

How to load data to Galaxy and convert the Genotype Grid file to Flapjack project (not split)

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Step 1: Create a user account in Galaxy

One time only step

Genotype-Grid file – Flapjack file Conversion

Step 1: open the Galaxy Server through this link

<http://13.250.212.83/>

or

<http://111.93.2.172:8088>

Create a user account here or log in

Create account

Email address:

Password:

Strength

Confirm password:

Public name:


Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least three characters in length and contain only lower-case letters, numbers, dots, underscores, and dashes ('.', '_', '-').



Workflow "Run Marker-assisted Backcrossing (MABC) analysis (Input: Intertek/LGC Genotype files)" has been imported.
You can [start using this workflow](#) or [return to the previous page](#).

Click here

- Tools
- search tools
- Get Data
 - Genomic Selection
 - Data Format Conversion
 - Marker Selection
 - Imputation
 - Cluster Analysis
 - GWAS tools
 - Text Manipulation
 - Collection Operations
 - Filter and Sort
 - Join, Subtract and Group
 - Extract Features
 - Fetch Sequences
 - Fetch Alignments
 - Statistics
 - Graph/Display Data
 - VCF intersect
 - HTPG TOOLS
 - Pre-genotyping
 - Post-genotyping
 - TOOLS FROM TOOLSHED
 - GOBII TOOLS



Excellence in Breeding PLATFORM

Welcome to Galaxy!

This instance is dedicated to host tools for the [GOBII](#) project, [HTPG](#) project and [EiB](#) platform.

Take an interactive tour: [Galaxy UI](#) [History](#) [Scratchbook](#)

History

search datasets

Unnamed history
(empty)

This history is empty. You can [load your own data](#) or [get data from an external source](#)

Step 2: Add HTPG Workflows


One time step

← → ↻ ⓘ Not secure | 13.250.212.83

Galaxy / EiB-demo Analyze Data Workflow **Shared Data** Visualization Help User Using 0%

Tools

- Get Data
 - Genomic Selection
 - Data Format Conversion
 - Marker Selection
 - Imputation
 - Cluster Analysis
 - GWAS tools
 - Text Manipulation
 - Collection Operations
 - Filter and Sort
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 **Intelligence in Breeding PLATFORM**

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History Using 0%

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Shared Data dropdown menu:

- Access published resources
- Histories
- Workflows**
- Visualizations
- Pages

Click on Shared data in the menu bar then workflows

- Tools
- Get Data
- Genomic Selection
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- GWAS tools
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- Post-genotyping
- TOOLS FROM TOOLSHED

Published Workflows

search name, annotation, owner, and tags

Advanced Search

Name	Annotation	Owner	Community Rating	Community Tags	Last Updated
Run Marker-assisted Backcrossing (MABC) analysis (Input: Intertek/LGC Genotype file)		wkigoni	★★★★★		~5 days ago
Run F1/Pedigree Verification (Input: HTPG Sample file and Intertek/LGC Genotype files)	Run this workflow to conduct an F1 or Pedigree verification	wkigoni	★★★★★		~5 days ago
Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file)	Run this workflow to get a Flapjack project file from Intertek/LGC file	wkigoni	★★★★★		~5 days ago
Create Split-groups/Populations in Flapjack (Input: Intertek/LGC Genotype grid and HTPG Sample files)	Run this workflow to create split your genotype data into groups/populations in Flapjack	wkigoni	★★★★★		~5 days ago

History

search datasets

Unnamed history (empty)

This history is empty. You can [load your own data](#) or [get data from an external source](#)

Click on import for all workflows

Click on Workflow to see imported workflows now in your user account

Galaxy / EiB-demo

Analyze Data **Workflow** Shared Data Visualization Help User Using 0%

Tools

search tools

Get Data

Genomic Selection

Data Format Conversion

Marker Selection

Imputation

Cluster Analysis

GWAS tools

Text Manipulation

Collection Operations

Filter and Sort

Join, Subtract and Group

Extract Features

Fetch Sequences

Fetch Alignments

Statistics

Graph/Display Data

VCF intersect

HTPG TOOLS

Pre-genotyping

Post-genotyping

TOOLS FROM TOOLSHED

Published Workflows

Chain tools into workflows

search name, annotation, owner, and tags

Advanced Search

Name	Annotation	Owner	Community Rating	Community Tags	Last Updated↓
Run Marker-assisted Backcrossing (MABC) analysis (Input: Intertek/LGC Genotype files)		wkigoni	★★★★★		~5 days ago
Run F1/Pedigree Verification (Input: HTPG Sample file and Intertek/LGC Genotype files)	Run this workflow to conduct an F1 or Pedigree verification	wkigoni	★★★★★		~5 days ago
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Create Split-groups/Populations in Flapjack (Input: Intertek/LGC Genotype grid and HTPG Sample files)	Run this workflow to create split your genotype data into groups/populations in Flapjack	wkigoni	★★★★★		~5 days ago

History

search datasets

Unnamed history

(empty)

This history is empty. You can [load your own data](#) or [get data from an external source](#)

Show all Workflows in the tool Panel

The screenshot shows the Galaxy / EiB-demo interface. The top navigation bar includes 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The left sidebar contains a 'Tools' panel with a search bar and various tool categories like 'Get Data', 'Genomic Selection', 'Data Format Conversion', etc. The main area is titled 'Your workflows' and contains a table of workflows. The right sidebar shows an empty 'History' panel.

Name	Tags	Owner	# of Steps	Published	Show in tools panel
imported: Intertek (HTPG) - Flapjack Analysis		You	4	No	<input checked="" type="checkbox"/>
imported: Create Split-groups/Populations in Flapjack (Input: Intertek/LGC Genotype grid and HTPG Sample files)		You	5	No	<input checked="" type="checkbox"/>
imported: Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file)		You	3	No	<input checked="" type="checkbox"/>
imported: Run F1/Pedigree Verification (Input: HTPG Sample file and Intertek/LGC Genotype files)		You	3	No	<input checked="" type="checkbox"/>
imported: Run Marker-assisted Backcrossing (MABC) analysis (Input: Intertek/LGC Genotype files)		You	3	No	<input checked="" type="checkbox"/>

A red box highlights the 'Show in tools panel' column, and a red arrow points to it from a text box that says 'Check this box for all workflows'.

