



Ted Liefeld
Cancer Informatics Development
Broad Institute of MIT and Harvard

Need: Insights through integrative studies

Gene mutation causing Leigh Syndrome French Canadian Type (LFSC) and 8 other mitochondrial diseases

Integrate: candidate genomic region, mitochondrial proteomic data, and cancer expression compendium

Authors: Mootha et al. 2003, Calvo et al. 2006

Subtle repression of oxphos genes in diabetic muscle: role for mitochondrial dysregulation in diabetes pathology; new computational approach Gene Set Enrichment Analysis

Integrate: Gene sets/pathways & processes with expression profiles

Authors: Mootha et al. 2003, Subramanian & Tamayo et al. 2005

IKBKE as a new breast cancer oncogene

Integrate: RNAi screens, transformation of activated kinases, and copy number from SNP arrays of cell lines

Authors: Boehm et al. 2007

Discovery of 3 new genes involved in Glioblastoma Multiforme (NF1, ERBB2, PIK3R1); Confirmation of TP53, PTEN, EGFR, RB1, PIK3CA

Integrate: DNA sequence, copy number, methylation aberrations and expression profiles in 206 glioblastomas

Authors: TCGA Research Network 2008

~3000 novel, large non-coding RNAs with functions in development, the immune response and cancer

Integrate: Genome sequences from 21 mammals, epigenomic maps, and expression profiles

Authors: Guttman, Rinn et al. 2009

Characterization of disease subtypes and improved risk stratification for medulloblastoma patients

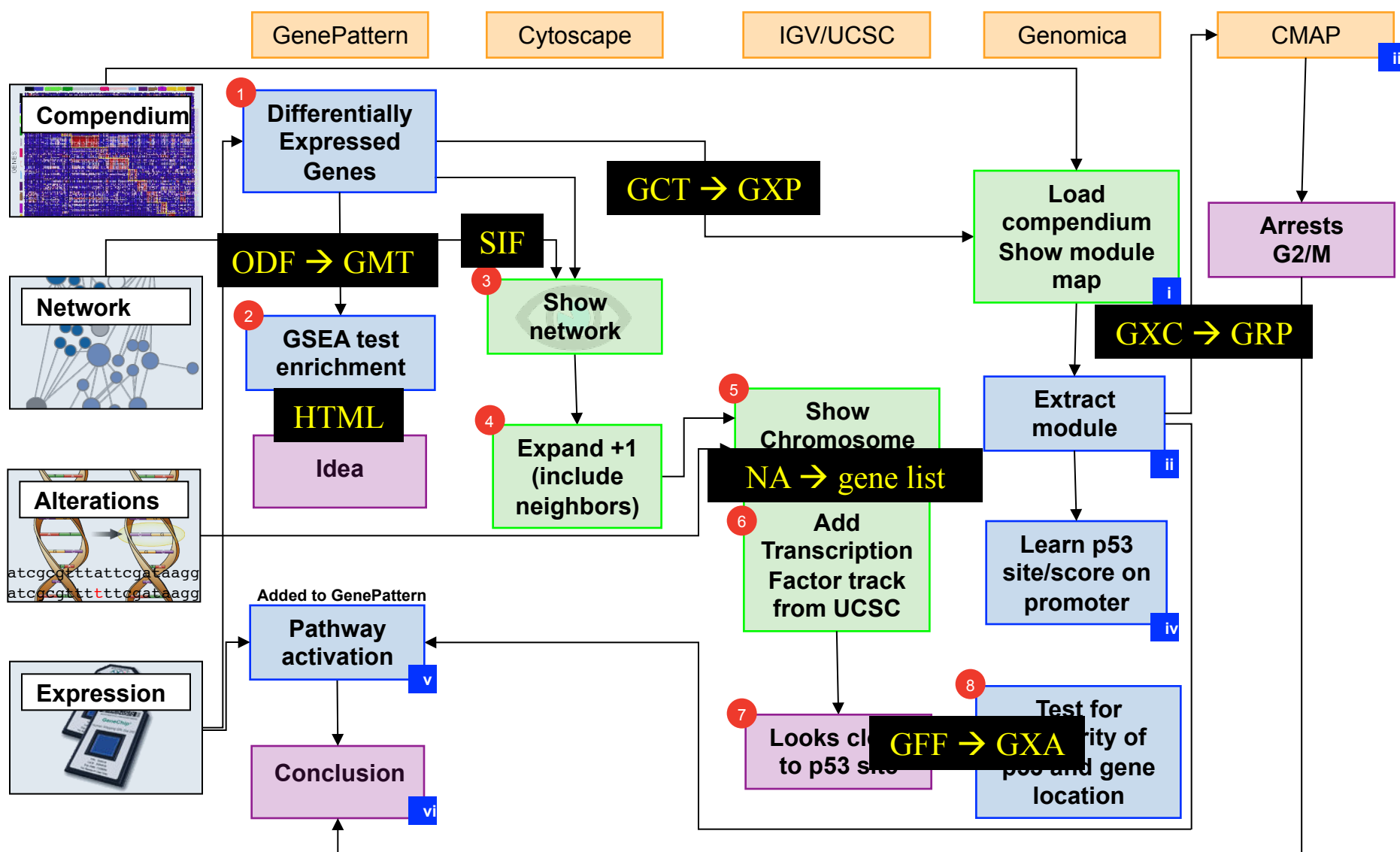
Integrate: Copy number, expression, clinical data for 96 medulloblastoma patients

