

REFINERY PLATFORM

**Integrating Visualization *and*
Analysis of Large-Scale
Biological Data**

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Harvard Medical School
Center for Biomedical Informatics

Broad Institute of MIT and Harvard
Cancer Program

REFINERY PLATFORM

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Department of Biostatistics *Winston Hide*



Funded in part by

Agilent Technologies

TCGA

The Cancer Genome Atlas

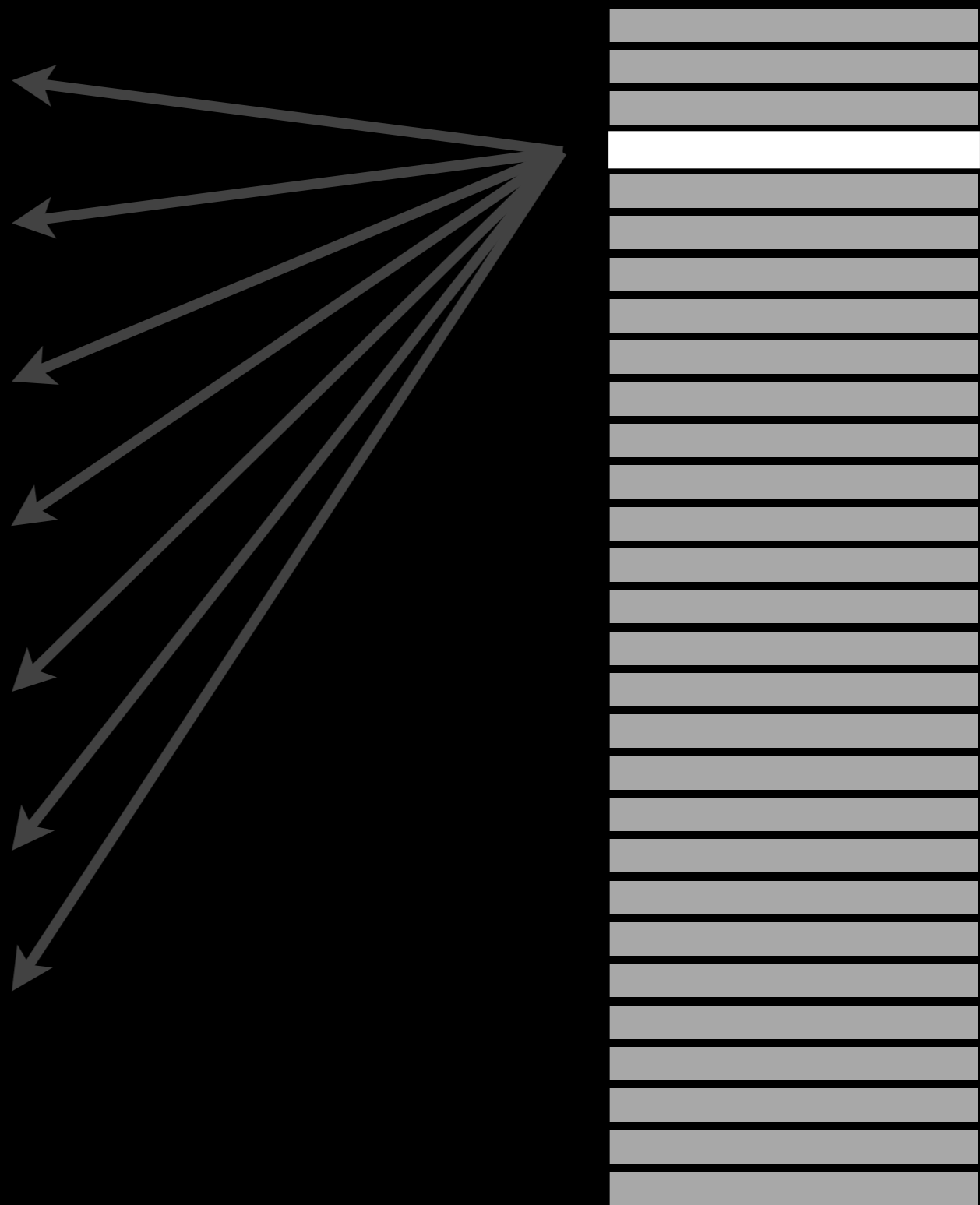
20 cancer types

×

500 patients

10,000 patients

mRNA expression
microRNA expression
DNA methylation
protein expression
copy number variants
mutation calls
clinical parameters



mRNA expression

microRNA expression

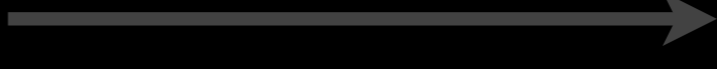
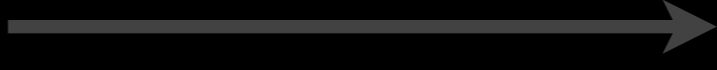
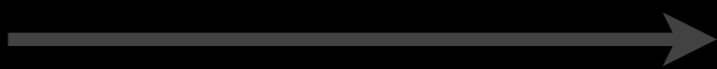
DNA methylation

protein expression

copy number variants

mutation calls

clinical parameters



ARTICLE doi:10.1038/nature11412

Comprehensive molecular portraits of human breast tumours

The Cancer Genome Atlas Network*

We analysed primary breast cancers by genomic DNA copy number arrays, DNA methylation, exome sequencing, messenger RNA arrays, microRNA sequencing and reverse-phase protein arrays. Our ability to integrate information across platforms provided key insights into previously defined gene expression subtypes and demonstrated the existence of four main breast cancer classes when combining data from five platforms, each of which shows significant molecular heterogeneity. Somatic mutations in only three genes (TP53, PIK3CA and GATA3) occurred at >10% incidence across all breast cancers; however, there were numerous subtype-associated and novel gene mutations including the enrichment of specific mutations in GATA3, PIK3CA and MAP3K1 with the luminal A subtype. We identified two novel protein-expression-defined subgroups, possibly produced by stromal/microenvironmental elements, and integrated analyses identified specific signalling pathways dominant in each molecular subtype including a HER2/phosphorylated HER2/EGFR/phosphorylated EGFR signature within the HER2-enriched expression subtype. Comparison of basal-like breast tumours with high-grade serous ovarian tumours showed many molecular commonalities, indicating a related aetiology and similar therapeutic opportunities. The biological finding of the four main breast cancer subtypes caused by different subsets of genetic and epigenetic abnormalities raises the hypothesis that much of the clinically observable

ARTICLE doi:10.1038/nature11192

Comprehensive molecular characterization of human colon and rectal cancer

The Cancer Genome Atlas Network*

To characterize somatic alterations in colorectal carcinomas, we conducted a genome-scale analysis of 276 samples, analysing exome sequences, DNA copy number, promoter methylation and messenger RNA and microRNA expression. A subset of these samples (97) underwent low-depth-of-coverage whole-genome sequencing. In total, 16% of colorectal carcinomas were found to be hypermutated; three quarters of these had the expected high microsatellite instability, usually with hypermethylation and MMR silencing, and one-quarter had somatic mismatch repair gene and polymerase ϵ (POLD1) mutations. Excluding the hypermutated cancers, colon and rectum cancers were found to have considerably similar patterns of genomic alteration. Twenty-four genes were significantly mutated, and in addition to the expected APC, TP53, SMAD4, PIK3CA and KRAS mutations, we found frequent mutations in ARID1A, SOX9 and FAM123B. Recurrent copy number alterations include potentially drug-targetable amplifications of ZNF217 and each chromosome 8 and 12. Recurrent chromosomal translocations were observed in 16% of 107

Vol 457, 23 October 2008 | doi:10.1038/nature07386

ARTICLES

Comprehensive genomic characterization defines human glioblastoma genes and core pathways

The Cancer Genome Atlas Research Network*

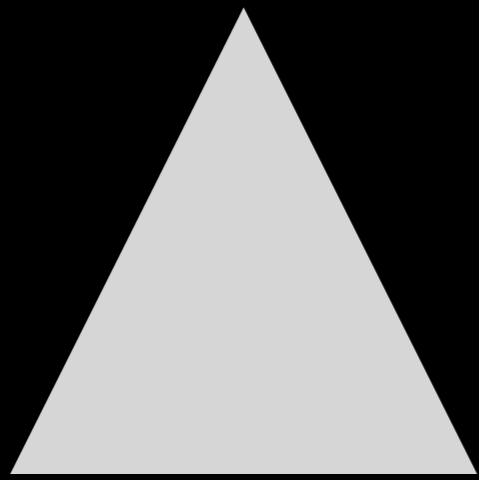
Human cancer cells typically harbour multiple chromosomal aberrations, nucleotide substitutions and epigenetic modifications that drive malignant transformation. The Cancer Genome Atlas (TCGA) pilot project aims to assess the value of large-scale multi-dimensional analysis of these molecular characteristics in human cancer and to provide the data rapidly to the research community. Here we report the interim integrative analysis of DNA copy number, gene expression and DNA methylation alterations in 206 glioblastomas—the most common type of primary adult brain cancer—and nucleotide sequence alterations in 91 of the 206 glioblastomas. This analysis provides new insights into the roles of ERBB2, NF1 and

ARTICLE doi:10.1038/nature10166

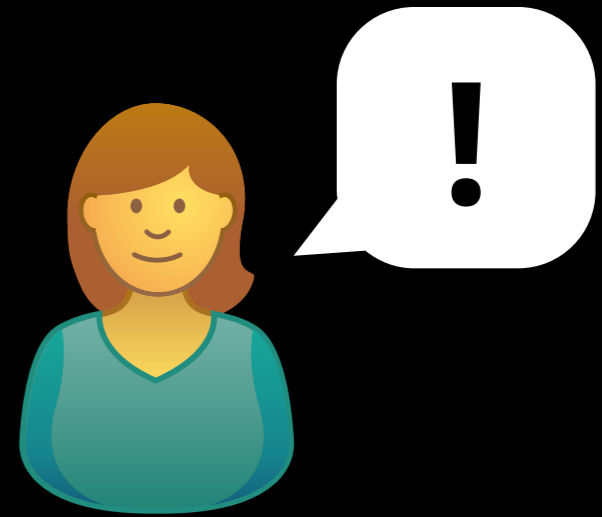
Integrated genomic analyses of ovarian carcinoma

The Cancer Genome Atlas Research Network*

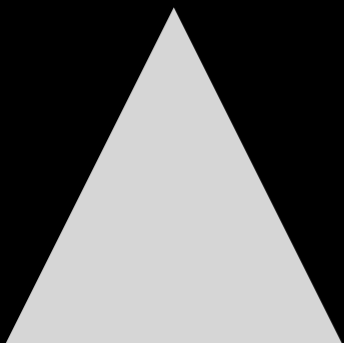
A catalogue of molecular alterations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 216 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic mutations in nine further genes including NF1, BRCA1, BRCA2, ERB and CTN21; 111 significant focal DNA copy number alterations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and/or CTN21 alterations, have on survival. Pathway analyses suggested that



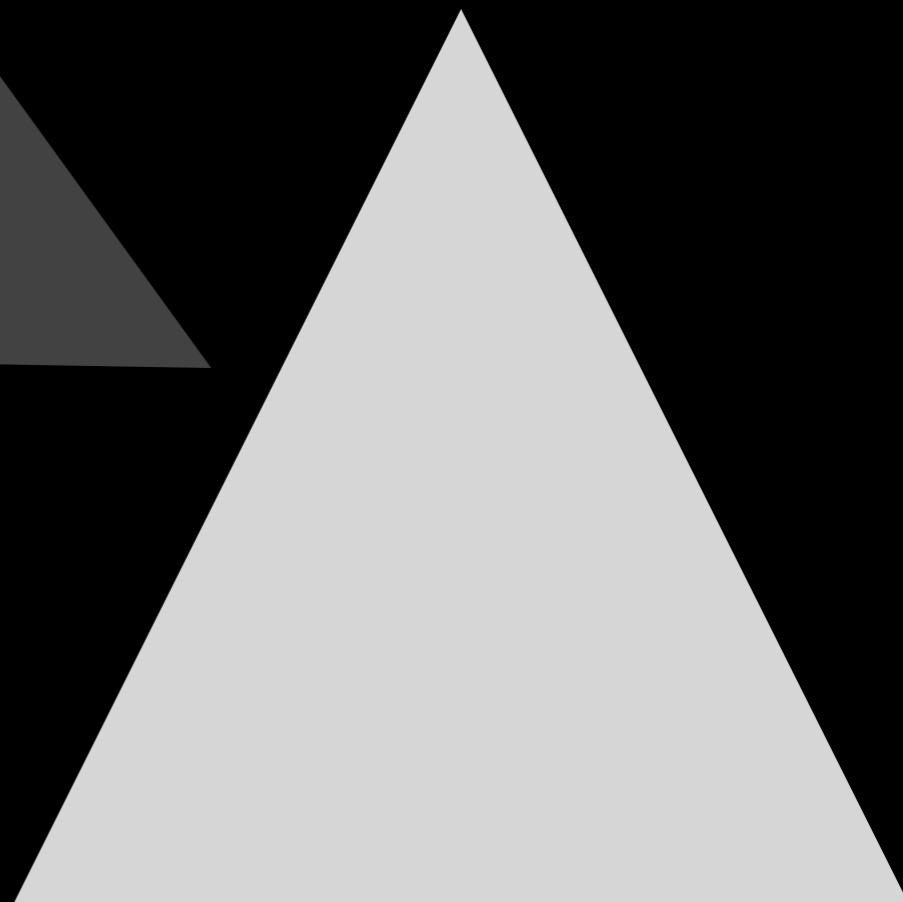
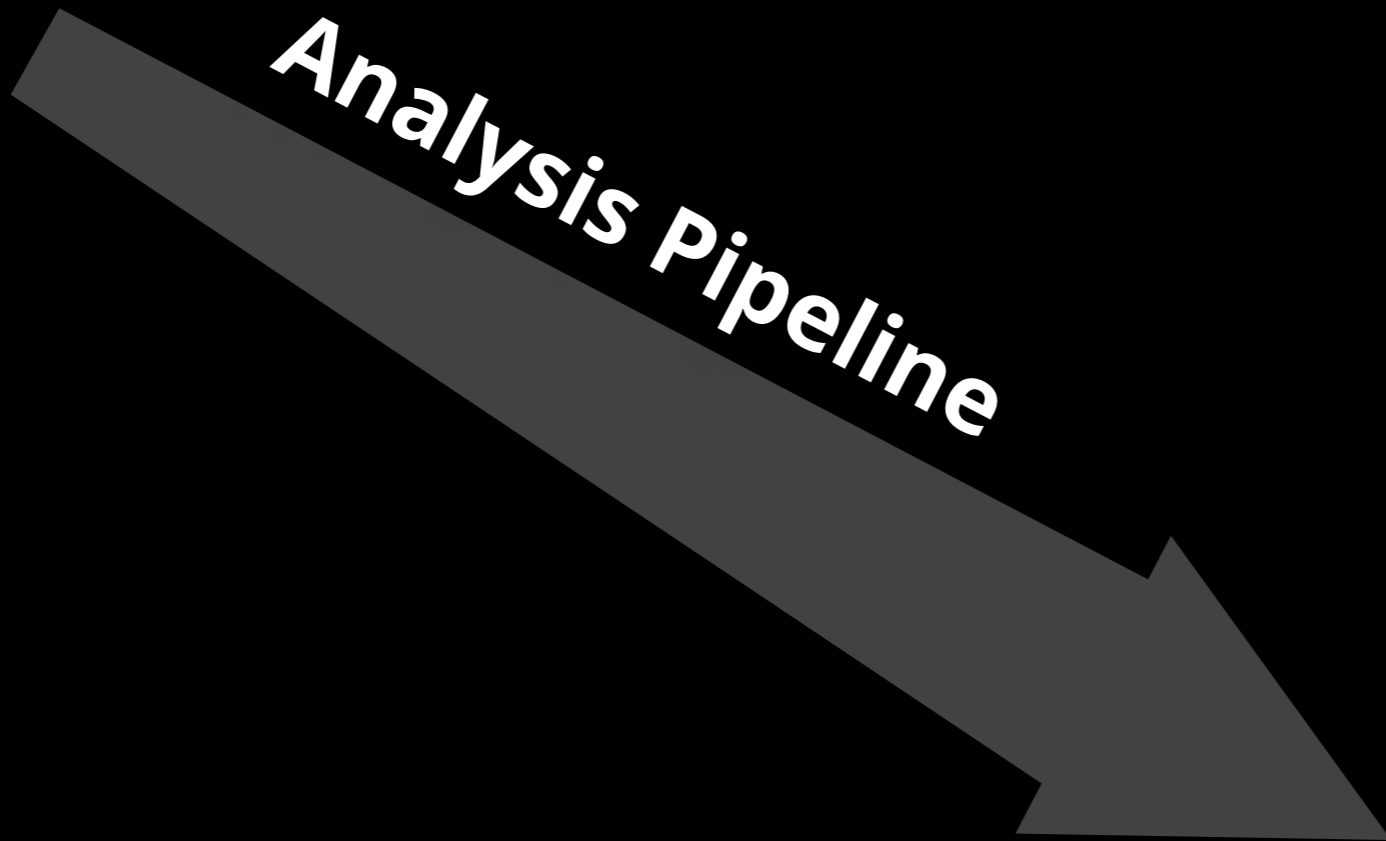
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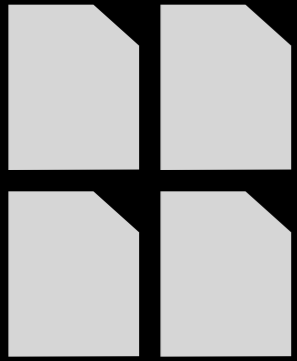