Click on Analyse data to see all the workflows in the tool panels

Galaxy / EiB-demo

Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools

TOOLS FROM TOOLSHED

search tools

GOBII TOOLS

Flapjack Tools

Workflows

- All workflows
- imported: Intertek (HTPG) - Flapjack Analysis
- imported: Create Split-groups/Populations in Flapjack (Input: Intertek/LGC Genotype_grid and HTPG Sample files).
- imported: Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file).
- imported: Run F1/Pedigree Verification (Input: HTPG Sample file and Intertek/LGC Genotype files).
- imported: Run Marker-assisted Backcrossing (MABC) analysis (Input: Intertek/LGC Genotype files).

Excellence in Breeding PLATFORM

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Take an interactive tour: [Galaxy UI](#) [History](#) [Scratchbook](#)

History

search datasets

Unnamed history (empty)

This history is empty. You can [load your own data](#) or [get data from an external source](#)

NB: In future, all these workflows will be present on the tools pane and hence whenever you log into your account

Step 1: Loading data into Galaxy

NB: This is a routine step whenever running an analysis in Galaxy that requires a file as the input

Galaxy Interphase

The screenshot shows the Galaxy web interface in a browser window. The browser address bar shows the URL 111.93.2.172:8083. The interface has a dark blue header with the Galaxy logo and navigation menus: Analyze Data, Workflow, Shared Data, Visualization, Help, and User. The main content area is divided into three panels:

- Tools panel (left):** A sidebar with a search bar and a list of tool categories including Get Data, Send Data, Collection Operations, Text Manipulation, Filter and Sort, Join, Subtract and Group, Convert Formats, Extract Features, Fetch Sequences, Fetch Alignments, Statistics, Graph/Display Data, HTPG Tools, NGS, Population Tools, and Workflows (with sub-items All workflows and HTPG Flapjack Analysis).
- Analysis Panel (center):** A large area with a light gray background. It displays a welcome message: "Hello, Galaxy is running!". Below this, it says "To customize this page edit static/welcome.html" and provides two buttons: "Configuring Galaxy »" and "Installing Tools »". It also offers an interactive tour with links for "Galaxy UI", "History", and "Scratchbook". At the bottom, it provides information about Galaxy being an open platform for data intensive research, developed by The Galaxy Team, and supported by various institutions.
- Data panel (right):** A sidebar with a search bar and a section titled "Unnamed history (empty)". A blue information box states: "This history is empty. You can load your own data or get data from an external source".

Tools panel:

This is where you find the tools and Workflows

Analysis Panel:

This is where the analysis is done when a tool or workflow is run.

Data panel:

This is where all Uploaded data and results files from analysis are found.

Click on Upload file

Galaxy / EiB-demo Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools search tools

Get Data
Upload File from your computer

Genomic Selection
Data Format Conversion
Marker Selection
Imputation
Cluster Analysis
GWAS tools
Text Manipulation
Collection Operations
Filter and Sort
Join, Subtract and Group
Extract Features
Fetch Sequences
Fetch Alignments
Statistics
Graph/Display Data
VCF intersect

HTPG TOOLS
Pre-genotyping
Post-genotyping

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History search datasets

Unnamed history
(empty)

i This history is empty. You can [load your own data](#) or [get data from an external source](#)

Tools

search tools

Get Data

Upload File from your computer

Genomic Selection

Data Format Conversion

Marker Selection

Imputation

Cluster Analysis

GWAS tools

Text Manipulation

Collection Operations

Filter and Sort

Join, Subtract and Group

Extract Features

Fetch Sequences

Fetch Alignments

Statistics

Graph/Display Data

VCF intersect

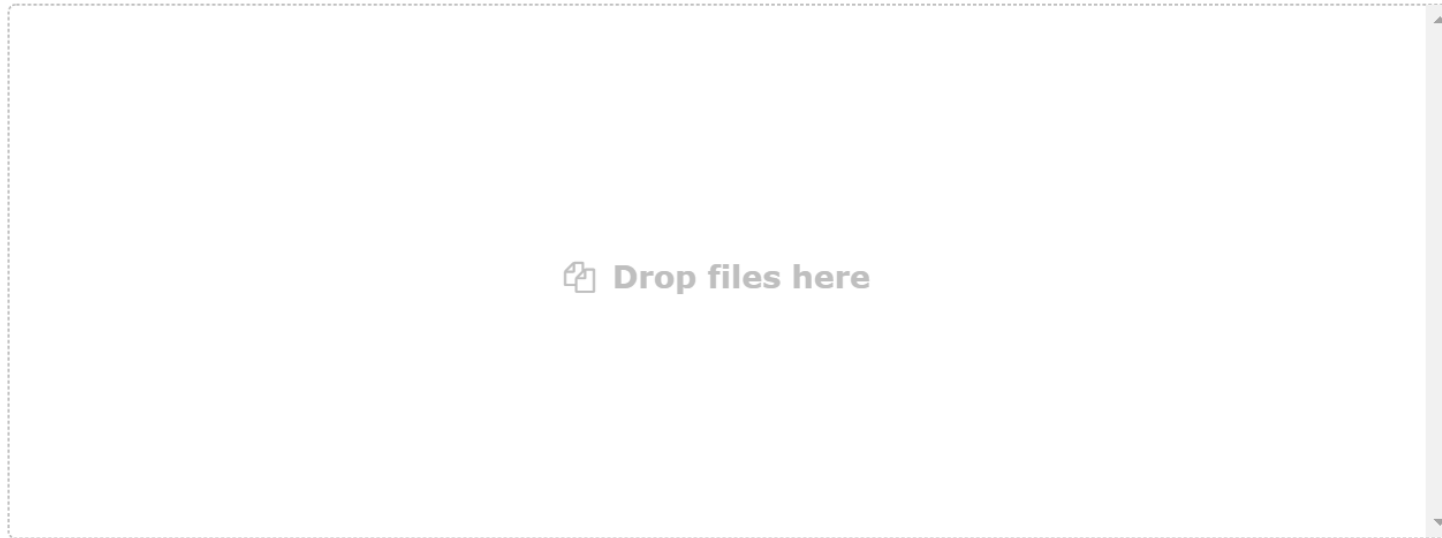
HTPG TOOLS

Pre-genotyping

Post-genotyping

Download from web or upload from disk

Regular Composite Collection



Type (set all): 🔍

Genome (set all):