Authors: Tamayo et al., Cho et al. 2011

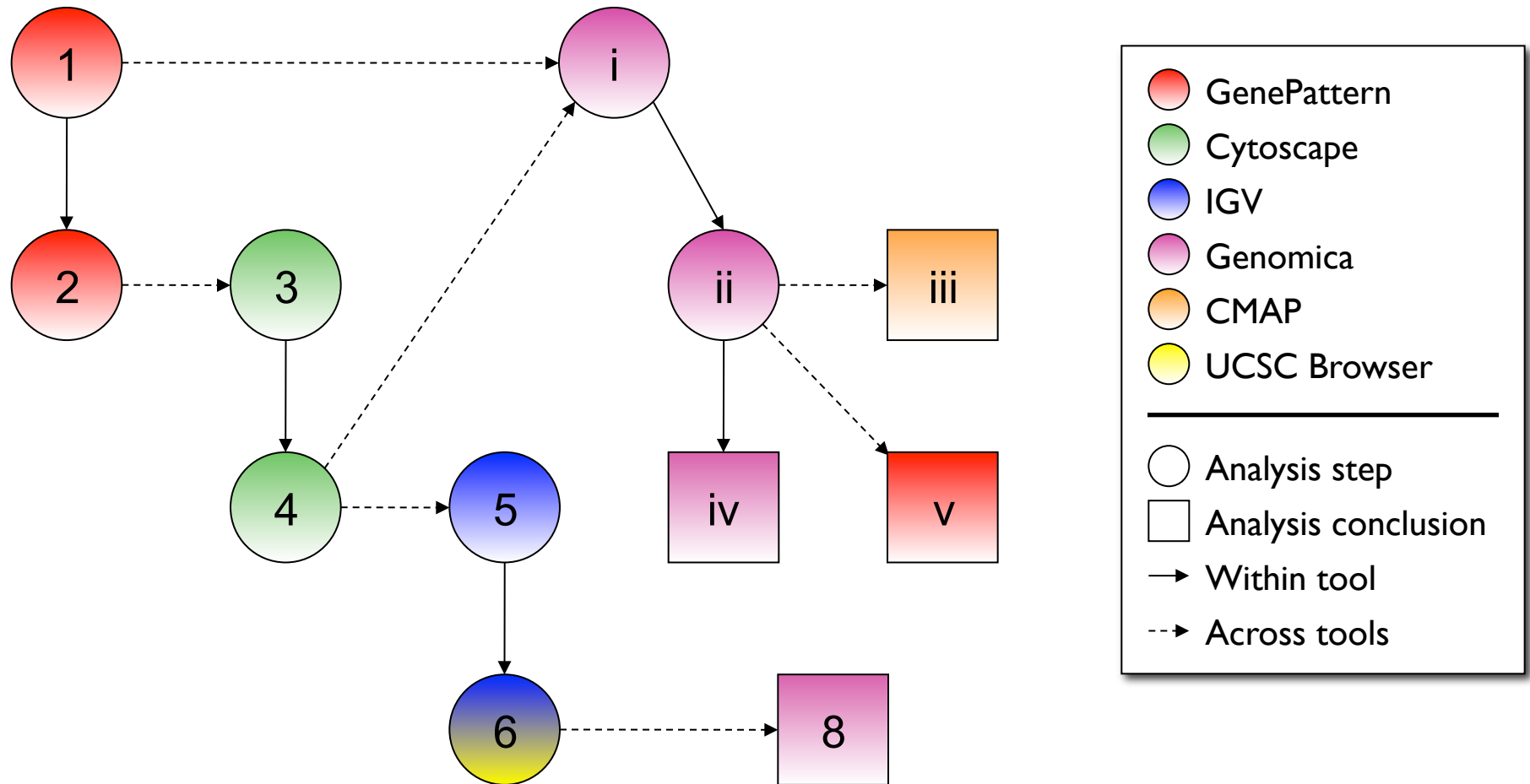
The Challenges

- **Flood of high throughput biological data**
genomic sequence, global mRNA expression profiles,
copy number and LOH, epigenetic data,
protein level and modification status,
metabolite profiles
- **Proliferation of tools**
Databases, visualization, and analysis
Difficulty of getting tools to work together
Access, analyze, visualize each data type separately

Integrative Genomics Use Case



12 steps, 6 tools, 7 transitions



The Need

- A lightweight “connection layer” for a wide variety of integrative genomic analyses
 - Support for all types of resource: Web-based, desktop, etc.
 - Automatic conversion of data formats between tools
 - Easy access to data from any location
 - Any tool that joins is automatically connected to the community of tools
 - Ease of entry into the environment

Cloud-based storage



API connectivity layer



Google™



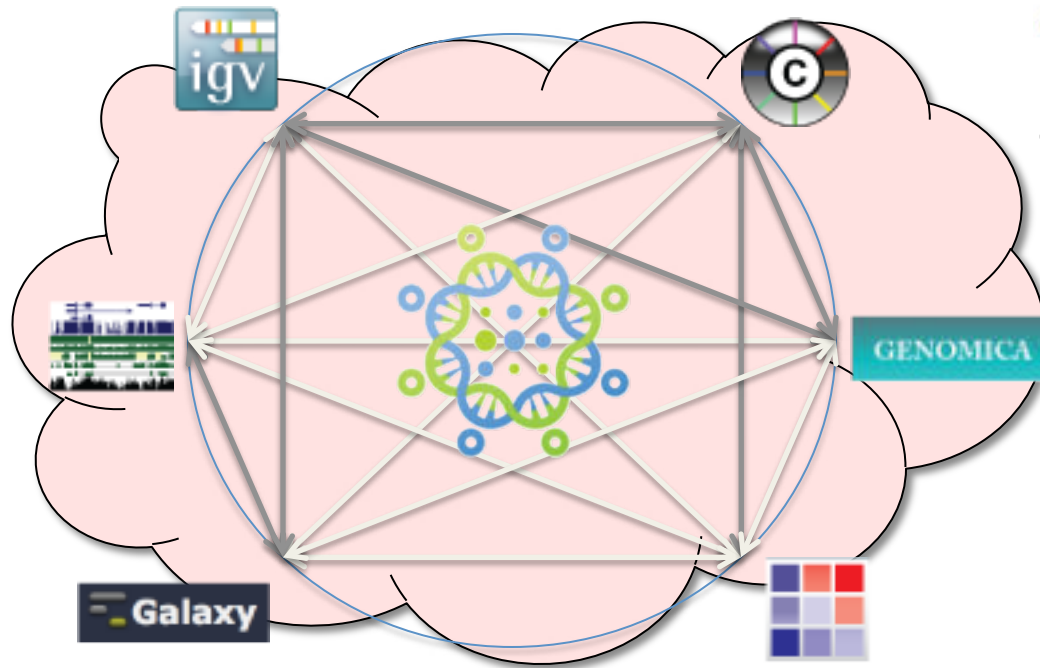
Online community to share diverse computational tools

GENOMESPACE



6 Seed Tools

Cytoscape
Galaxy
GenePattern
Genomica
IGV
UCSC Browser



3 Driving Biological Projects

lincRNAs
Cancer stem cells
Patient Stratification

Outreach: new
tools

www.genomespace.org

Outreach: new
DPBs

UC SANTA CRUZ



National Human
Genome Research
Institute



GenomeSpace Principles

- Aimed towards non-programming users
- Support interoperability through automatic cross-tool data transfer
- Requires minimal changes to tools