Insight

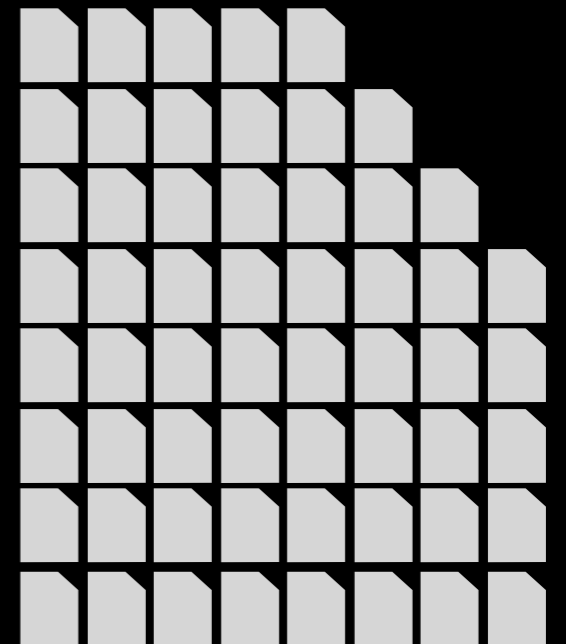


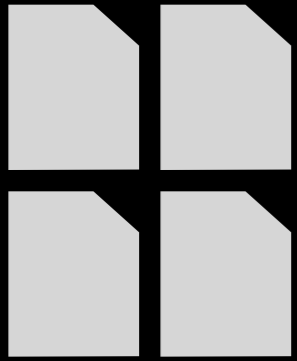
Analysis Pipeline



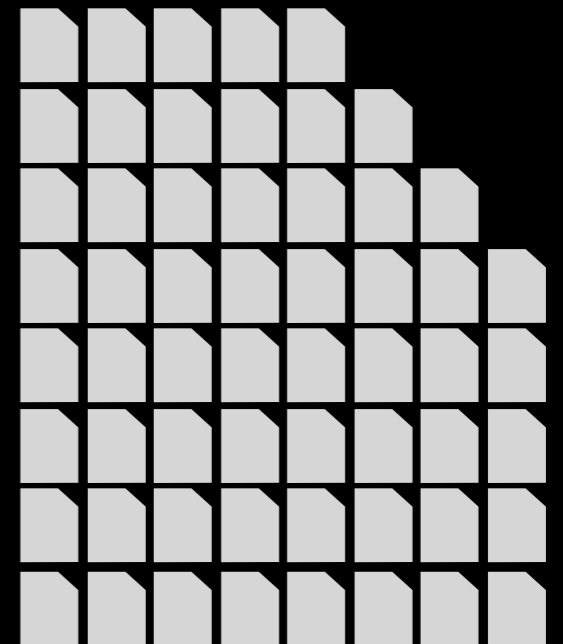


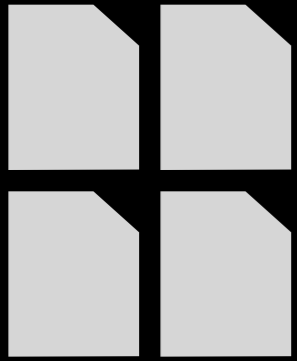
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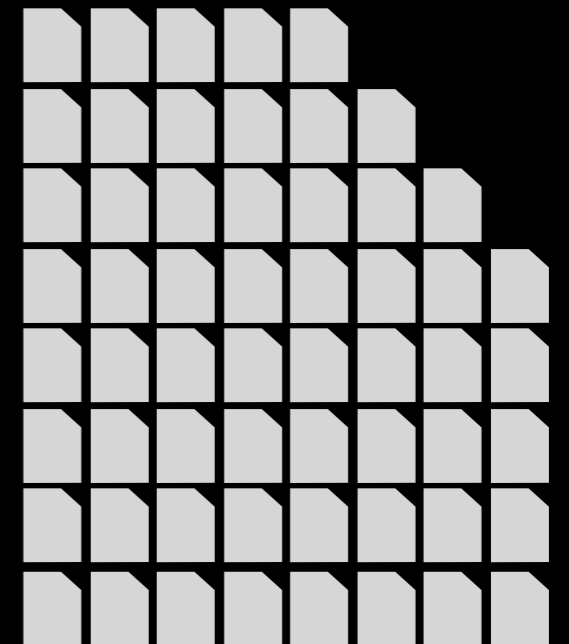
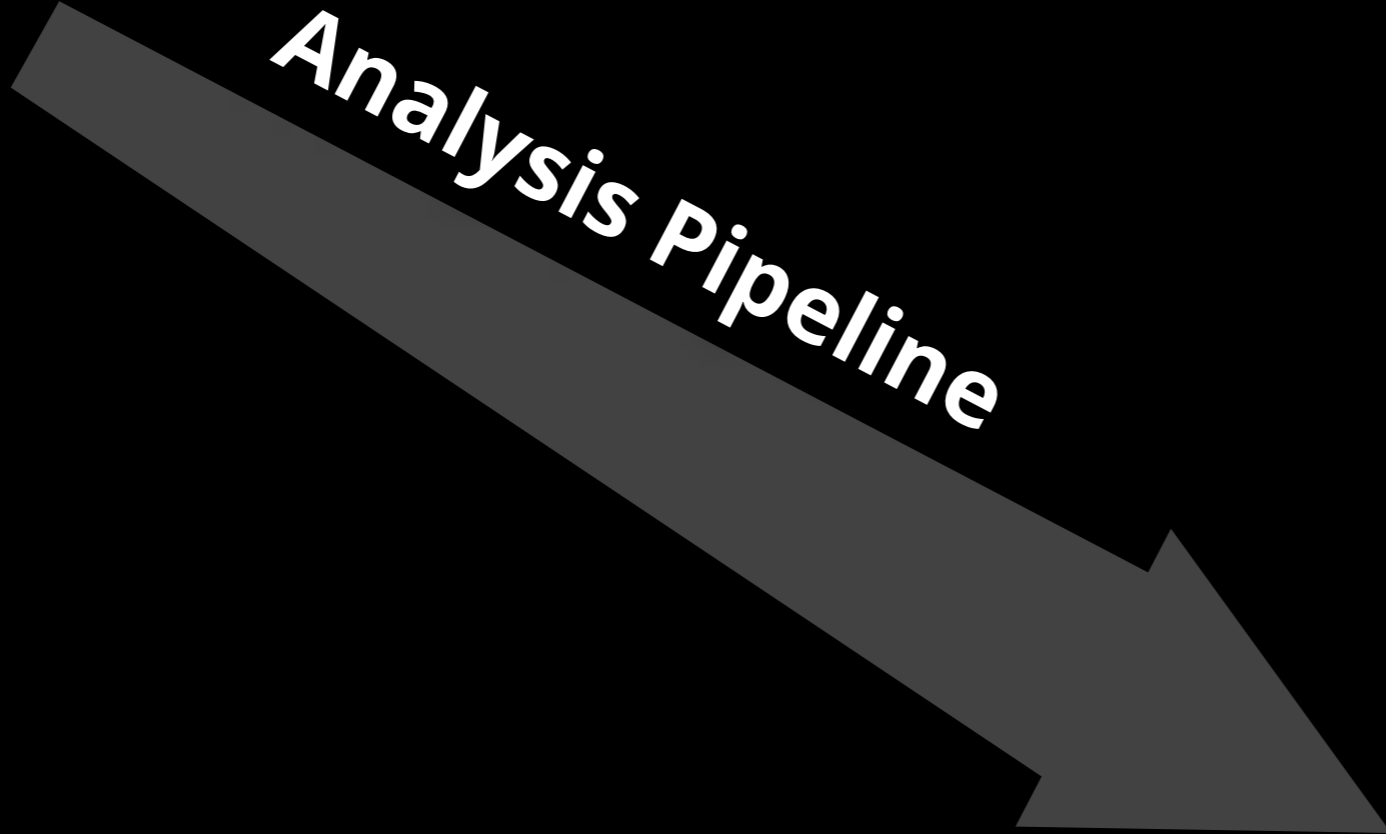


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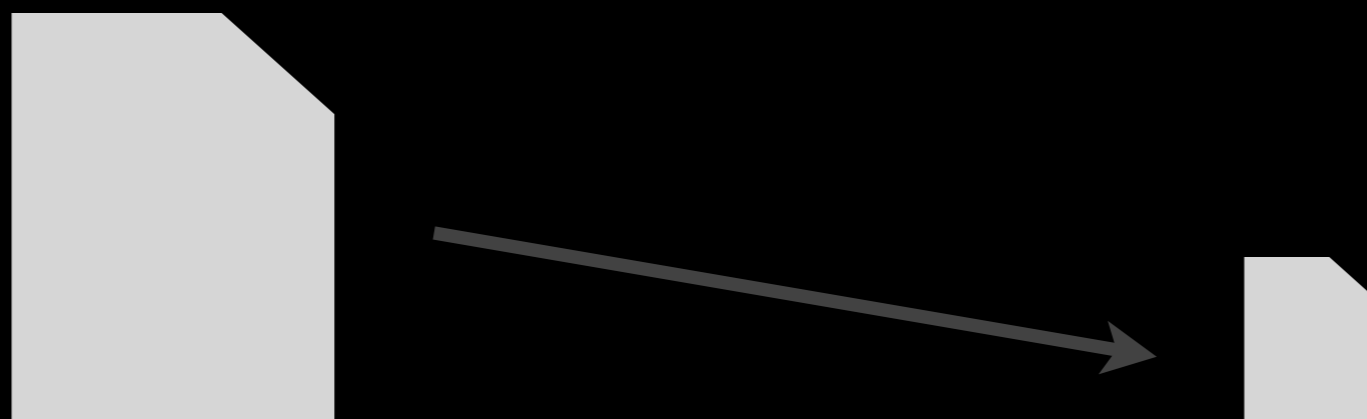


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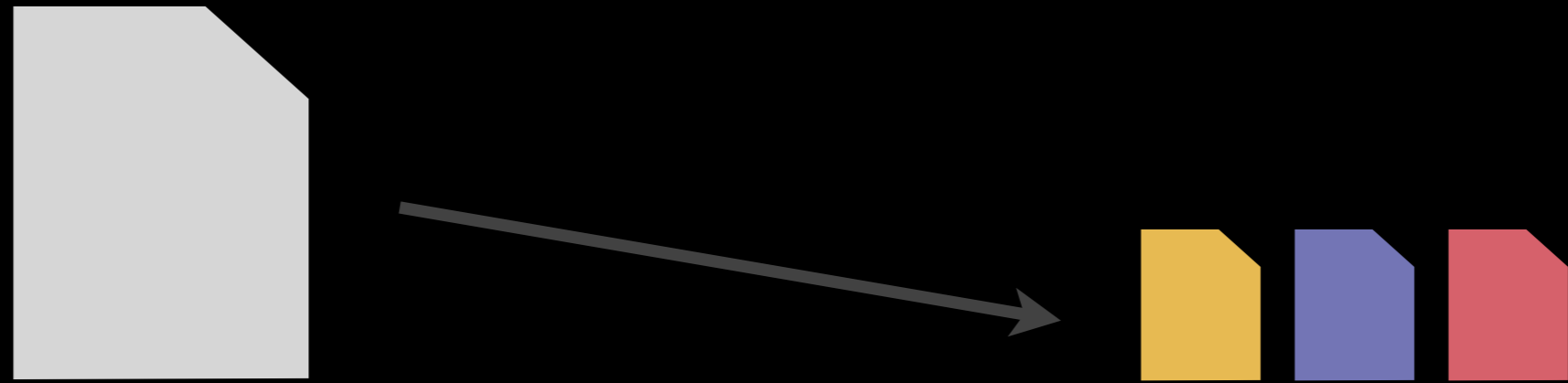


Multiple Steps

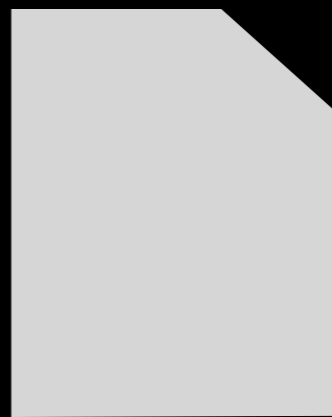
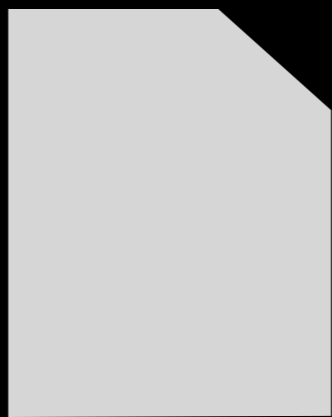
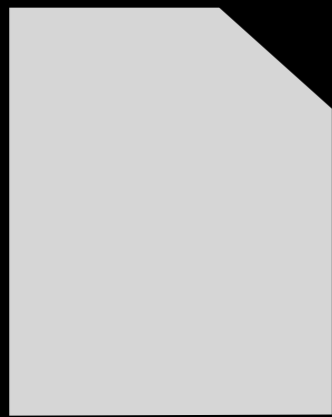
Long Runtime

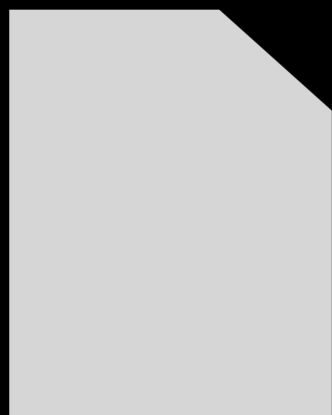
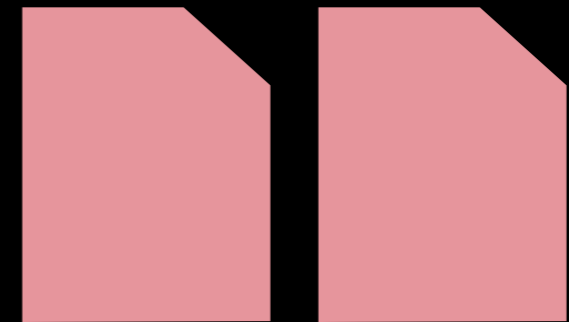
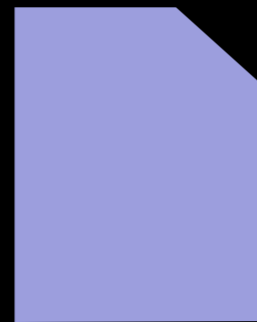
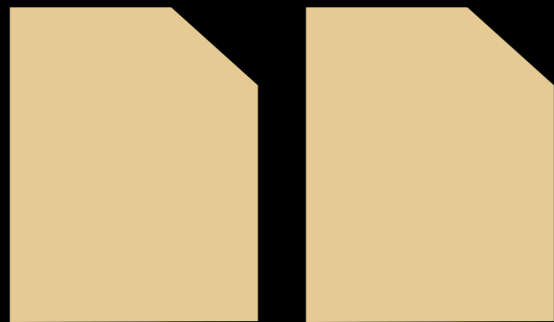
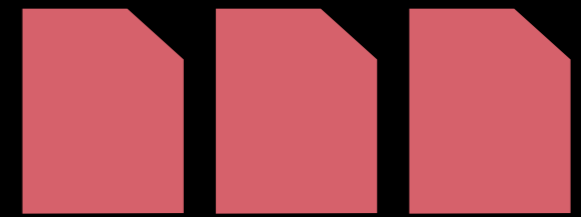
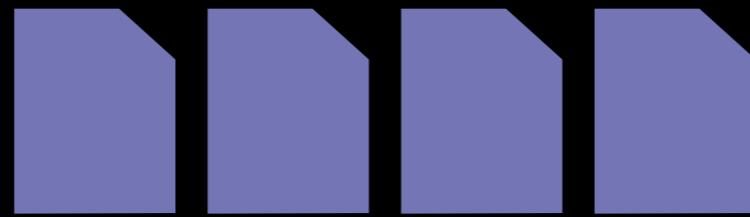
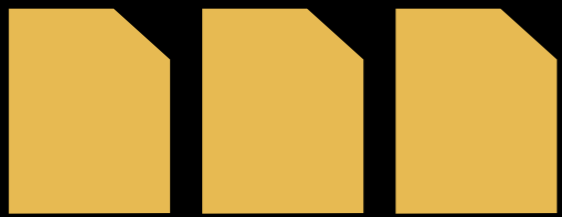
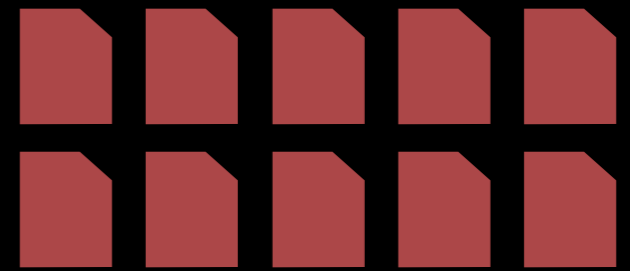
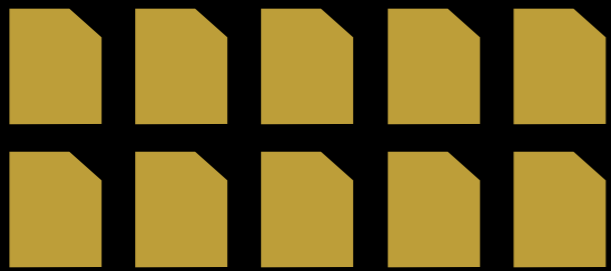


