

Assembly tutorial

Alt-text Figure 9 - Galaxy homepage

Screenshot of Galaxy's homepage. A red arrow points to "Login or Register". Details in the main text.

Alt-text Figure 10 - Rename history

Screenshot of Galaxy's homepage. A red arrow points to "Rename history". Details in the main text.

Alt-text Figure 11 - Upload data

Screenshot of Galaxy's homepage. A red arrow points to "Upload Data". Details in the main text.

Alt-text Figure 12 - Upload window

Screenshot of Galaxy upload window. A red arrow points to "Paste/Fetch data". Details in the main text.

Alt-text Figure 13 - Start upload

Screenshot of Galaxy upload window with a list of files in it. A red arrow points to "Start". Details in the main text.

Alt-text Figure 14 - Uploaded files

Screenshot of Galaxy upload window. The window is green to indicate it is ready. A red arrow points to "Close". Details in the main text.

Alt-text Figure 15 - Processing files

Screenshot of Galaxy homepage. A red arrow points to the uploaded data highlighted in yellow in the "History" menu. Details in the main text.

Alt-text Figure 16 - Files processed

Screenshot of Galaxy homepage. A red arrow points to the uploaded data highlighted in green in the "History" menu. Details in the main text.

Alt-text Figure 17 - Enabling file selection

Screenshot of Galaxy homepage. A red arrow points to the "operations on multiple datasets" tick-box in the "History" menu. Details in the main text.

Alt-text Figure 18 - Selecting files

Screenshot of Galaxy homepage. A red arrow points to the tick-boxes in front of the datasets in the "History" menu. Details in the main text.

Alt-text Figure 19 - Building list of dataset pairs

Screenshot of Galaxy homepage. One red arrow points to the "For all selected" in the "History" menu and another red arrow points to "Build List of Dataset Pairs". Details in the main text.

Alt-text Figure 20 - Creating a collection

Screenshot of Galaxy "Create a collection of paired datasets" window. One red arrow points to a field containing "_1", and a second arrow points to a field containing "_2". At the bottom of the window, a red arrow points to "Name" and another red arrow points to "Create collection". Details in the main text.

Alt-text Figure 21 - Disabling operation in multiple datasets

Screenshot of Galaxy homepage. A red arrow points to the “operations on multiple datasets” tick-box in the “History” menu. Details in the main text.

Alt-text Figure 22 - Choosing alignment tool

Screenshot of Galaxy “Edit dataset attributes” window. A red arrow points to the search field in the “Tools” menu. The field contains the query “bwa-mem”. Another red arrow points to “Map with BWA” in the “Tools” menu. Details in the main text.

Alt-text Figure 23 - Setting up the alignment

Screenshot of Galaxy analyses window. A red arrow points to the field “Will you select a reference genome from your history” with the information “Use a genome from history” selected in the field. A second red arrow points to the field “Single or pair-end reads” with the information “Paired collection” selected in the field. A third red arrow points to the field “Select analysis mode” with the information “1_Simple Illumina mode” selected in the field. Details in the main text.

Alt-text Figure 24 - How to view the results

Screenshot of Galaxy’s output window. A red arrow points to “View data” in the “History” menu. Details in the main text.

Alt-text Figure 25 - Snippet of the BAM file - part 1

Screenshot of a BAM file output. It has the columns QNAME, FLAG, RNAME, POS, MAPQ, CIGAR, MRNM and MPOS. Details in the text.

Alt-text Figure 26 - Snippet of the BAM file - part 2

Screenshot of a BAM file output. It has the columns ISIZE and SEQ. Details in the text.