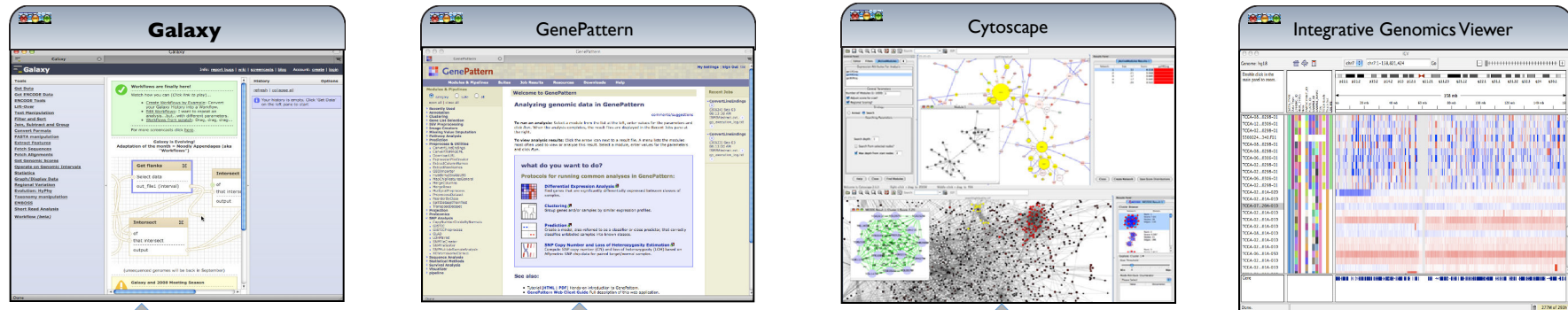


Open Source, LGPL

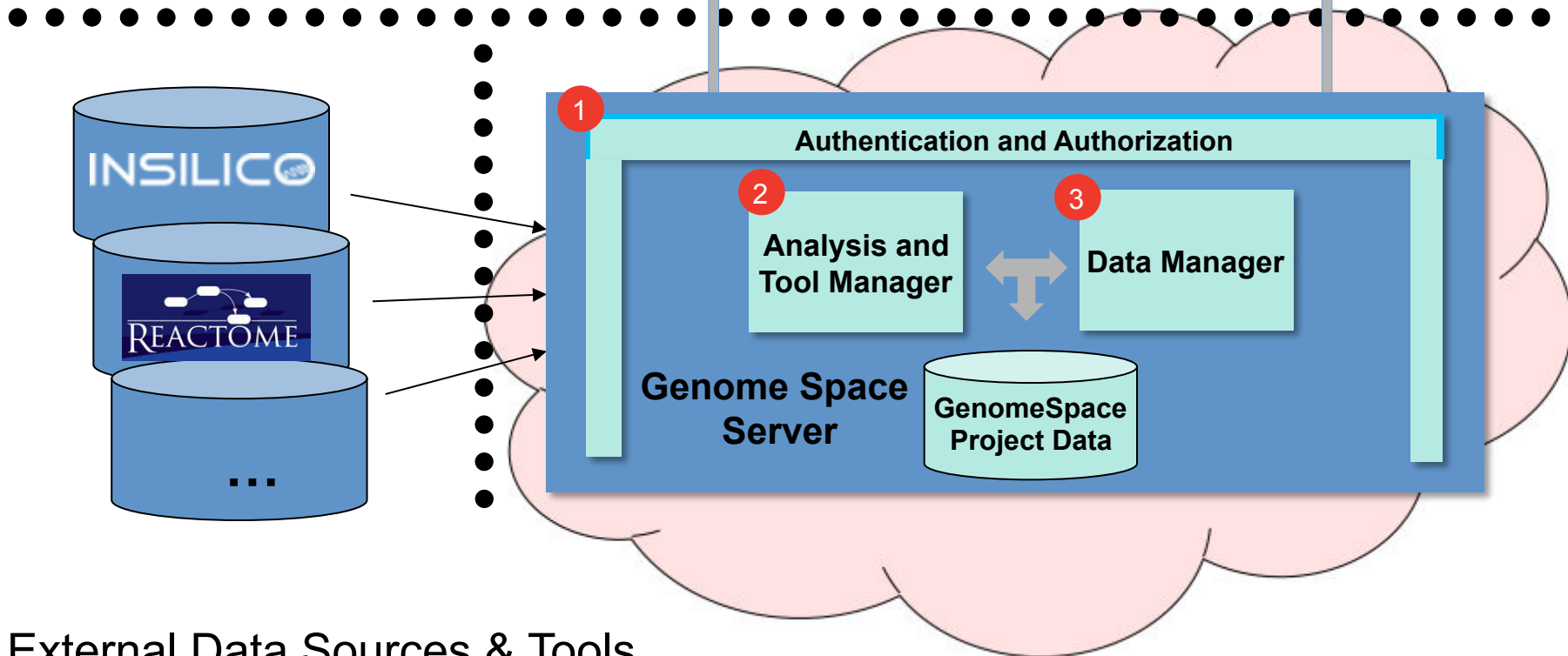
@genomespace

www.genomespace.org

GenomeSpace Components

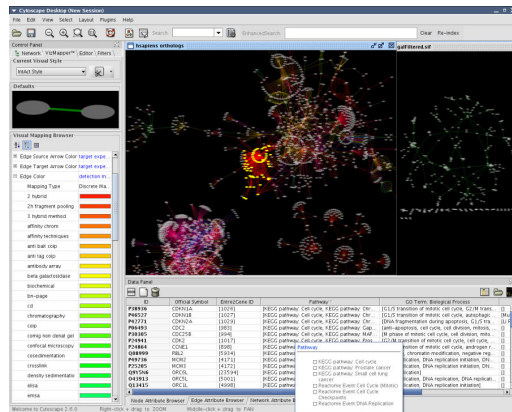


GS Enabled Tools

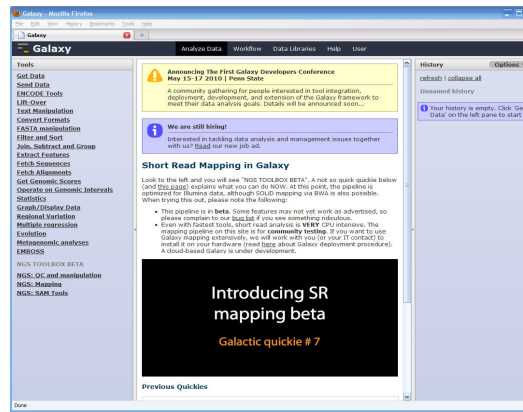


External Data Sources & Tools

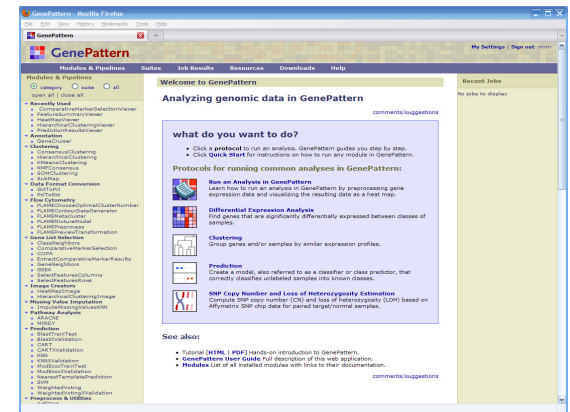
Seed Tools



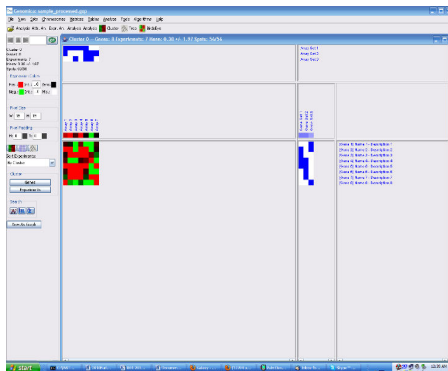
Cytoscape



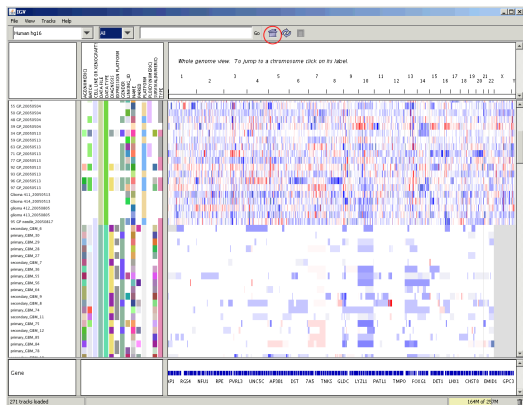
Galaxy



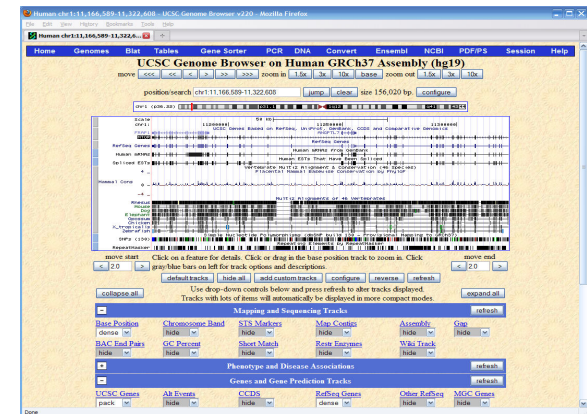
GenePattern



Genomica



IGV



UCSC Genome Browser

Using GenomeSpace

The screenshot displays the GenomeSpace web interface. At the top, a browser window shows the URL <https://gsui.genomespace.org/jsui/#>. Below the browser, the GenomeSpace logo and a user profile 'ted' are visible. A red box highlights the 'Tools' and 'Data Sources' sections. The 'Tools' section includes icons for Cistrome, IGV, GenePattern, Cytoscape, Galaxy, and Genomica. The 'Data Sources' section includes icons for InSilicoDB and UCSC Table Browser. Below these, a menu bar contains 'File', 'Launch', 'View', 'System', and 'Help'. A red box also highlights the 'Directories' and 'File List' sections. The 'Directories' section on the left shows a tree structure with 'Home', 'ted', and several sub-directories. The 'File List' section on the right shows a table of files with columns for 'Filename', 'Owner', 'Size', and 'Last Modified'.

Filename	Owner	Size	Last Modified
asdf	ted		
subdirAAAAA4	ted		
subdircccc3	ted		
testAdd2	ted		
testChromosome	ted		
CCELE_Expression_Entrez_2010-09-29.res	ted	152.68 Mb	2 months ago
HSCRegulatorsGeneSet.gmt	ted	63 bytes	5 months ago
Regulators.bed.bed	ted	47 Kb	5 months ago
SUV_chooser.xlsx	ted	38 Kb	2 months ago
TF.data.comp.marker.HSC.vs.Rest.attr	ted	134 Kb	6 months ago
TF.data.genesymbol.gct	ted	1.31 Mb	4 months ago
data.sort.comp.marker.HSC.vs.Rest.filt5.UP.outputDOWN.cys	ted	20 Kb	4 months ago
galFiltered.xgmml	ted	1.59 Mb	2 months ago
geneManiaQuery.txt	ted	1 Kb	8 months ago
human_interactome_cyt.cys	ted	5 bytes	5 months ago
input_breastcancer_BN_L0_KD_blue.cys	ted	16 Kb	4 months ago
input_breastcancer_BN_L0_KD_green.cys	ted	13 Kb	4 months ago
searchGenes2.txt	ted	532 bytes	5 months ago
searchGenes3.txt	ted	532 bytes	5 months ago

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Tools and
Data
Sources
Actions