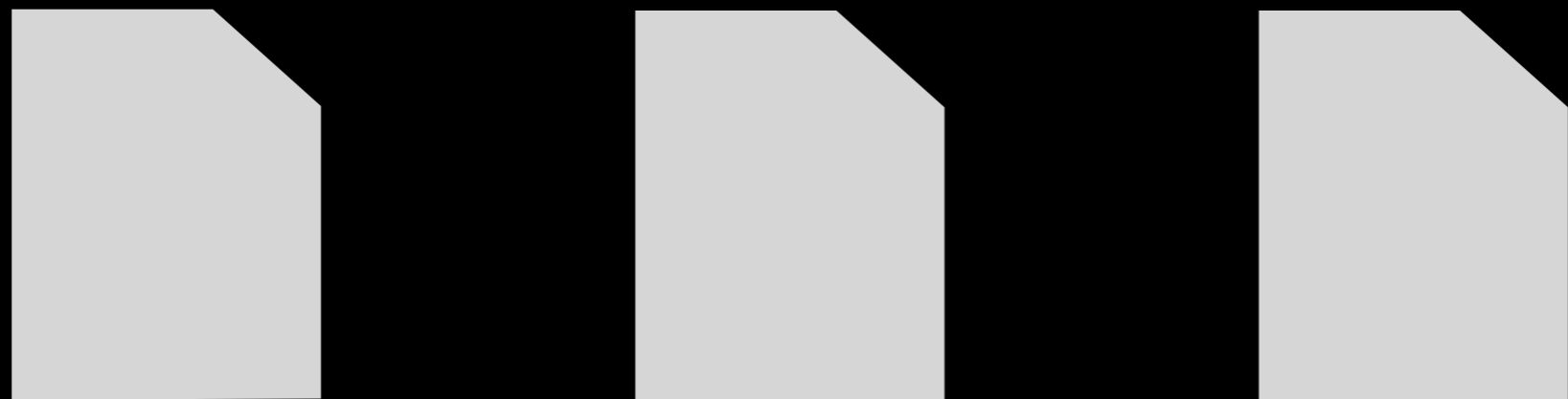
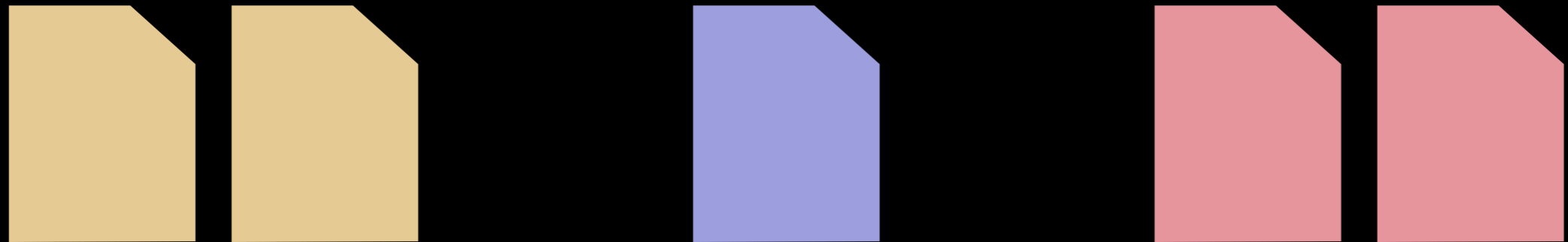
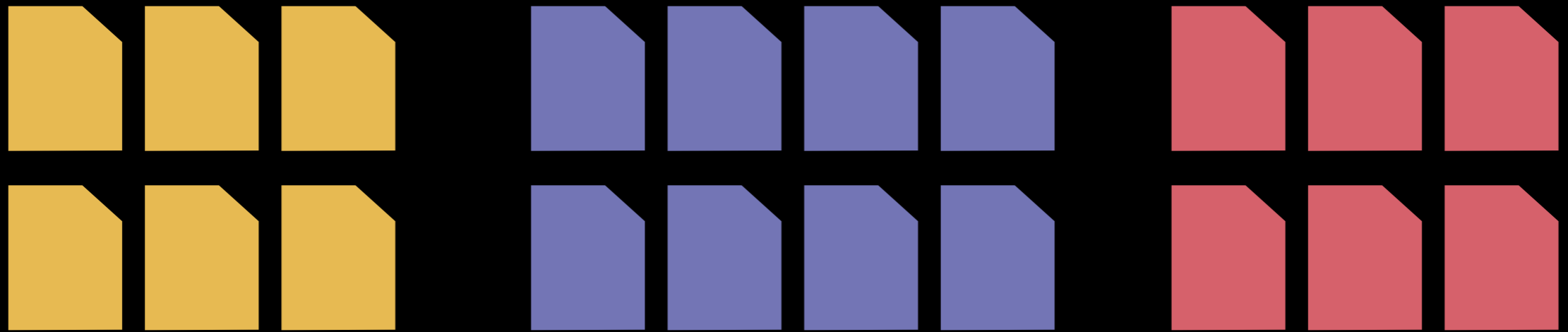
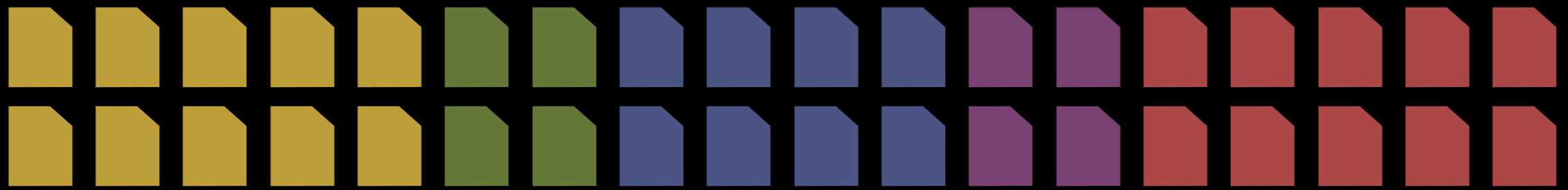
Decreasing Size



Increasing Heterogeneity









INTEGRATION

INTEGRATION



Horizontal Integration across Data Types

Biological Insight



Vertical Integration across Data Levels

Confirmation & Troubleshooting

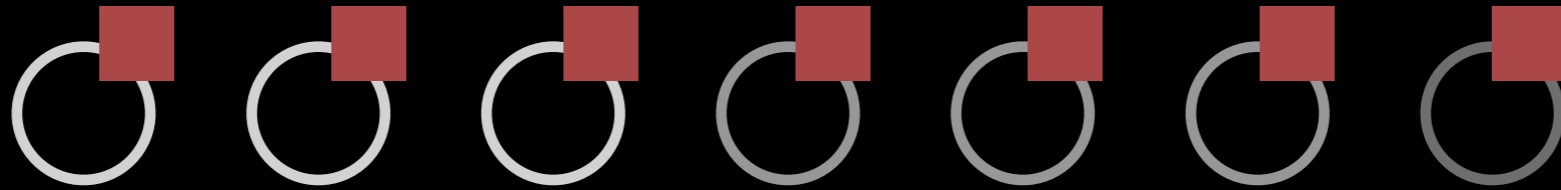
REFINERY PLATFORM





Repository

Meta data annotation





Repository

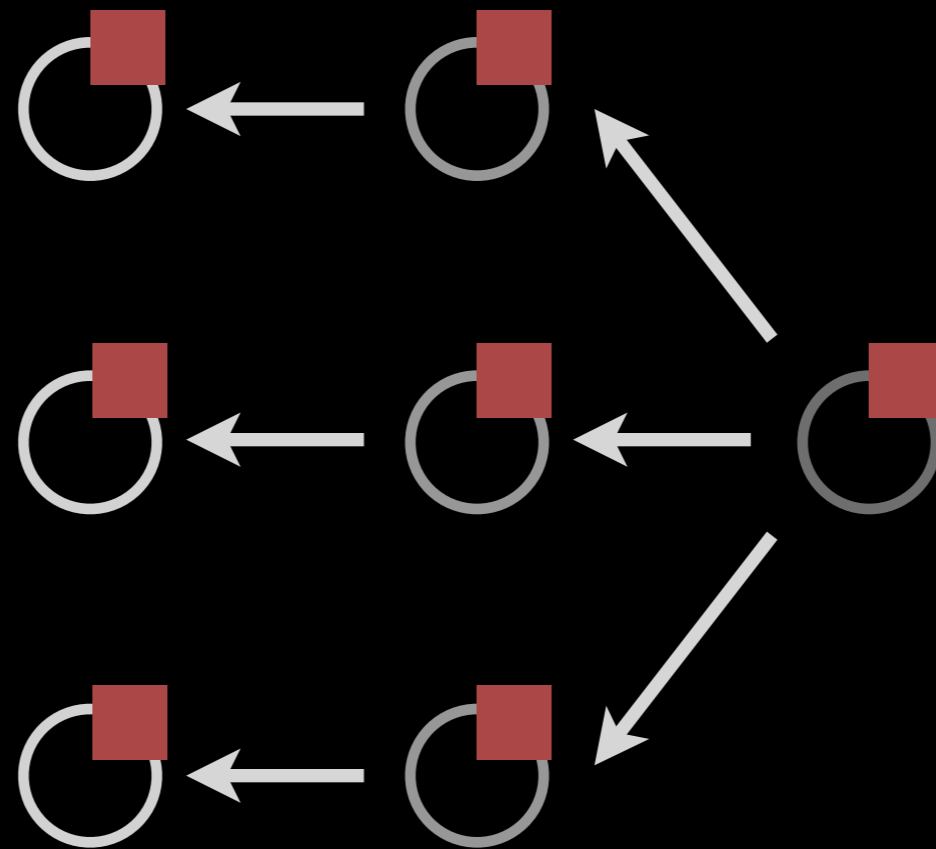
Meta data annotation





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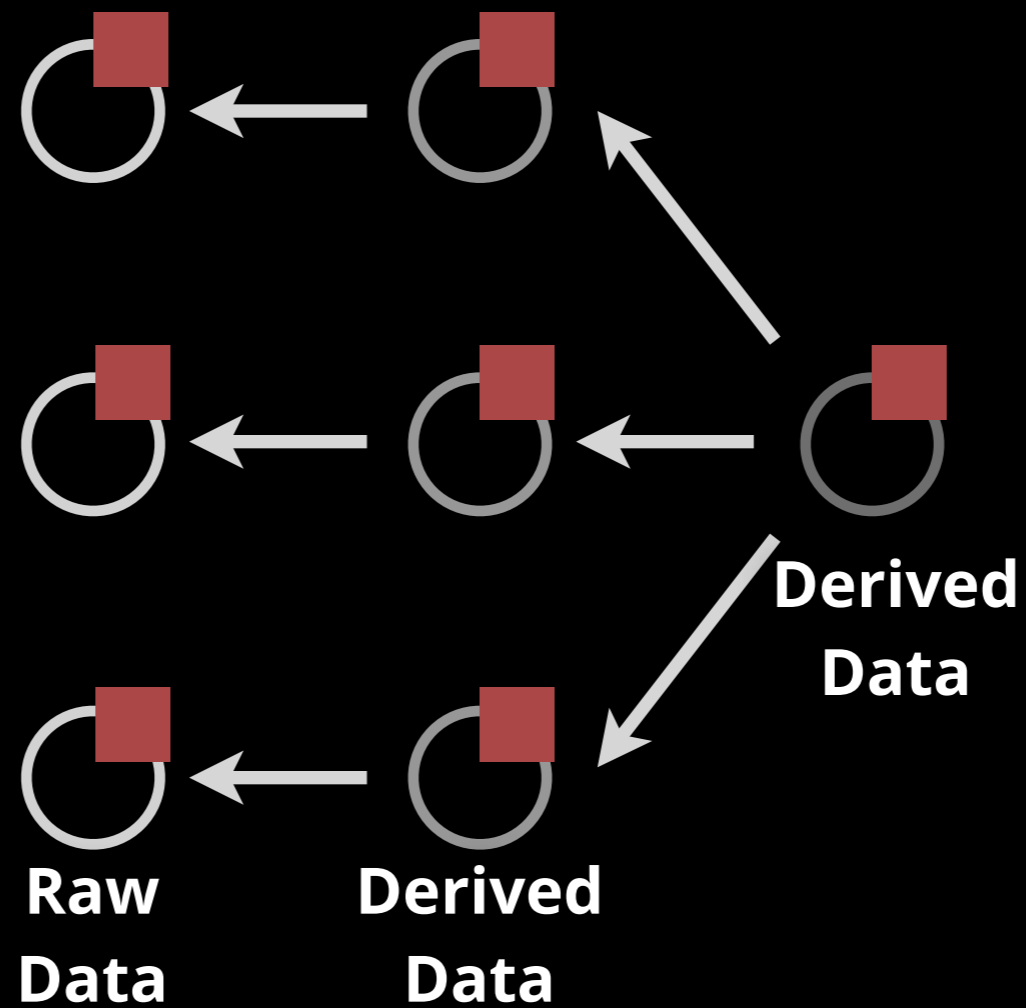
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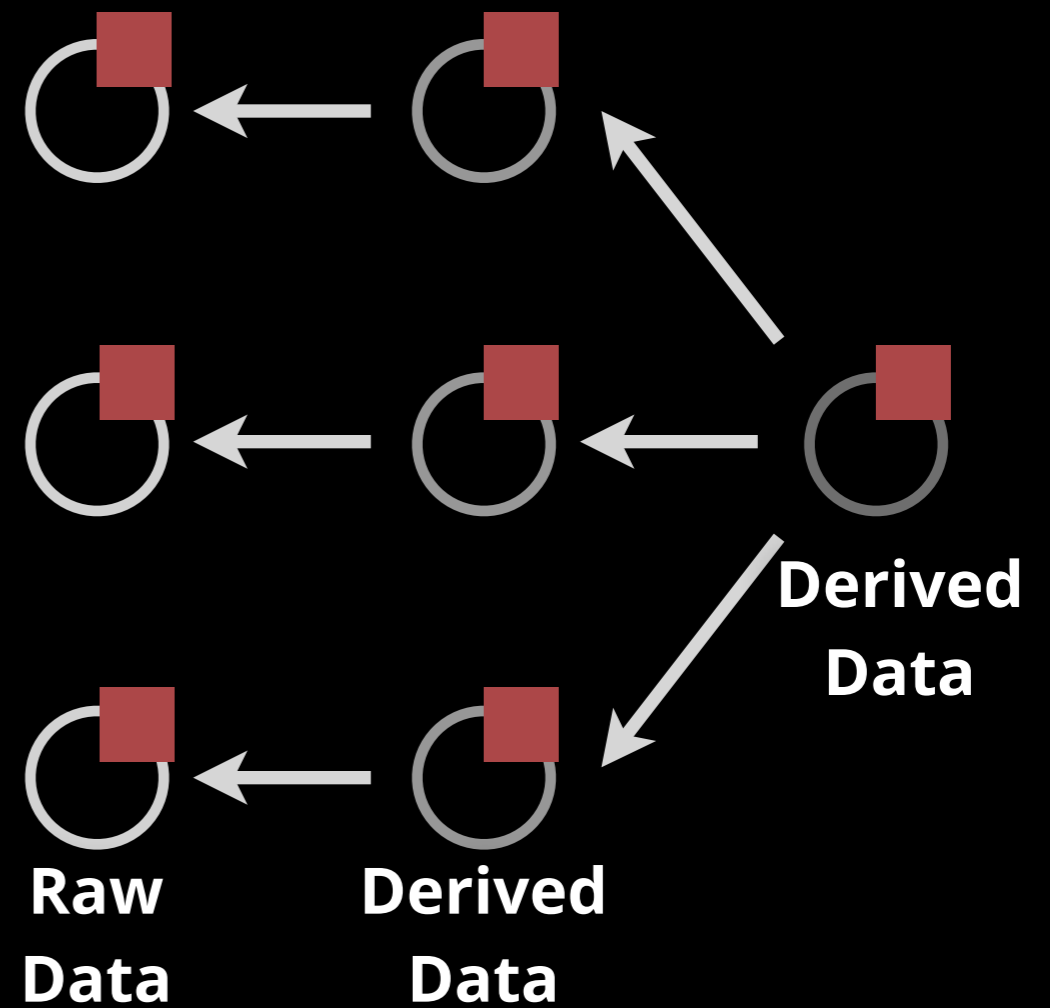
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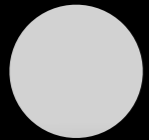
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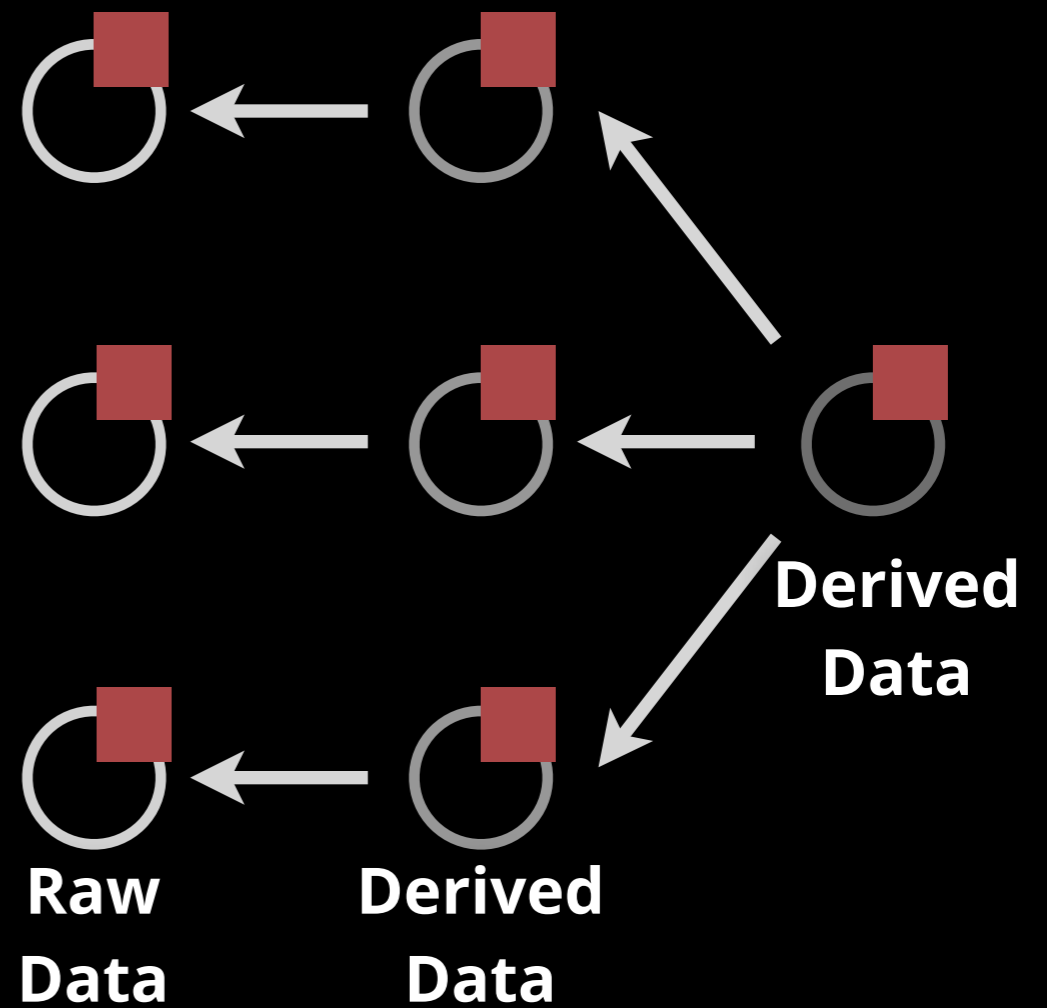


