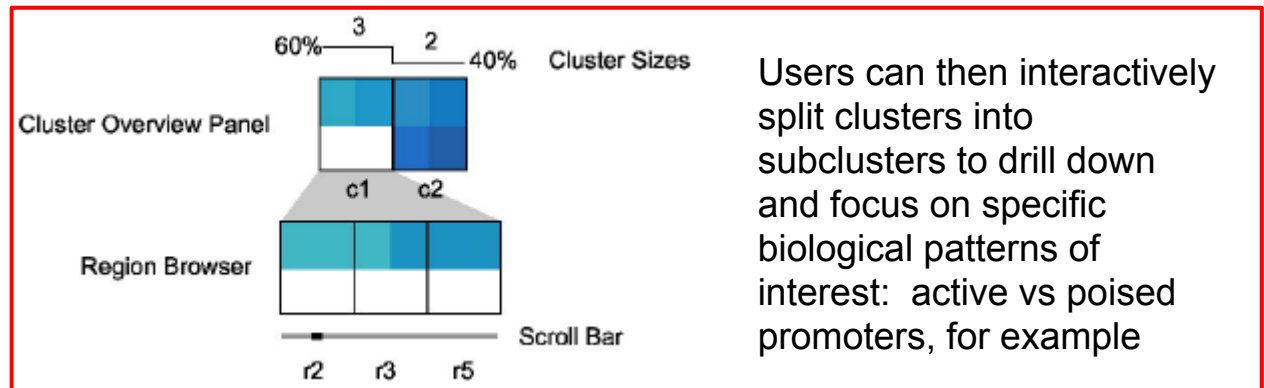
I. Preprocessing (ROIs = r1 - r5)



II. Clustering (C1, C2)



III. Interactive Visualization



Methodology: GREAT & HOMER

The patterns identified by Spark require further investigation to assess biological meaning

- GREAT² (Genomic Regions Enrichment of Annotations Tool) analysis
 - Assesses functional significance of cis-regulatory regions, here identified by Spark
 - Associates both proximal and distal binding events (Chip-Seq) with putative target genes
 - Uses gene annotation from several ontologies to associate the cis-regulatory regions with the annotations
 - Calculates statistical enrichments for associations between cis-regulatory regions and the annotations
 - Outputs annotation terms significantly associated with input cis-regulatory regions
- HOMER³ analysis:
 - Utilizes a de novo motif discovery algorithm
 - Scores motifs by looking for motifs with differential enrichment between two sets of sequences
 - Enrichment measured using the cumulative hypergeometric distribution (or cumulative binomial distribution for large data sets)
 - Motifs with p-values below 1e-10 are typically reasonable candidates for further investigation. Motifs with a p-value greater than 1e-10 or even 1e-12 are likely false positives

²McLean et al. "GREAT improves functional interpretation of cis-regulatory regions". Nature Biotechnology, 28: 495-503 (2010).

³Heinz et al. "Simple Combinations of Lineage-determining transcription factors prime cis-regulatory elements required for macrophage and B cell identities". Molecular Cell, 28: 576-589 (2010).

Welcome to the Genboree Workbench! [Getting Started]

Data Selector

Refresh Data Filter: Select a

- Epigenome ToolSet Demo Input Data
 - Databases
 - ASHG 2013 Demo
 - All Annotations in Database
 - Tracks
 - Lists & Selections
 - Lists of Tracks
 - HL60_Tracks
 - HSC_Tracks
 - Immune_HL60_H3K4me1**
 - Myeloid_Tracks
 - release9_H3K27me3
 - release9_H3K36me3
 - release9_H3K4me1
 - release9_H3K4me3
 - release9_H3K9me3
- Sample Sets
- Samples
- Files
- Queries
- Binding Sites Demo
- Brain

Details

Input Data

- Immune_HL60_H3K4me1
- ChromHMM:Enhancers

Output Targets

- GenboreeUser_database
- Use_Case_20_GU

Step 1 - Drag "Immune_HL60_H3K4me1". Drag "ChromHMM:Enhancers" from "ROI Repository" > Databases > "ROI Repository - hg19" > Tracks > "Class:Enhancer".

Step 2 - Drag your database and project page to the output targets

Note the “Epigenome” menu turns green when “Input Data” and “Output Targets” are properly populated.

Step 3 - Click on “Epigenome”
- Click on “Compute Similarity Matrix (heatmap)”

The screenshot shows the Genboree web interface. On the left is a navigation tree with categories like 'Lists & Selections', 'SampleSets', 'Samples', 'Files', 'Queries', 'Binding Sites Demo', and 'Brain'. The 'Epigenome' menu is highlighted in green in the top navigation bar. A dropdown menu is open under 'Epigenome', showing options: 'Random Forest', 'QIIME', 'QC', 'Search for Similar Signals by Correlation', 'Analyze Signals', 'Compute Similarity Matrix (heatmap)', 'Create Track Lists from Irewick Tree', 'Slice Epigenomic Data', and 'Analyze Signals in the Context of Epigenome Atlas'. The 'Compute Similarity Matrix (heatmap)' option is highlighted with a red box. Below the navigation bar, the 'Input Data' section contains 'Immune_HL60_H3K4me1' and 'ChromHMM:Enhancers'. The 'Output Targets' section contains 'GenboreeUser_database' and 'Use_Case_20_GU'.

Tool Settings

Compute Similarity Matrix (heatmap) BETA

Tool Overview

Input Entity Lists(s)/ROI-Track:

Items: Immune_HL60_H3K4me1 (Track Entity List)
ChromHMM:Enhancers (Track)

Output Database/Project:

Database/Projects: GenboreeUser_database Group: GenboreeUser_group
Of Interest: Use_Case_20_GU Group: GenboreeUser_group

labelLeave data matrix unchanged

Epigenomic Experiment Heatmap Tool

Analysis Name: Heatmap_HL60_Immune_2013

Normalization: Quantile

Aggregating Function: Avg

Distance Function: Pearson's Correlation

Hierarchical Clustering Function: Average

Key:

Key Size: 0.75

Height: 8

Width: 10

Trace: None

Density: Histogram

Dendrograms to display on heatmap: Both

No Data Regions

No Data Value: 0

Remove No Data Regions?

If EITHER track has no data for that region:

If BOTH tracks have no data for that region:

Submit Cancel

Step 4 - A default "Analysis Name" is generated by Genboree. It is recommended that all text and the time stamp be kept, and that you append some unique text to the beginning to help you distinguish different jobs run from the same tool.

Step 5 - Select Pearson's Correlation as distance function and Average as hierarchical clustering function

Step 6 - Select to remove data if both tracks have no data for that region

You will see this message upon successful submission of your heatmap job:

Job Submission Status

Compute Similarity Matrix (heatmap) BETA

Job Id: wbJob-epigenomicsHeatmap-MJCS03-4497

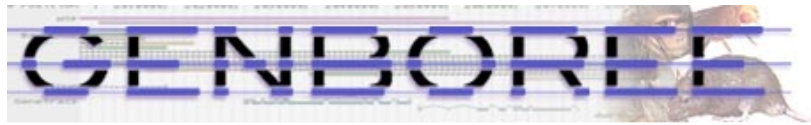
Your job has been successfully submitted. You will be notified by email when your job has completed.