Cloud-
based
filesystem

GenomeSpace Actions

Welcome to GenomeSpace

https://gsui.genomespace.org/jsui/#

GENOMESPACE^{BETA}

ted

Tools

Cistrome IGV GenePattern Cytoscape Galaxy Genomica

Data Sources

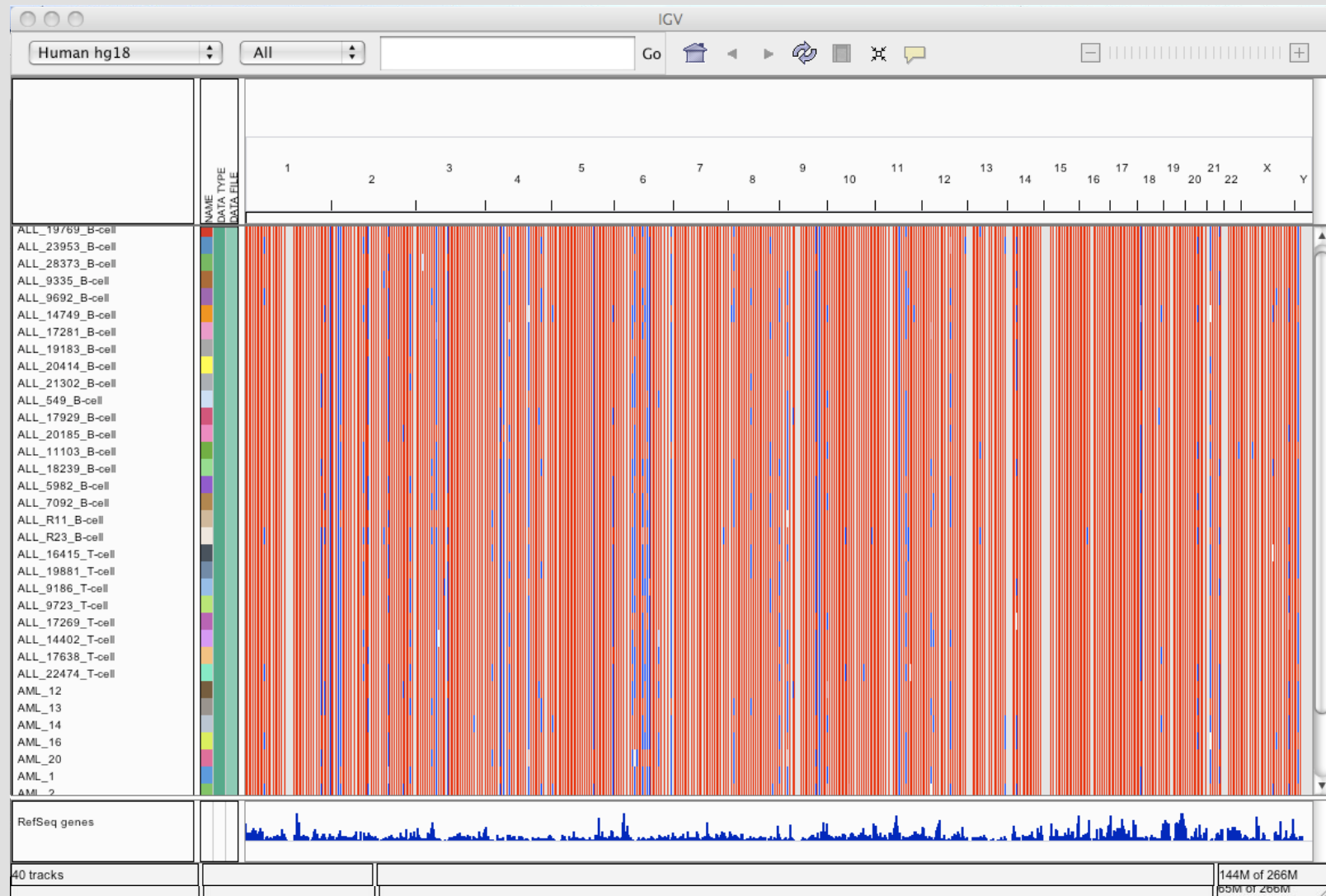
InSilicoDB UCSC Table Browser

File Launch View System Help

Directories	Filename	Owner	Size	Last Modified
Home	asdf	ted		
ted	subdirAAAAA4	ted		
GP_cytoscape_demo	subdircccc3	ted		
GSE1000GPL96_RNA_FRMAGENE_8127	testAdd2	ted		
demo	testChrome	ted		
foo	CCLE_Expression_Entrez_2010-09-29.res	ted	152.68 Mb	2 months ago
galaxy_export	HSC	ted	63 bytes	5 months ago
working dir	Regu	ted	47 Kb	5 months ago
Shared to ted	SUV	ted	38 Kb	2 months ago
Public	TF.d	ted	134 Kb	6 months ago
	TF.d	ted	1.31 Mb	4 months ago
	data	ted	20 Kb	4 months ago
	galFile	ted	1.59 Mb	2 months ago
	gene	ted	1 Kb	8 months ago
	human_interactome_cyt.cys	ted	5 bytes	5 months ago
	input_breastcancer_BN_L0_KD_blue.cys	ted	16 Kb	4 months ago
	input_breastcancer_BN_L0_KD_green.cys	ted	13 Kb	4 months ago
	searchGenes2.txt	ted	532 bytes	5 months ago
	searchGenes3.txt	ted	532 bytes	5 months ago

https://dm.genomespace.org/datamanager/file/Hom...ape_demo/CCLE_Expression_Entrez_2010-09-29.res d by the National Human Genome Research Institute (NHGRI)

GenomeSpace Tool Enablement: IGV



GenomeSpace Tool Enablement: Galaxy

The screenshot displays the Galaxy web interface. The browser window has tabs for 'Welcome to GenomeSpace' and 'Galaxy'. The address bar shows 'https://test.g2.bx.psu.edu/root'. The Galaxy logo is in the top left, and navigation links like 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Cloud', 'Help', and 'User' are in the top right. A 'Log out ted' button is also present. The left sidebar contains a 'Tools' panel with a list of tool categories. The main workspace on the right shows a file browser with a table of files.

Tools Panel (Left Sidebar):

- Get Microbial Data
- BioMart Central server
- BioMart Test server
- CBI Rice Mart rice mart
- GrameneMart Central server
- modENCODE fly server
- Flymine server**
- Flymine test server**
- modENCODE modMine server**
- YeastMine server
- metabolicMine server
- modENCODE worm server
- WormBase server
- Wormbase test server
- EuPathDB server
- EncodeDB at NHGRI
- EpiGRAPH server
- EpiGRAPH test server
- HbVar Human Hemoglobin Variants and Thalassemias
- GenomeSpace import from file browser**
- SNP Eff
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation

Main Workspace (Right):

Name	Send As	Last Modified
.. (To Parent)		
ted		
Shared to ted		
Public		

GenomeSpace Data Source Integration: InSilico DB

The screenshot displays the InSilico DB web application interface. The browser address bar shows the URL <https://insilico.ulb.ac.be/app/browse>. The application header includes the InSilico logo, the tagline "Select and export your results to analysis tools", and navigation links for "Report Bug", "Samples basket", and a user profile "michaelr@broadinstitute.org".

Filters Panel (Left):

- DataSets source:** ☒ My safe [2/2], ☒ Public [5/5]
- Curation:** ☒ Manually curated, ☒ To curate
- Platforms:** ☒ MicroArray [11/11], ☒ High Throughput Sequencing [10/10]
- Measurement type:** ☒ MicroArray [1/1], ☒ High Throughput Sequencing [2/2]
- Data pre-processing:** ☒ MicroArray [2/2], ☒ High Throughput Sequencing [2/2]

Main Content Area:

Search query eg: lung cancer | Datasets displayed 1 - 25 of 6428 | Available samples: 205263 | Page 1 of 25

Dataset	Sharing	#Samples
GEO GSE1000 Osteosarcoma TE85 cell tissue culture study [Edit/Show clinical annotation] [Download] [Export]	Public	10
GEO GSE10000 Age-dependent aorta transcriptomes [Edit/Show clinical annotation] [Download]	Public	18
GEO GSE10006 Decreased Expression of Intelectin 1 Nonsmokers [Edit/Show clinical annotation] [Download]	Public	87
GEO GSE1001 retina injury timecourse [Edit/Show clinical annotation] [Download] [Export]	Public	18
GEO GSE10011 Expression data from NIH-3T3 cells used for half-life determination [Edit/Show clinical annotation] [Download] [Export]	Public	45
GEO GSE10015 Expression data from rat tissues dosed with AMG A or AMG B [Edit/Show clinical annotation] [Download] [Export]	Public	108
GEO GSE10017 Podocytes use FcRn to clear IgG from the glomerular basement membrane [Edit/Show clinical annotation] [Download] [Export]	Public	2

