

XCout - User Manual

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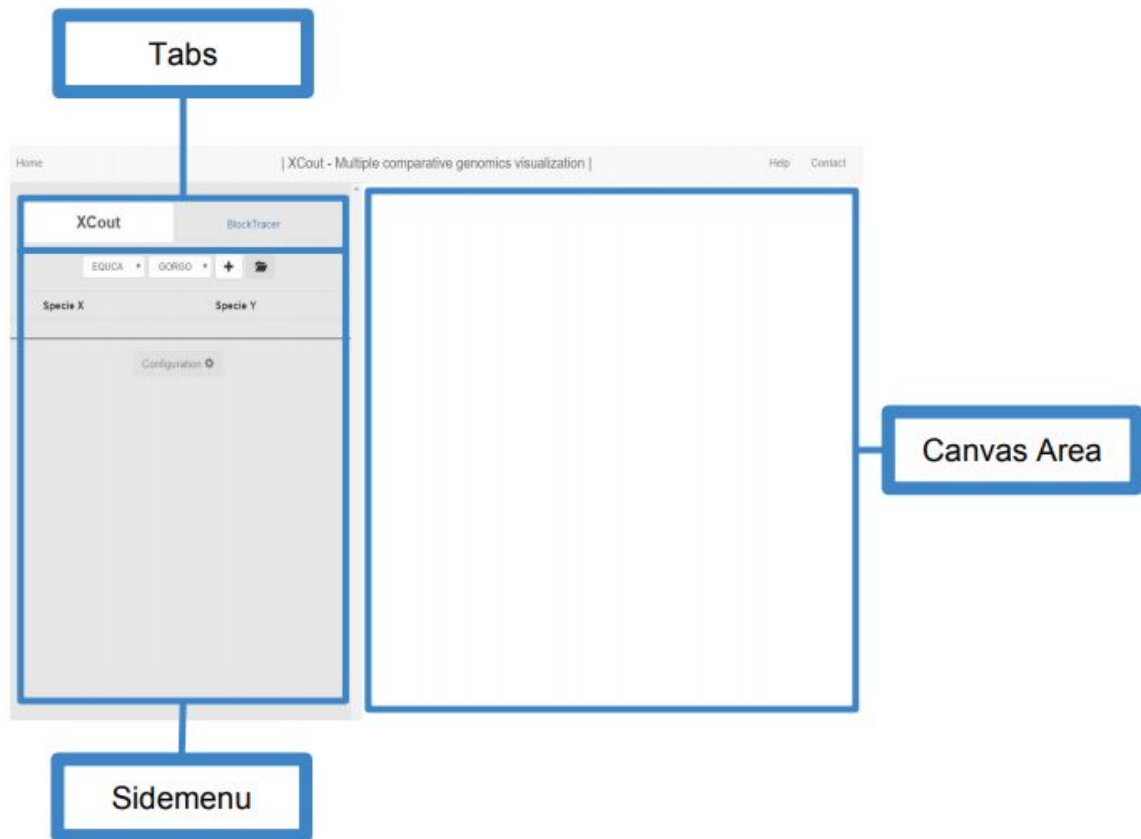
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General Module

XCout is composed of two main modules: XCout (multiple pairwise visualization) and BlockTracer (CSB tracking visualization). Independent to the active module, the web application interface is split in 3 main areas, as explained in the following image:

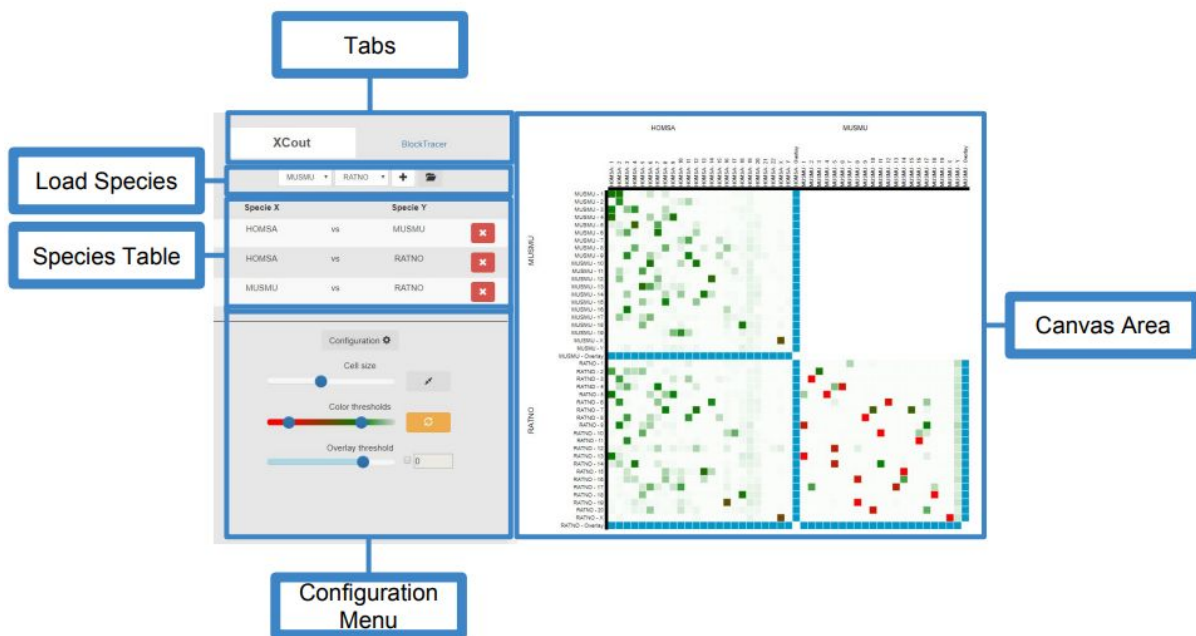


Tabs: Main modules of the XCout client, either XCout (multiple pairwise visualization) or BlockTracer (CSB tracking across species)

Canvas Area: Space used by the currently active module to draw the canvas of the visualization



Side Menu: Zone reserved to configure the active module and additional information is presented.

XCout: Main overview



Tabs: XCout is the currently active tab

Side Menu:

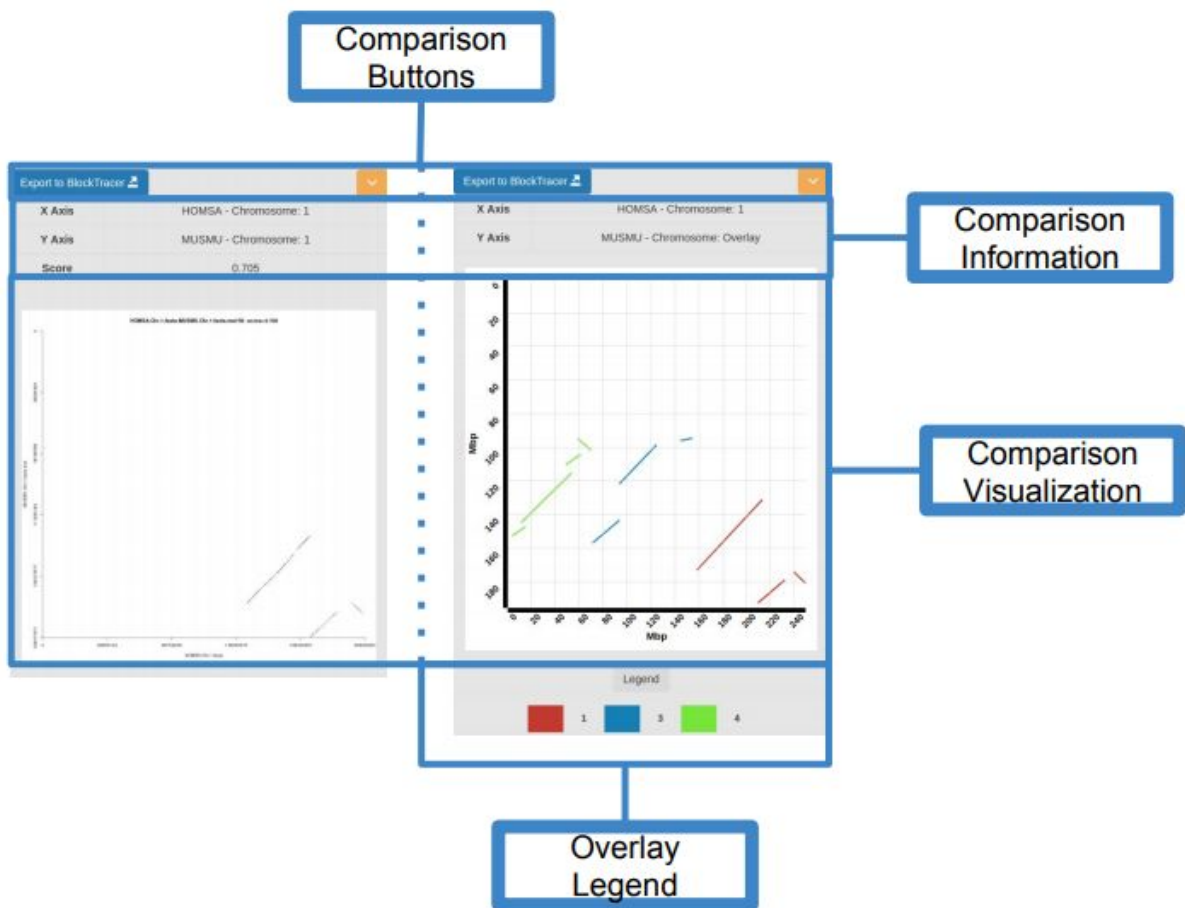
- **Load species:** Selection of two species to visualize their full genome comparison in the Canvas Area
- **Species Table:** Currently loaded species in the Canvas Area
- **Configuration Menu:** User is able to control the:
 - **Cell Size:** The slider bar controls the size of each of the comparison boxes. The 'Fit to Screen' button () will adapt the visualization size to the current window size, and if clicked again it will return to the previous (original) size.
 - **Color Thresholds:** The slider bar allows the user to manually color gradient in the visualization. The 'Suggested Thresholds' button () will send automatically change it towards the most appropriate values to detect interesting comparisons with a quick glance.
 - **Overlay Threshold:** This controls the number of comparisons to be overlaid when visualizing the Overlay of detected Collinear Synteny Blocks (CSB). The user may also activate the 'Overlay Threshold' checkbox in the configuration menu, and type the number of comparisons he wants to overlay, which will select the lowest score comparisons.

Canvas Area: Grid display which facilitates the detection of comparisons of interest out of a huge number of comparisons by presenting an interactive matrix canvas in which each row and column represent a chromosome of a specie and the cells represent the comparisons between them.

User can hover the mouse through the boxes and obtain the distance score calculated from Chromeister (0 to 1 - lower is better).



The color is directly related to the metric of chromeister, enabling a quick detection of conserved signal comparisons.

XCout: Sidemenu



After clicking on a cell in the main canvas, a new section will appear in the Side Menu. The image of the left corresponds to a single pairwise comparison, and the right one to an Overlay canvas (multiple pairwise CSB overlaid). This visualizations are exclusive

Comparison Buttons: There are two buttons.

