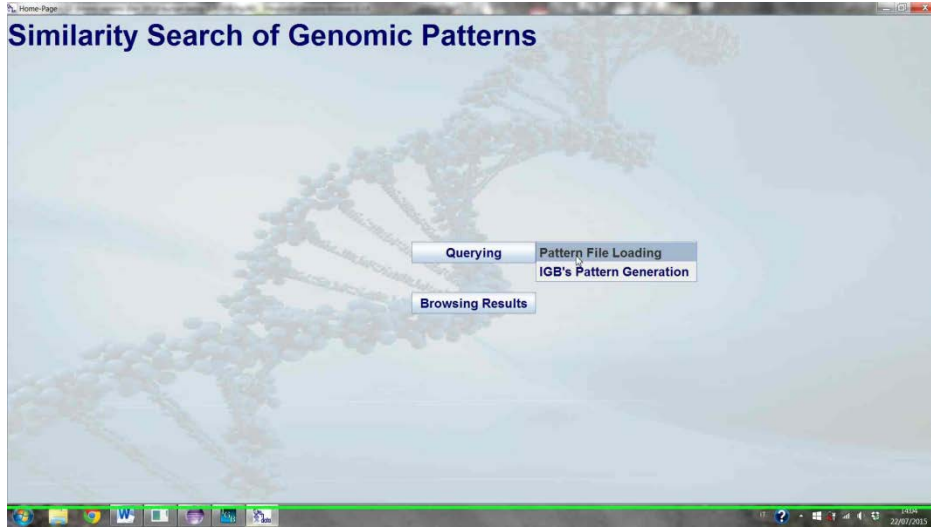
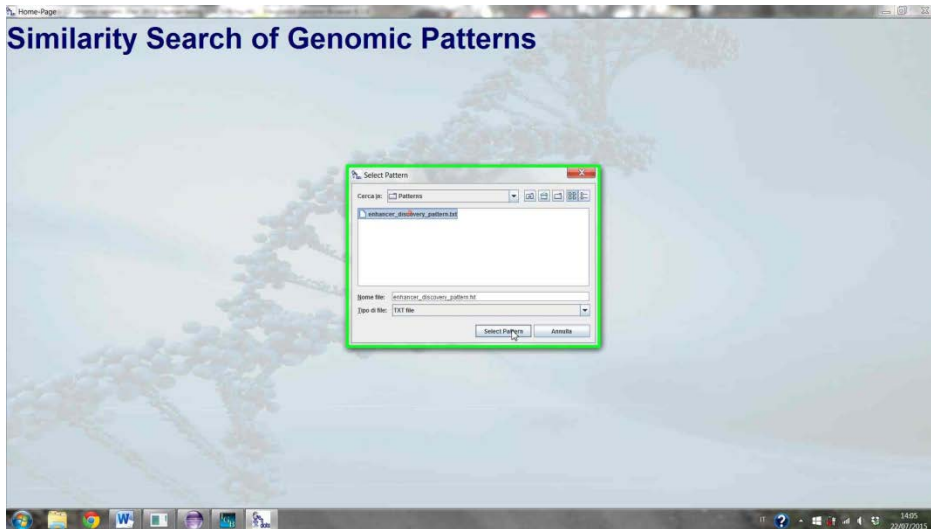