You can track the progress of your job using the 'Job Summary' tool under System/Network/Jobs.

If you have questions, please contact genboree_admin@genboree.org for assistance.

OK

Status of the jobs submitted can be obtained through Job Summary



The screenshot shows the Genboree Workbench interface. At the top, there is a navigation bar with tabs for System/Network, Data, QC and Pre-processing, Genome, Transcriptome, Cistrome, Epigenome, Metagenome, Visualization, and Help. Below this is a sidebar menu with options like User Profile, Groups, Hosts, Jobs, and Request Feature. The 'Jobs' menu is expanded, and 'Job Summary' is highlighted with a red box. A red arrow points from this box to a 'Job Summary' tool settings window. This window has a 'Settings' tab and contains fields for Start Date (2013/7/18), End Date (YYYY/MM/DD), Sort Order (Newest first), and Group By (None). At the bottom of the settings window, there are 'Generate Report' and 'Cancel' buttons, with a red box around the 'Generate Report' button and a red arrow pointing to it. A larger red box at the bottom of the screenshot contains the text: "Select 'Generate Report' to see Job Summary".



Genboree is built & maintained by the **Bioinformatics Research Laboratory** at **Baylor College of Medicine**.

Genboree is a hosted service. Code is available **free for academic use**.



You will receive an email with the following message when your job is finished:

Hello

Your Compute Similarity Matrix (heatmap) job completed successfully.

Job Summary:

JobID - wbJob-epigenomicsHeatmap-e3CshO-5730
Analysis Name - EpigenomeExpHeatmap2013-10-09-00:42:01

Inputs:

1. Entitylist -
2. Trk -
3. Entitylist -

Outputs:

1. Db -
2. Prj -

Settings:

analysisName - EpigenomeExpHeatmap2013-10-09-00:42:01
dendograms - both
density - histogram
distfun - cor
hclustfun - average
height - 8
key - TRUE
keySize - 0.75

Clicking on the link will take you to the project page containing your results

- The Genboree Team

Result File Location in the Genboree Workbench:

<http://genboree.org/java-bin/project.jsp?projectName=Roadmap%20Epigenome%20Data%20Analysis>

GENBOREE

BCM
Baylor College of Medicine

Home Workbench Browser Profile Groups Projects Databases Tools Log Out Help

(This is a recently added feature. Report issues to Genboree Admin.)

Edit Mode

Project Page

Project News:

2013/10/10: Genboree User ran Epigenomic Heatmap Tool (Heatmap HL60 Immune 2013-10-10-18 20 45) and the results are available at the link below.

- Study Name: Heatmap HL60 Immune 2013-10-10-18 20 45
- Link to results

Genboree is built & maintained by the Bioinformatics Research Laboratory at Baylor College of Medicine.

Genboree is a hosted service. Code is available free for academic use.

B
R
L

HGSC

Click on the "Link to results" in your Project page

Table of Content: Epigenomic HeatMap

Study Name: Heatmap HL60 Immune 2013-10-10-18 20 45

User: Genboree User

Date: 2013/10/10 19:13 CDT

Epigenomic HeatMap Plots

[Heatmap](#)

[Correlation plot](#)

Click on the heatmap to see which reference epigenome profiled in the NIH Roadmap Epigenome Project does HL60 cluster with

Newick Tree Visualizations

Equal Branch Lengths

Rows [\[PNG\]](#) [\[SVG\]](#)

Columns [\[PNG\]](#) [\[SVG\]](#)

Scaled Branch Lengths

Rows [\[PNG\]](#) [\[SVG\]](#)

Columns [\[PNG\]](#) [\[SVG\]](#)

Natural Log Scaled Branch Lengths

Rows [\[PNG\]](#) [\[SVG\]](#)

Columns [\[PNG\]](#) [\[SVG\]](#)

Log10 Scaled Branch Lengths

Rows [\[PNG\]](#) [\[SVG\]](#)

Columns [\[PNG\]](#) [\[SVG\]](#)

Step 7 - Drag “HL60_Tracks”, “Myeloid_Tracks”, “HSC_Tracks”, and “Limma:Myeloid_comb” from “Epigenome ToolSet Demo Input Data”

System/Network Data

Visualization Help

Welcome to the

Data Selector

Refresh Data Filter: Select a filter...

- Epigenome ToolSet Demo Input Data
 - Databases
 - ASHG 2013 Demo
 - All Annotations in Database
 - Tracks
 - Class: Enhancer
 - Limma:Myeloid_comb
 - Class: Gene
 - Class: Marker
 - Class: Sequence
 - Lists & Selections
 - Lists of Tracks
 - HL60_Tracks
 - HSC_Tracks
 - Immune_HL60_H3K4me1
 - Myeloid_Tracks
 - release9_H3K27me3
 - release9_H3K36me3
 - release9_H3K4me1
 - release9_H3K4me3
 - release9_H3K9me3

Details

Attribute	Value
Group	GenboreeUser_group
Role	administrator
Name	GenboreeUser_database
Description	Template for Human Genome, UCSC Build Hg19

Input Data

- Limma:Myeloid_comb
- HL60_Tracks
- HSC_Tracks
- Myeloid_Tracks

Output Targets

- GenboreeUser_database

Step 8 - Drag your database to Output Targets



Step 9 -Expand "Epigenome" --> "Analyze Signals" --> select "Cluster by Spark"

The screenshot shows the Genboree Workbench interface. At the top, there are navigation tabs: System/Network, Data, QC and Pre-processing, Genome, Transcriptome, Cistrome, Epigenome, and Metagenome. The 'Epigenome' tab is selected. A red box highlights the 'Epigenome' menu, which is expanded to show options: Random Forest, QIIME, QC, Search for Similar Signals by Correlation, Analyze Signals (highlighted in green), Compute Similarity Matrix (heatmap), Create Track Lists from Newick Tree, Slice Epigenomic Data, and Analyze Signals in the Context of Epigenome Atlas. A red arrow points from the 'Analyze Signals' option to the 'Cluster by Spark' option in a sub-menu. The 'Cluster by Spark' option is also highlighted in green and has a red box around it. The main interface shows a 'Data Selector' on the left with a tree view of data sets, including 'Epigenome ToolSet Demo Input Data' and 'Databases'. The 'Input Data' section on the right lists 'Limma:Myeloid_comb', 'HL60_Tracks', 'HSC_Tracks', and 'Myeloid_Tracks'. The 'Output Targets' section lists 'GenboreeUser_database'.