Export Options Menu (Overlaid):

- ☐ Genepattern
- ☒ Genomespace
- Normalization options:**
 - ☐ Original normalization
 - ☒ fRMA normalization
- Gene/probe options:**
 - ☒ genes
 - ☐ probes

Other collaborating projects

- Cistrome (*Dana Farber Cancer Institute*)
- Reactome (*Ontario Institute for Cancer Research*)
- geWorkbench (*Columbia University*)
- Taverna/MyExperiment (*University of Manchester*)
- ArrayExpress (*European Bioinformatics Institute*)
- National Center for Biomedical Ontology (*Stanford University*)
- ISA-TOOLS (*Oxford University*)
- Archon Genomics X-Prize

DBP3: Studying the regulatory control of human hematopoiesis



Cell

Resource

Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis

Noa Novershtern,^{1,2,3,11} Aravind Subramanian,^{1,11} Lee N. Lawton,⁴ Raymond H. Mak,¹ W. Nicholas Haining,⁵ Marie E. McConkey,⁶ Naomi Habib,³ Nir Yosef,¹ Cindy Y. Chang,^{1,6} Tal Shay,¹ Garrett M. Frampton,^{2,4} Adam C.B. Drake,^{2,7} Ilya Leskov,^{2,7} Bjorn Nilsson,^{1,6} Fred Pfeffer,⁸ David Dombkowski,⁸ John W. Evans,⁵ Ted Liefeld,¹ John S. Smutko,⁹ Jianzhu Chen,^{2,7} Nir Friedman,³ Richard A. Young,^{2,4} Todd R. Golub,^{1,5,10} Aviv Regev,^{1,2,10,12,*} and Benjamin L. Ebert^{1,5,6,12,*}

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⁴Whitehead Institute for Biomedical Research, 9 Cambridge Center, Cambridge, MA 02142, USA

⁵Dana-Farber Cancer Institute, Boston, MA 02115, USA

⁶Brigham and Women's Hospital, Boston, MA 02115, USA

⁷Koch Institute for Integrative Cancer Research, Massachusetts Institute of Technology, Cambridge, MA 02139

⁸Massachusetts General Hospital, Boston, MA 02114, USA

⁹Nugen Technologies, San Carlos, CA 94070, USA

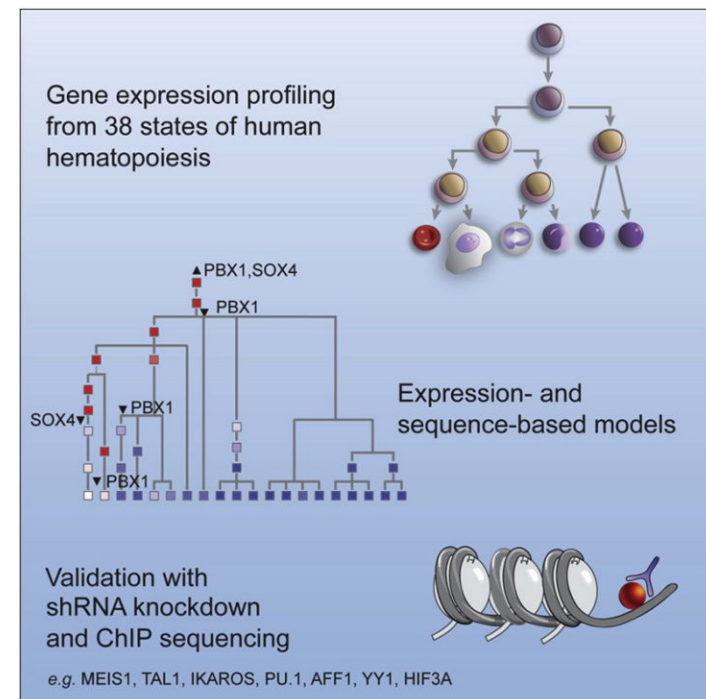
¹⁰Howard Hughes Medical Institute, Chevy Chase, MD 20815-6789, USA

¹¹These authors contributed equally to this work

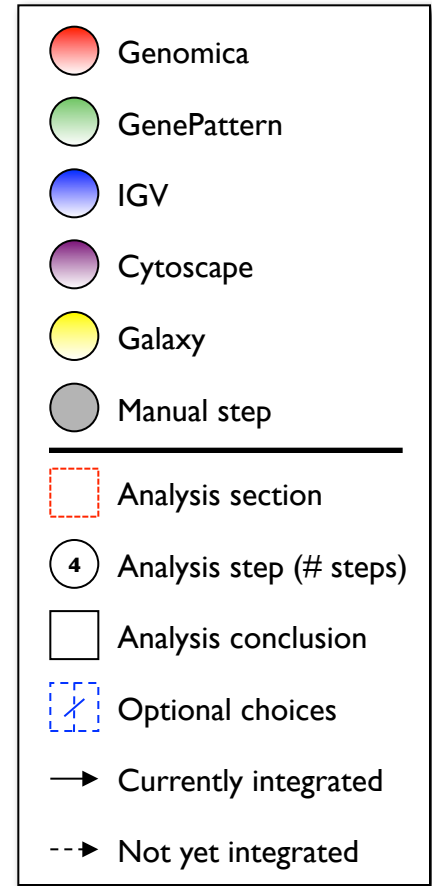
¹²These authors contributed equally to this work

*Correspondence: aregev@broad.mit.edu (A.R.), bebert@partners.org (B.L.E.)

DOI 10.1016/j.cell.2011.01.004

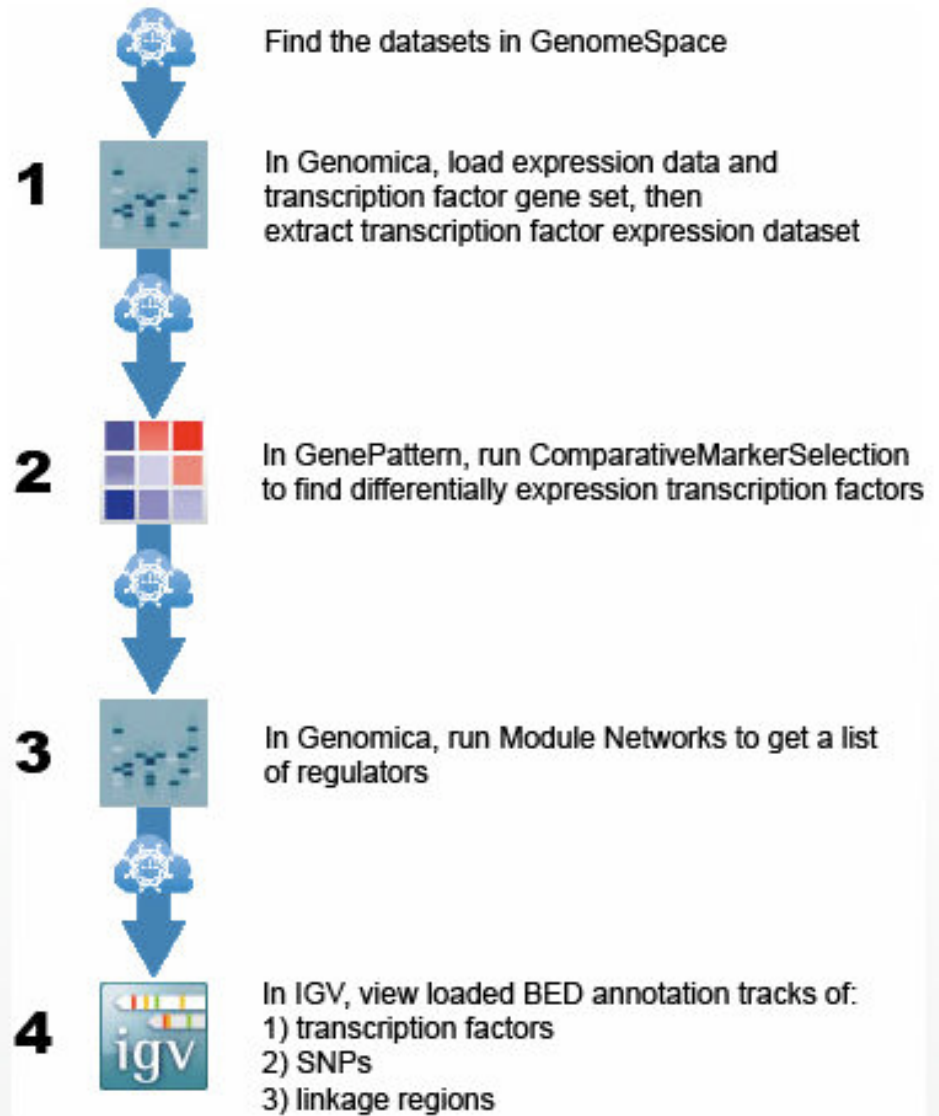
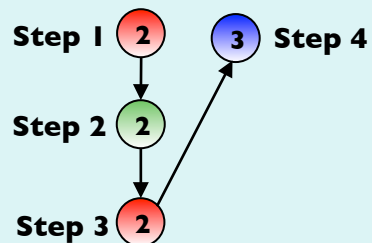