Select your genotype Grid file in your computer

The image shows a web browser window with a file selection dialog box open. The dialog box is titled "Open" and shows the contents of a folder named "direct_Intertek-Fj". The file "example_grid_file" is selected, and its name is entered in the "File name:" field. The "Open" button is highlighted with a red box. The background interface includes a sidebar with menu items: "Fetch Sequences", "Fetch Alignments", "Statistics", "Graph/Display Data", "VCF intersect", "HTPG TOOLS", "Pre-genotyping", and "Post-genotyping". The main area has a search bar with "Type (set all):" set to "Auto-detect" and "Genome (set all):" set to "---- Additional Species A...". At the bottom, there are buttons for "Choose local file", "Paste/Fetch data", "Pause", "Reset", "Start", and "Close".

Name	Date modified
direct_intertek-Fj_conversion_example_output	8/15/2018 11:45 AM
<input checked="" type="checkbox"/> example_grid_file	8/15/2018 11:44 AM

File name: example_grid_file All Files

Open Cancel

Type (set all): Auto-detect Q Genome (set all): ---- Additional Species A...

Choose local file Paste/Fetch data Pause Reset Start Close

Tools

search tools

Get Data

Upload File from your
computer

Genomic Selection

Data Format Conversion

Marker Selection

Imputation

Cluster Analysis

GWAS tools

Text Manipulation

Collection Operations

Filter and Sort

Join, Subtract and Group

Extract Features

Fetch Sequences

Fetch Alignments

Statistics

Graph/Display Data

VCF intersect

HTPG TOOLS

Pre-genotyping







Post-genotyping

Download from web or upload from disk


Regular

Composite



Collection

Name	Size	Type	Genome	Settings	Status
 example_grid_file.xlsx	234.5 KB	Auto-dete...  	----- Additional Sp... 		100% 

Type (set all):

Auto-detect 

Genome (set all):

----- Additional Species A...  Choose local file Paste/Fetch data

Pause

Reset

Start

Close

Click on Start to upload
the file to Galaxy then
Close

Tools

search tools

Get Data
Upload File from your computer

Genomic Selection

Data Format Conversion

Marker Selection

Imputation

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GWAS tools

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Pre-genotyping

Post-genotyping



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History

search datasets

Unnamed history
1 shown

234.53 KB

**1: example_grid_file.x
lsx**

Your file will be added to the data panel

Click on the desired workflow for your data conversion

The screenshot displays the Galaxy / EiB-demo interface. The top navigation bar includes 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The left sidebar contains a 'Tools' section with a search bar and categories like 'Pre-genotyping', 'Post-genotyping', and 'Flapjack Tools'. Under 'Workflows', three items are listed, with the first two highlighted in red boxes. The main content area features the 'Excellence in Breeding PLATFORM' logo and a 'Welcome to Galaxy!' message. The right sidebar shows a 'History' section with a search bar and a list of datasets, including '1: example_grid_file.x'.

Galaxy / EiB-demo

Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools

search tools

HTPG TOOLS

Pre-genotyping

Post-genotyping

TOOLS FROM TOOLSHED

GOBII TOOLS

Flapjack Tools

Workflows

- All workflows
- imported: Intertek (HTPG) - Flapjack Analysis
- imported: Create Split-groups/Populations in Flapjack (Input: Intertek/LGC Genotype_grid and HTPG Sample_files)
- imported: Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file)
- imported: Run F1/Pedigree Verification (Input: HTPG Sample file and Intertek/LGC Genotype_files)

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History

search datasets

Unnamed history

1 shown

234.53 KB

1: example_grid_file.x
lsx

To create a Flapjack file with split populations

To convert a single Genotype file directly to Fj project file

Step 2:

Running the “Directly convert a Genotype Grid File to a Flapjack Project”
Workflow

Information about what the workflow does and the required input is available here

Galaxy / EiB-demo Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools search tools

Workflow: imported: Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file) Run workflow

History Options
Send results to a new history
Yes No

1: Intertek/LGC Genotype Grid file (Galaxy Version 1.0.0)
excel_workbook
1: example_grid_file.xlsx
1: example_grid_file.xlsx

2: Intertek-Flapjack Converter (Galaxy Version 1.0.0)

3: Flapjack Project File (Galaxy Version 0.0.1)
Flapjack genotype file
Output dataset 'out_file' from step 2
Flapjack map file
Nothing selected
Flapjack-formatted (tab-delimited text) input file of map data
Flapjack phenotype file

History search datasets
Unnamed history
1 shown
234.53 KB
1: example_grid_file.xlsx

Choose your input data here

Tools

search tools

- Get Data
- Genomic Selection
- Data Format Conversion
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- Statistics
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- VCF intersect
- HTPG TOOLS
- Pre-genotyping
- Post-genotyping
- TOOLS FROM TOOLSHED

Workflow: imported: Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file)

Run workflow

Click here to run analysis

History Options

Send results to a new history

Yes No

1: Intertek/LGC Genotype Grid file (Galaxy Version 1.0.0)

excel_workbook

1: example_grid_file.xlsx

Select an excel file

Job Post Actions

Hide output 'sheet2'. Hide output 'sheet3'. Hide output 'sheet1'.

2: Intertek-Flapjack Converter (Galaxy Version 1.0.0)

3: Flapjack Project File (Galaxy Version 0.0.1)

Flapjack genotype file

Output dataset 'out_file' from step 2

Flapjack map file

Nothing selected

Flapjack-formatted (tab-delimited text) input file of map data

Flapjack phenotype file

History

search datasets

Unnamed history

1 shown

234.53 KB

1: example_grid_file.xlsx

Area for displaying workflow history and results, currently empty.