Cluster by Spark (Analyze Signals)

Tool Overview

Inputs:

Data Tracks/Files: Limma:Myeloid_comb
 Group: Epigenome ToolSet Demo Data, Database: ASHG 2013 Demo
 Group: Epigenome ToolSet Demo Input Data, Database: ASHG 2013 Demo
 Group: Epigenome ToolSet Demo Input Data, Database: ASHG 2013 Demo
 Group: Epigenome ToolSet Demo Input Data, Database: ASHG 2013 Demo

Output Database:
 Database: GenboreeUser_database Group: GenboreeUser_group

Spark Analysis Settings

Analysis Name: Spark-HL60_CD14_HSC

Select ROI Track: MCD34:H3K9me3 28
 Limma:Myeloid_comb
 CD14:H3K27ac 21 26
 CD14:H3K27me3 21 05
 CD14:H3K36me3 21 06

Region Label: MyROIs

Statistics Type: global

of Clusters: 16

of Bins: 20

Data Track Colors:

CD14:H3K27ac 21 26	blue
CD14:H3K27me3 21 05	blue
CD14:H3K36me3 21 06	blue
CD14:H3K4me1 21 03	blue
CD14:H3K4me3 01 07	blue
CD14:H3K9me3 21 04	blue
HL-60:H3K27ac-SET-A23124	blue
HL-60:H3K27me3-SET-A23122	blue
HL-60:H3K36me3-SET-A23123	blue
HL-60:H3K4me1-SET-A23119	blue
HL-60:H3K4me3-SET-A23120_1	blue
HL-60:H3K9me3-SET-A23121	blue
Limma:Myeloid_comb	blue
MCD34:H3K27ac 36 52	blue
MCD34:H3K27me3 17	blue
MCD34:H3K36me3 28	blue
MCD34:H3K4me1 28	blue
MCD34:H3K4me3 17	blue
MCD34:H3K9me3 28	blue

Submit **Cancel**

Step 10 - Add identifier text at beginning of analysis name

Step 11 - Select ROI (Region of Interest) Track "Limma:Myeloid_comb"

Step 12 - Enter the # of Clusters "16". During visualization, User can change number of clusters based on their expert knowledge.

You will see this message upon successful submission of your Spark job:

Job Submission Status

Cluster by Spark (Analyze Signals)

Job Id: wbJob-spark-qq6exj-5176

Your job has been successfully submitted. You will be notified by email when your job has completed.

You can track the progress of your job using the 'Job Summary' tool under System/Network/Jobs.

If you have questions, please contact genboree_admin@genboree.org for assistance.

OK

You will receive an email with the following message when your Spark job has finished:

Your Spark job completed successfully.

Job Summary:

JobID - wbJob-spark-AsqKIJ-9045

Analysis Name -

Inputs:

of Data Tracks -

ROI Track -

Outputs:

Output DB -

Output Host - genboree.org

Settings:

k -

normType - exp

numBins - 20

regionLabel -

statsType - global

Additional Info:

To view your results in the Spark GUI:

(a) download and unzip the results archive and then

(b) launch Spark via Java Web Start and open the analysis folder.

Spark Java Web Start Link:

<http://www.bcgsc.ca/downloads/spark/current/start.jnlp>

Step 13 - Download Spark GUI



- The Genboree Team

Result File Location in the Genboree Workbench:

(Direct links to files are at the end of this email)

Host: genboree.org

Grp:

Db:

Files Area:

*
*
*

Step 14 - Download Spark Results and UNZIP the Folder



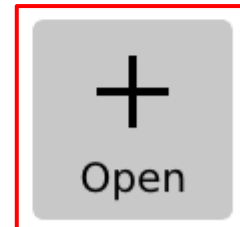
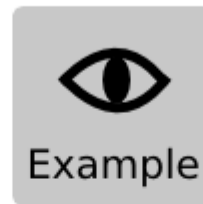
Result File URLs (click or paste in browser to access file):

FILE: !

URL:

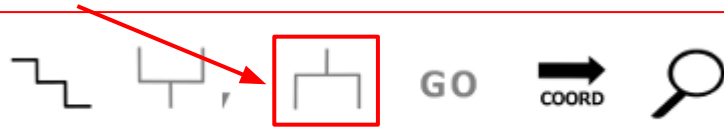
http://genboree.org/java-bin/apiCaller.jsp?srcPath=http%3A%2F%2Fgenboree.org%2FREST%2Fv1%2Fgrp%2Fvamin_group%2Fdb%2FUseCase%2Ffile%2FSpark%2520-%2520Results%2FSpark_Myeloid_HSC%2FSpark_Myeloid_HSC.zip%2Fdata%3F&fileDownload=true&promptForLogin=true&errorFormal=html

SPARK GUI



Step 15 - Select Open and choose the unzipped folder

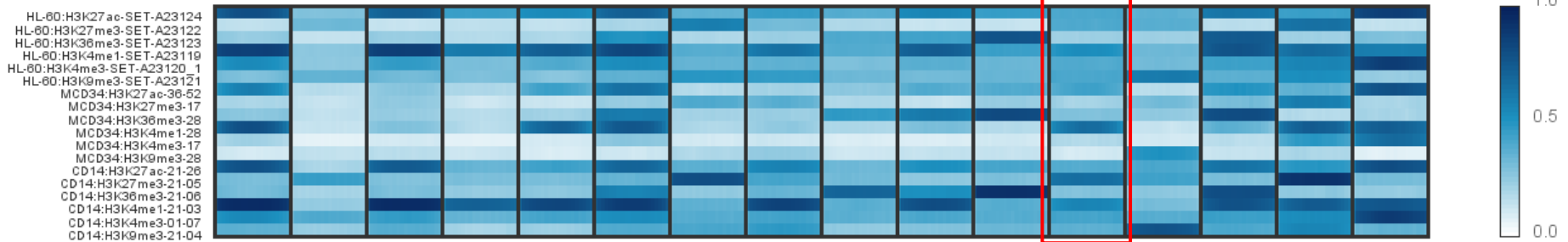
Step 16: Split the cluster to find enhancers that have active enhancer profile in HL60



Cluster Sizes (37013 regions clustered)



