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GBOT upgrade : a loci comparison tool dedicated to the exploration of duplications and synteny

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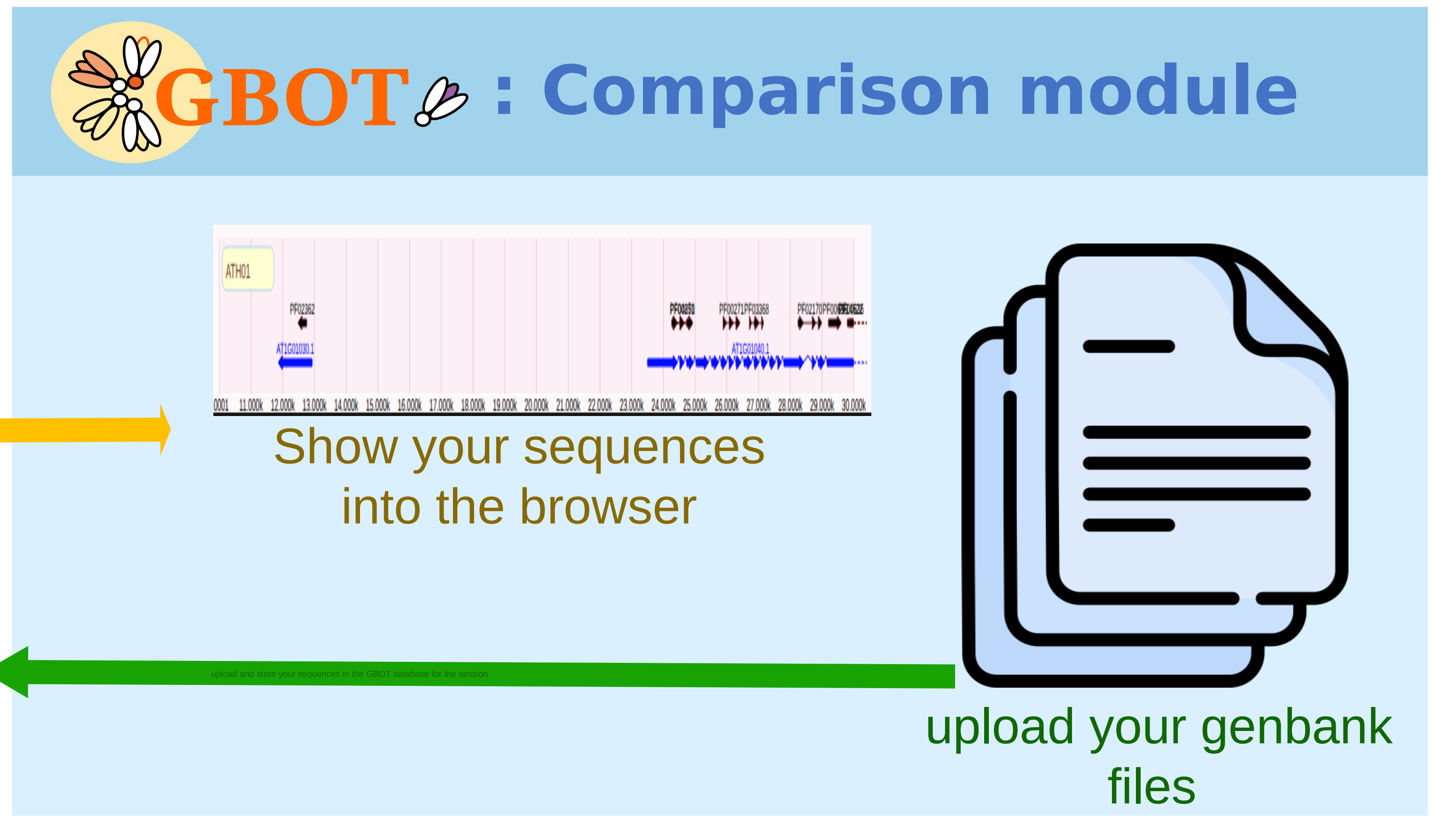
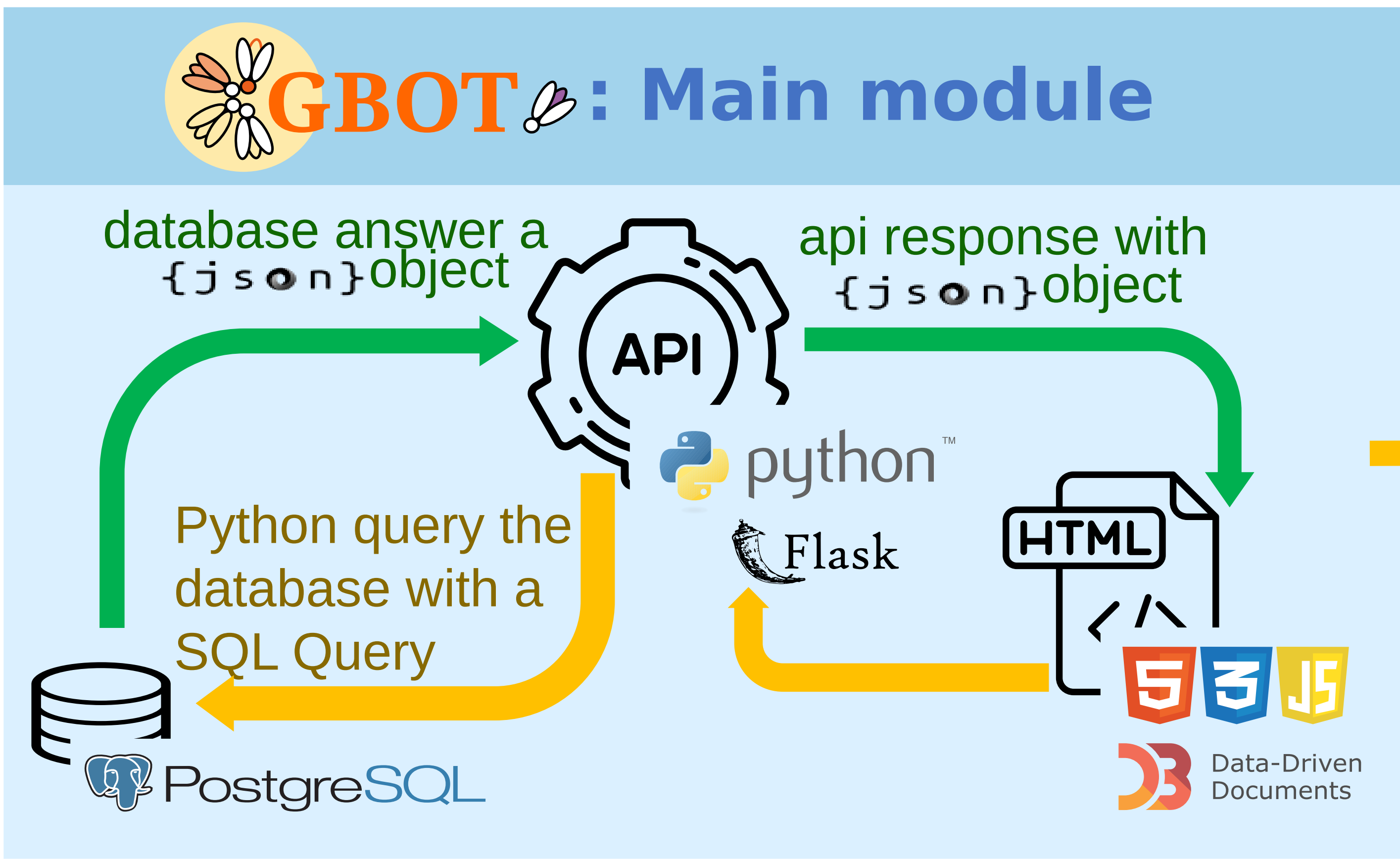


