



## GScope: a clipped fisheye viewer effective for highly complicated biomolecular network graphs

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### ABSTRACT

**Summary:** A graphical tool to visualize highly complicated biomolecular network graphs is described. It helps us to understand the graphs from macroscopic and microscopic viewpoints by incorporating continuous transition from global to clipped hyperbolic projection. GScope also helps us to find a molecule in the graphs by offering several searching functions. It is useful to publish biomolecular network graphs on the internet.

**Availability:** GScope is available at <http://gscope.gsc.riken.go.jp>

**Contact:** [gscope@gsc.riken.go.jp](mailto:gscope@gsc.riken.go.jp)

Biomolecular networks extracted from various sorts of biological data tend to be highly complicated and incomprehensible because those connections found among the molecules are far from simple, but intercrossed with many other connecting lines (Marcotte *et al.*, 1999). Fisheye visualization technique is one of the solutions to focus on local details in a global context of graphs, and useful for the computer display of large information structures (Furnas, 1986; Sarkar and Brown, 1992). Robinson and Flores (1997) emphasized such 'Focus+Context' display is effective to understand structures of biological data. Although the fisheye view is valuable for phylogenetic trees in which closely related items are placed in a neighborhood (Fischer *et al.*, 1999), it often fails to give comprehensible presentations for multi-linked network graphs. In biomolecular networks, molecules are not always linked in a simple tree structure but sometimes in a multi-linked complex, where linked molecules are placed distantly.

To cope with the above-mentioned problem, we hereby present a new visualization tool named 'GScope (Genomic Science Center Open Pathway Explorer)' to analyze complicated biomolecular network graphs by combining advantages of fisheye conversion function and clipping of linked local structures.

The visualization scheme is defined as follows: First, for each molecule a distance  $r$  from a focused point is

calculated. In Figure 1, a focused point (molecule) is colored in red. Second, a mapping distance  $r'$  is calculated by the following conversion function:

$$r' = r(d + 1)/(dr + s),$$

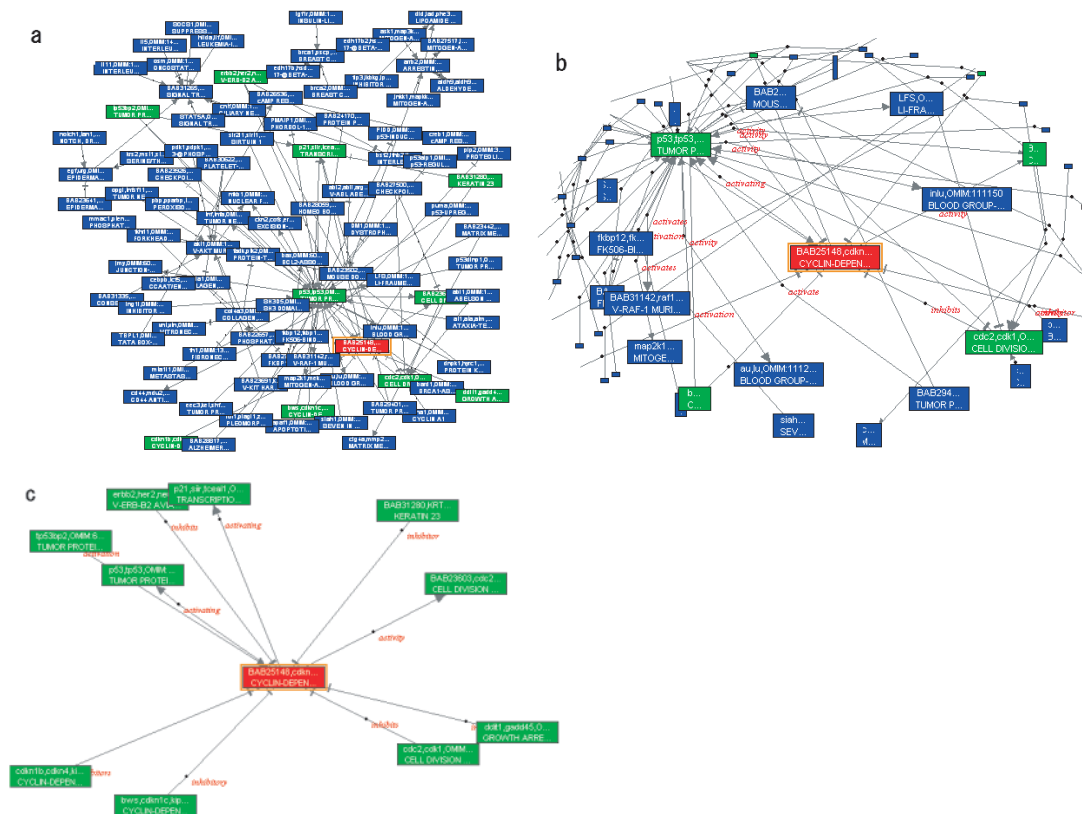
where  $d$  and  $s$  are parameters for the conversion function. Third, each molecule is drawn at a place  $r'$  from the center of the screen. As the parameter  $d$  is gradually enlarged from zero, a global view (Fig. 1a) changes to a fisheye view (Fig. 1b), where the neighborhood of the focused position is displayed in great detail and remote molecules are shown only as small landmarks. Rectangles representing molecules are drawn smaller as  $r'$  increases.

For biological molecules, it is very important to understand the relationship between molecules. Unfortunately some relationships between the focused molecule (red) and linked molecules (green) are difficult to see in the fisheye view (Fig. 1b) because the green molecules are placed remotely from the red molecule. As seen in Figure 1c, clipping only green molecules without geometrical change is suitable for confirmation of the local relationships. Since Figure 1b and c are correspond geometrically and viewed in turn by a simple mouse operation, the neighborhood and related molecules are easily checked by users of the viewer.

It is often difficult for a user to search for a molecule from a complicated network graph. GScope helps one to find a molecule by offering 'keyword search' and 'a list view' of all molecules in the graph. By using a regular expression as a query in the keyword search, it enables them to set focus on the molecule, to change the color of the molecule, and to show the molecule in bold letters. All molecules are listed up in an alphabetical order in the list view of GScope: It is very easy for a user to find a molecule from the list view.

It is occasionally the case that multiple molecules having the same name appear in a network graph. GScope automatically creates links among those molecules, and allow a user to learn that molecules with the same name exist somewhere in the network. A user can be easily

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**Fig. 1.** A biomolecular network graph representing molecular relationships extracted from OMIM database (<http://www.ncbi.nlm.nih.gov/omim/>) is represented by rectangles (molecules) and arrows (relationships). (a) A global view of the graph in which a red-colored molecule is directly connected with green molecules. (b) A fisheye view of the graph where molecules neighbor to the red molecule are displayed in great detail and remote molecules are shown as small rectangles. (c) A clipped view of the graph where directly linked molecules (green) to the red molecule are shown in great detail. This view (c) geometrically corresponds to the fisheye view (b).

navigated through those molecules by clicking triangle navigating icons in the rectangles of the molecules.

Data of a network graph is represented by XML-based schema (SRML: Simple Result Markup Language) which is suitable to represent gene–gene interaction relationships by a software ‘KnowledgeEditor’ (Toyoda and Konagaya, 2002). GScope is implemented as a plug-in component for web browsers based on ActiveX technology of Microsoft (<http://msdn.microsoft.com>) and help us to publish network graphs through the web, and offers many programmable interface methods. Elaborate manuals and tutorials are available on our web site (<http://gscope.gsc.riken.go.jp>).

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