Research Paper – Circos: An information aesthetic for comparative genomics

Improvements in data acquisition are outpacing our techniques for processing that data. Innovations in visualization will be necessary to keep up with the complexity of the information being displayed.

Effective Visualizations:

* Clarity
* High data-to-ink ratio
* Favorable scaling

Circos is useful for drawing in various orders and orientations, visualizing scale transitions (as depicted in Figure 6, where sections of graphs are blown up onto other areas of the circle, called breakout diagrams), magnitudes of connectedness between different groups (also within sub-perimeters within those groups), etc. Transparent ribbons allow for one-to-many relationships between groups which are easier to visualize.

Perhaps most importantly, Circos constructs visualizations which are as intriguing to look at as the data they attempt to distill, promoting prolonged inspection.

*filterlinks –* parses link file and selects only those links that pass positional criteria

*orderchr* – applies simulated annealing to a link dataset to generate an ideogram order that minimizes or maximizes the number of links that cross in the image

*bundlelinks* – used to identify links that are corroborated by other adjacent links

*binlinks* – used to generate density tracks, suitable for scatter/line/histogram tracks, based on the number of links within a sliding window

*tableviewer –* a collection of tools that is used to o parse tabular data and generate data and configuration files for visualizing tables with Circos

Research Paper – OmicCircos: A Simple-toUse R Package for the Circular Visualization of Multidimensional Omics Data

Doughnut tracks are effective in displaying relationships among genes or genomic intervals.

Java-based circular plot tools include CGView and DNAPlotter. Keep these in mind in case the R package being used is bottlenecked in places where other tools are more highly optimized. This assumes that the R plotter supports incremental function calls, not only one-and-dones.

The three main functions in OmicCircos are:

*segAnglePo()*, which specifies the circle size, the number of segments, and segment width.

*circos(),* allows images to be superimposed on the circle plot, for example, a heat map generated using the *apply()* R function.

*sim.circos()*, which allows a simulation of styles of circular plots using randomly generated data. Allows for dry runs.