1938 Enhancers (out of the 37013) have this profile of epigenomic marks.



C12

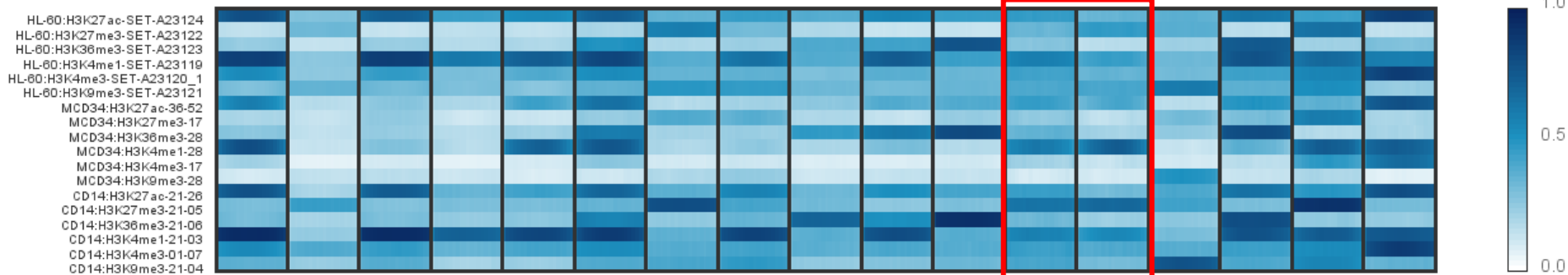
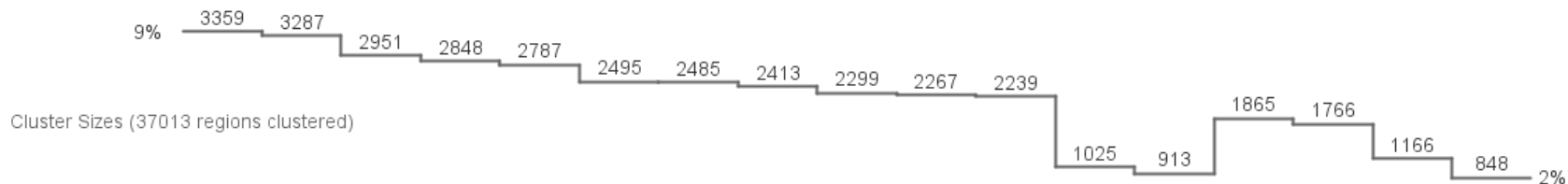
CD34 CD14 HL-60



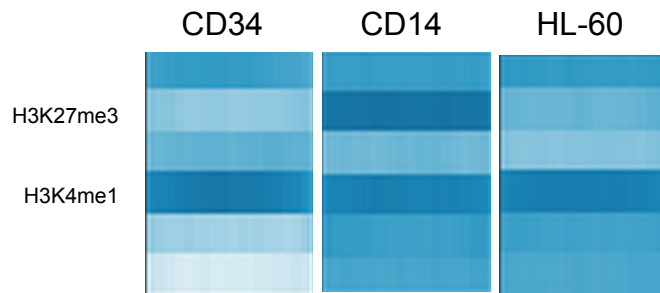
Epigenomic transitions of 1938 enhancers

Clustering (C12) reveals a shift from active epigenomic marks in human immune stem cells (MD34) to poised epigenomic marks in myeloid cells (CD14) and then active in HL-60

Upon splitting cluster C12 into two clusters, notice that the cluster with 1025 enhancer regions show a clear shift of HL60 in the active state (H3K4me1 and H3K27ac), while the cluster with 913 shows a poised state (H3K4me1 and H3K27ac).

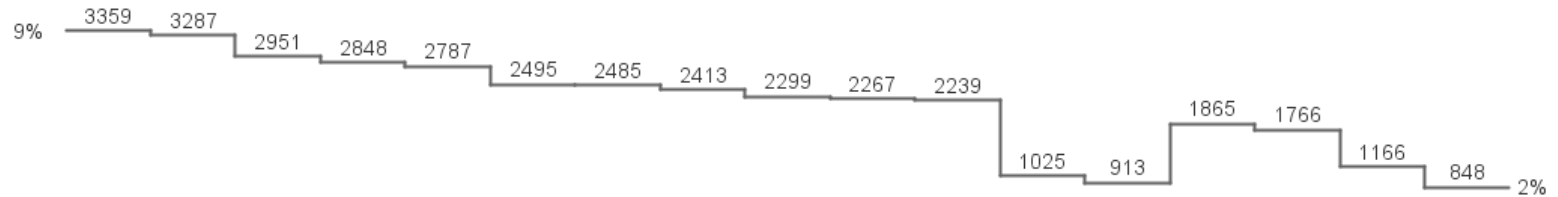
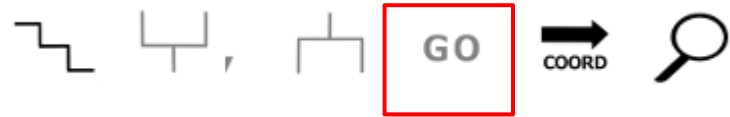


C12

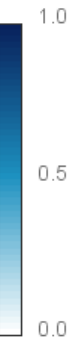
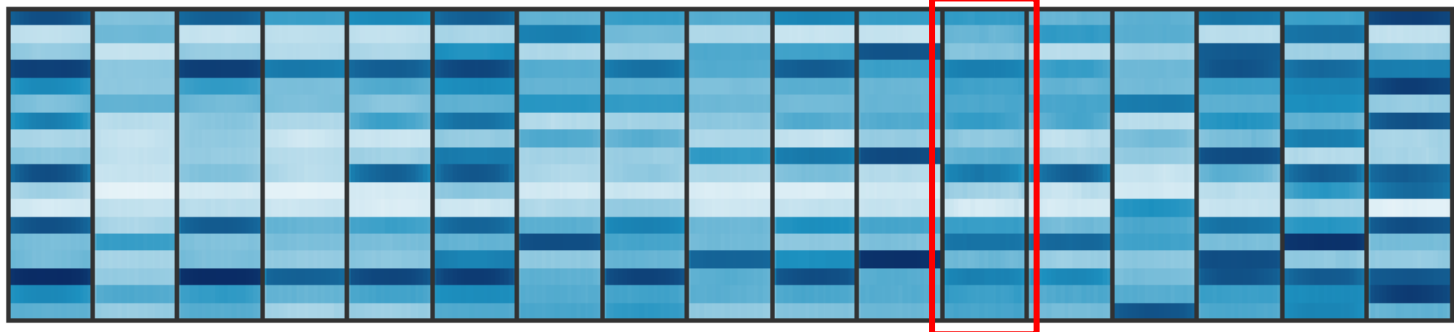


Epigenomic transitions of 1025 enhancers

The next few slides will walk you through some data manipulations in Excel which are required to generate BED files. BED files will supply the annotations for subsequent steps



HL-60:H3K27ac-SET-A23124
HL-60:H3K27me3-SET-A23122
HL-60:H3K36me3-SET-A23123
HL-60:H3K4me1-SET-A23119
HL-60:H3K4me3-SET-A23120_1
HL-60:H3K9me3-SET-A23121
MCD34:H3K27ac-36-52
MCD34:H3K27me3-17
MCD34:H3K36me3-28
MCD34:H3K4me1-28
MCD34:H3K4me3-17
MCD34:H3K9me3-28
CD14:H3K27ac-21-26
CD14:H3K27me3-21-05
CD14:H3K36me3-21-06
CD14:H3K4me1-21-03
CD14:H3K4me3-01-07
CD14:H3K9me3-21-04



Step 17 - Select Copy and Launch. Web-browser will be launched. We will do Motif and GREAT analysis via Genboree. We will not use DAVID as regions are enhancers and not genes.

Warning [X]

? Too many IDs to query in a single URL. Click 'Copy and Launch' to copy these IDs to the clipboard and launch the DAVID website. Once loaded, paste your ID list into the 'Upload Tab'.