GENOMESPACE

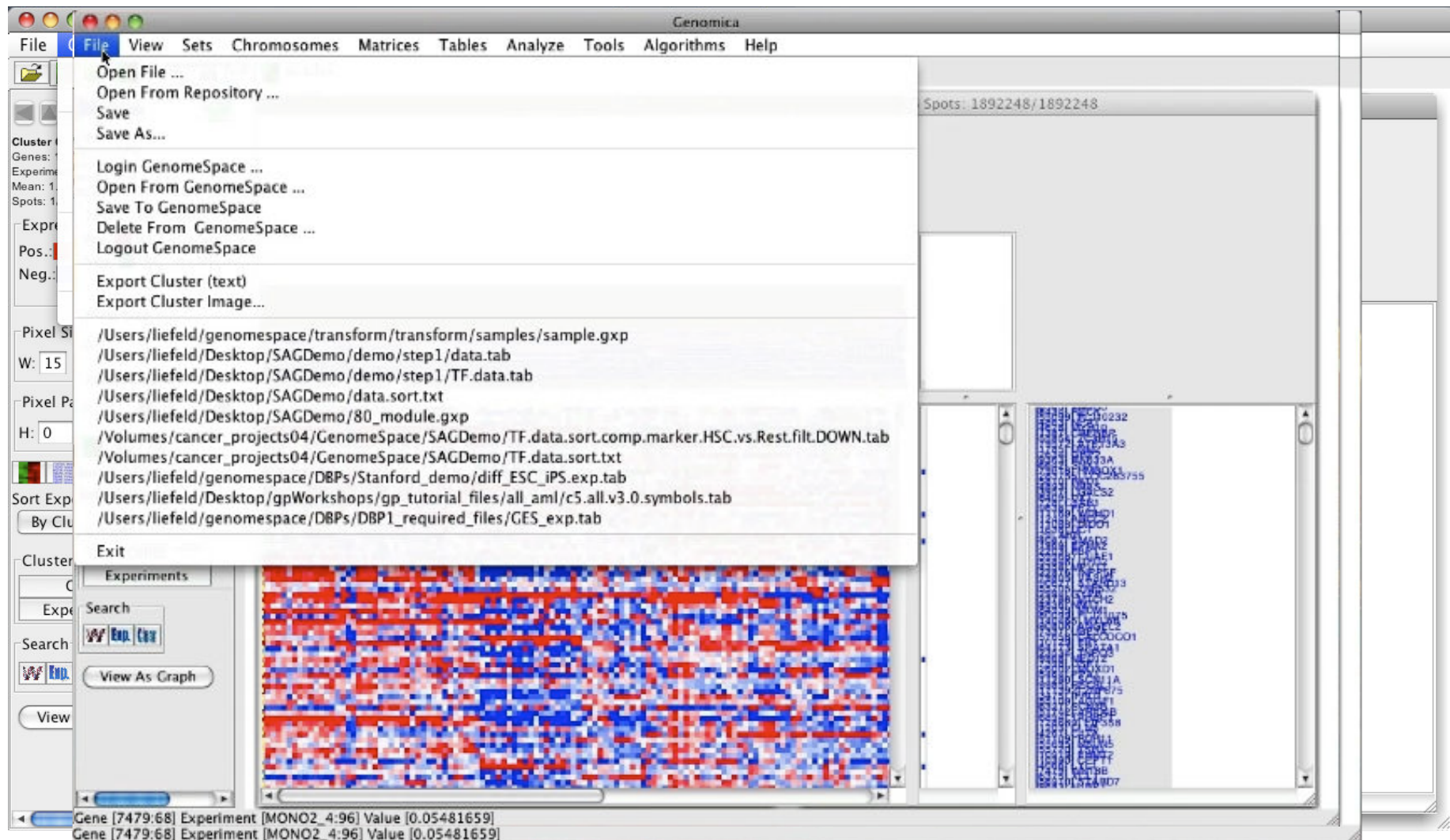


Part 5: Finding new transcription factor regulators

From part 4



Step 1: Create transcription factor dataset in Genomica and save to GenomeSpace



Step 2: Send transcription factor datasets into GenePattern

Receive GenomeSpace File

gpami.broadinstitute.org:8080/gp/pages/genomespace/receiveFile.jsf?files=https%3A%2F%2Fdm.genomesp

Wikipedia (erQ)

Receive GenomeSpace File

My Settings | Sign out mmm

Modules & Pipelines Suites Job Results Resources Downloads Administration Help GenomeSpace

GenomeSpace has sent you a file

DMAP.classes.cls

1. Save a Copy: Upload Directory Submit
2. Send to Module as cls: CART Submit

TF.data.tab *Converted to gct*

1. Save a Copy: Upload Directory Submit
2. Send to Module as tab: Submit
3. Send to Module as gct: ARACNE Submit

About GenePattern | Contact Us

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Step 2: Perform differential expression analysis in GenePattern

The screenshot displays the GenePattern web interface in a browser window. The address bar shows the URL `gpami.broadinstitute.org:8080/gp/pages/genomespace/receiveFile.jsf#`. The page title is "GenePattern - ComparativeMarkerSelection". The interface includes a navigation bar with links for "Modules & Pipelines", "Suites", "Job Results", "Resources", "Downloads", "Administration", "Help", and "GenomeSpace". A sidebar on the left lists various modules under "Recently Used", including "Annotation", "Clustering", "Data Format Conversion", "Flow Cytometry", and "Gene List Selection". The main content area shows the configuration for the "ComparativeMarkerSelection" module (version 8). The configuration includes fields for "input file*", "cls file*", "confounding variable cls file", "test direction*", "test statistic*", "min std", and "number of permutations*". The "input file*" field is set to `ispace.org/datamanager/dataformat/gct` with the "Specify URL" option selected. The "cls file*" field is set to `https://dm.genomespace.org/datamana` with the "Specify URL" option selected. The "test direction*" is set to "2 Sided" and the "test statistic*" is set to "T-Test". The "number of permutations*" is set to "1000". A "Run" button is visible. On the right, a "Recent Jobs" panel shows a list of jobs, including "shipp_lymphoma" and "step4", with details on their status and file sizes. The footer of the page contains the copyright information: "©2012 The Broad Institute of MIT and Harvard" and "Funded by the National Human Genome Research Institute (NHGRI)".

GenePattern - ComparativeMarkerSelection

gpami.broadinstitute.org:8080/gp/pages/genomespace/receiveFile.jsf#

Receive GenomeSpace File x GenePattern - ComparativeMar... x +

GenePattern My Settings | Sign out mmr

Modules & Pipelines Suites Job Results Resources Downloads Administration Help GenomeSpace

Modules & Pipelines

category suite all
open all | close all

Recently Used

- Annotation
 - GeneCruiser
- Clustering
 - ConsensusClustering
 - HierarchicalClustering
 - KMeansClustering
 - NMFConsensus
 - SOMClustering
 - SparseHierarchicalClustering
 - SubMap
- Data Format Conversion
 - BamToSam
 - BedToGtf
 - CsvToFcs
 - ExprToGct
 - FastqToSam
 - FcsToCsv
 - Fpkm_trackingToGct
 - GctToPcl
 - PclToGct
 - SamToBam
 - SamToFastq
 - TmapToGct
- Flow Cytometry
 - AddFCSEventIndex
 - AddFCSPParameter
 - AddNoiseToFCS
 - ExtractFCSDataSet
 - ExtractFCSKeywords
 - ExtractFCSParameters
 - PreviewFCS
 - SetFCSKeywords
- Gene List Selection
 - ClassNeighbors
 - ComparativeMarkerSelection
 - ExtractComparativeMarkerResults
 - GeneNeighbors
 - GSEA
 - SelectFeaturesColumns

ComparativeMarkerSelection version 8

Show parameter descriptions

* required field Run Reset properties | export | help

input file* ispace.org/datamanager/dataformat/gct Batch Parameter

Specify URL Basic Upload

The input file - .res, .gct. Note that if your data is log transformed, you will need to set the "log transformed data" parameter below to "yes".

cls file* https://dm.genomespace.org/datamana Batch Parameter

Enter a URL to the file you wish to input.