Tools



search tools

**Get Data****Genomic Selection****Data Format Conversion****Marker Selection****Imputation****Cluster Analysis****GWAS tools****Text Manipulation****Collection Operations****Filter and Sort****Join, Subtract and Group****Extract Features****Fetch Sequences****Fetch Alignments****Statistics****Graph/Display Data****VCF intersect**

HTPG TOOLS

Pre-genotyping**Post-genotyping**

TOOLS FROM TOOLSHED



Successfully invoked workflow **imported: Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file)**.

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

History

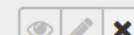
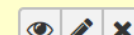
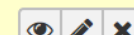
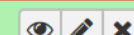


search datasets

**Unnamed history**

6 shown

234.53 KB

**6: Flapjack CreateP
roject on data 5****5: Flapjack_file.gen
otype****4: Worksheet3_file.
txt****3: Worksheet2_file.
txt****2: Worksheet1_file.
txt****1: example_grid_file.x
lsx**

Check here for the progress. All output files should turn green when the analysis is over



Tools



search tools



Get Data

Genomic Selection

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TOOLS FROM TOOLSHED



Successfully invoked workflow **imported: Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file).**

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

History



search datasets



Unnamed history

3 shown, 3 hidden

1.44 MB



6: Flapjack CreateProject on data 5



589.0 KB

format: **flapjack**, database: ?

Map/marker cache created in 3ms

Reading line 100 (7ms)

Reading line 200 (6ms)

Reading line 300 (4ms)

Reading line 400 (2ms)

Reading line 500 (3ms)

Reading line 600 (2ms)

Reading line 700 (2ms)

Reading line 800 (2ms)

Reading line 900 (2ms)

Reading line 10



Display in Flapjack: [View](#) ([Help](#))

binary data

Click on the Flapjack file to see details

5: Flapjack_file.gen





Tools



search tools



Get Data

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HTPG TOOLS

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TOOLS FROM TOOLSHED



Successfully invoked workflow **imported: Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file).**

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

History



search datasets



Unnamed history

3 shown, 3 hidden

1.44 MB



6: Flapjack CreateProject on data 5



589.0 KB

format: **flapjack**, database: ?

Map/marker cache created in 3ms
Reading line 100 (7ms)
Reading line 200 (6ms)
Reading line 300 (4ms)
Reading line 400 (2ms)
Reading line 500 (3ms)
Reading line 600 (2ms)
Reading line 700 (2ms)
Reading line 800 (2ms)
Reading line 900 (2ms)
Reading line 10



Download in Flapjack: [View \(Help\)](#)

binary data

Save As

« Desk > IRR1_August_Breeders_... Search IRR1_August_Breeders_...

Organize New folder

Name	Date modified	Type
galaxy_demo	8/22/2018 6:39 AM	File

File name: Galaxy6-[Flapjack_CreateProject_on_data_5]

Save as type: Flapjack Project

Save Cancel

Visualization Help User

Using 0%

Convert Genotype file to a Flapjack project (Input: ...)

the resulting data by refreshing the History pane. When the job 'finished' if completed successfully or 'error' if problems

History

search datasets

Unnamed history
3 shown, 3 hidden

1.44 MB

6: Flapjack CreateProject on data 5
589.0 KB
format: flapjack, database: ?

Map/marker cache created in 3ms

- Reading line 100 (7ms)
- Reading line 200 (6ms)
- Reading line 300 (4ms)
- Reading line 400 (2ms)
- Reading line 500 (3ms)
- Reading line 600 (2ms)
- Reading line 700 (2ms)
- Reading line 800 (2ms)
- Reading line 900 (2ms)
- Reading line 10

Display in Flapjack: View (Help)

binary data

5: Flapjack_file.gen

Open the save file in Flapjack and run analysis

direct_intertek-Fj_conversion_example_output.flapjack - Flapjack - 1.18.06.29

File Edit View Visualization Analysis Data Help

New Project Open Project Import Data Find Genotypes Chromosomes

Chromosome: 1 1,728 lines, 34 markers, length: 33

dataset_2038 1728x34
Trait Data
Default View

sample_1 G C G T C T A C A A C T G T A G G T A C T T A C G C A A G A T G T T G G A
sample_2 G C G T C C A C A A C T G T T G G T A C T T A C G G A A G A T G T T G G A C
sample_3 C T
sample_4 G C G T C C A C A A C T A T T A G G T A C T T A C G G A A G A T G T T G G A C
sample_5 G C G T C C A C A A C T A T T A G G T A C T T A C G G A A G A T G T T G G A C
sample_6 G C G T C C A C A A C T A G T T A G G T A C T T A C G G A A G A T G T T G G A C
sample_7 G C G T C C A C A A C T A G T T A G G T A C T T A C G G A A G A T G T T G G A C
sample_8 G C G T C C A C A A C T A G T T A G G T A C T T A C G G A A G A T G T T G G A C
sample_9 G C G T C C A C A A C T A G T T A G G T A C T T A C G G A A G A T G T T G G A C
sample_10 G C G T C C A C A A C T A T T G G T A C T T A C G G A A G A T G T T G G A C
sample_11 G C G T C T G C A A C T G T T G G T A C C T A C G C A A G A T G T T G G A C
sample_12 G C G T C T G C A A C T G T A G G T A C C T A C G C A A G A T G T T G G A C
sample_13 G C G T C T G C A A C T G T T A G G T A C C T A C G C A A G A T G T T G G A C
sample_14 G C G T C T G C A A C T G T T A G G T A C C T A C G C A A G A T G T T G G A C
sample_15 G C G T C T G C A A C T G T T G G T A C C T A C G C A A G A T G T T G G A C
sample_16 G C G T C T G C A A C T G T T G G T A C C T A C G C A A G A T G T T G G A C
sample_17 G C G T C T G C A A C T G T T G G T A C C T A C G C A A G A T G T T G G A C
sample_18 G C G T C C A C A A C T A T T G G T A C C T A C G C A A G A T G T T G G A C
sample_19 G C G T C C A C A A C T A T T G G T A C C T A C G C A A G A T G T T G G A C
sample_20 G C G T C C A C A A C T A T T G G T A C C T A C G C A A G A T G T T G G A C