Repository

Meta data annotation



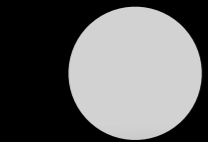
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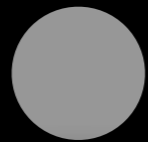


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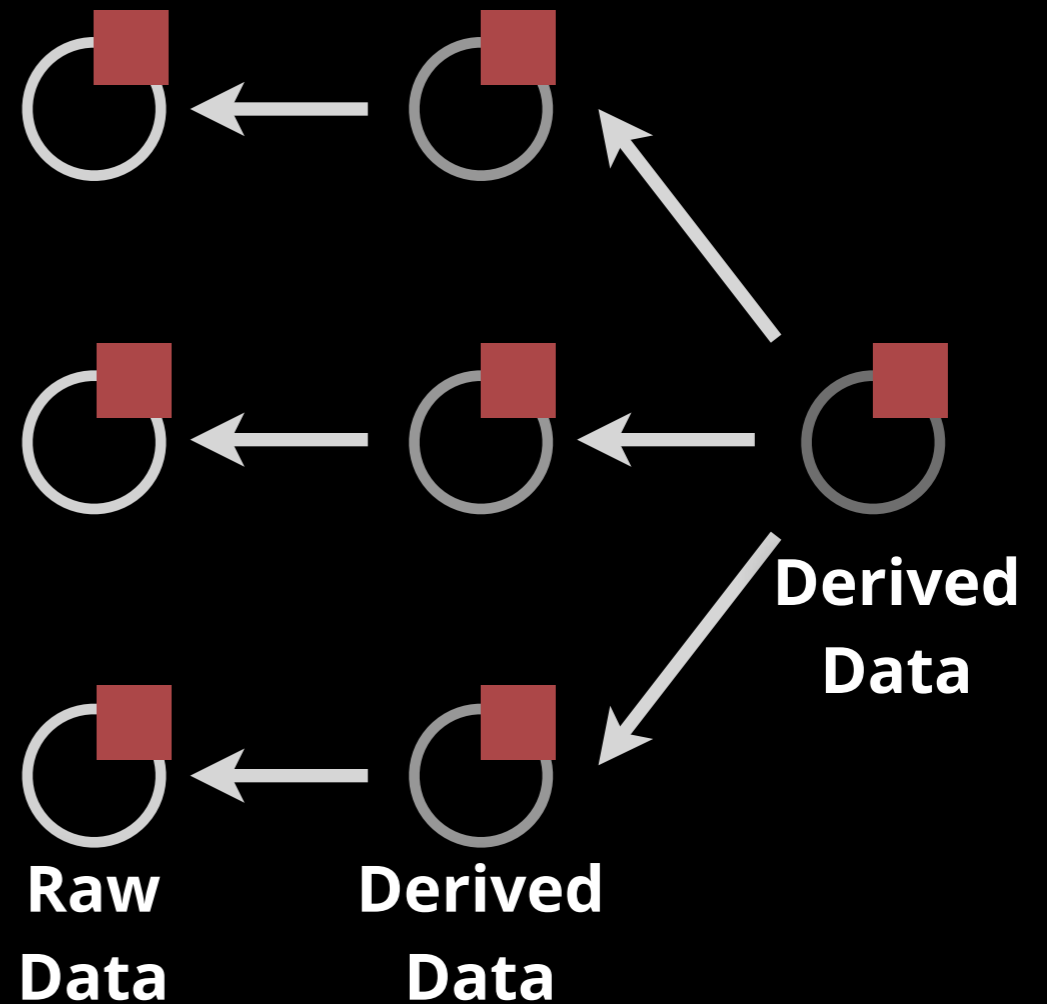
Meta data annotation



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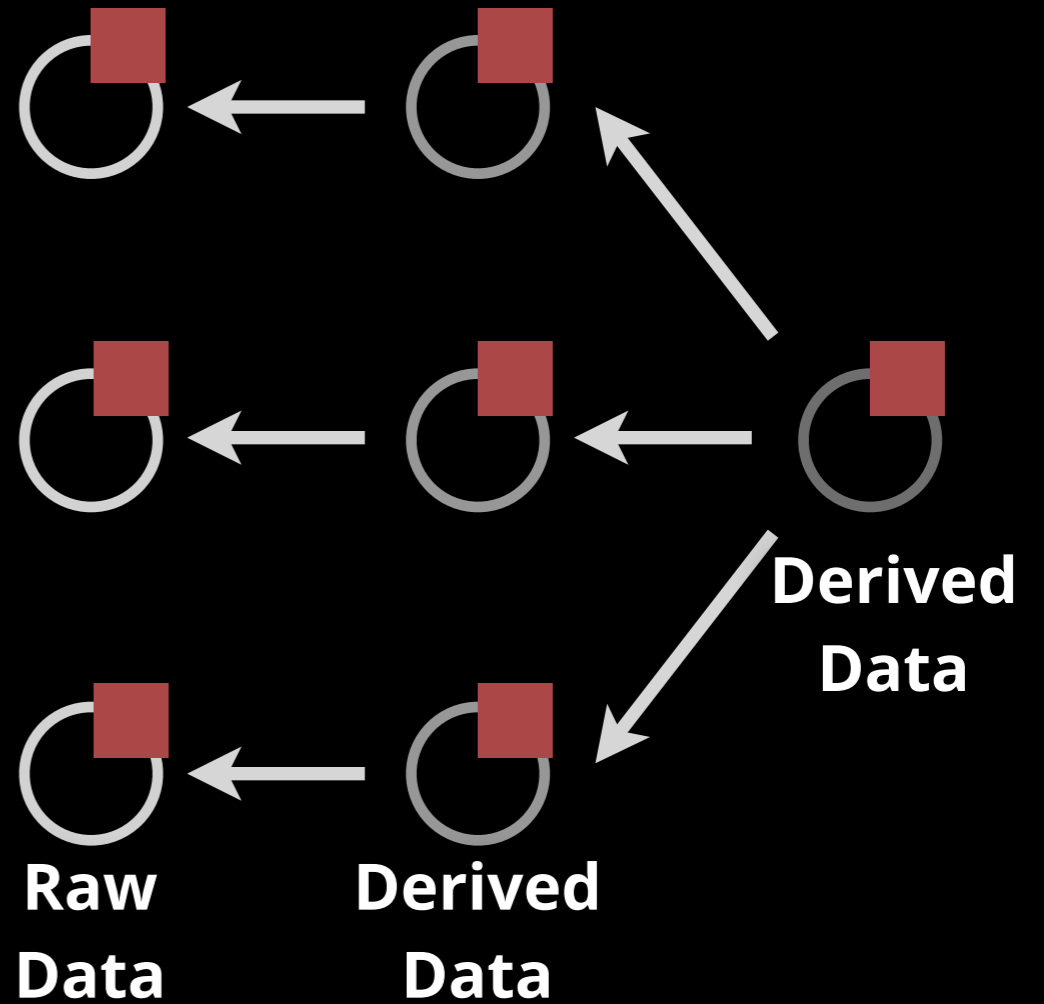
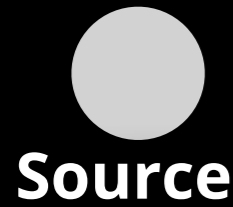
Sample





Repository

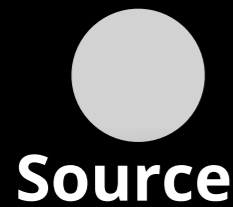
Meta data annotation





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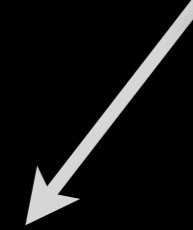
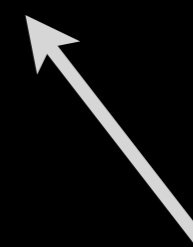
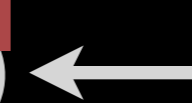
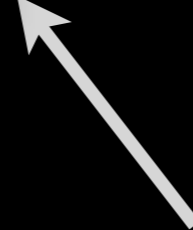
Meta data annotation



Derived
Data

Raw
Data

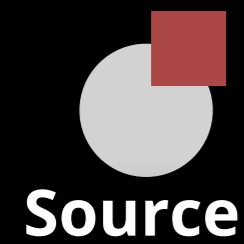
Derived
Data





Repository

Meta data annotation



Source



Sample



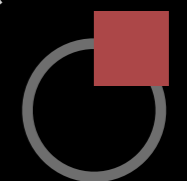
Assay



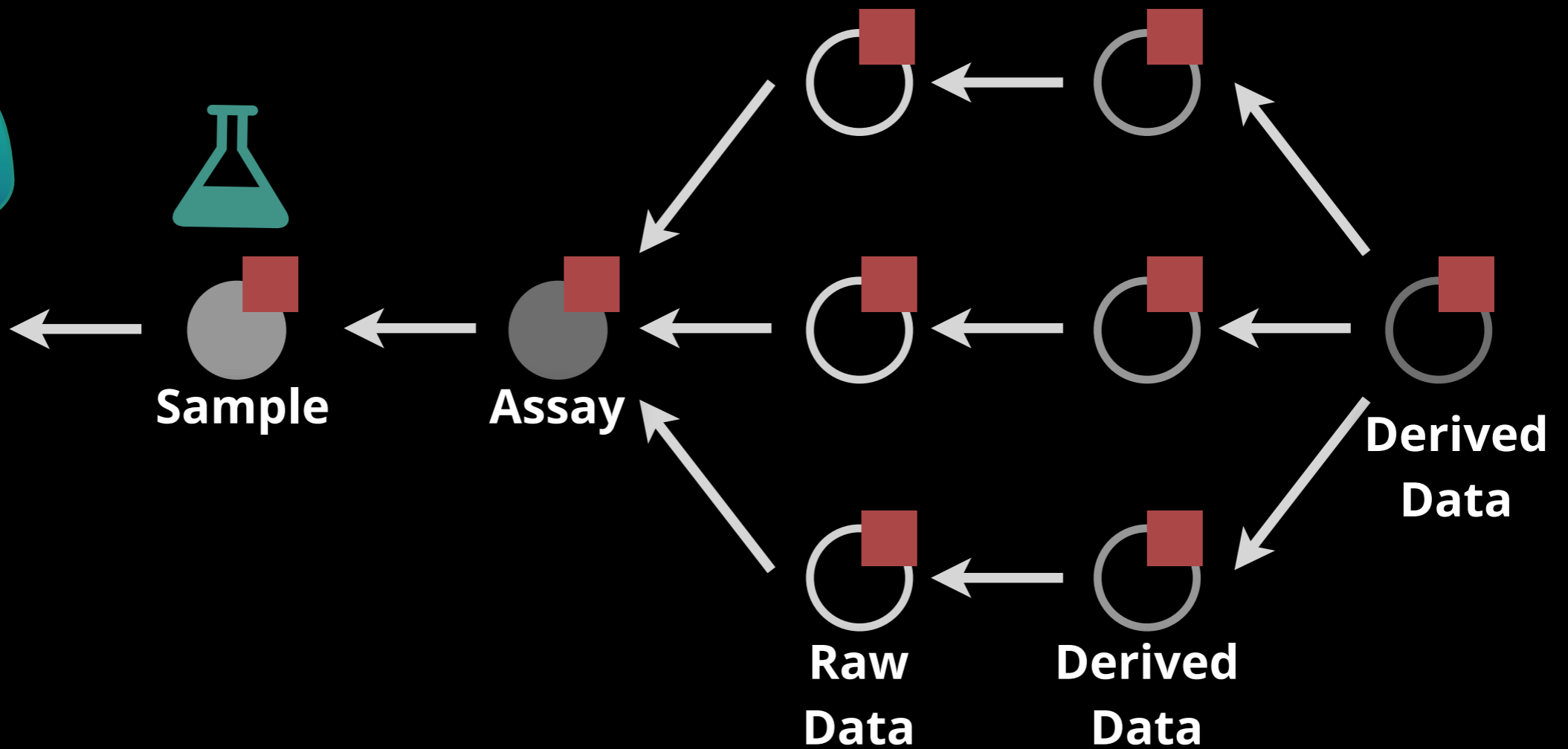
Raw
Data



Derived
Data



Derived
Data



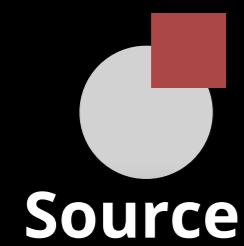


Repository

Meta data annotation

Provenance tracking

ISA-Tab



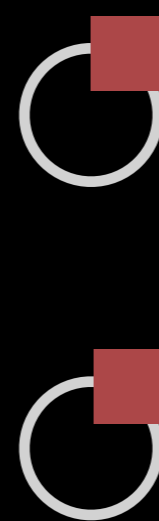
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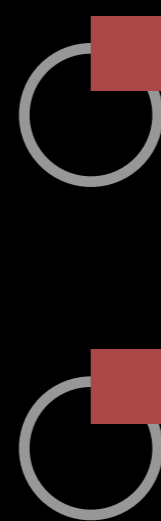
Sample



Assay



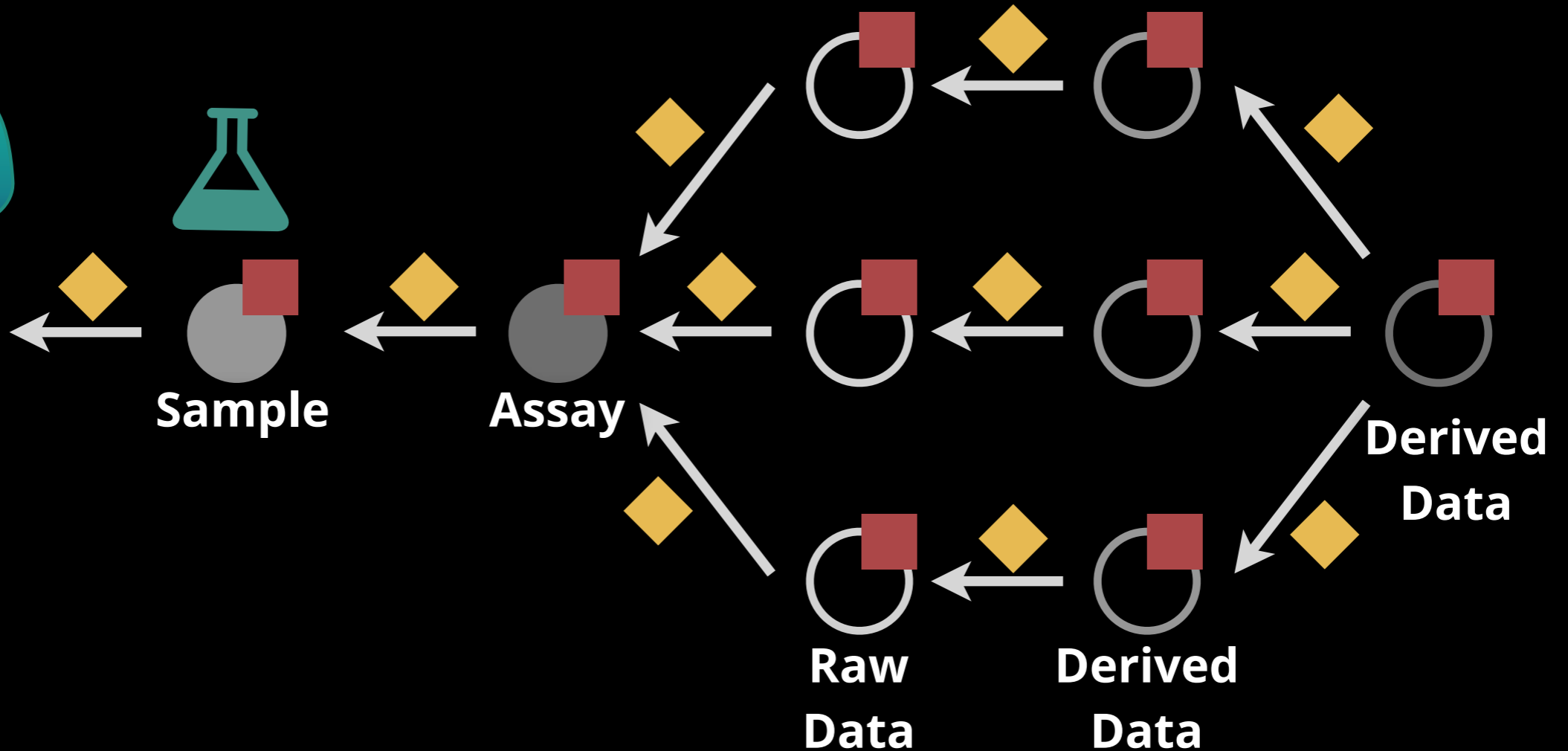
Raw
Data



Derived
Data



Derived
Data





Repository

Meta data annotation
Provenance tracking \rangle **ISA-Tab**

Meta data and provenance import: ISA-Tab



Repository

Meta data annotation
Provenance tracking \rangle **ISA-Tab**

Meta data and provenance import: ISA-Tab

Meta data import: tabular files

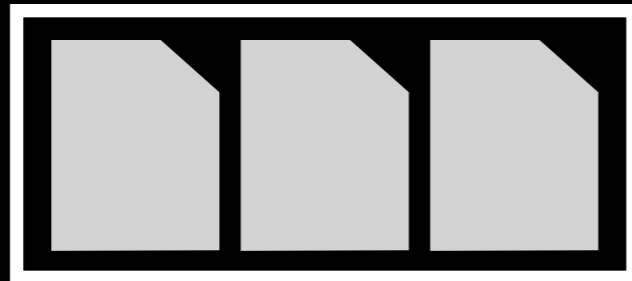
Data stored locally

Data stored remotely: download on demand



Repository

Sample Browsing



Data Set ENCODE-X Chromatin

Samples Attributes Analyses Downloads Details Sharing

1328 of 1328 [View in IGV](#) Showing **Data** **Annotation** Selection Save Load Workflow

