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Introduction

The **Assembler Viewer** software is developed to visualize the genomes assembly results.

!Note! The program operates large amount of data, which may cause delay in displaying. Please be patient.

Application window
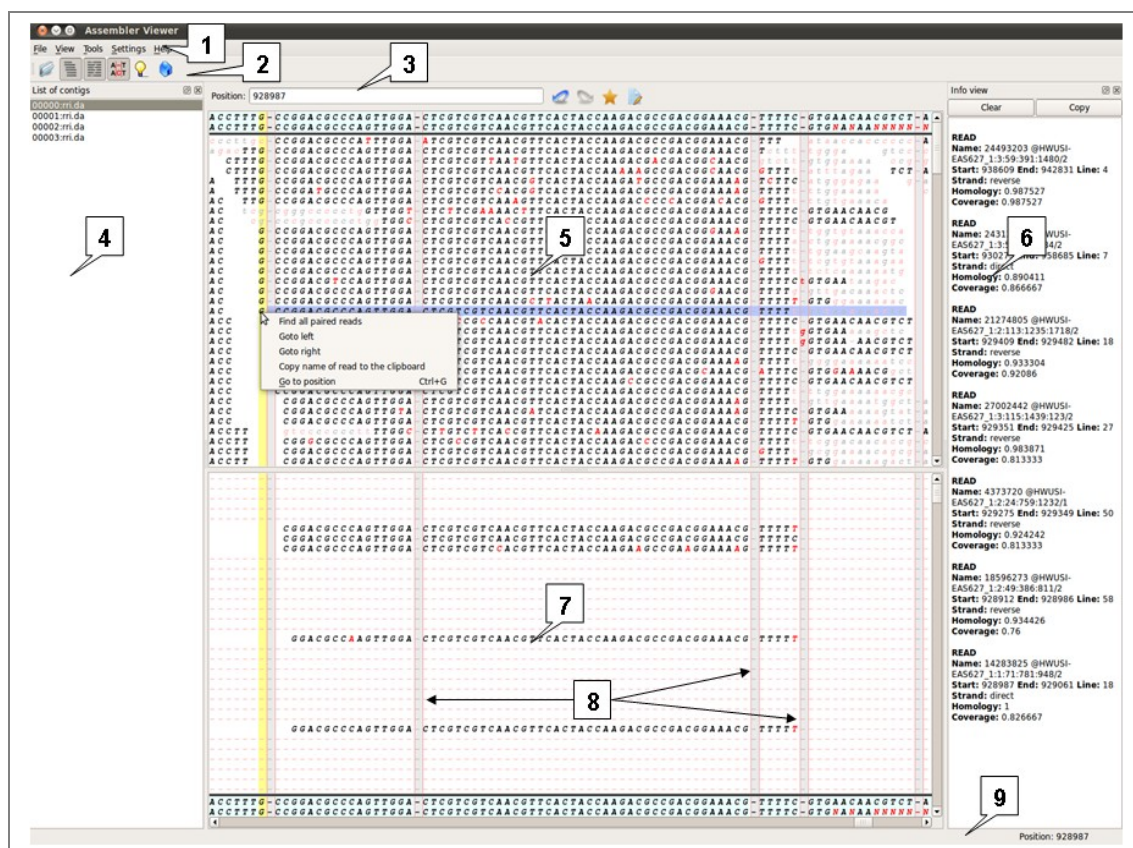
1. Main menu. 2. Toolbar. 3. Navigation toolbar. 4. List of contigs window. 5. Unspliced reads window. 6. Info view window 7. Spliced reads window. 8. Inserts. 9. Status bar.

Main Menu

File:

Open reads — open one or more files with reads. For correct information displaying, the folder with *.da file should contain all corresponding raw data files.

Save image — save image from main window in .png format.

Close all — close all opened data.

Exit — quit the program.

View:

- **Show inserts** — display inserts in reads and corresponding gaps in reference sequences in the middle of Unspliced reads window and Spliced reads window. Insertion is marked with vertical red line.
- **Save bookmarks to file** — save current bookmarks into a file in plain text format, each position number is saved in a separate file row.
- **Load bookmarks from file** — load bookmarks from a file.
- **Go to position** — jump to a specified position in the Structure view window, Unspliced reads window and Spliced reads window.
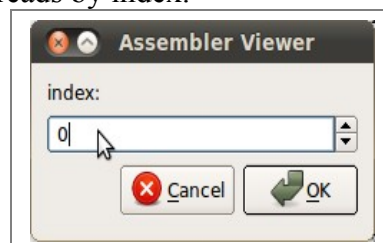

- **Show unspliced reads** — display the Unspliced reads window, option is enabled by default.
- **Show spliced reads** - display the Spliced reads window, option is enabled by default.
- **List of contigs** — display the List of contigs window.
- **Info view** — display the Info view window.

Tools:

Find reads by name – search for reads by name.
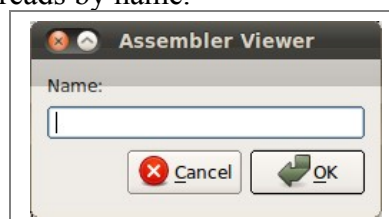
Find reads by index – search for reads by index.

Settings:

Set Font – open the "Select Font" dialog.

Help:
Content... - show the Help window
About — show the program info window
Visit Website — link to http://www.softberry.com/berry.phtml

Main toolbar

Buttons at the Main toolbar duplicate the often used menu items.

|		
		File → Open reads
		View → Show unspliced reads
		View → Show spliced reads
		View → Show inserts
		Help → About
		Help → Visit Website

List of contigs

There is a list of contigs on the left. To the right, at **Unspliced reads window** and **Spliced reads window,** the reads mapped onto contig chosen from the list are displayed.