Overview

Line:
Marker:
Genotype:

Zoom:

Flapjack Tip: Hold CTRL while clicking and dragging lines or markers to move them to new positions

21x36, 4C, 7T, 118.62MB

How to create a Split-populations Flapjack project file

Step 1. Create the following analysis file

Clipboard: Paste, Cut, Copy, Format Painter
Font: Calibri, 11, Bold, Italic, Underline, Text Color, Background Color, Font Color
Alignment: Wrap Text, Merge & Center
Number: General, \$, %, .00, .00
Styles: Conditional Formatting, Format as Table, Cell Styles
Cells: Insert, Delete, Format
Editing: AutoSum, Fill, Clear, Sort & Find & Filter, Select

	A	B	C	D	E	F	G	H	I	K	L	M	N	O	P	
1	KBiosciences grid report															
2	Grid version 1.03															
3	More information is available in the Genotyping-.csv file. This file lists only the calls for each SNP on each well with a subject ID. When a subject ID is duplicated and the calls don't match															
4	Project number											0				
5	Order number											0				
6	Plates											17970-01	17970-02	17970-03	17970-04	17970-05
7																
8	DNA \ Assay	snpOS0089	snpOS0096	snpOS0061	snpOS0054	snpOS0002	snpOS0007	snpOS0005	snpOS0024	snpOS0040	snpOS0295	snpOS0296	snpOS0297	snpOS0298	snpOS0299	
9	2db17703b53a	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
10	494d342c5de2	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
11	43b60a8864c4	G:G	C:C	G:G	C:C	A:A	?	A:A	A:A	C:C	C:C	?	C:C	A:A	A:A	
12	eb3c0afb963c	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
13	041e37041746	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
14	ed19fd708927	G:G	?	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
15	66324c99753e	G:G	?	C:C	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
16	33b8a0f69eea	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
17	45d4e08a7b57	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
18	edff59da7d58	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
19	f3d1fb26c36c	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
20	e55de89d3d4c	?	?	C:G	?	?	?	A:T	?	?	?	?	?	?	A:T	
21	a0b87f5b99c5	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	
22	9ca31f064b28	G:G	C:C	G:G	C:C	A:A	G:G	A:A	A:A	C:C	C:C	G:G	C:C	A:A	A:A	

Worksheet 1: Genotype Grid file

File Home Insert Page Layout Formulas Data Review View Tell me what you want to do... Kigoni, Milcah (ICRISAT-Nairobi)

Clipboard: Paste, Copy, Format Painter, Cut

Font: Calibri, 11, Bold, Italic, Underline, Text Color, Background Color, Font Color

Alignment: Wrap Text, Merge & Center

Number: General, Currency, Percentage, Decimals

Styles: Conditional Formatting, Table, Cell Styles

Cells: Insert, Delete, Format

Editing: AutoSum, Fill, Clear, Sort & Find & Filter, Select

	A	B	C	D	E	F	G	H	I	J	K	L
1	dnarun_name	germplasm_name	dnasample_name	germplasm_pedigree	germplasm_type	germplasm_par1	germplasm_par1_type	germplasm_par2	germplasm_par2_type	dnasample_sample_group	dnasample_sample_group_cycle	dnasample_UUID
2	2db17703b53a	XBL-167-s1		inbred	parent					xbl-2018-P3		142cf886-a065-11e8-98d0-52
3	494d342c5de2	XBL-167-s2		inbred	parent					xbl-2018-P3		142cf5a-a065-11e8-98d0-52
4	43b60a8864c4	XBL-167-s3		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142cfec6-a065-11e8-98d0-52
5	eb3c0afb963c	XBL-167-s4		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d0164-a065-11e8-98d0-52
6	041e37041746	XBL-167-s5		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d03d0-a065-11e8-98d0-52
7	ed19fd708927	XBL-167-s6		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d05f6-a065-11e8-98d0-52
8	66324c99753e	XBL-167-s7		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d0b82-a065-11e8-98d0-52
9	33b8a0f69eea	XBL-167-s8		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d0de4-a065-11e8-98d0-52
10	45d4e08a7b57	XBL-167-s9		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d1000-a065-11e8-98d0-52
11	edff59da7d58	XBL-167-s10		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d123a-a065-11e8-98d0-52
12	f3d1fb26c36c	XBL-167-s11		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d14ce-a065-11e8-98d0-52
13	e55de89d3d4c	XBL-167-s12		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d17d0-a065-11e8-98d0-52
14	a0b87f5b99c5	XBL-167-s13		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d2374-a065-11e8-98d0-52
15	9ca31f064b28	XBL-167-s14		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d2608-a065-11e8-98d0-52
16	f174d75ed456	XBL-167-s15		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d2856-a065-11e8-98d0-52
17	87d7e26e0a7f	XBL-167-s16		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d2aa4-a065-11e8-98d0-52
18	83aafcd2e60d	XBL-167-s17		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d2cca-a065-11e8-98d0-52
19	6769870c098a	XBL-167-s18		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d368e-a065-11e8-98d0-52
20	7d580709fcd7	XBL-167-s19		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d3bc0-a065-11e8-98d0-52
21	773ff9f46a82	XBL-167-s20		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d3eae-a065-11e8-98d0-52
22	b2c61fea53f3	XBL-167-s21		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d414c-a065-11e8-98d0-52
23	79fe18e33844	XBL-167-s22		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d43ea-a065-11e8-98d0-52
24	132c1ded06a1	XBL-167-s23		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d4f3e-a065-11e8-98d0-52
25	21ddd729df9	XBL-167-s24		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d51a0-a065-11e8-98d0-52
26	c0d2d40b80a3	XBL-167-s25		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d53e4-a065-11e8-98d0-52
27	b4ff5601f33a	XBL-167-s26		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d55f6-a065-11e8-98d0-52
28	1b8badb4e7ac	XBL-167-s27		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d5858-a065-11e8-98d0-52
29	31250a1658c4	XBL-167-s28		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d5a74-a065-11e8-98d0-52
30	bf813c051e0e	XBL-167-s29		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d5ca4-a065-11e8-98d0-52
31	405d291372bc	XBL-167-s30		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d68de-a065-11e8-98d0-52
32	9e0dcf8473ee	XBL-167-s31		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d6b36-a065-11e8-98d0-52
33	222cf749a76	XBL-167-s32		KR-104/Sika-105	F1	KR 104	DP	SIKA	RP	xbl-2018-P3		142d7a2c-a065-11e8-98d0-52