Facets

-
- ▶ Cell Or Tissue
- ▶ Platform
- ▶ Species
- ▶ Factor Function
- ▶ Factor
- ▶ Treatment
- ▶ Data Source
- ▶ Genome Build
- ▶ Antibody
- ▶ Data Type
- ▶ Lab

List Matrix

Columns 10 20 50 100 500

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Data Set ENCODE-X Chromatin

Samples Attributes Analyses Downloads Details Sharing

1328 of 1328 [View in IGV](#) Showing **Data** **Annotation** Selection Save Load Workflow

Facets

Reset All

Cell Or Tissue

- S2 cell line 124
- Third instar larvae (L3) 124
- BG3 cell line 92
- K562 90
- Larvae stage 3 (L3) 67
- Late embryo 14-16hr (EL) 65
- Kc cell line 63
- Adult head (AH) 54
- Early embryo (EE) 42
- H1-hESC 42
- Early embryo 2-4hr (EE) 38
- HepG2 34
- GM12878 32
- HeLa-S3 28
- Mixed embryo (MXEMB) 27
- HUVEC 24
- K562 + A549 24
- Clone 8 cell line 21
- NHEK 20
- A549 19
- UMCC 16

List Matrix

Columns 10 20 50 100 500

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<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Histone modification active	H3K9ac	ENCODE	H3K9ac	Histone CHIP-seq	Broad
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Histone modification active	H3K4me3	ENCODE	H3K4me3	Histone CHIP-seq	UW
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Histone modification active	H3K4me3	ENCODE	H3K4me3	Histone CHIP-seq	Broad
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Enhancer associated	CEBPB	ENCODE	CEBPB	non-Histone CHIP-seq	Stanford
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2	non-Histone CHIP-seq	HudsonAlpha
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2	non-Histone CHIP-seq	HudsonAlpha
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Insulator	CTCF	ENCODE	CTCF	non-Histone CHIP-seq	UW
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Enhancer associated	P300	ENCODE	p300	non-Histone CHIP-seq	HudsonAlpha
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2(phosphoS2)	non-Histone CHIP-seq	Stanford
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2	non-Histone CHIP-seq	UT-A
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Insulator	CTCF	ENCODE	CTCF	non-Histone CHIP-seq	UT-A
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Insulator	CTCF	ENCODE	CTCF_(SC-5916)	non-Histone CHIP-seq	HudsonAlpha
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Insulator	CTCF	ENCODE	CTCF_(SC-5916)	non-Histone CHIP-seq	HudsonAlpha
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Histone modification active	H3K4me3	ENCODE	H3K4me3	Histone CHIP-seq	Broad
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Histone modification active	H3K79me2	ENCODE	H3K79me2	Histone CHIP-seq	Broad
<input checked="" type="checkbox"/>	A549	Illumina sequencing	H. sapiens	Histone modification active	H3K4me3	ENCODE	H3K4me3	Histone CHIP-seq	Broad

Data Set ENCODE-X Chromatin

Samples Attributes Analyses Downloads Details Sharing

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Facets

Reset All

- ▶ Cell Or Tissue
 - K562 28
- ▶ Platform
- ▶ Species
 - H. sapiens 28
- ▶ Factor Function
 - Transcription 13
 - Histone methyltransferase 9
 - Enhancer associated 6
- ▶ Factor
- ▶ Treatment
- ▶ Data Source
- ▶ Genome Build
- ▶ Antibody
- ▶ Data Type
- ▶ Lab

List Matrix

Columns 10 20 50 100 500

<input checked="" type="checkbox"/>	Cell Or Tissue	Platform	Species	Factor Function	Factor	Data Source	Antibody	Data Type	Lab
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Transcription	PolIISSP	Ram et al	RNAPIISSP	non-Histone CHIP-seq	Bernstein
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Histone methyltransferase	RBBP5	Ram et al	RBBP5	non-Histone CHIP-seq	Bernstein
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Enhancer associated	CBP/CBP1	Ram et al	KAT3A-CBP	non-Histone CHIP-seq	Bernstein
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Enhancer associated	P300	Ram et al	P300	non-Histone CHIP-seq	Bernstein
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Histone methyltransferase	ESET/SETDB1	Ram et al	ESET	non-Histone CHIP-seq	Bernstein
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Histone methyltransferase	RBBP5	ENCODE	RBBP5	non-Histone CHIP-seq	Broad
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2	non-Histone CHIP-seq	Broad
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Enhancer associated	P300	ENCODE	p300	non-Histone CHIP-seq	Broad
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Enhancer associated	CEBPB	ENCODE	CEBPB	non-Histone CHIP-seq	Stanford
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Enhancer associated	CEBPB	ENCODE	CEBPB_(SC-150)	non-Histone CHIP-seq	HudsonAlpha
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Histone methyltransferase	ESET/SETDB1	ENCODE	SETDB1	non-Histone CHIP-seq	USC
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Histone methyltransferase	ESET/SETDB1	ENCODE	SETDB1	non-Histone CHIP-seq	USC
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Enhancer associated	P300	ENCODE	p300	non-Histone CHIP-seq	Stanford
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2(phosphoS2)	non-Histone CHIP-seq	Stanford
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2	non-Histone CHIP-seq	Stanford
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2(phosphoS2)	non-Histone CHIP-seq	Stanford
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2	non-Histone CHIP-seq	Yale
<input checked="" type="checkbox"/>	K562	Illumina sequencing	H. sapiens	Transcription	PolII	ENCODE	Pol2	non-Histone CHIP-seq	Stanford

Data Set ENCODE-X Chromatin

Samples Attributes Analyses Downloads Details Sharing

1328 of 1328

View in IGV



Showing

Data

Annotation



Selection

Save

Load

Workflow

Facets

List

Matrix

Reset All

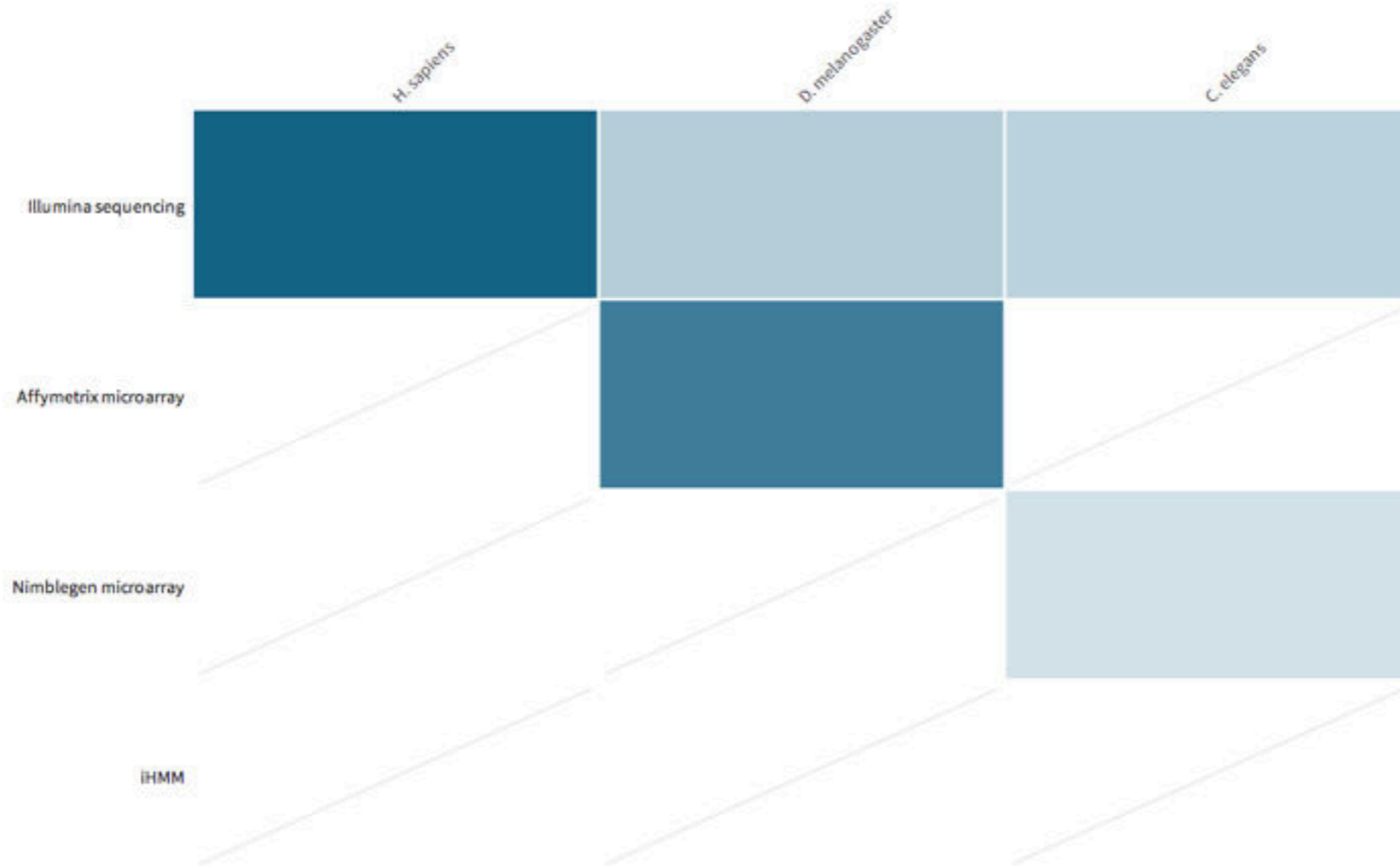
Rows

Platform (4)

Columns

Species (3)

- ▶ Cell Or Tissue
- ▶ Platform
- ▶ Species
- ▶ Factor Function
- ▶ Factor
- ▶ Treatment
- ▶ Data Source
- ▶ Genome Build
- ▶ Antibody
- ▶ Data Type
- ▶ Lab



Data Set ENCODE-X Chromatin

Samples Attributes Analyses Downloads Details Sharing

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View in IGV



Showing

Data

Annotation



Selection

Save

Load

Workflow

Facets

List

Matrix

Reset All

Rows Species (3)

Columns Factor Function (23)

- Cell Or Tissue
- Platform
- Species
 - D. melanogaster
- Factor Function
- Factor
- Treatment
- Data Source
- Genome Build
- Antibody
- Data Type
- Lab

593



Data Set ENCODE-X Chromatin

Samples Attributes Analyses Downloads Details Sharing

143 of 1328 View in IGV Showing Data Annotation Selection Save Load Workflow

Facets

List Matrix

Reset All

Rows Species (3) Columns Factor Function (23)

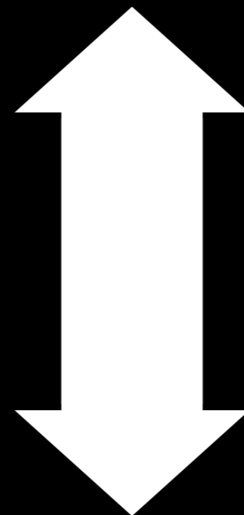
- Cell Or Tissue
- Platform
- Species
 - D. melanogaster 143
- Factor Function
 - Histone modification active 143
- Factor
- Treatment
- Data Source
- Genome Build
- Antibody
- Data Type
- Lab





Workflow Engine

Galaxy



Tools
Toolshed
Workflow Editor
API





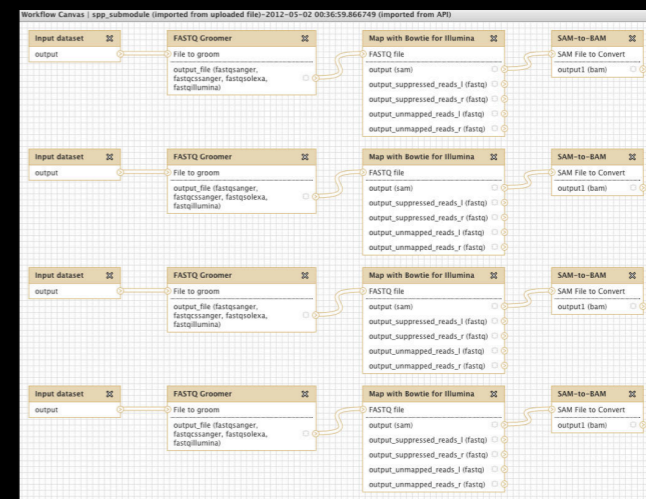
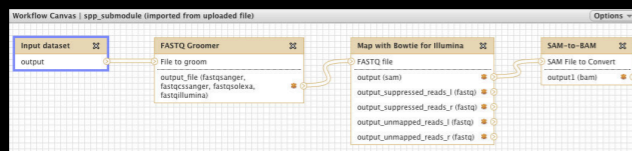
Workflow Engine

Galaxy

Workflow
Template

API

Workflow
Instance

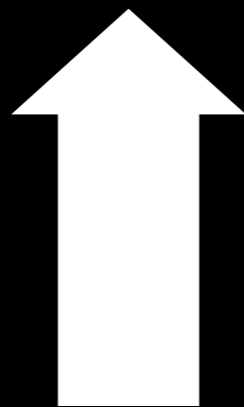




Workflow Engine

Galaxy

Workflow
Inputs



API



Workflow
Outputs



Data Set Test 1: Request for Comments (RFC) Test

Samples Attributes Analyses Downloads Details Sharing

23 of 23 View in IGV Showing Data Annotation Selection Save Load Workflow

Facets

Reset All

- ▶ Author
- ▶ Month
- ▶ Year
- ▶ Type
- ▶ File Type

▶ Analysis

List Matrix

Columns 10 20 50 100 500

<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Title	Author	Month	Year	Type	File Type	Name
<input checked="" type="checkbox"/>	Device independent graphical display description	McConnell	June	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc177.txt
<input checked="" type="checkbox"/>	Graphics Facilities at Ames Research Center	McConnell	April	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc126.txt
<input checked="" type="checkbox"/>	Network Graphics meeting	Veza	April	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc134.txt
<input checked="" type="checkbox"/>	Network graphic attention handling	Cotton	June	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc178.txt
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test tool out
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_02
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_04
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc111.txt
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test tool out
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test tool out
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_03
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_01
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Proposal for a Network Standard Format for a Data Stream to Control	Crocker	January	1971	Raw Data File	txt	http://eehlenborg.com/wp-

Data Set Test 1: Request for Comments (RFC) Test

Samples Attributes Analyses Downloads Details Sharing

23 of 23 View in IGV Showing Data Annotation Selection Save Load Workflow

Workflow dropdown menu:

- Test workflow: SPP analog
- Test workflow: 5 steps without branching

Facets

Reset All

- Author
- Month
- Year
- Type
- File Type

Analysis

List Matrix

Columns 10 20 50 100 500

<input checked="" type="checkbox"/>	Title	Author	Month	Year	Type	File Type	Name
<input checked="" type="checkbox"/>	Device independent graphical display description	McConnell	June	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc177.txt
<input checked="" type="checkbox"/>	Graphics Facilities at Ames Research Center	McConnell	April	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc126.txt
<input checked="" type="checkbox"/>	Network Graphics meeting	Veza	April	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc134.txt
<input checked="" type="checkbox"/>	Network graphic attention handling	Cotton	June	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc178.txt
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test tool out
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_02
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_04
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc111.txt
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test tool out
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test tool out
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_03
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_01
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Proposal for a Network Standard Format for a Data Stream to Control	Crocker	January	1971	Raw Data File	txt	http://eehlenborg.com/wp-

Data Set Test 1: Request for Comments (RFC) Test

Samples Attributes Analyses Downloads Details Sharing

23 of 23 View in IGV Showing Data Annotation Selection Save Load Workflow Test workflow: 5 steps without branching

Facets

Reset All

- ▶ Author
- ▶ Month
- ▶ Year
- ▶ Type
- ▶ File Type

▶ Analysis

List Matrix

Columns 10 20 50 100 500

<input checked="" type="checkbox"/>	↓ Title	Author	Month	Year	Type	File Type	Name
<input checked="" type="checkbox"/>	Device independent graphical display description	McConnell	June	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc177.txt
<input checked="" type="checkbox"/>	Graphics Facilities at Ames Research Center	McConnell	April	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc126.txt
<input checked="" type="checkbox"/>	Network Graphics meeting	Veza	April	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc134.txt
<input checked="" type="checkbox"/>	Network graphic attention handling	Cotton	June	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc178.txt
<input checked="" type="checkbox"/>	<input type="radio"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test tool out
<input checked="" type="checkbox"/>	<input type="radio"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_02
<input checked="" type="checkbox"/>	<input type="radio"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_04
<input checked="" type="checkbox"/>	<input type="radio"/> Pressure from the Chairman	Crocker	March	1971	Raw Data File	txt	http://gehlenborg.com/wp-content/uploads/rfc/rfc111.txt
<input checked="" type="checkbox"/>	<input type="radio"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test tool out
<input checked="" type="checkbox"/>	<input type="radio"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test tool out
<input checked="" type="checkbox"/>	<input type="radio"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_03
<input checked="" type="checkbox"/>	<input type="radio"/> Pressure from the Chairman	Crocker	March	1971	Derived Data File	txt	1_test_01
<input checked="" type="checkbox"/>	<input type="radio"/> Proposal for a Network Standard Format for a Data Stream	Crocker	January	1971	Raw Data	txt	http://eehlenborg.com/wo-

Run Analysis

Set1

Crocker after

Run Analysis

Analysis Test workflow: 5 steps without branching 2013-07-19 @ 03:20:53

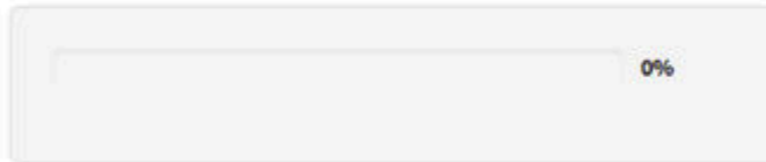
Status

⚙ Test workflow: 5 steps without branching started on July 19, 2013, 3:20 a.m.. (View in Galaxy)

Preprocessing

Finished File upload is complete.

