

HiveR: 2 and 3D Hive Plots of Networks

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HiveR is an *R* package for creating and plotting 2D and 3D hive plots. Hive plots are a unique method of displaying networks of many types; the concept was developed by [Martin Krzywinski](#) at the Genome Sciences Center. The key innovation in a hive plot is that nodes are deliberately assigned to an axis rather than being positioned by an algorithm whose results depend upon the position of the other nodes. Thus a node is plotted on a particular axis, has a radius along that axis, and may have color and size. Assignment to an axis is based upon the context of the problem, for instance membership in a certain category, while radius, color and size can be a function of network properties, or any other quantitative measure appropriate to the problem. The advantage of this approach is that deletion or addition of a node does not cause the entire layout to change and as a result, comparison of related networks using is straightforward (and implemented in a hive panel). Finally, edges connecting nodes may have a width and a color. The net result is that hive plots are rational and predictable as the layout depends only on the structural properties of the network. They are also very flexible and may be tuned to show particular properties of interest: the mapping of network properties is primarily limited by one's creativity, insight, and the particular knowledge domain. **HiveR** is a fresh *R* implementation of Krzywinski's *Perl* program. It extends the original notion of 2D hive plots to include interactive 3D plots using **rgl**, which can also be made into animations. Examples of 2D and 3D hive plots from a range of fields will be presented. **HiveR** is available on CRAN. In the event you can't attend the talk or wish to chat, there is also a poster on **HiveR**. Stop by and share your ideas, as there are many features that could be added to **HiveR**.

References

M. Krzywinski, I. Birol, S. Jones & M. Marra (2011). Hive Plots - Rational Approach to Visualizing Networks. *Briefings in Bioinformatics* [doi:10.1093/bib/bbr069](https://doi.org/10.1093/bib/bbr069)