Genotype_Grid_file **Sample_file** SNP_info_Summary_file

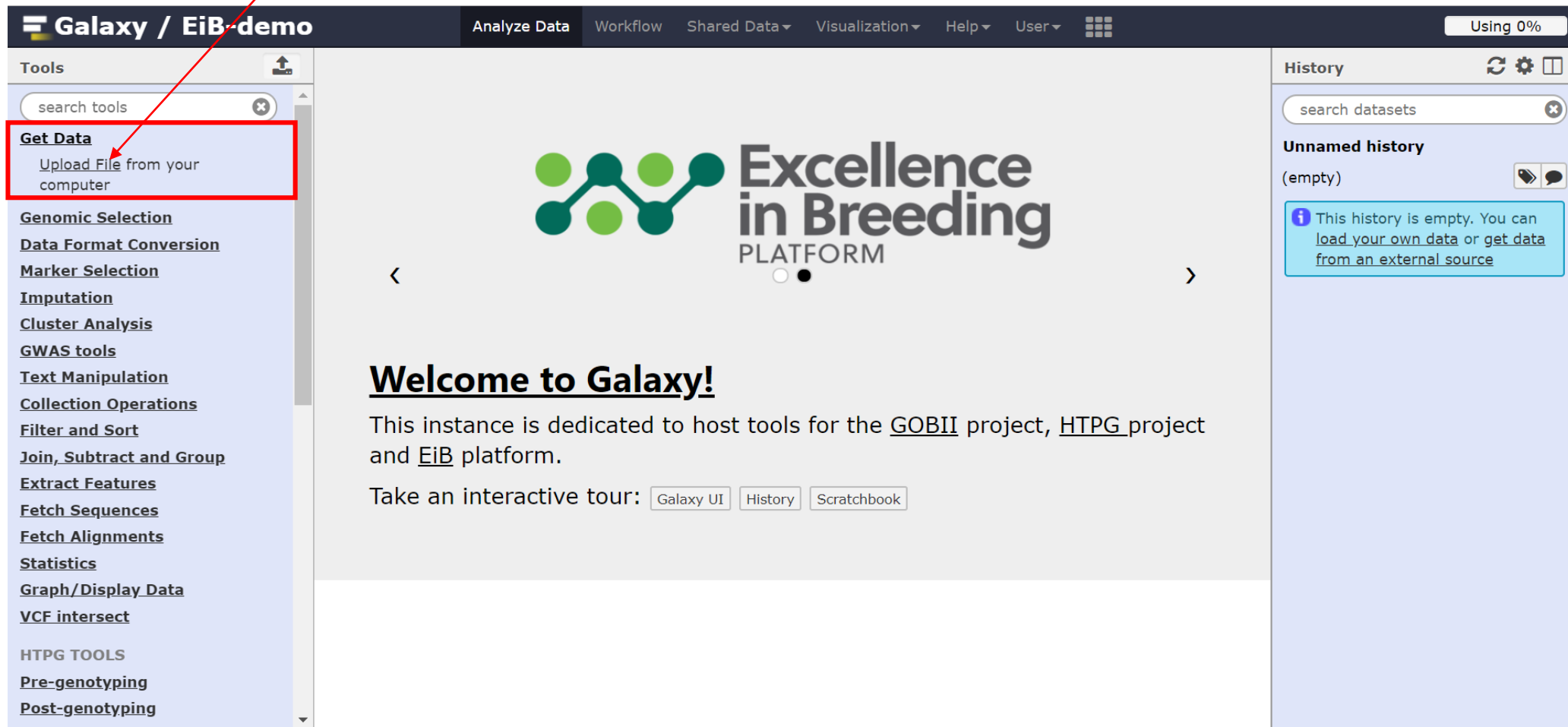
Worksheet 2: Your filled HTPG Sample file
 NB: Splitting will be done according to how samples are group in column (dnasample_sample_group). See a completed example above

	A	B	C	D	E	F	G
1	Intertek SNP ID	Customer_SNP_ID	Trait/Gene	Favorable_Allele	Unfavorable_Allele		
2	snpOS0089	MSU7_3_31323659_[C/G]	Drought/DTY3.1	C	T		
3	snpOS0096	S12_17618268	Drought/DTY12.1	AG	TC		
4	snpOS0061	Xa21_SKEP	BLB/Xa21	A	C		
5	snpOS0054	xa5-S1_SKEP	BLB/xa5	G	A		
6	snpOS0002	S8_27520607	BLB/xa13	A	G		
7	snpOS0007a	Pi9-1a	Blast/Pi9	A	G		
8	snpOS0009	Pi2-1	Blast/Pi2	A	T		
9	snpOS0024	chalk5_576	Chalky/Chalk5	T	C		
10	snpOS0031	BadH2_3bp_E12	Fragrance/BADH2	T	C		
11	snpOS0040	s9_6774928	Submergence/Submergence	G	A		
12							
13							
14							
15							
16							
17							
18							
19							
20							
21							
22							

worksheet 3: Your SNP/Marker summary information in (optional)


Step 2. Upload your analysis file in Galaxy


Click on Upload file



The screenshot displays the Galaxy / EiB-demo web interface. The top navigation bar includes 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The left sidebar contains a 'Tools' section with a search bar and a list of tool categories. The 'Get Data' category is highlighted with a red box, and the 'Upload File from your computer' option is selected. The main content area features the 'Excellence in Breeding PLATFORM' logo and a 'Welcome to Galaxy!' message. The right sidebar shows the 'History' section, which is currently empty.