Step-to-step example of use of our application

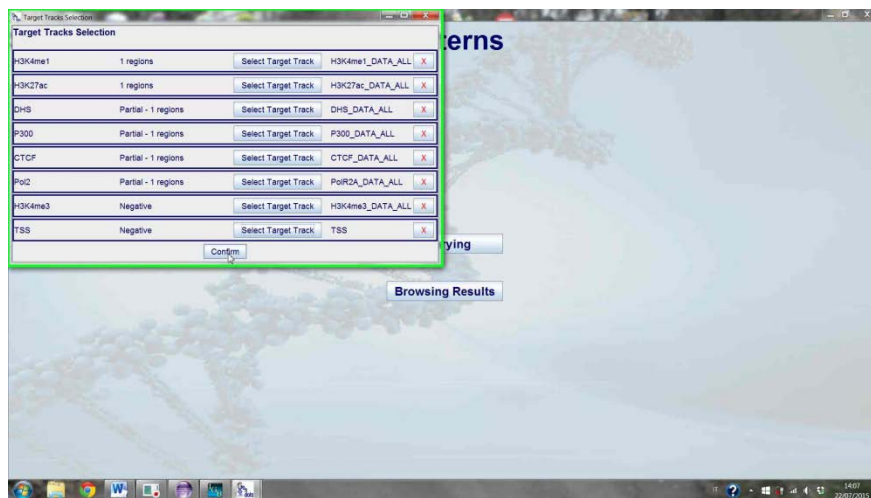
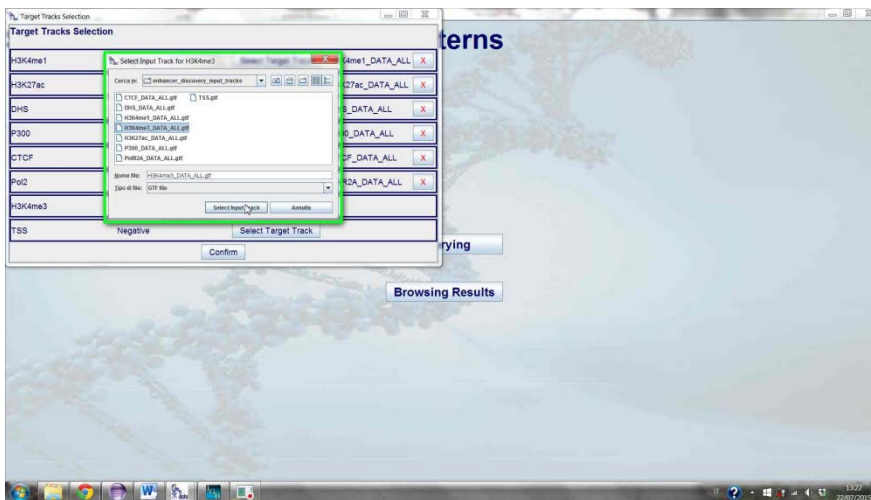
1. Run the application (IGB should start too; if it does not run IGB manually and load the human genome).
2. In the main window, select *Querying >> Pattern File Loading*.



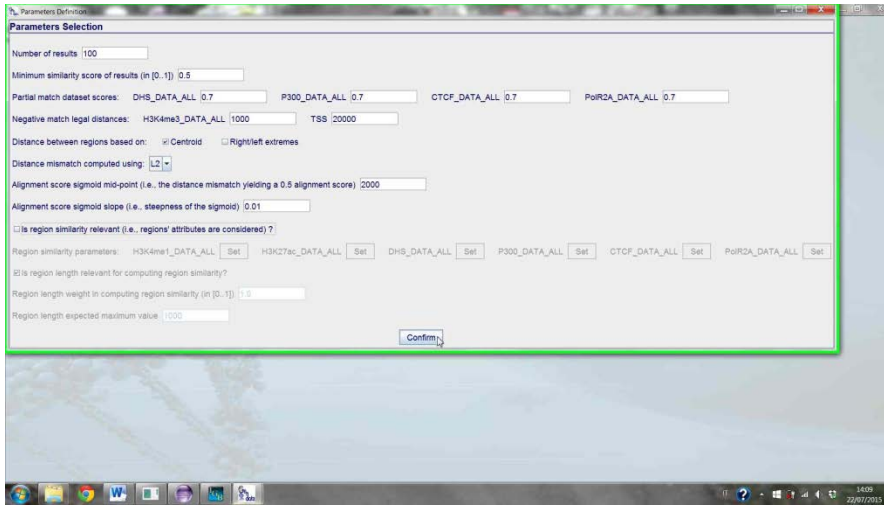
3. Load the *enhancer_discovery_pattern* file.