Execution



Postprocessing

Waiting File download is pending.

Data Set Test 1: Request for Comments (RFC) Test

Samples

Attributes

Analyses

Downloads

Details

Sharing

2 of 23

View in IGV



Showing

Data

Annotation



Selection

Save

Load

Workflow

Facets

Reset All

▶ Author

▶ Month

▶ Year

▶ Type

▶ File Type

▶ Analysis

Test workflow: 5 steps

 without branching 2013-06-20 @ 13:32:08

List

Matrix

Columns 10 20 50 100 500

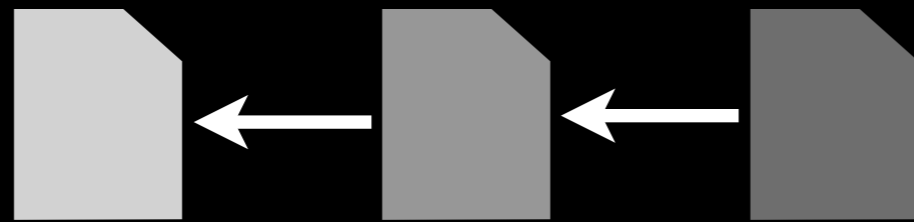
 Title Pressure from the Chairman Proposal for a Network Standard Format for a Data Stream to Control Graphics Display
 1 2 3 4 5

Author	Month	Year	Type	File Type	Name
Crocker	March	1971	Derived Data File	txt	1_test tool out
Crocker	January	1971	Derived Data File	txt	2_test tool out