Galaxy / EiB-demo Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools 

search tools 

Get Data

Upload File from your computer

Genomic Selection

Data Format Conversion

Marker Selection

Imputation

Cluster Analysis

GWAS tools

Text Manipulation

Collection Operations

Filter and Sort

Join, Subtract and Group

Extract Features

Fetch Sequences

Fetch Alignments

Statistics


Graph/Display Data

VCF intersect

HTPG TOOLS

Pre-genotyping




Post-genotyping


 **Excellence in Breeding**
PLATFORM



Welcome to Galaxy!

This instance is dedicated to host tools for the [GOBII](#) project, [HTPG](#) project and [EiB](#) platform.

Take an interactive tour: [Galaxy UI](#) [History](#) [Scratchbook](#)

History   

search datasets 

Unnamed history
(empty)  

i This history is empty. You can [load your own data](#) or [get data from an external source](#)

Galaxy

111.93.2.172:8083

Galaxy

Analyze Data Workflow Shared Data Visualization Help User

Tools

search tools

Get Data

plink - Filter large VCF file

Upload File from your computer

UCSC Main table browser

UCSC Test table browser

UCSC Archaea table browser

EBI SRA ENA SRA

Get Microbial Data

BioMart Ensembl server

CBI Rice Mart rice mart

GrameneMart Central server

modENCODE fly server

Flymine server

Flymine test server

modENCODE modMine server

MouseMine server

Ratmine server

YeastMine server

Download from web or upload from disk

Regular Composite Collection

Name	Size	Type	Genome	Settings	Status
File3_HTPG_analysis_file(Galaxy_input).xlsx	697.6 KB	Auto-dete...	---- Additional Sp...	⚙️	100% ✓

Type (set all): Auto-detect Q Genome (set all): ---- Additional Species A...

Choose local file Paste/Fetch data Pause Reset Start Close

1. Click here to browse for excel file in your computer

2. Click on start to load, then close

Click on the Create Split-groups/populations workflow or Intertek (HTPG) Flapjack Analysis

Galaxy / EiB-demo Analyze Data Workflow Shared Data Visualization Help User Using 0%

Tools

search tools

HTPG TOOLS

Pre-genotyping

Post-genotyping

TOOLS FROM TOOLSHED

GOBII TOOLS

Flapjack Tools

Workflows

- All workflows
- imported: Intertek (HTPG) - Flapjack Analysis**
- imported: Create Split-groups/Populations in Flapjack (Input: Intertek/LGC Genotype_grid and HTPG Sample files)
- imported: Directly Convert Genotype file to a Flapjack project (Input: Intertek/LGC grid file)
- imported: Run F1/Pedigree Verification (Input: HTPG Sample file and Intertek/LGC Genotype files)

Excellence in Breeding PLATFORM

Welcome to Galaxy!

This instance is dedicated to host tools for the GOBII project, HTPG project and EiB platform.

Take an interactive tour: [Galaxy UI](#) [History](#) [Scratchbook](#)

History

search datasets

Unnamed history

1 shown

234.53 KB

1: example_grid_file.xlsx

To create a Flapjack file with split populations Click here

Click Run Workflow

The screenshot displays the Galaxy web interface for configuring a workflow. The browser address bar shows the URL `111.93.2.172:8083/workflow/run?id=ebfb8f50c6abde6d`. The main header includes the Galaxy logo and navigation tabs for 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The top right corner indicates 'Using 4.6 MB'.

The left sidebar contains a 'Tools' section with a search bar and a list of tool categories: Get Data, Send Data, Collection Operations, Text Manipulation, Filter and Sort, Join, Subtract and Group, Convert Formats, Extract Features, Fetch Sequences, Fetch Alignments, Statistics, Graph/Display Data, HTPG Tools, NGS, Population Tools, and Workflows. Under 'Workflows', there is a link to 'HTPG/Intertek-Flapjack_analysis'.

The main content area is titled 'Workflow: HTPG/Intertek-Flapjack_analysis' and features a 'Run workflow' button. The workflow is composed of four steps:

- Step 1: excel to txt extractor (Galaxy Version 1.0.0)**
 - Input: `2: File3_HTPG_analysis_file(Galaxy_input).xlsx`
 - Output: `2: File3_HTPG_analysis_file(Galaxy_input).xlsx`
- Step 2: Intertek to Flapjack converter (Galaxy Version 1.0.0)**
- Step 3: Intertek / Flapjack - SNP Sample File Processor (Galaxy Version 0.0.1)**
 - Output dataset 'output' from step 3
- Step 4: Flapjack Split By Sample (Galaxy Version 0.0.1)**
 - Output dataset 'sampleFile_sheet2' from step 1

Below the steps, there are sections for 'Flapjack genotype file', 'Flapjack phenotype file', and 'Flapjack map file', each with a dropdown menu currently set to 'Nothing selected'.

The right sidebar shows the 'History' panel with a search bar and a list of datasets. The current history is 'Unnamed history' with 1 shown and 1 deleted, totaling 1.36 MB. A dataset is listed: `2: File3_HTPG_analysis_file(Galaxy_input).xlsx`.

A red arrow points from the text 'Click Run Workflow' to the 'Run workflow' button.

Galaxy x milcah - [Icons] x

111.93.2.172:8083/workflow/run?id=ebfb8f50c6abde6d

Galaxy Analyze Data Workflow Shared Data Visualization Help User Using 5.9 MB

Tools [Upload Icon]

search tools [Close]

- Get Data
- Send Data
- Collection Operations
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Statistics
- Graph/Display Data
- HTPG Tools
- NGS
- Population Tools

Workflows

- All workflows
- HTPG/Intertek-Flapjack_analysis

✓ Successfully invoked workflow **HTPG/Intertek-Flapjack_analysis**.