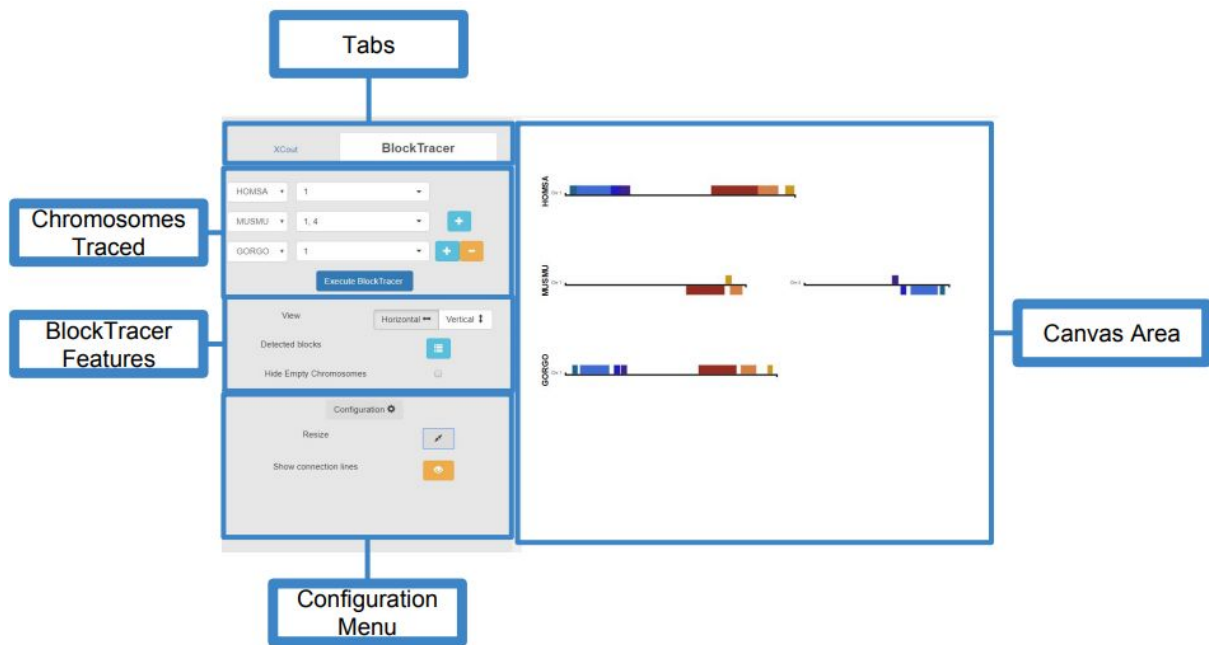
- **Export to BlockTracer:** Clicking this button () will export current comparison to BlockTracer module.
- **Hide arrow:** Press this button () to hide this section of the Side Menu

Comparison Information: Table with information regarding the current comparison.

Comparison Visualization: Either a single pairwise comparison image, or an overlay of multiple pairwise comparisons. Based on the selected cell.


Overlay Legend: Available only if currently viewing an overlaid comparison. User can toggle the visualization of the chromosomes by clicking on their color or number.

BlockTracer



Tabs: BlockTracer is the active tab

Side Menu:

- **Chromosomes Traced:** This represents the species and chromosomes from which the user wants to track CSBs.
- **Blocktracer Features:** Features available for block tracer.
 - **View:** User selects the main axis for the visualization, either horizontal or vertical.
 - **Detected blocks:** Clicking this button () will open a modal that provides information regarding the currently visualized CSBs and specific zones for each chromosome.
 - **Hide Empty Chromosomes:** This checkbox controls whether the selected chromosomes that do not have any CSB tracked along the set species are visualized.
- **Configuration Menu:** User is able to control the:
 - **Cell Size:** The

Canvas Area: Visualization of the tracked CSBs of the selected chromosomes and species.

Each chromosome can have blocks above or below the chromosome line. Their position implies the blocks relationship to the previous organism: above means the strand is forward (5'-3') and below means it is reversed (3'-5').

All the blocks in the first species will always be forward. Hence, it will be our baseline reference genome.

Analogous colors tend to belong to the same pairwise comparison