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GBOT database (<http://stat.genopole.cnrs.fr/server/GBOT/index.html>) was presented at the previous JOBIM as an original and modular genome browser with graphical tools dedicated to exploring gene families and orthology relationships. Today, we are introducing a new module derived from GBOT's development, designed to visualize and compare large genomic regions, facilitating the study of duplications and synteny conservation. The associated tools also enable expert structural annotation of the visualized loci while leveraging other GBOT's modules.



Use case : comparison module

The screenshot shows the GBOT comparison module interface. It includes a navigation bar with 'Config.', 'New Analyse', and 'Add Sequence'. Below the navigation bar, there are sliders for 'E-value' and 'Hits'. The main area displays a complex network of lines representing relationships between sequences. Annotations include:

- 1**: A purple arrow pointing to the 'Local View' and 'blastN same size' options.
- 2**: A purple arrow pointing to the 'Upload Manager' dialog box, which shows a table of uploaded files.
- 3**: A purple arrow pointing to the 'blastN' radio button in the interface.
- PFAM motifs automatically detected and displayed**: A callout box pointing to a specific motif in the sequence visualization.
- Zoom through genomic sequences and their features.**: A callout box pointing to a zoomed-in view of a genomic sequence.

The 'Upload Manager' dialog box contains the following table:

Files	Uploaded	Stored in db	Blast banks
ClusterA_Ambrosiana_120010tp	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
ClusterA_Camelinasativa_chr11.nbk	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

The result is a visualization of your sequences and blast results, automatically calculated and stored in the GBOT database, for an interactive and dynamic visualization of the relationships between genes in your sequences. Numerous options allow the user to optimize visualization in order to highlight synteny conservation : zoom level, sequence inversion, choice of sequence order, selective display of available annotations... Such analyses also enable the structural annotations to be confirmed, refined and inferred from one sequences to others.