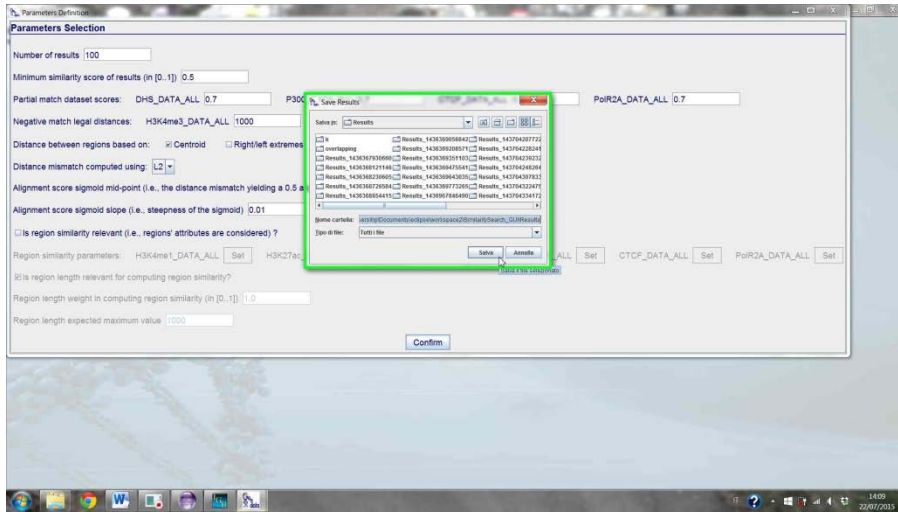
4. In the window that pops up, for each track of the pattern select the corresponding input track from the folder *enhancer_discovery_input_tracks* and then press *confirm*.



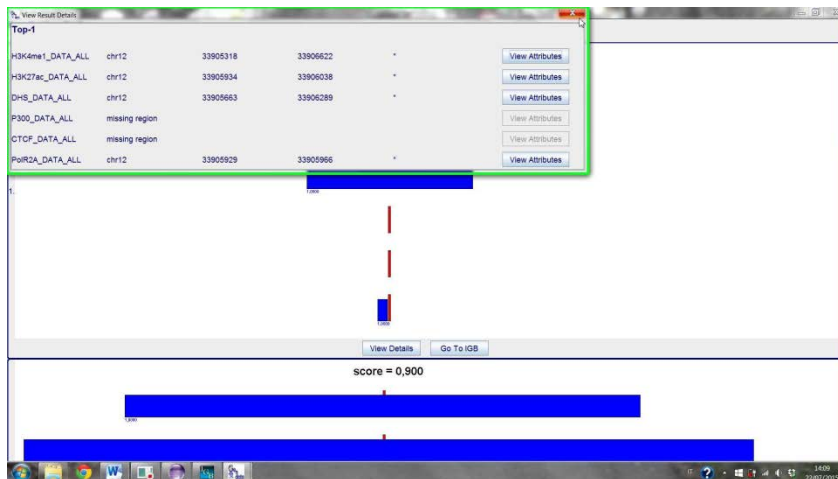
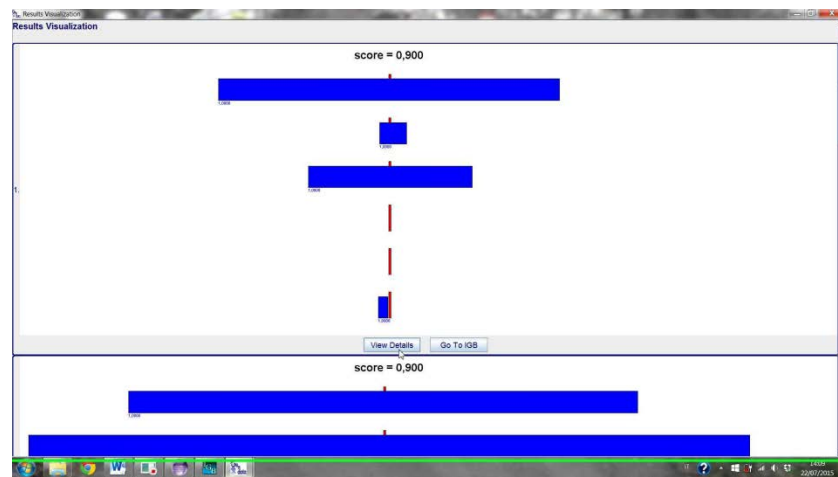
5. Select the parameters of the query (to have interesting results use the configuration of parameters shown in the figure below) and then press *confirm*.