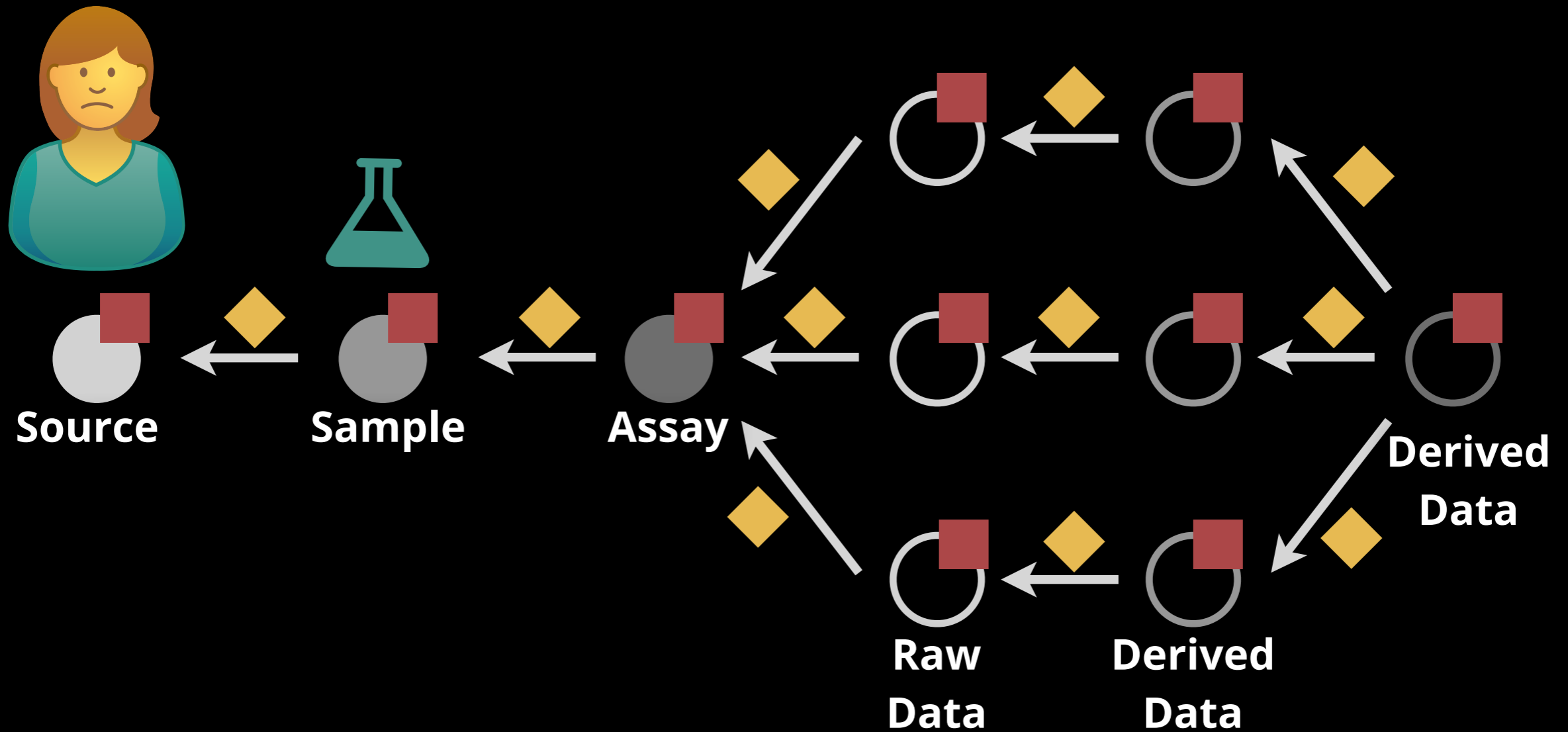
Workflow Engine

Provenance Tracking



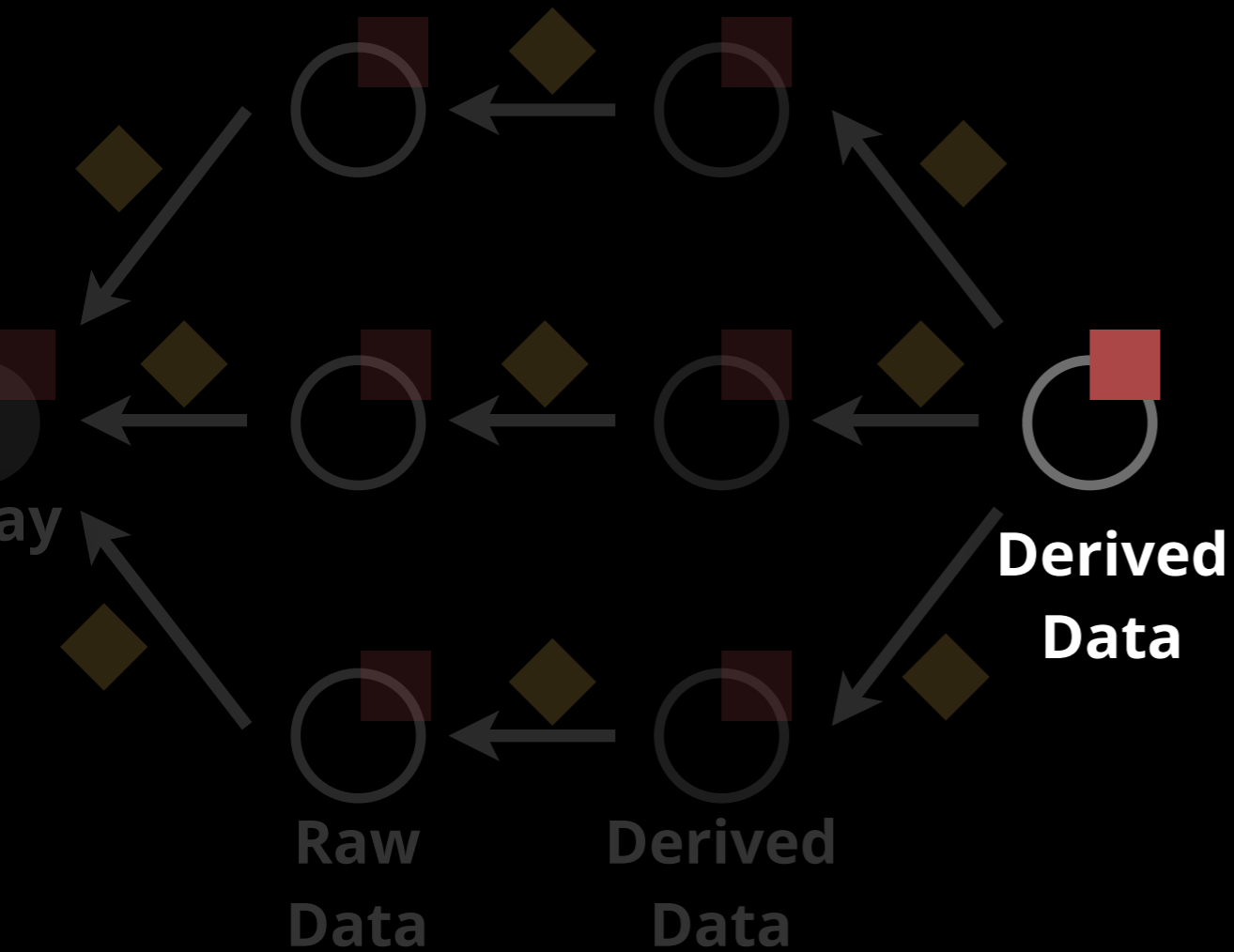


Workflow Engine



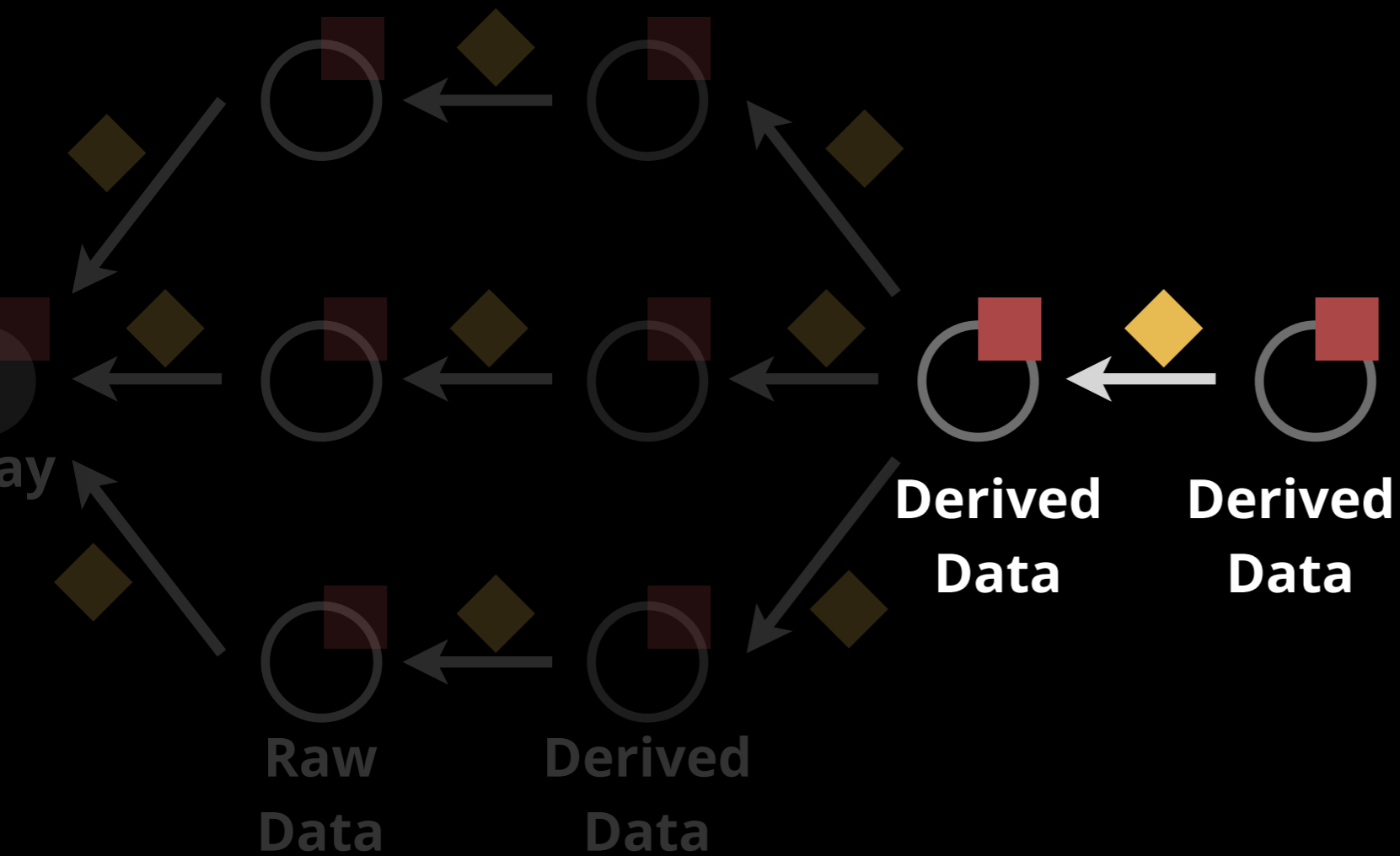


Workflow Engine



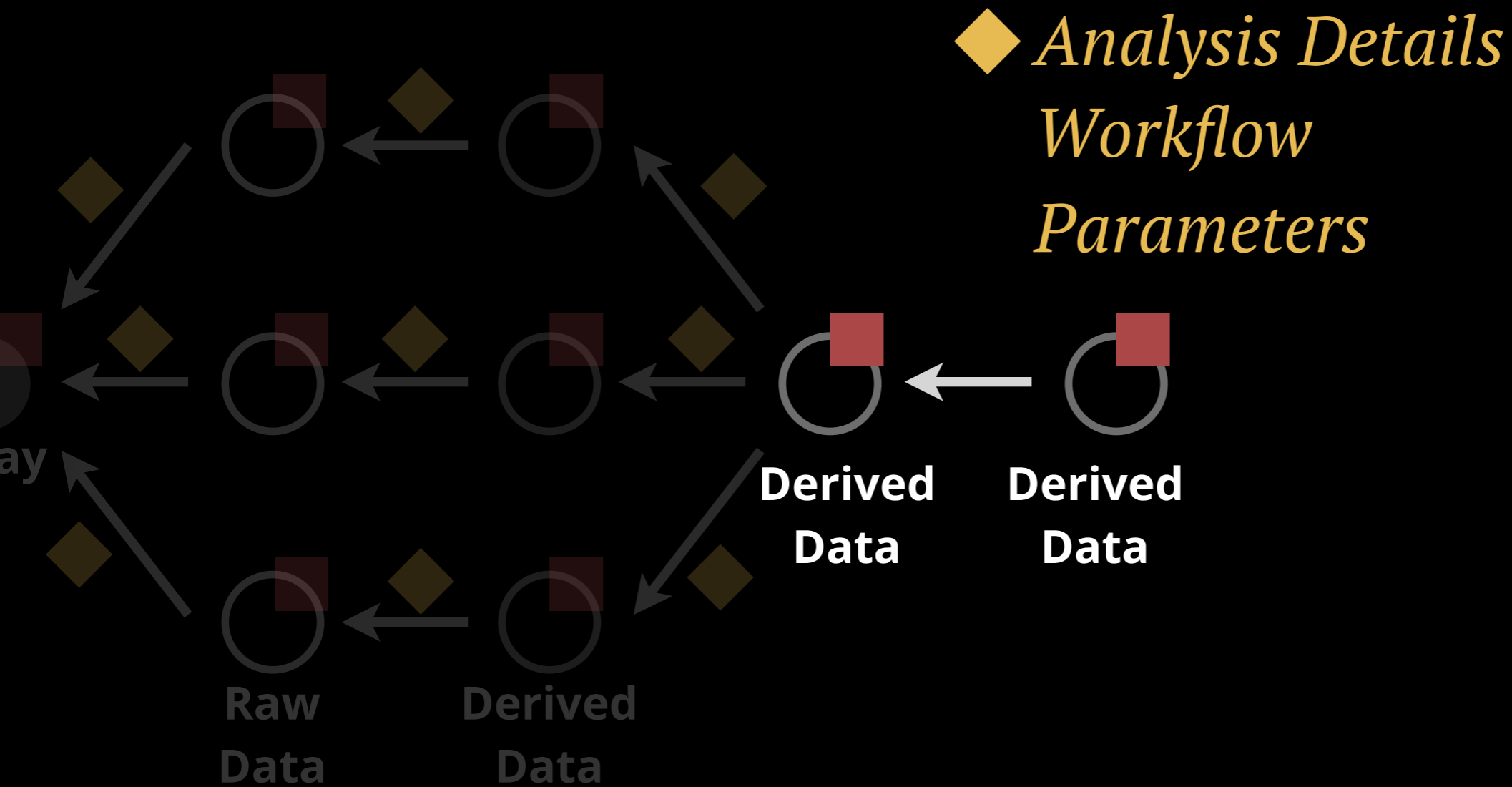


Workflow Engine





Workflow Engine



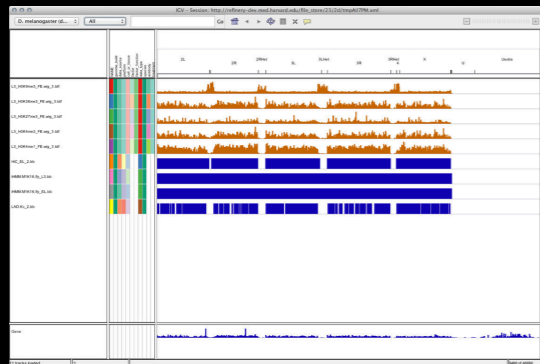


Visualization



file-driven

database-driven



Java Webstart tools *or*
built-in Refinery tools

built-in Refinery tools

D. melanogaster (d...)

All

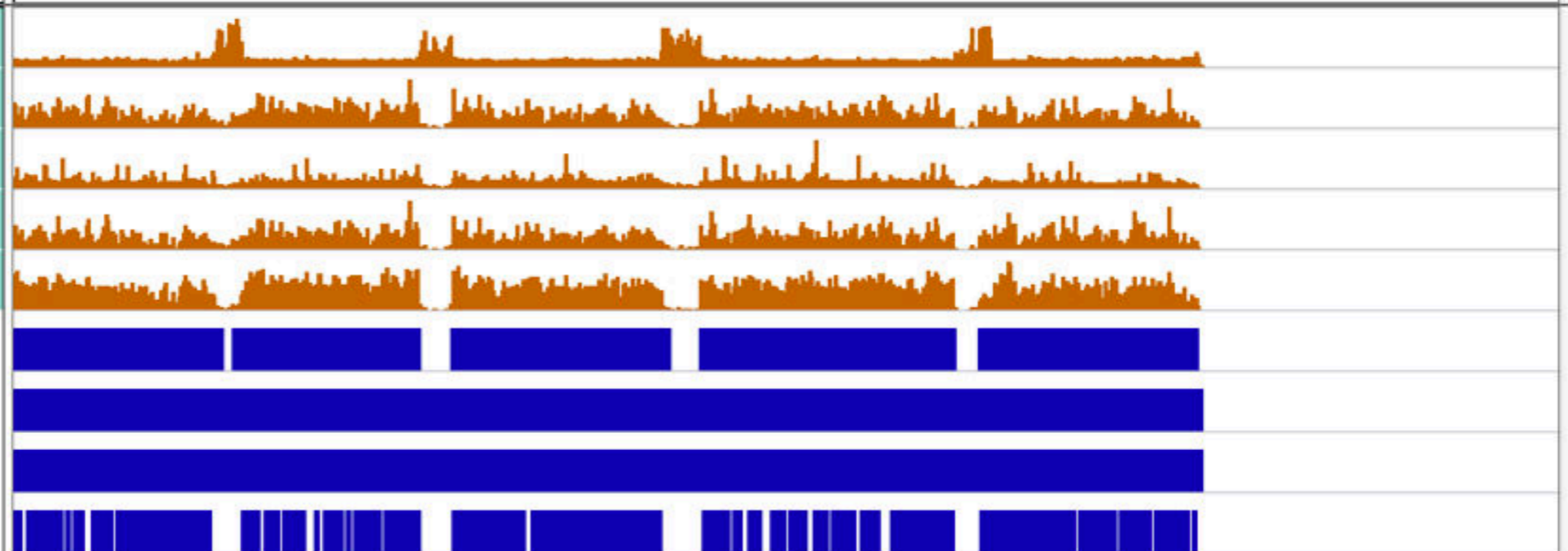
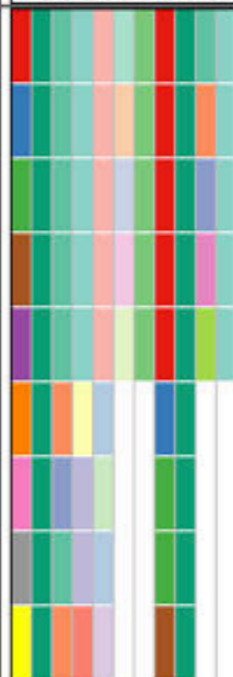
Go



NAME
genome_build
data_source
platform
cell_or_tissue
factor
factor_function
data_type
species
antibody
treatment

2L 2R 2Rhet 3L 3Lhet 3R 3Rhet 4 X U Uextra

L3_H3K9me3_FE.wig_3.tdf
L3_H3K36me3_FE.wig_3.tdf
L3_H3K27me3_FE.wig_3.tdf
L3_H3K4me3_FE.wig_3.tdf
L3_H3K4me1_FE.wig_3.tdf
HiC_EL_2.bb
iHMM.M1K16.fly_L3.bb
iHMM.M1K16.fly_EL.bb
LAD.Kc_2.bb



Data Set ENCODE-X Chromatin

Samples Details Sharing

5 of 1298 selected View in IGV Download as Archive Showing Data Annotation

Facets

Reset All

- Species
 - D. melanogaster 5
- Cell Or Tissue
 - Third instart larvae (L3) 5
- Factor Function
- Factor
 - H3K27me3 1
 - H3K36me3 1
 - H3K4me1 1
 - H3K4me3 1
 - H3K9me3 1
- Antibody
- Treatment
- Data Type
- Platform
 - Illumina sequencing 5
- Data Source
- Genome Build

List Matrix

Columns 10 20 50 100

<input checked="" type="checkbox"/> ↓ Species	Cell Or Tissue	Factor Function	Factor	Antibody	Treatment	Data Type	Platform	Data Source	Genome Build
<input checked="" type="checkbox"/> D. melanogaster	Third instart larvae (L3)	Histone modification	H3K9me3	H3K9me3	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3
<input checked="" type="checkbox"/> D. melanogaster	Third instart larvae (L3)	Histone modification	H3K36me3	H3K36me3	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3
<input checked="" type="checkbox"/> D. melanogaster	Third instart larvae (L3)	Histone modification	H3K27me3	H3K27me3	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3
<input checked="" type="checkbox"/> D. melanogaster	Third instart larvae (L3)	Histone modification	H3K4me3	H3K4me3	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3
<input checked="" type="checkbox"/> D. melanogaster	Third instart larvae (L3)	Histone modification	H3K4me1	H3K4me1	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3

D. melanogaster (d...)

All

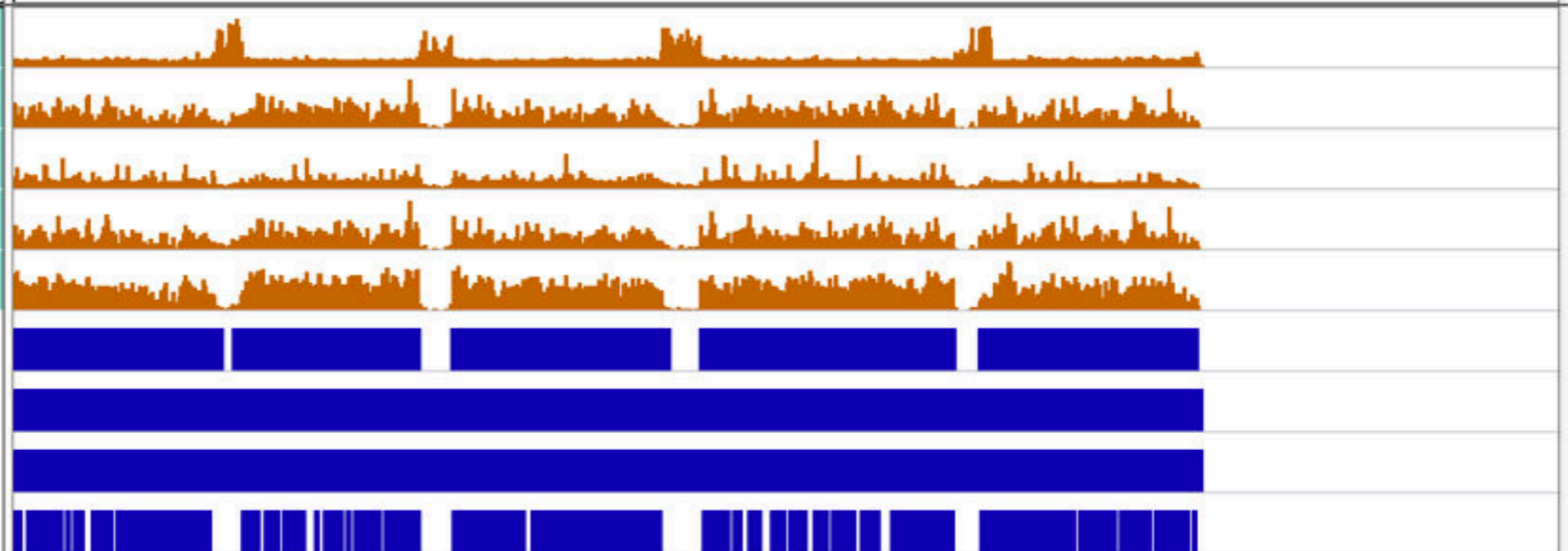
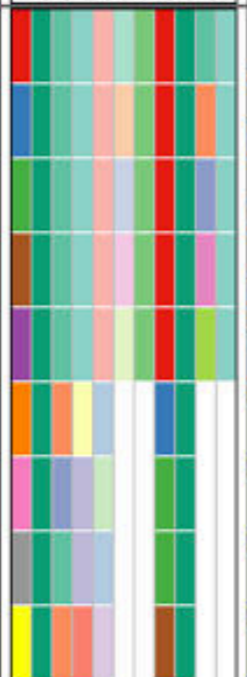
Go



NAME
genome_build
data_source
platform
cell_or_tissue
factor
factor_function
data_type
species
antibody
treatment

2L 2R 2Rhet 3L 3Lhet 3R 3Rhet 4 X U Uextra

L3_H3K9me3_FE.wig_3.tdf
L3_H3K36me3_FE.wig_3.tdf
L3_H3K27me3_FE.wig_3.tdf
L3_H3K4me3_FE.wig_3.tdf
L3_H3K4me1_FE.wig_3.tdf
HiC_EL_2.bb
iHMM.M1K16.fly_L3.bb
iHMM.M1K16.fly_EL.bb
LAD.Kc_2.bb



Gene



D. melanogaster (d...)

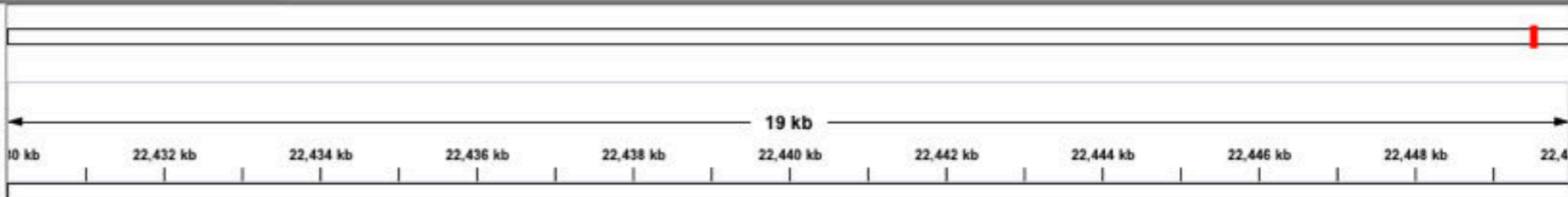
chr2L

chr2L:22,430,000-22,450,000

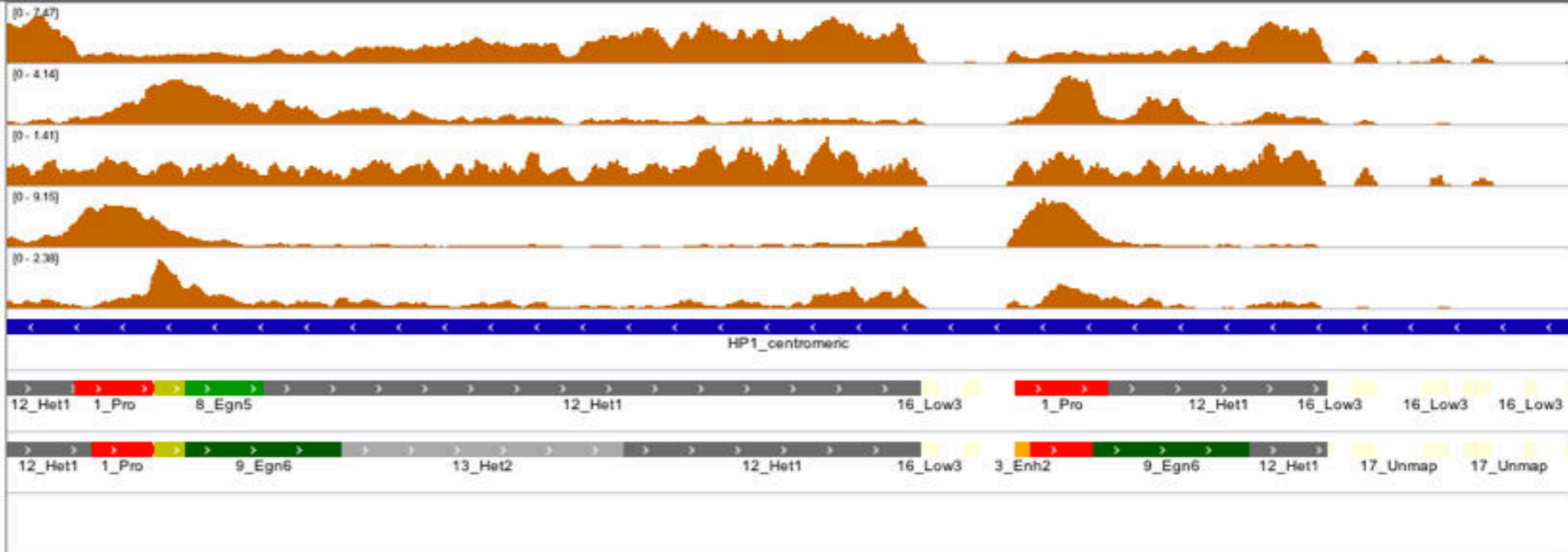
Go



NAME
genome_build
data_source
platform
cell_or_tissue
factor
factor_function
data_type
species
antibody
treatment



L3_H3K9me3_FE.wig_3.tdf
L3_H3K36me3_FE.wig_3.tdf
L3_H3K27me3_FE.wig_3.tdf
L3_H3K4me3_FE.wig_3.tdf
L3_H3K4me1_FE.wig_3.tdf
HiC_EL_2.bb
iHMM.M1K16.fly_L3.bb
iHMM.M1K16.fly_EL.bb
LAD.Kc_2.bb



Gene



Data Set ENCODE-X Chromatin

Samples Attributes Analyses Details Sharing

12 of 12 selected View in IGV Download as Archive Showing Data Annotation

Facets

Reset All

- Species
- Cell Or Tissue
- Factor Function
- Factor
- Antibody
- Treatment
- Data Type
- Platform
- Data Source
- Genome Build

List Matrix

Columns 10 20 50 100

<input checked="" type="checkbox"/>	Species	Cell Or Tissue	Factor Function	Factor	Antibody	Treatment	Data Type	Platform	Data Source	Genome Build
<input checked="" type="checkbox"/>	C. elegans	Larvae stage 3 (L3)					Chromatin state map	hiHMM	modENCODE	WS220
<input checked="" type="checkbox"/>	C. elegans	Early embryo (EE)					Chromatin state map	hiHMM	modENCODE	WS220
<input checked="" type="checkbox"/>	C. elegans	MXEMB					Lamina associated domains	LAD	modENCODE	WS220
<input checked="" type="checkbox"/>	D. melanogaster	Late embryo 14-16hr (EL)					HiC topological domains	HiC	Others	dm3
<input checked="" type="checkbox"/>	D. melanogaster	Third instar larvae (L3)					Chromatin state map	hiHMM	modENCODE	dm3
<input checked="" type="checkbox"/>	D. melanogaster	Late embryo 14-16hr (EL)					Chromatin state map	hiHMM	modENCODE	dm3
<input checked="" type="checkbox"/>	D. melanogaster	Kc					Lamina associated domains	LAD	Others	dm3
<input checked="" type="checkbox"/>	H. sapiens	H1-hESC					HiC topological domains	HiC	Others	hg19
<input checked="" type="checkbox"/>	H. sapiens	H1-hESC					Chromatin state map	hiHMM	ENCODE	hg19
<input checked="" type="checkbox"/>	H. sapiens	GM12878					Chromatin state map	hiHMM	ENCODE	hg19

Data Set ENCODE-X Chromatin

Samples Details Sharing

13 of 1298 selected View in IGV Download as Archive Showing Data Annotation

Facets

Reset All

- Species**
 - H. sapiens 8
 - D. melanogaster 5
- Cell Or Tissue**
 - GM12878 8
 - Third instart larvae (L3) 5
- Factor Function**
- Factor**
 - H3K27me3 3
 - H3K36me3 3
 - H3K4me3 3
 - H3K4me1 2
 - H3K9me3 2
- Antibody**
- Treatment**
- Data Type**
- Platform**
 - Illumina sequencing 13
- Data Source**

List Matrix

Columns 10 20 50 100

<input checked="" type="checkbox"/>	Species	Cell Or Tissue	Factor Function	Factor	Antibody	Treatment	Data Type	Platform	Data Source	Genome Build
<input checked="" type="checkbox"/>	D. melanogaster	Third instart larvae (L3)	Histone modification	H3K9me3	H3K9me3	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3
<input checked="" type="checkbox"/>	D. melanogaster	Third instart larvae (L3)	Histone modification	H3K36me3	H3K36me3	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3
<input checked="" type="checkbox"/>	D. melanogaster	Third instart larvae (L3)	Histone modification	H3K27me3	H3K27me3	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3
<input checked="" type="checkbox"/>	D. melanogaster	Third instart larvae (L3)	Histone modification	H3K4me3	H3K4me3	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3
<input checked="" type="checkbox"/>	D. melanogaster	Third instart larvae (L3)	Histone modification	H3K4me1	H3K4me1	None	Histone ChIP-seq	Illumina sequencing	modENCODE	dm3
<input checked="" type="checkbox"/>	H. sapiens	GM12878	Histone modification	H3K36me3	H3K36me3	None	Histone ChIP-seq	Illumina sequencing	ENCODE	hg19
<input checked="" type="checkbox"/>	H. sapiens	GM12878	Histone modification	H3K27me3	H3K27me3	None	Histone ChIP-seq	Illumina sequencing	ENCODE	hg19
<input checked="" type="checkbox"/>	H. sapiens	GM12878	Histone modification	H3K4me3	H3K4me3	None	Histone ChIP-seq	Illumina sequencing	ENCODE	hg19
<input checked="" type="checkbox"/>	H. sapiens	GM12878	Histone modification	H3K4me1	H3K4me1	None	Histone ChIP-seq	Illumina sequencing	ENCODE	hg19
<input checked="" type="checkbox"/>	H. sapiens	GM12878	Histone modification	H3K36me3	H3K36me3	None	Histone ChIP-seq	Illumina sequencing	ENCODE	hg19
<input checked="" type="checkbox"/>	H. sapiens	GM12878	Histone modification	H3K27me3	H3K27me3	None	Histone ChIP-seq	Illumina sequencing	ENCODE	hg19
<input checked="" type="checkbox"/>	H. sapiens	GM12878	Histone modification	H3K4me3	H3K4me3	None	Histone ChIP-seq	Illumina sequencing	ENCODE	hg19
<input checked="" type="checkbox"/>	H. sapiens	GM12878	Histone modification	H3K9me3	H3K9me3	None	Histone ChIP-seq	Illumina sequencing	ENCODE	hg19

Data Set ENCODE-X Chromatin

Samples Details Sharing

13 of 1298 selected

View in IGV

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Showing

Data

Annotation

Facets

List

Matrix

Reset All

Columns

10 20 50 100

Species

 H. sapiens 8 D. melanogaster 5

Cell Or Tissue

 GM12878 8 Third instart larvae (L3) 5

Factor Function

Factor

 H3K27me3 3 H3K36me3 3 H3K4me3 3 H3K4me1 2 H3K9me3 2

Antibody

Treatment

Data Type

Platform

 Illumina sequencing 13

Data Source

Launch IGV

You selected samples from 2 different genome builds. To view the samples, open IGV with the corresponding genome.