Copy and Launch Cancel

Once selected "Copy and Launch", open excel and paste the region IDs to make BED file



FILE HOME INSERT PAGE LAYOUT FORMULAS DATA REVIEW VIEW

From Access From Web From Text From Other Sources Existing Connections Refresh All Connections Sort Filter Filter Reapply Advanced Text to Columns Flash Fill Remove Duplicates Data Validation Consolidate

Get External Data Connections Sort & Filter Data Tools

A1 : chr1:152490602-152493200

	A	B	C	K	L	M	I
1	chr1:152490602-152493200						
2	chr2:44376002-44376600						
3	chr2:60475802-60476000						
4	chr2:66148202-66150600						
5	chr2:74765202-74766400						
6	chr2:202894202-202897400						
7	chr3:126216002-126216200						
8	chr3:126654202-126655200						
9	chr4:114675002-114682000						
10	chr4:175502402-175502800						
11	chr4:18710202-187111800						
12	chr5:64395602-64399200						
13	chr5:143554602-143572000						
14	chr6:2618002-26184000						
15	chr6:4186002-41862400						
16	chr6:44039002-44040800						
17	chr6:134272402-134273200						
18	chr6:157094602-157098000						
19	chr6:158934802-158936400						
20	chr6:167134002-167185200						
21	chr7:25935802-25937600						
22	chr7:14164602-141616200						
23	chr8:11274002-11274200						
24	chr9:71625802-71628600						
25	chr9:11655602-116567000						
26	chr9:120504602-120508200						
27	chr10:96303402-96305000						
28	chr11:46542002-46542200						
29	chr11:46542002-46542200						
30	chr11:46542002-46542200						

**Step 18 - Paste and Select the column.
Under "Data", select "Text to Columns"**

Convert Text to Columns Wizard - Step 1 of 3

The Text Wizard has determined that your data is Delimited.

If this is correct, choose Next, or choose the data type that best describes your data.

Original data type

Choose the file type that best describes your data:

- Delimited - Characters such as commas or tabs separate each field.
- Fixed width - Fields are aligned in columns with spaces between each field.

Preview of selected data:

```
1 chr1:152490602-152493200
2 chr2:44376002-44376600
3 chr2:60475802-60476000
4 chr2:66148202-66150600
5 chr2:74765202-74766400
6 chr2:202894202-202897400
```

**Step 19 - Select Delimited
and select "Next"**

Cancel

< Back

Next >

Finish

Convert Text to Columns Wizard - Step 2 of 3



This screen lets you set the delimiters your data contains. You can see how your text is affected in the preview below.

Delimiters

Tab

Semicolon

Comma

Space

Other:

Treat consecutive delimiters as one

Text qualifier:

Step 20 - Select Delimiters as Others and enter a semi-colon ":". Select "Finish".

Data preview

chr1	152490602-152493200
chr2	44376002-44376600
chr2	60475802-60476000
chr2	66148202-66150600
chr2	74765202-74766400
chr2	202894202-202897400

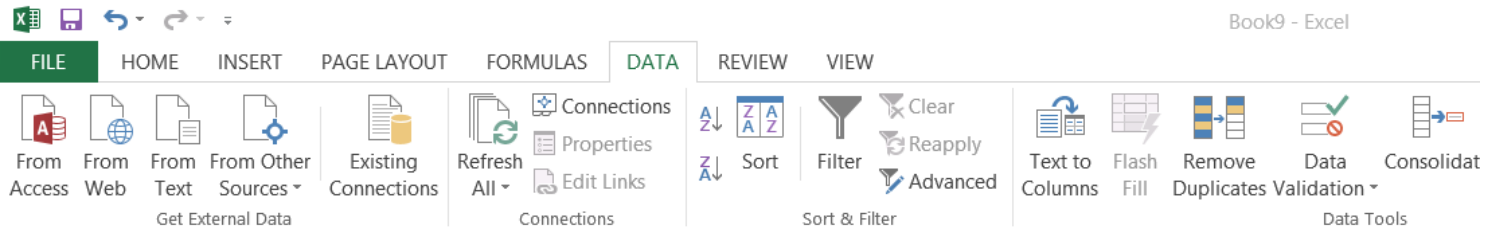
Perform similar steps to separate Chromosome Start and Stop into different columns, but instead of entering a semi-colon, you will enter hyphen.

Cancel

< Back

Next >

Finish



B1 : 152490602

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	chr1	1.52E+08	1.52E+08										
2	chr2	44376002	44376600										
3	chr2	60475802	60476000										
4	chr2	66148202	66150600										
5	chr2	74765202	74766400										
6	chr2	2.03E+08	2.03E+08										

Step 21 - Select column B and C and format the cells by right click and choose "Format Cells". Select category as "Number" with 0 decimal place

? X

Format Cells

Number Alignment Font Border Fill Protection

Category:

- General
- Number
- Currency
- Accounting
- Date
- Time
- Percentage
- Fraction
- Scientific
- Text
- Special
- Custom

Sample: 152490602

Decimal places: 0

Use 1000 Separator (,)

Negative numbers:

- 1234
- 1234
- (1234)
- (1234)

Number is used for general display of numbers. Currency and Accounting offer specialized formatting for monetary value.

OK Cancel

Step 22 - Save the file as "Spark_C12_1.txt" in Tab-delimited format

Welcome to the Genboree Workbench! [Getting Started]

Step 24 -Expand "Data" > "Tracks" > "Import" > "Upload Track Annotations"

Data Selector

Refresh

- genboree.org
 - Atlas Tools Access
 - BRL AUTO TEST
 - EDACC
 - Epigenome Informatics Demo Output Data
 - Epigenome Informatics Workshop (May 2012)
 - Epigenome ToolSet Demo Input Data
 - Epigenomics Roadmap Repository
 - GenboreeUser_group
 - Databases
 - GenboreeUser_database**
 - Projects
 - GMT_Tutorial
 - JonathanMill_Lab
 - Public
 - ROI Repository
 - Targeted Atlases
 - vamin_group
 - genboree.bcgsc.ca
 - genboree.cbrc.jp
 - www.brain-research-lab.org

Attribute	Value
Group	GenboreeUser_group
Role	administrator
Name	GenboreeUser_database
Description	Template for Human Genome, UCSC Build Hg19

Input Data

⬆️ ⬇️ ✖️ 🗑️

Output Targets

⬆️ ⬇️ ✖️ 🗑️

- GenboreeUser_database

Step 23 -To upload track annotations, drag your database



Tool Settings

Upload Track Annotations

Tool Overview

Input Data:
Data File: *n/a*

Output Location:
Database: *GenboreeUser_database* Group: *GenboreeUser*

Settings

Select File: Spark-C12_1.txt

Input Format:

Track Class:

Track Name: :

Skip non-assembly chromosomes
 Skip out-of-range annotations
 0 based and half open
 1 based and fully closed

Step 25 - Choose File "Spark-C12_1.txt" to upload

Step 26 - Select Bed

Step 27 - Name Track Class as "Enhancer", Track Name as "Spark:HL60_active_C12"

You will see this message upon successful submission of your Upload Track Annotations job:

Job Submission Status

Upload Track Annotations

Job Id: *wbJob-uploadTrackAnnos-rHaHFD-3024*

Your job has been successfully submitted. You will be notified by email when your job has completed.