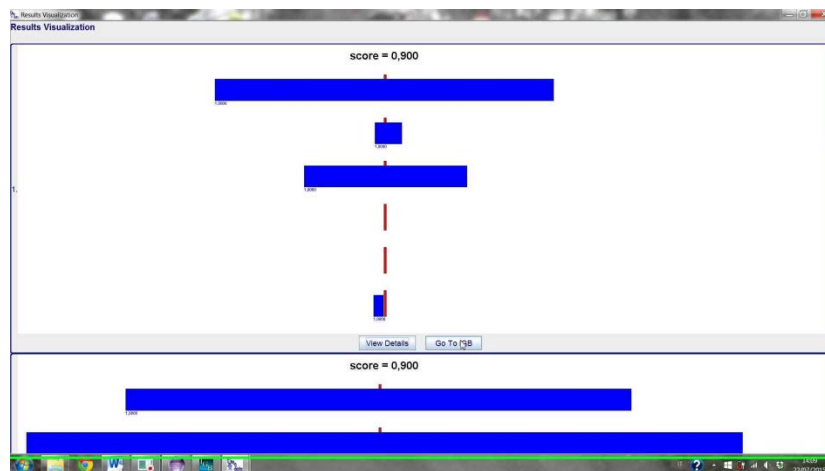
6. Select in which directory you want to save the results of the query.



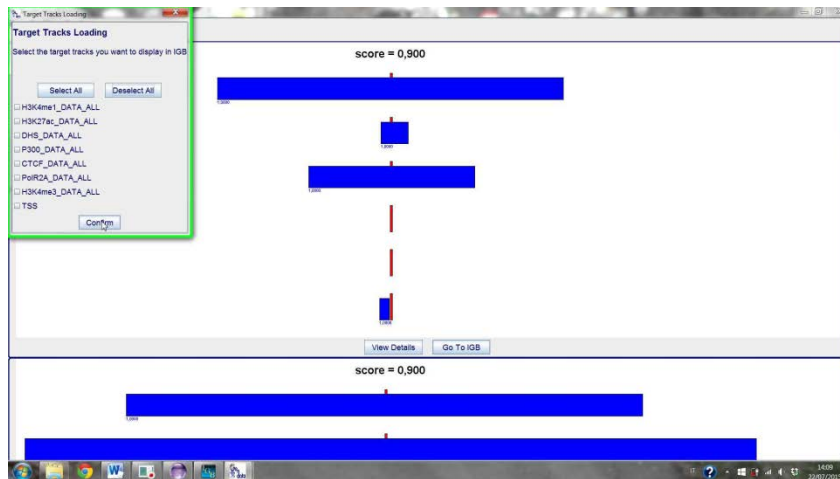
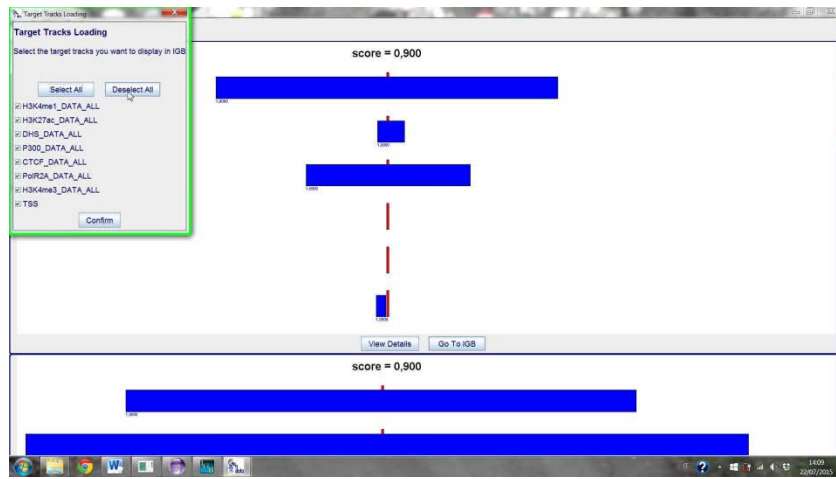
- When the results of the query are available a new window pops up in which it is possible to browse such results. For instance, use the button *view details* of a result to have some information on the genomic regions that form it.