Specify URL Basic Upload

The class file - .cls

confounding variable cls file Browse...

Select a single file under 2GB to upload.

Specify URL Basic Upload

The class file containing the confounding variable.

test direction* 2 Sided

The test to perform

test statistic* T-Test

The statistic to use

min std

The minimum standard deviation if test statistic includes min std option

number of permutations* 1000

The number of permutations to perform (use 0 to calculate asymptotic p-values using the standard independent two-sample t-test)

Recent Jobs Uploads GenomeSpace

Logged in as: mmr

- mmr
 - shipp_lymphoma
 - dbol_outcome.cls Apr 23 07:48:23 PM; 1.0 KB
 - dbol_outcome.res Apr 23 07:48:23 PM; 2.8 MB
 - dbol_vs_fsc.res Apr 23 07:48:24 PM; 3.6 MB
 - dbol_vs_fsc.cls Apr 23 07:48:23 PM; 1.0 KB
 - step4
 - igv_snapshot.IRF4.png Mar 14 10:37:43 PM; 1.0 KB
 - snps.bed Mar 14 10:38:26 PM; 143.0 KB
 - Galaxy SNPsLinkageRegionsTFs.xls Mar 14 10:37:26 PM; 1.0 KB
 - linkage_regions.bed Mar 14 10:36:39 PM; 147.0 KB
 - RefSeq_Hg17.TFs.GS.bed Mar 14 10:38:11 PM; 28.0 KB
 - step2
 - TF.data.txt Mar 14 10:30:12 PM; 1.3 MB
 - TF.data.tab Apr 25 12:34:40 PM; 1.3 MB
 - TF.data.comp.marker.HSC vs. Rest.f Mar 14 10:29:21 PM; 619.0 KB
 - TF.data.comp.marker.HSC vs. Rest.f Mar 14 10:29:05 PM; 2.0 KB
 - TF.data.comp.marker.HSC vs. Rest.c Mar 14 10:29:38 PM; 126.0 KB
 - DMAP.classes.cls Mar 14 10:30:28 PM; 1.0 KB
 - TF.data.gct Mar 14 10:29:55 PM; 1.3 MB
 - genomics_output

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Step 3: Send differentially expressed genes to Genomica

The screenshot shows the GenePattern web interface in a browser window. The address bar displays `gpami.broadinstitute.org:8080/gp/pages/index.jsf`. The page has a navigation bar with tabs for Modules & Pipelines, Suites, Job Results, Resources, Downloads, Administration, Help, and GenomeSpace. On the left, a sidebar lists various modules under categories like Recently Used, Annotation, Clustering, Data Format Conversion, Flow Cytometry, and Gene List Selection. The main content area is titled 'Welcome to GenePattern' and 'Analyzing genomic data in GenePattern', with a section 'what do you want to do?' providing links to protocols for running analyses. On the right, a 'Recent Jobs' panel lists various analysis jobs. A red rectangle highlights the 'Send to Genomica as gxp' option in the 'Recent Jobs' panel.

GenePattern

gpami.broadinstitute.org:8080/gp/pages/index.jsf

Welcome to GenomeSpace

GenePattern

Modules & Pipelines Suites Job Results Resources Downloads Administration Help GenomeSpace

Modules & Pipelines

category suite all

open all | close all

Recently Used

- ComparativeMarkerSelection

Annotation

- GeneCruiser

Clustering

- ConsensusClustering
- HierarchicalClustering
- KMeansClustering
- NMFConsensus
- SOMClustering
- SparseHierarchicalClustering
- SubMap

Data Format Conversion

- BamToSam
- BedToGtf
- CsvToFcs
- ExprToGct
- FastqToSam
- FcsToCsv
- Fpkms_trackingToGct
- GctToPcl
- PclToGct
- SamToBam
- SamToFastq
- TmapToGct

Flow Cytometry

- AddFCSEventIndex
- AddFCSParameter
- AddNoiseToFCS
- ExtractFCSDataSet
- ExtractFCSKeywords
- ExtractFCSParameters
- PreviewFCS
- SetFCSKeywords

Gene List Selection

- ClassNeighbors
- ComparativeMarkerSelection
- ExtractComparativeMarkerResults
- GeneNeighbors
- GSEA
- SelectFeaturesColumns
- SelectFeaturesRows

Welcome to GenePattern

Analyzing genomic data in GenePattern

what do you want to do?

- Click a **protocol** to run an analysis. GenePattern guides you step by step.
- Click **Quick Start** for instructions on how to run any module in GenePattern.

Protocols for running common analyses in GenePattern:

Run an Analysis in GenePattern
Learn how to run an analysis in GenePattern by preprocessing gene expression data and visualizing the resulting data as a heat map.

Differential Expression Analysis
Find genes that are significantly differentially expressed between classes of samples.

Clustering
Group genes and/or samples by similar expression profiles.

Prediction
Create a model, also referred to as a classifier or class predictor, that correctly classifies unlabeled samples into known classes.

SNP Copy Number and Loss of Heterozygosity Estimation
Compute SNP copy number (CN) and loss of heterozygosity (LOH) based on Affymetrix SNP chip data for paired target/normal samples.

See also:

<http://gpami.broadinstitute.org:8080/gp/pages/index.jsf#>

Recent Jobs

Up

Delete

Save

Send to Genomica as gxp

Send to IGV as gct

Send to Galaxy as gct

Sent by GenomeSpace as gct

ARACNE

CART

CARTXValidation

CisFileCreator

CollapseDataset

ComparativeMarkerSelection

ComparativeMarkerSelectionViewer

ConsensusClustering

ConvertToMAGETAB

CytoscapeViewer

ExtractComparativeMarkerResults

ExtractRowNames

GctToPcl

GeneCruiser

GeneNeighbors

GSEA

HeatMapImage

HeatMapView

HierarchicalClustering

IGV

ImputeMissingValues.KNN

KMeansClustering

KNN

KNNXValidation

MergeColumns

MergeRows

MetageneProjection

MINDY

MINDYViewer

MultiplotPreprocess

NMF

Step 3: perform module network analysis in Genomica



Step 4: Visualize regulators with known SNPs and linkage regions

Welcome to GenomeSpace

https://gsui.genomespace.org/jsui/gsui.html#

Wikipedia (en)

Logout mmr

Tools

IGV Genomica GenePattern Galaxy Cytoscape

Data Sources

UCSC Table Browser InSilicoDB

Send to: --select tool-- Launch Download Sharing Delete

Directories

- mmr
 - all_aml
 - genomica_output
 - shipp_lymphoma
 - step1
 - step2
 - step3
 - step4**