You can track the progress of your job using the 'Job Summary' tool under System/Network/Jobs.

If you have questions, please contact genboree_admin@genboree.org for assistance.

Welcome to the Genboree Workbench! [Getting Started]

Data Selector

Refresh

- GenboreeUser_group
 - Databases
 - GenboreeUser_database
 - All Annotations in Database
 - Tracks
 - Class: BranchSpecificROI
 - Class: Class
 - Class: Enhancer
 - Spark:HL60_active_C12
 - Class: Gene
 - Class: High Density Score Data
 - Class: MACS
 - Class: Marker
 - Class: Sequence
 - Class: SPARK
 - Lists & Selections
 - SampleSets
 - Samples
 - Files
 - Queries
 - Projects
 - GenboreeUser_project

Select "Refresh" to view the uploaded track

Details

Attribute	Value
View Link	Link to Project
Group	GenboreeUser_group
Name	Use_Case_20_GU

Input Data

Spark:HL60_active_C12

Step 28 - Drag Spark: HL60_active_C12 from your database in Input Data. Drag Your Database and Project Page in Output Targets

Output Targets

- GenboreeUser_database
 - Use_Case_20_GU

Welcome to the Genboree Workbe

Data Selector

Refresh Data Filter: S

- GenboreeUser_group
 - Databases
 - GenboreeUser_database
 - All Annotations in Database
 - Tracks
 - Class: BranchSpecificROI
 - Class: Class
 - Class: Enhancer
 - Spark:HL60_active_C12
 - Class: Gene
 - Class: High Density Score Data
 - Class: MACS
 - Class: Marker
 - Class: Sequence
 - Class: SPARK
 - Lists & Selections
 - SampleSets
 - Samples
 - Files
 - Queries
 - Projects
 - GenboreeUser_project

- Analyze Structural Variants
- Find Motifs**
- SNPs
- GREAT

HOMER

Step 29 - Expand "Genome" > "Find Motifs" > "HOMER"

View Link	Value
Group	GenboreeUser_group
Name	Use_Case_20_GU

Input Data

Spark:HL60_active_C12

Output Targets

- GenboreeUser_database
- Use_Case_20_GU

Tool Settings

HOMER BETA

⊕ **Tool Overview**

Input Track:

Genes/Peaks of Interest: Spark:HL60_active_C12 Group: GenboreeUser_group, Database: GenboreeUser_database

Output Database/Project:

Database/Projects Of Interest: GenboreeUser_database Group: GenboreeUser_group
Use_Case_20_GU Group: GenboreeUser_group

Settings

Analysis Name Homer-2013-10-11-17:54:29

Genome Version hg19

Run against Genome
 Run against Promoters

Promoter Set human

⊕ **Basic Options**
⊕ **Advanced Options**
⊕ **Known Motif Options/Visualizations**


Submit **Cancel**

You will see this message upon successful submission of your HOMER job:

Job Submission Status

HOMER BETA

Use_Case_20_GU

 **Job Id:** wbJob-homer-DsBoDo-8944

Your job has been successfully submitted. You will be notified by email when your job has completed.

You can track the progress of your job using the 'Job Summary' tool under System/Network/Jobs.

If you have questions, please contact genboree_admin@genboree.org for assistance.

OK

You will get following e-mail message when job is completed

Hello

Your HOMER job completed successfully.

Job Summary:

JobID - wbJob-homer-hsthEq-0654

Additional Info:

Target Group:

Target Database:

Clicking on the link will take you to the project page containing your results

from HOMER un

Result File Location in the Genboree Workbench:

<http://genboree.org/java-bin/project.jsp?projectName=Roadmap%20Epigenome%20Data%20Analysis>

Project Page

Project News:

2013/10/11:

Genboree User ran a GREAT (Genomic Regions Enrichment of Annotations Tool) job (wbJob-great-DqocDC-0173). Click the link below to perform live analysis with GREAT:

- **Peform GREAT anlysis**

2013/10/11:

Genboree User ran a HOMER job (wbJob-homer-DsBoDo-8944) and the results are available at the link below.

- **Link to Homer Results**

Links to HOMER results of motifs that are enriched for the regions chosen in Spark cluster.

Welcome to the Genboree Workbe

Data Selector

Refresh

Data Filter: S

- Analyze Structural Variants
- Find Motifs
- G/A
c/A SNPs
- GREAT**

Step 31 - Expand "Genome" > select "GREAT"

- GenboreeUser_group
 - Databases
 - GenboreeUser_database
 - All Annotations in Database
 - Tracks
 - Class: BranchSpecificROI
 - Class: Class
 - Class: Enhancer
 - Spark:HL60_active_C12
 - Class: Gene
 - Class: High Density Score Data
 - Class: MACS
 - Class: Marker
 - Class: Sequence
 - Class: SPARK
 - Lists & Selections
 - SampleSets
 - Samples
 - Files
 - Queries
 - Projects
 - GenboreeUser project

View Link

Group	GenboreeUser_group
Name	Use_Case_20_GU

Input Data

Spark:HL60_active_C12

Step 30 - Drag Spark: HL60_active_C12 from your database in Input Data. Drag Your Database and Project Page in Output Targets

Output Targets

GenboreeUser_database
Use_Case_20_GU

Tool Settings

GREAT BETA

Tool Overview

Tracks of Interest:

Track: *Spark:HL60_active_C12* Group: *GenboreeUser_group*,
Database: *GenboreeUser_database*

Output Database/Project:

Database/Projects Of Interest: *GenboreeUser_database* Group: *GenboreeUser_group*
Use_Case_20_GU Group: *GenboreeUser_group*

Settings


Analysis Name

You will see this message upon successful submission of your GREAT job:

Job Submission Status

GREAT BETA

Job Id: *wbJob-great-DqocDC-0173*

 Your job has been successfully submitted. You will be notified by email when your job has completed.

You can track the progress of your job using the 'Job Summary' tool under System/Network/Jobs.

If you have questions, please contact genboree_admin@genboree.org for assistance.

You will receive an email with the following message when job is finished

Hello

Your GREAT job completed successfully.

Job Summary:

JobID - wbJob-great-AC73IN-8111

Additional Info:

Target Group:

Target Database

Clicking on the link will take you to the project page containing your results

Result File Location in the Genboree Workbench:

<http://genboree.org/java-bin/project.jsp?projectName=Roadmap%20Epigenome%20Data%20Analysis>

Project Page

Project News:

2013/10/11:

Genboree User ran a GREAT (Genomic Regions Enrichment of Annotations Tool) job (wbJob-great-DqocDC-0173). Click the link below to perform live analysis with GREAT:

- [Perform GREAT analysis](#)

2013/10/10:

Genboree User ran Epigenomic Heatmap Tool (Heatmap HL60 Immune 2013-10-10-18 20 45) and the results are available at the link below.