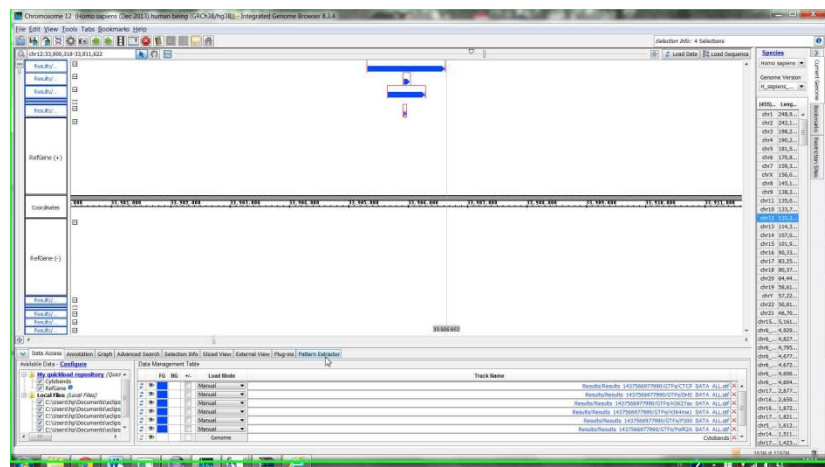
- Let us now use IGB to visualize a specific result. For instance, press the button *go to igb* corresponding to the Top-1 result.



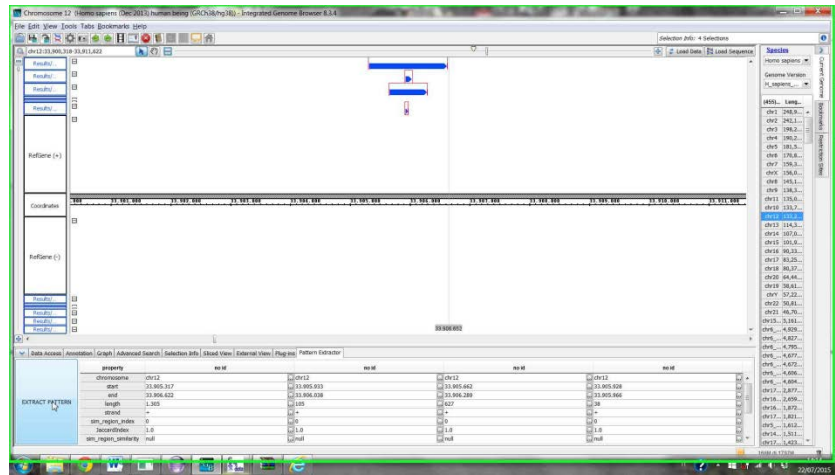
- In the window that pops up you can select if you want to visualize on IGB also the input tracks, besides the tracks of the selected result. For this example, deselect all the input tracks.



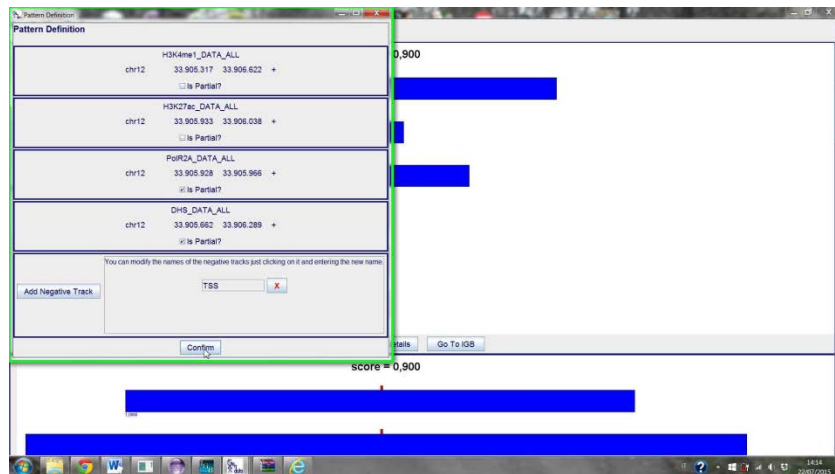
- Wait for IGB to load all the tracks and, then, select some regions of the result (for this example select all the regions). Then, open the *PatternExtractor* tab at the bottom of the page.



- In the PatternExtractor tab you can examine the details of the selected regions and eventually, through the button *Extract Pattern*, use these regions as pattern for a new query (basically restart the cycle query-results-query).



- A new window pops up in which you can define some parameters of the extracted regions. For instance, select that tracks *PolR2A_DATA_ALL*, and *DHS_DATA_ALL* are partial (as they were in the original query), and add a negative track called *TSS*. Finally, press confirm.



13. Select where to save the new pattern you just created. At this point, you can select again input tracks and the parameters of the query and so on...