Filename

- ☐ Galaxy
- ☒ RefSeq
- ☐ igv_snp
- ☒ linkage
- ☒ snps.be

Launch IGV

Currently Selected Files

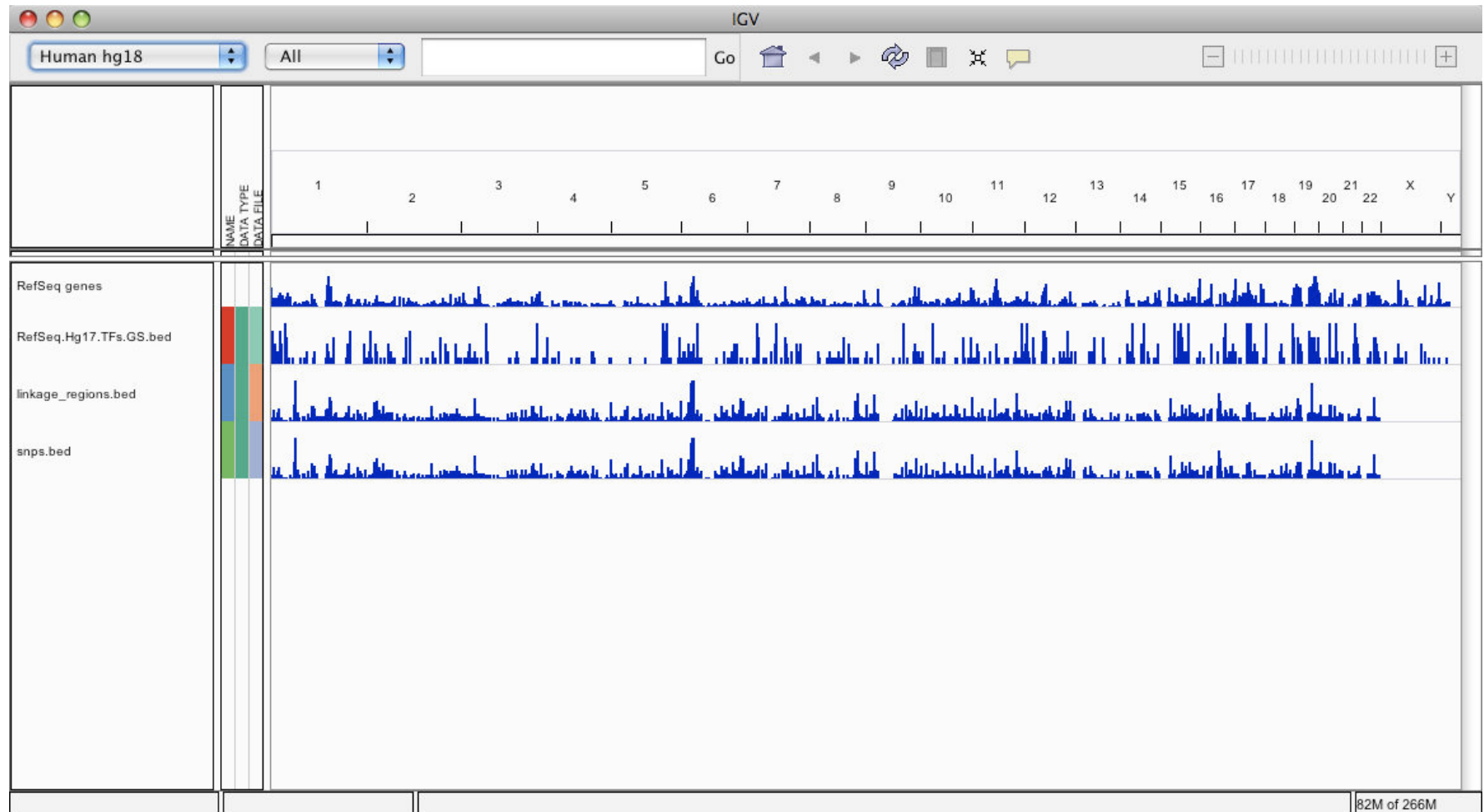
- /step4/RefSeq.Hg17.TFs.GS.bed
- /step4/linkage_regions.bed
- /step4/snps.bed

Drop files here

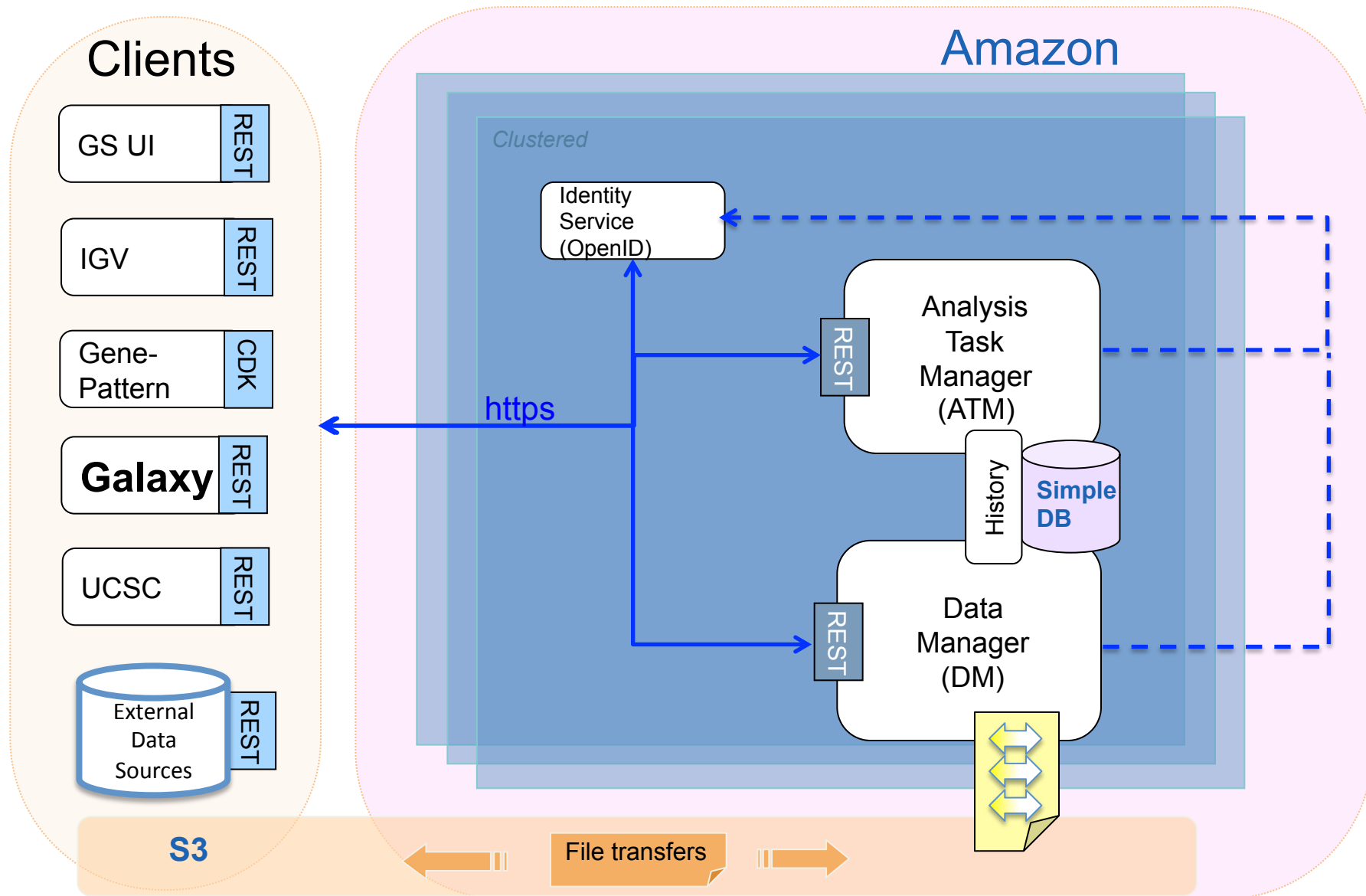
Launch Close

	Owner	Size	Last Modified
	mmr	8 bytes	2 months ago
	mmr	27 Kb	2 months ago
	mmr	8 bytes	2 months ago
	mmr	147 Kb	2 months ago
	mmr	143 Kb	2 months ago

Step 4: Visualize regulators with known SNPs and linkage regions



GenomeSpace Architecture



Adding it to your Galaxy

<http://wiki.g2.bx.psu.edu/GenomeSpace>

1. Pull the changesets
2. Add GenomeSpace to your toolbox
3. Enable OpenID in your config file
4. Restart





Join the GenomeSpace community

We're looking for

- ✓ Researchers with driving biological projects
- ✓ Developers & Data providers
 - Add your tools
 - Contribute format converters
 - Build new infrastructure

Acknowledgements

GenomeSpace Collaborators

Cytoscape: Trey Ideker Lab, UCSD

Galaxy: Anton Nekrutenko Lab, Penn State University

Genomica: Eran Segal Lab, Weizmann Institute

UCSC Browser Team

GenePattern Team

IGV Team

Driving Biological Projects

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Questions?