FISH Oracle: a web server for flexible visualization of DNA copy number data in a genomic context

Malte Mader[1], Ronald Simon[1], Sascha Steinbiss[2] and Stefan Kurtz[2]

[1] *Department of Pathology, University Medical Center Hamburg-Eppendorf, Martinistrasse 52, 20246 Hamburg, Germany*

[2] *Center for Bioinformatics, University of Hamburg, Bundesstrasse 43, 20146 Hamburg, Germany*

The rapidly growing amount of array comparative genomic hybridization (array CGH) data requires improved visualization software supporting the process of identifying candidate cancer genes. Optimally, such software should work across multiple microarray platforms, should be able to cope with data from different sources and should be easy to operate.

We have developed a web-based software *FISH Oracle* [1] to visualize data from multiple array CGH experiments in a genomic context. Its fast visualization engine [2] and advanced web [3] and database technology [4] supports highly interactive use. FISH Oracle comes with a convenient data import mechanism, powerful search options for genomic elements (e.g. gene names or karyobands), quick navigation and zooming into interesting regions, and mechanisms to export the visualization into different high quality formats. These features make the software especially suitable for the needs of life scientists. Figure 1 shows a screenshot of the application running in a standard web browser.

FISH Oracle offers a fast and easy to use visualization tool for array CGH and SNP array data. It allows for the identification of genomic regions representing minimal common changes based on data from one or more experiments. FISH Oracle will be instrumental to identify candidate onco and tumor suppressor genes based on the frequency and genomic position of DNA copy number changes. The FISH Oracle application and an installed demo web server are available at `http://www.zbh.uni-hamburg.de/fishoracle`.

References

[1] Malte Mader, Ronald Simon, Sascha Steinbiss, and Stefan Kurtz. FISH Oracle: a web server for flexible visualization of DNA copy number data in a genomic context. *Journal of Clinical Bioinformatics*, 1(1):20, 2011.

[2] Sascha Steinbiss, Gordon Gremme, Christin Schärfer, Malte Mader, and Stefan Kurtz. AnnotationSketch: a genome annotation drawing library. *Bioinformatics*, 25(4):533–534, 2009.

[3] Google Web Toolkit. `http://code.google.com/webtoolkit/`.

[4] MySQL. `http://www.mysql.com/`.

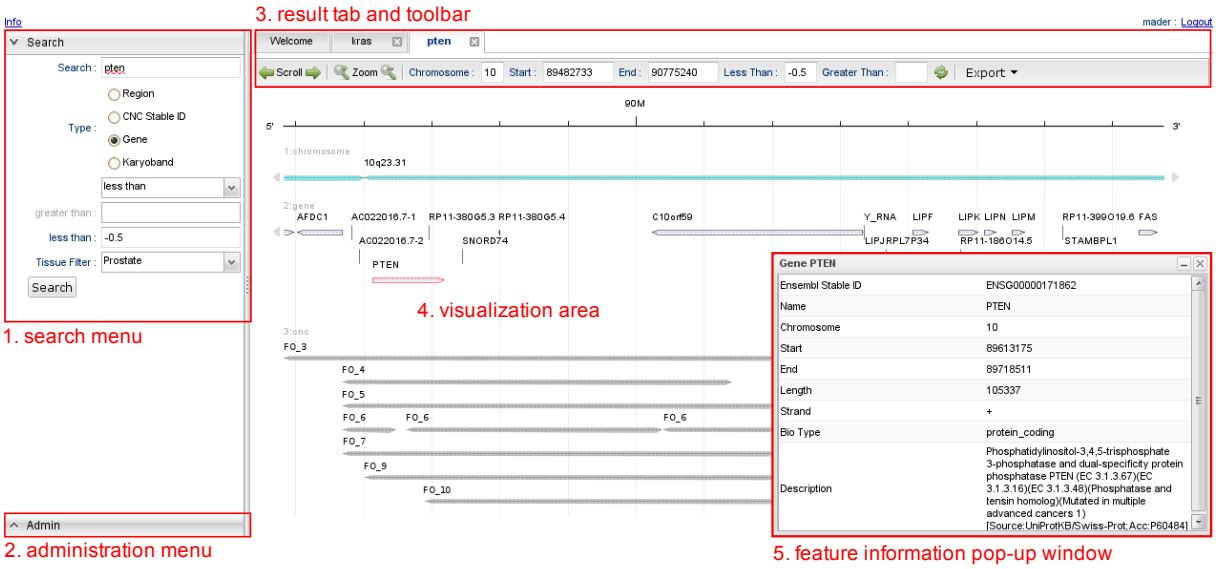

Figure 1: The FISH Oracle user interface. (1) The search menu is on the left hand side. It allows to specify a region, segment IDs, gene names and karyobands as search keys. Segments describe genomic deletions or amplifications. A threshold for the segment mean intensity values can be specified with the “less than” (search for deleted genomic regions) or “greater than” (search for amplified genomic regions) option. The tissue type filter restricts the display to segments for one or more specific tissue types. (2) The administration menu (lower left corner) provides functionality for data import and user account administration. (3) Each search opens a new tab that can be identified by the search query appearing as the caption of the tab. Each open tab has its own toolbar, showing chromosomal positions and buttons for navigation and image export. (4) The visualization, according to the current toolbar settings, is displayed below the toolbar. In this case, the image shows segment data and annotations in the region 10p23. A minimally overlapping region of deleted chromosomal regions with the known tumor suppressor gene *PTEN* is recognizable. (5) Clicking on the symbol representing a gene or a segment triggers a pop-up window containing corresponding detailed information.