- **Study Name:** Heatmap HL60 Immune 2013-10-10-18 20 45
- [Link to results](#)

GREAT - Genomic Regions Enrichment of Annotations Tool

Host	Group	Database	Track	Link for live analysis
genboree.org	GenboreeUser_group	GenboreeUser_database	Spark:HL60_active_C12	Click here

GREAT version 2.0.2 current (04/03/2012 to now) ▼

Job Description

Job ID: 20131011-public-2.0.2-BkWIIV

Display name:

Test set: external data (1,025 genomic regions)
[Show in UCSC genome browser.](#) *How do I look at my regions in the genome?*

Background: Whole genome background

Assembly: Human: GRCh37 ([UCSC hg19, Feb 2009](#)) *What gene set does GREAT use?*

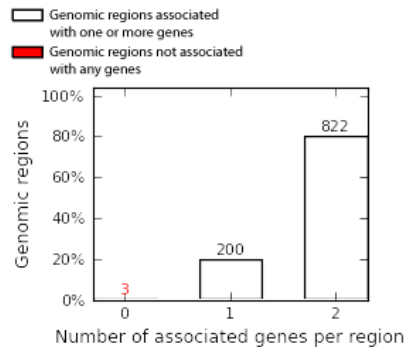
Associated genomic regions: Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included. 3 of all 1,025 genomic regions (0.3%) are not associated with any genes.
[View all genomic region-gene associations.](#) *Which genes are my regions associated with?*
[Revise the region-gene association rule.](#) *How are my regions associated with genes?*

Region-Gene Association Graphs

What do these graphs illustrate?

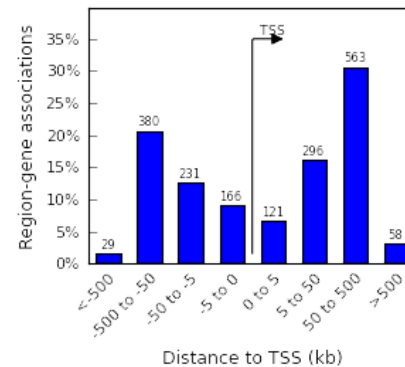
Number of associated genes per region

[Download as PDF.](#)



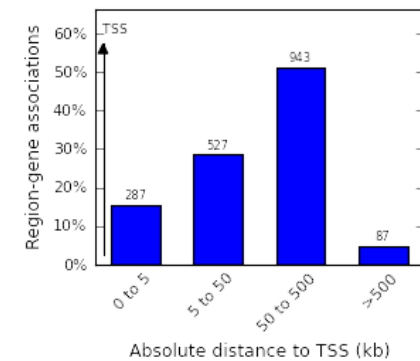
Binned by orientation and distance to TSS

[Download as PDF.](#)



Binned by absolute distance to TSS

[Download as PDF.](#)



When should I use a background set?
What should my background regions file contain?

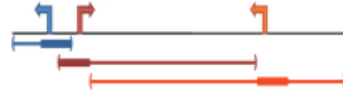
Association rule settings

Hide settings »

Associating genomic regions with genes

GREAT calculates statistics by associating genomic regions with nearby genes and applying the gene annotations to the regions. Association is a two step process. First, every gene is assigned a regulatory domain. Then, each genomic region is associated with all genes whose regulatory domain it overlaps.

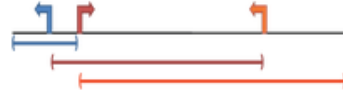
Basal plus extension



Proximal: kb upstream, kb downstream, plus Distal up to kb

Gene regulatory domain definition: Each gene is assigned a basal regulatory domain of a minimum distance upstream and downstream of the TSS (regardless of other nearby genes). The gene regulatory domain is extended in both directions to the nearest gene's basal domain but no more than the maximum extension in one direction.

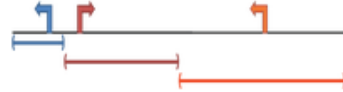
Two nearest genes



within kb

Gene regulatory domain definition: Each gene is assigned a regulatory domain that extends in both directions to the nearest gene's TSS but no more than the maximum extension in one direction.

Single nearest gene



within kb

Gene regulatory domain definition: Each gene is assigned a regulatory domain that extends in both directions to the midpoint between the gene's TSS and the nearest gene's TSS but no more than the maximum extension in one direction.



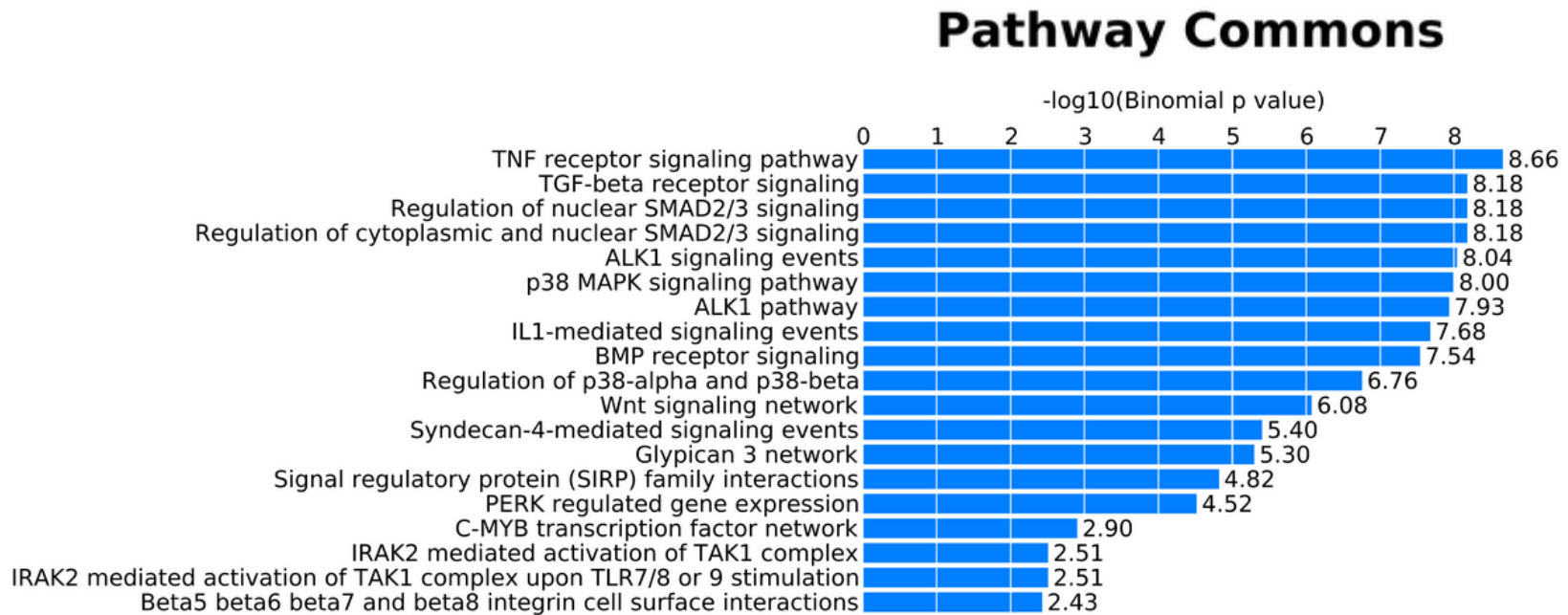
Gene Transcription Start Site (TSS)