H. sapiens (hg19) **D. melanogaster (dm3)**

Close

 Species D. melanogaster Third D. melanogaster Third D. melanogaster Third D. melanogaster Third instart larvae (L3) D. melanogaster Third instart larvae (L3) H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878 H. sapiens GM12878

Platform Data Source Genome Build

ChIP-seq Illumina sequencing modENCODE dm3

ChIP-seq Illumina sequencing modENCODE dm3

ChIP-seq Illumina sequencing modENCODE dm3

Histone modification H3K4me3 H3K4me3 None Histone ChIP-seq Illumina sequencing modENCODE dm3

Histone modification H3K4me1 H3K4me1 None Histone ChIP-seq Illumina sequencing modENCODE dm3

Histone modification H3K36me3 H3K36me3 None Histone ChIP-seq Illumina sequencing ENCODE hg19

Histone modification H3K27me3 H3K27me3 None Histone ChIP-seq Illumina sequencing ENCODE hg19

Histone modification H3K4me3 H3K4me3 None Histone ChIP-seq Illumina sequencing ENCODE hg19

Histone modification H3K4me1 H3K4me1 None Histone ChIP-seq Illumina sequencing ENCODE hg19

Histone modification H3K36me3 H3K36me3 None Histone ChIP-seq Illumina sequencing ENCODE hg19

Histone modification H3K27me3 H3K27me3 None Histone ChIP-seq Illumina sequencing ENCODE hg19

Histone modification H3K4me3 H3K4me3 None Histone ChIP-seq Illumina sequencing ENCODE hg19

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Histone modification H3K9me3 H3K9me3 None Histone ChIP-seq Illumina sequencing ENCODE hg19

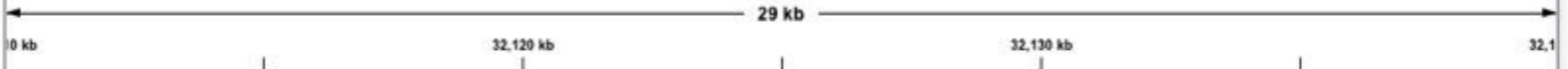
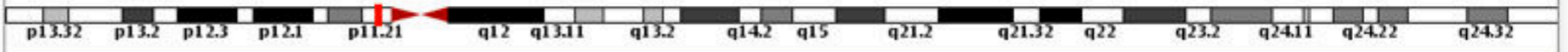
1 2 3 4 5

Human hg19

chr12

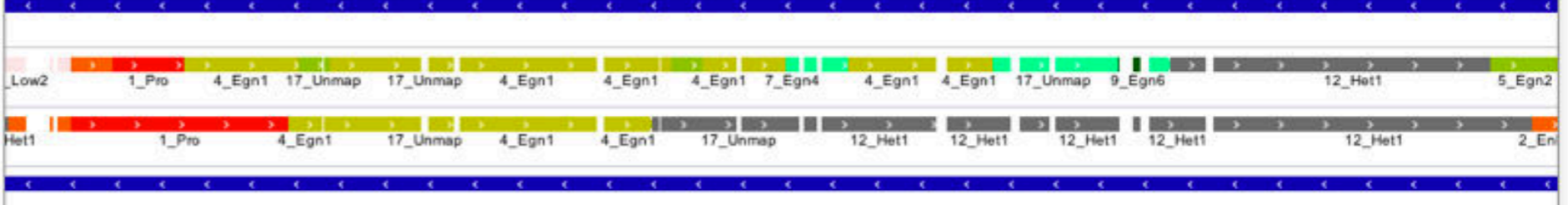
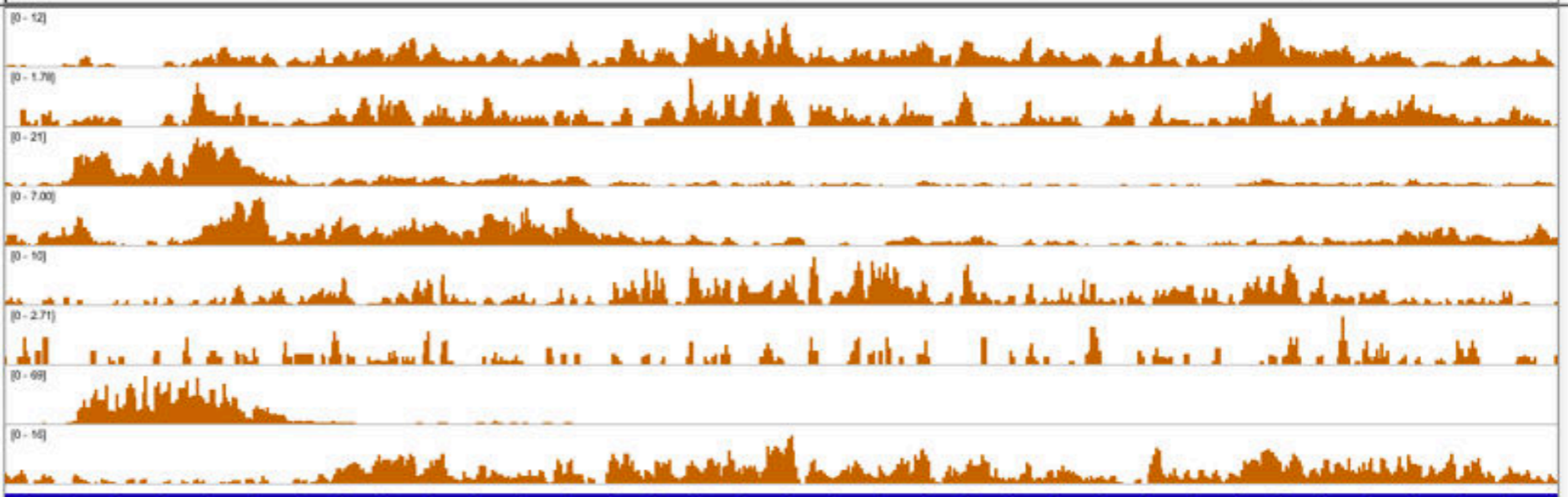
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Go



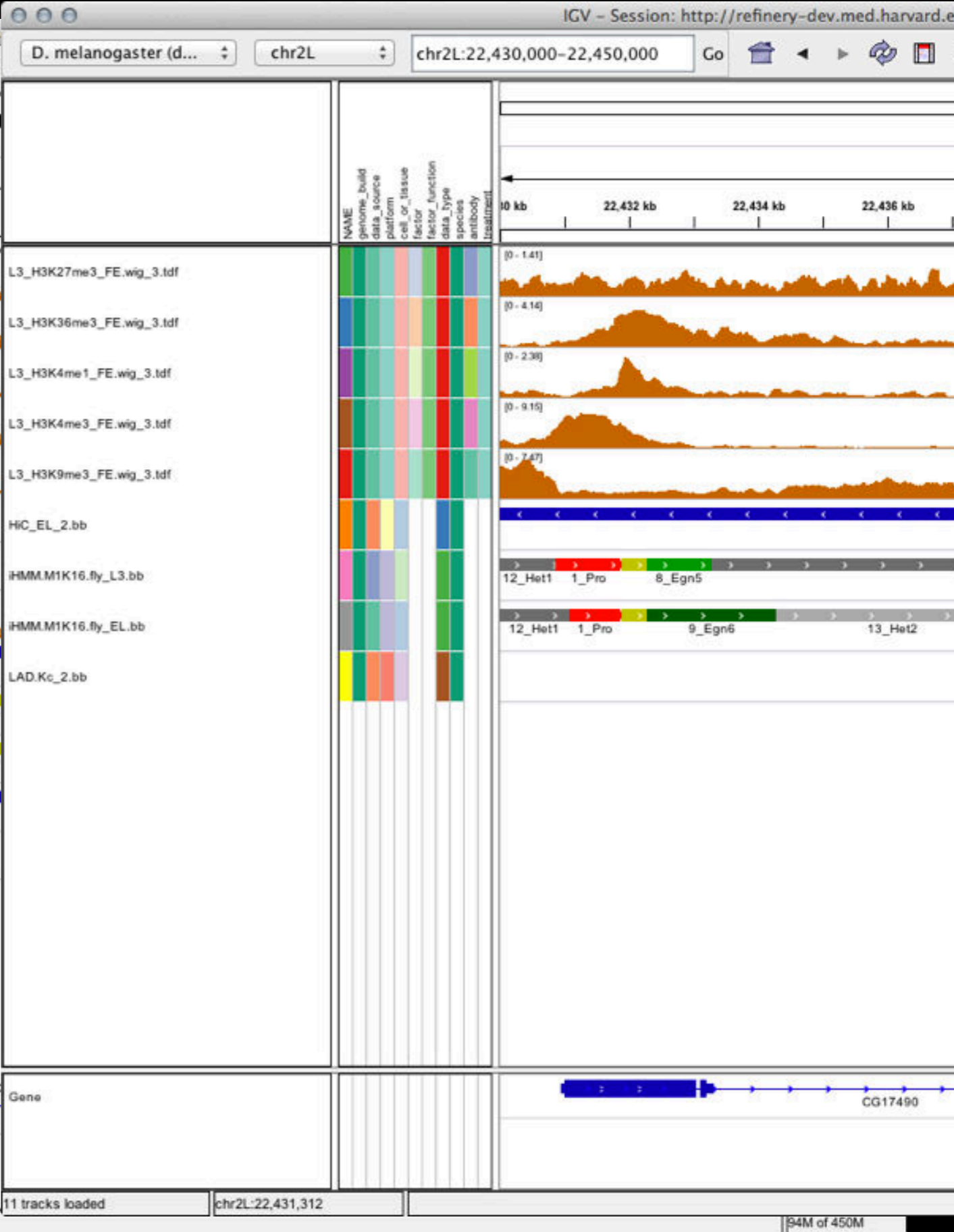
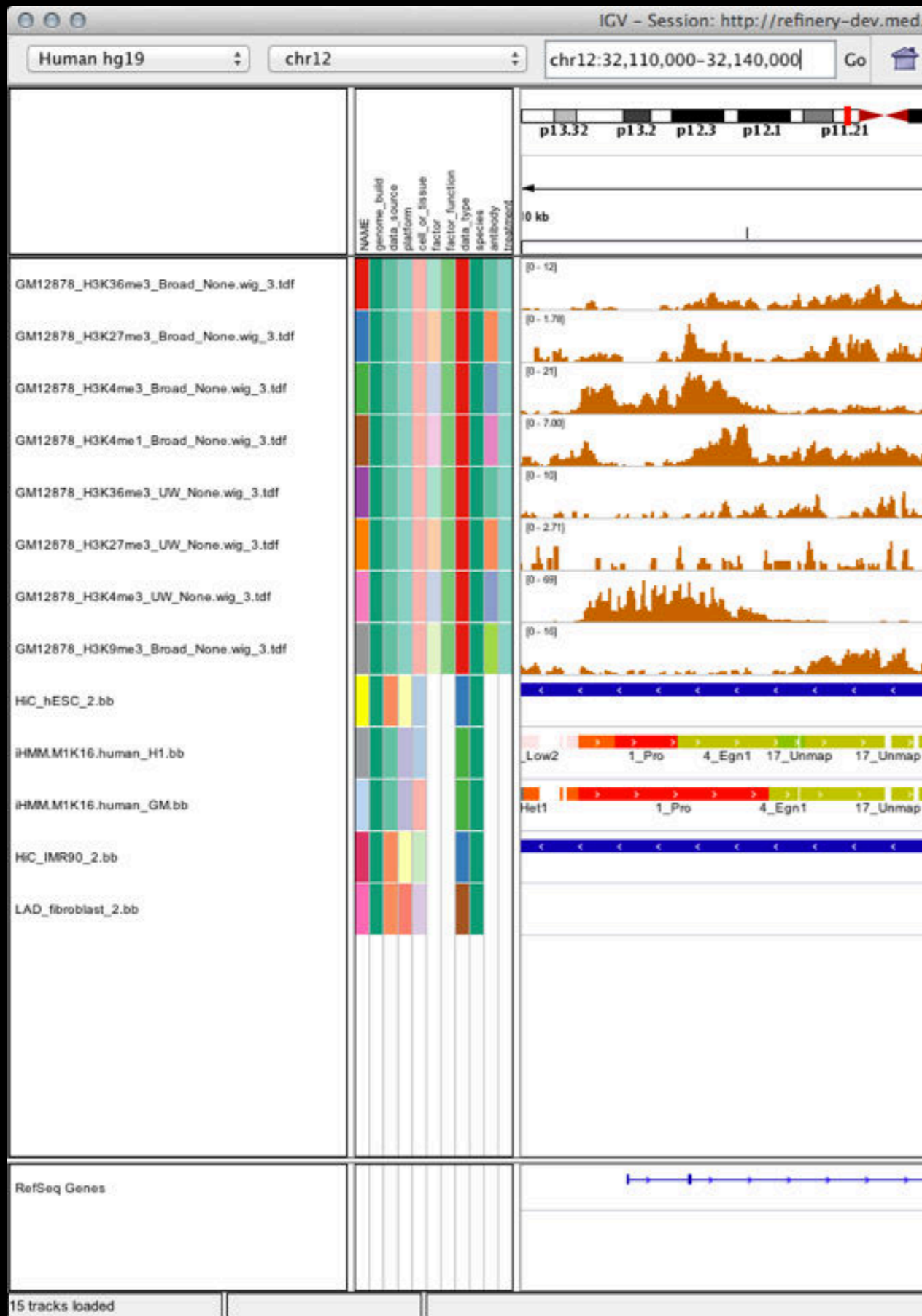
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- GM12878_H3K4me1_Broad_None.wig_3.tdf
- GM12878_H3K36me3_UW_None.wig_3.tdf
- GM12878_H3K27me3_UW_None.wig_3.tdf
- GM12878_H3K4me3_UW_None.wig_3.tdf
- GM12878_H3K9me3_Broad_None.wig_3.tdf
- H3C_hESC_2.bb
- iHMM.M1K16.human_H1.bb
- iHMM.M1K16.human_GM.bb
- H3C_IMR90_2.bb
- LAD_fibroblast_2.bb

NAME	genome_build	data_source	platform	cell_or_issue	factor	factor_function	data_type	species	antibody	treatment
GM12878_H3K36me3_Broad_None.wig_3.tdf	hg19	ChIP-seq	ILLUMINA	GM12878	H3K36me3	Chromatin state	ChIP-seq	Human	Anti-H3K36me3	None
GM12878_H3K27me3_Broad_None.wig_3.tdf	hg19	ChIP-seq	ILLUMINA	GM12878	H3K27me3	Chromatin state	ChIP-seq	Human	Anti-H3K27me3	None
GM12878_H3K4me3_Broad_None.wig_3.tdf	hg19	ChIP-seq	ILLUMINA	GM12878	H3K4me3	Chromatin state	ChIP-seq	Human	Anti-H3K4me3	None
GM12878_H3K4me1_Broad_None.wig_3.tdf	hg19	ChIP-seq	ILLUMINA	GM12878	H3K4me1	Chromatin state	ChIP-seq	Human	Anti-H3K4me1	None
GM12878_H3K36me3_UW_None.wig_3.tdf	hg19	ChIP-seq	ILLUMINA	GM12878	H3K36me3	Chromatin state	ChIP-seq	Human	Anti-H3K36me3	UW
GM12878_H3K27me3_UW_None.wig_3.tdf	hg19	ChIP-seq	ILLUMINA	GM12878	H3K27me3	Chromatin state	ChIP-seq	Human	Anti-H3K27me3	UW
GM12878_H3K4me3_UW_None.wig_3.tdf	hg19	ChIP-seq	ILLUMINA	GM12878	H3K4me3	Chromatin state	ChIP-seq	Human	Anti-H3K4me3	UW
GM12878_H3K9me3_Broad_None.wig_3.tdf	hg19	ChIP-seq	ILLUMINA	GM12878	H3K9me3	Chromatin state	ChIP-seq	Human	Anti-H3K9me3	None
H3C_hESC_2.bb	hg19	Hi-C	Hi-C	hESC	Chromatin state	Hi-C	Hi-C	Human	None	None
iHMM.M1K16.human_H1.bb	hg19	Hi-C	Hi-C	Human	Chromatin state	Hi-C	Hi-C	Human	None	None
iHMM.M1K16.human_GM.bb	hg19	Hi-C	Hi-C	Human	Chromatin state	Hi-C	Hi-C	Human	None	None
H3C_IMR90_2.bb	hg19	Hi-C	Hi-C	IMR90	Chromatin state	Hi-C	Hi-C	Human	None	None
LAD_fibroblast_2.bb	hg19	LAD	LAD	Fibroblast	Chromatin state	LAD	LAD	Human	None	None



RefSeq Genes





REFINERY PLATFORM

<http://www.refinery-platform.org>

<http://www.github.com/parklab/refinery-platform>

Work in progress!

First release scheduled for late summer

**Thank you open source
developers for your code!**

PP57 | Visual Exploration for Cancer Subtype Analysis (w/ StratomeX)
Tuesday, 10:30 am - Hall 7

WK6 | Integrated Visualization and Computing for Biomedical Research
Tuesday, 2:10 pm - Roof Garden (w/ Jeremy Goecks & Dave Clements)