Navigation toolbar

Position — when a number is entered, it is the same as "View → Go to position", when the mouse pointer is moved in Structure view window, Unspliced reads window and Spliced reads window, the current position is displayed.
In the right part of Navigation toolbar there are buttons for managing bookmarks.

		Jump to previous bookmark
		Jump to next bookmark
		Set a bookmark
		Open "Save bookmarks" dialog.

Saving and loading bookmarks can be performed through the View menu items.
"Save bookmarks" dialog
Manage bookmarks: view the list of bookmarks, obsolete bookmarks can be deleted by "Remove" button. To jump to bookmark select it and press "OK" button. To the list at the top part of the window, the search results (search by name or index, or search for paired reads) are being committed.
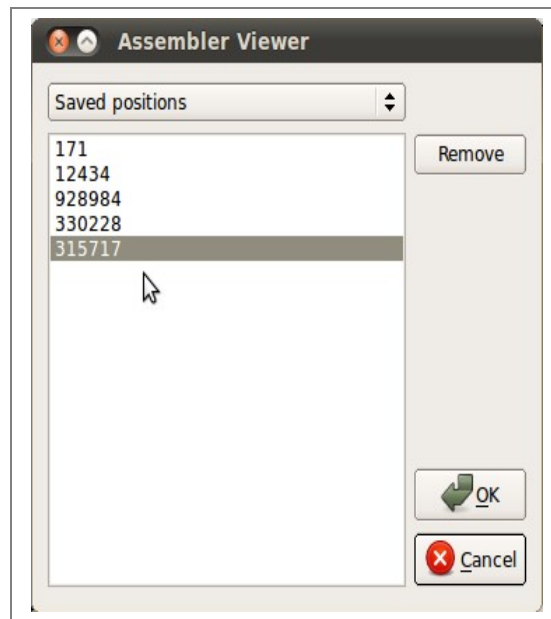
Reads windows

Unspliced reads window
In this window, top upper row shows the contig, the next row represents the consensus, all following rows represent reads.
Positions, in which an assembled sequence and/or read(s) differ from the reference sequence, are marked red. Non-significant reads' positions are pale and in lowercase. The information on this read is displayed when the mouse pointer hovers over a read.

Spliced reads window
Same rules as above are used to display reads in Spliced reads window. The consensus is shown in the last row, and the contig is shown in the row before that.

Mouse click inside Unspliced reads window or Spliced reads window causes yellow highlighting of a column that corresponds to current position of the mouse pointer. If necessary, information is automatically scrolled to move the position into visible area. The current feature itself is highlighted blue.
Scrollbar located below the Unspliced reads window and Spliced reads window allows to scroll the information in these windows.
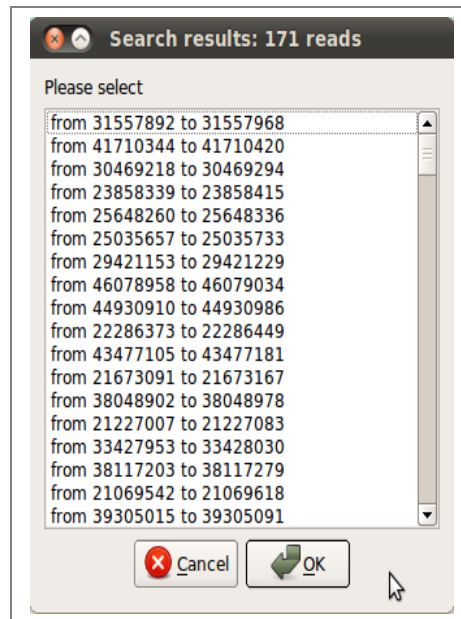Double click over the read sequence returns the cursor to the read starting position.

Contextual menu of the Spliced reads and Unspliced reads windows
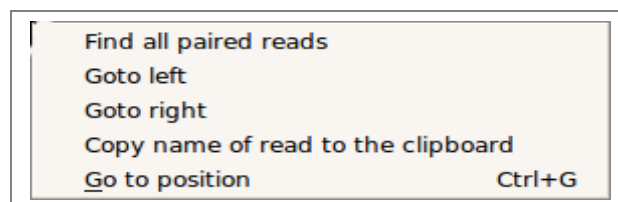
- **Find all paired reads** – find all paired reads for the currently selected one. For this read, the list of paired reads is being created. To jump to the paired read just double click on it. If only

the one paired read is found, the list is not appeared and cursor is instantly moved to the found read. The list of found reads is automatically being saved and can be viewed repeatedly in the "Saved bookmarks" dialogue.

Search results: 171 reads

Please select

from 31557892 to 31557968
from 41710344 to 41710420
from 30469218 to 30469294
from 23858339 to 23858415
from 25648260 to 25648336
from 25035657 to 25035733
from 29421153 to 29421229
from 46078958 to 46079034
from 44930910 to 44930986
from 22286373 to 22286449
from 43477105 to 43477181
from 21673091 to 21673167
from 38048902 to 38048978
from 21227007 to 21227083
from 33427953 to 33428030
from 38117203 to 38117279
from 21069542 to 21069618
from 39305015 to 39305091

Cancel   OK

- **Goto left** – move to the left, to the region covered with reads. The command is intended for quick scrolling of the regions not covered with reads.
- **Goto right** – move to the right, to the region covered with reads. The command is intended for quick scrolling of the regions not covered with reads.
- **Copy name of read to the clipboard** – copy the name of selected read to the clipboard.
- **Go to position** — jump to a specified position in the Unspliced reads window and Spliced reads window.

Go To Position

Go to position [   ]

Cancel   OK

Info view

The window displays information on selected reads.

Status bar

Displays the current cursor position.