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

History [Refresh] [Settings] [List Icon]

search datasets [Close]

Unnamed history
2 shown, 4 deleted, 2 hidden

2.63 MB [Check] [Trash] [Comment]

8: Flapjack Split By Sample on data 4 and data 7 [Eye] [Edit] [Close]

2: File3_HTPG_analysis_file(Galaxy_input).xlsx [Eye] [Edit] [Close]

Click on the top file

The screenshot shows the Galaxy web interface. At the top, the browser address bar displays the URL `111.93.2.172:8083/workflow/run?id=ebfb8f50c6abde6d`. The Galaxy header includes navigation tabs for **Analyze Data**, **Workflow**, **Shared Data**, **Visualization**, **Help**, and **User**, along with a **Using 5.9 MB** indicator.

On the left, the **Tools** sidebar is visible, listing categories such as **Get Data**, **Send Data**, **Collection Operations**, **Text Manipulation**, **Filter and Sort**, **Join, Subtract and Group**, **Convert Formats**, **Extract Features**, **Fetch Sequences**, **Fetch Alignments**, **Statistics**, **Graph/Display Data**, **HTPG Tools**, **NGS**, **Population Tools**, and **Workflows**. Under **Workflows**, the workflow `HTPG/Intertek-Flapjack_analysis` is listed.

The main workspace contains a green notification box with a checkmark icon, stating: **Successfully invoked workflow HTPG/Intertek-Flapjack_analysis.** Below this, a message explains that the workflow status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

On the right, the **History** sidebar shows a search bar and a list of datasets. The selected entry is **8: Flapjack Split By Sample on data 4 and data 7**, with a size of 1.0 MB and format `flapjack`. The details for this entry include: `Map/marker cache created in 1ms`, `Map All Chromosomes has length 9.0`, `Importing traits from /data/galaxy-data/galaxy/database/tmp/tmp...`, `No SQLite format 3 header`, `DB Serialization Cache: 0ms`, `Project saved in 736ms`, `Project created`, `got entry: null`, and `Project`. At the bottom of the history entry, there is a **Download** icon (a floppy disk) and a **Help** icon (a question mark).

Click on Download icon and save file

Save As

« IRRI_... » Sample_tracking and G... Search Sample_tracking and G...

Organize New folder

This PC

- 3D Objects
- Desktop
- Documents
- Downloads
- Music
- Pictures
- Videos
- Windows (C:)
- LENOVO (D:)

Name	Date modified	Type
galaxy_demo	8/23/2018 1:45 PM	File

File name: Split-flapjack_project-file-irri

Save as type: Flapjack Project

Save Cancel

Visualization Help User

Split-groups/Populations in Flapjack (Input: files).

the resulting data by refreshing the History pane. When the job 'finished' if completed successfully or 'error' if problems

History

search data

Unnamed I
7 shown, 28

3.55 MB

35: Flapjack
ample on c
data 34

258.0 KB
format: flap

Map/marke
Map All Chr
23.0
Importing t
/home/gala

No SQLite f
DB Serializ
Project sav
Project cre
got entry: i

Display in F
binary data

Split populations

Split-flapjack_project-file-irri.flapjack - Flapjack - 1.18.06.29

File Edit View Visualization Analysis Data Help

New Project Open Project Import Data Find Genotypes Chromosomes

Data Sets

- xbl-2018-P3 60x24
 - Trait Data
 - Default View
- RRN-2018-P1 40x24
 - Trait Data
 - Default View

Chromosome: All Chromosomes 60 lines, 24 markers, length: 23

45d4e08a...	XBL-167-s9	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T	G	T	A	G	G	G	C	
edff59da...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T	G	T	A	G	G	G	C	
f3d1fb26...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T	G	T	A	G	G	G	C	
e55de89d...	XBL-167...	KR-104/Sika...			C	G	F	U										A	T			T	G	T	G	
a0b87f5b...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T		T	A	G	G	G	C	
9ca31f06...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T	A	G	T	A	G	G	G	C
f174d75e...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T		A	A	G	G	G	C	
87d7e26e...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T	G	T	A	G	G	G	C	
83aafcd2...	XBL-167...	KR-104/Sika...	G	C	C	U	A	U	U	A	U	C	C	G	C	A	A	T		T	A		G	G	C	
6769870c...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T			A	G	G	G	C	
7d580709...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T	G	T	A	G	G	G	C	
773ff9f4...	XBL-167...	KR-104/Sika...	G	C			U	U	U	A	U	C	C	G	C	A	A	T		T	A	G	G	G	C	
b2c61fea...	XBL-167...	KR-104/Sika...	G	C			U	A	U		A	U	C	C	G	C	A	A	T	A	G	T	A	G	G	C
79fe18e3...	XBL-167...	KR-104/Sika...	G		G	U	A	U	U	A	U	C	C	G	C	A	A	T		T	A		G	G	C	
132c1ded...	XBL-167...	KR-104/Sika...	G	C	C	U	A	U	U	A	U	C			C	A	A	T	G	T	A	G	G	G	C	
21ddd72...	XBL-167...	KR-104/Sika...	G		G	U	A	U	U	A	U	C	C	G	C	A	A	T		T	A	G	G	G	C	
c0d2d40b...	XBL-167...	KR-104/Sika...	G		G	U	A	U	U	A	U	C	C	G	C	A	A	T	A	G	T	A	G	G	G	C
b4ff5601...	XBL-167...	KR-104/Sika...	G		G	U	A	U	U	A	U	C	C		C	A	A	T		T	A	G	G	G	C	
1b8badb4...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C		C	A	A	T	G	T	A		G	G	C	
31250a16...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T	G	T	A	G	G	G	C	
bf813c05...	XBL-167...	KR-104/Sika...	G	C	G	U	A	U	U	A	U	C	C	G	C	A	A	T	G	T	A	G	G	G	C	



Line:
Marker:
Genotype:

Zoom:



Flapjack Tip: Quickly track locations of interest by right-clicking on the display and selecting 'Bookmark location'

22x29, 4C, 7T, 102.00MB

Next step: Flapjack analysis

<https://media.readthedocs.org/pdf/flapjack/latest/flapjack.pdf>