Include curated regulatory domains [What are curated regulatory domains?](#)

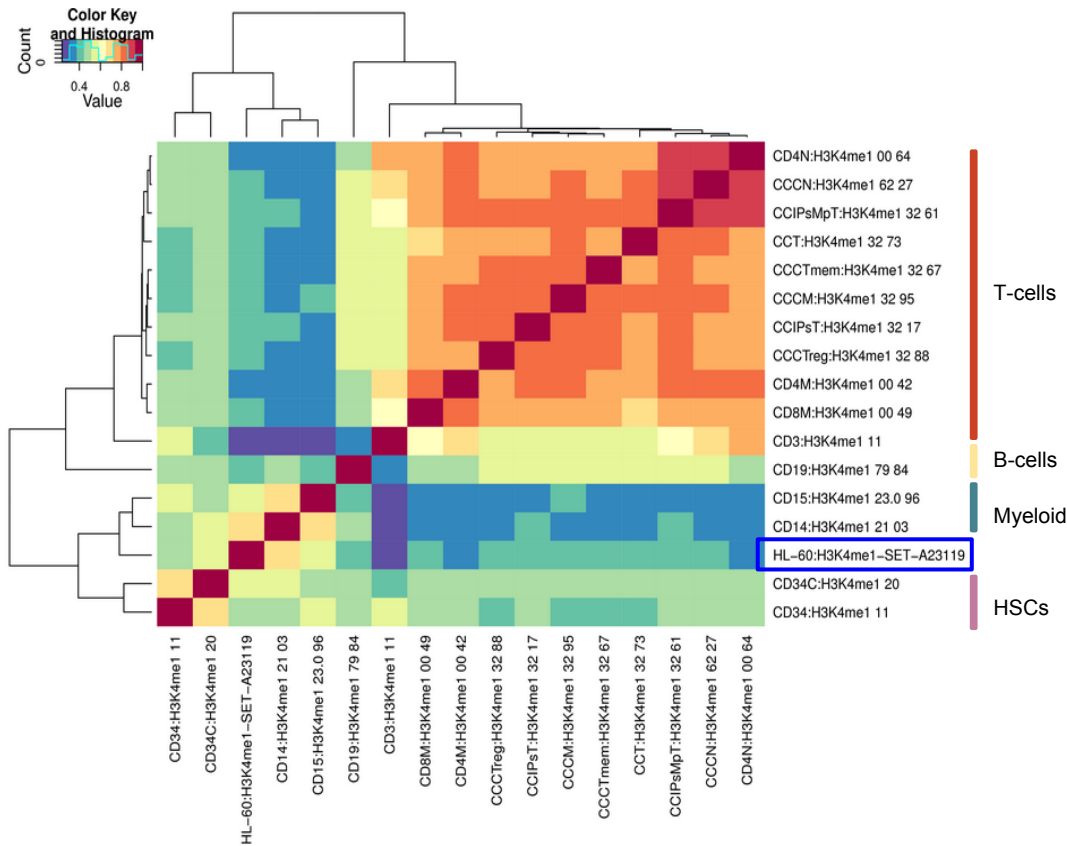
Submit

Reset

Pathways commons that are enriched using GREAT tool

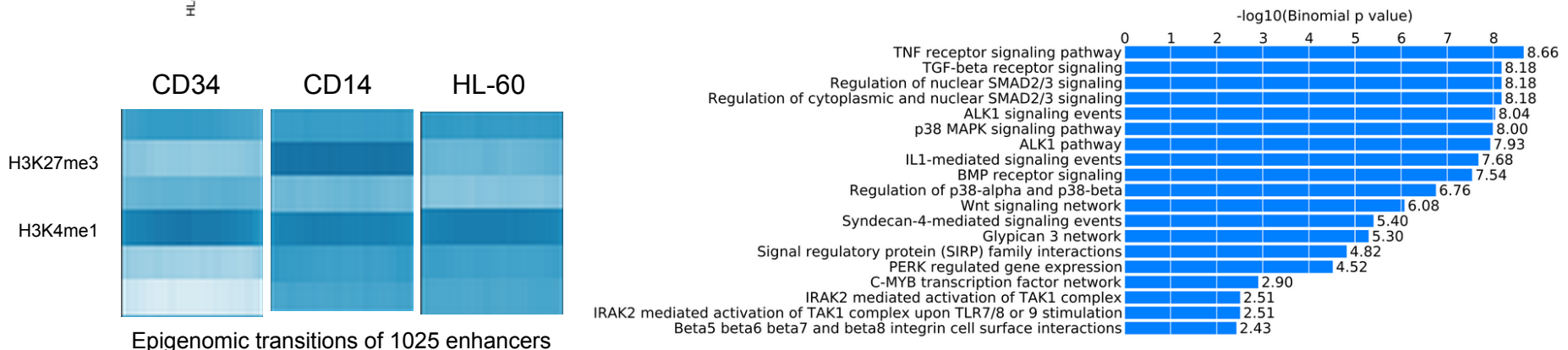


Summary and Interpretation of Results



Results: Comparison of reference epigenomes with HL60 histone modifications correctly identify HL60 as being of myeloid origin, suggesting one may perform an initial characterization of cell lines/tissues of unknown origin by virtual comparison to reference epigenomes. Further identifying enhancer regions that are undergoing epigenomic changes, Spark tool determined 1025 enhancers that underwent epigenomic transition. GREAT tool was used to determine pathways that these cis-regulatory regions are associated with. C-MYB, previously known, transcriptional regulator was found to be significantly enriched.

Pathway Commons



Help us improve Genboree. Please provide a comment or request feature.

The screenshot displays the Genboree Workbench interface. At the top, the 'GENBOREE' logo is on the left, and the 'BCM Baylor College of Medicine' logo is on the right. Below the logo is a navigation bar with tabs for 'System/Network', 'Data', 'QC and Pre-processing', 'Genome', 'Transcriptome', 'Cistrome', 'Epigenome', 'Metagenome', 'Visualization', and 'Help'. A sidebar on the left contains a tree view with categories like 'User Profile', 'Groups', 'Hosts', 'Jobs', and 'Request Feature' (which is highlighted with a red box). The main content area shows 'Genboree Workbench! [Getting Started]' with a 'Data Filter' dropdown. A 'Details' table is visible on the right. A 'Tool Settings' dialog box is open in the foreground, titled 'Request Feature'. It has a 'Settings' tab and contains the following fields: 'User Name' (Genboree User), 'User Email' (andrewj@bcm.edu), and a 'Message' text area. 'Submit' and 'Cancel' buttons are at the bottom of the dialog. At the bottom of the page, there is a logo for 'BRL' (Baylor Research Laboratory) on the left, a footer text stating 'Genboree is built & maintained by the Bioinformatics Research Laboratory at Baylor College of Medicine.' and 'Genboree is a hosted service. Code is available free for academic use.', and the 'HGSC HUMAN GENOME SEQUENCING CENTER' logo on the right.