Circos plot: a colourful depiction of highly knotty and convoluted scientific data.

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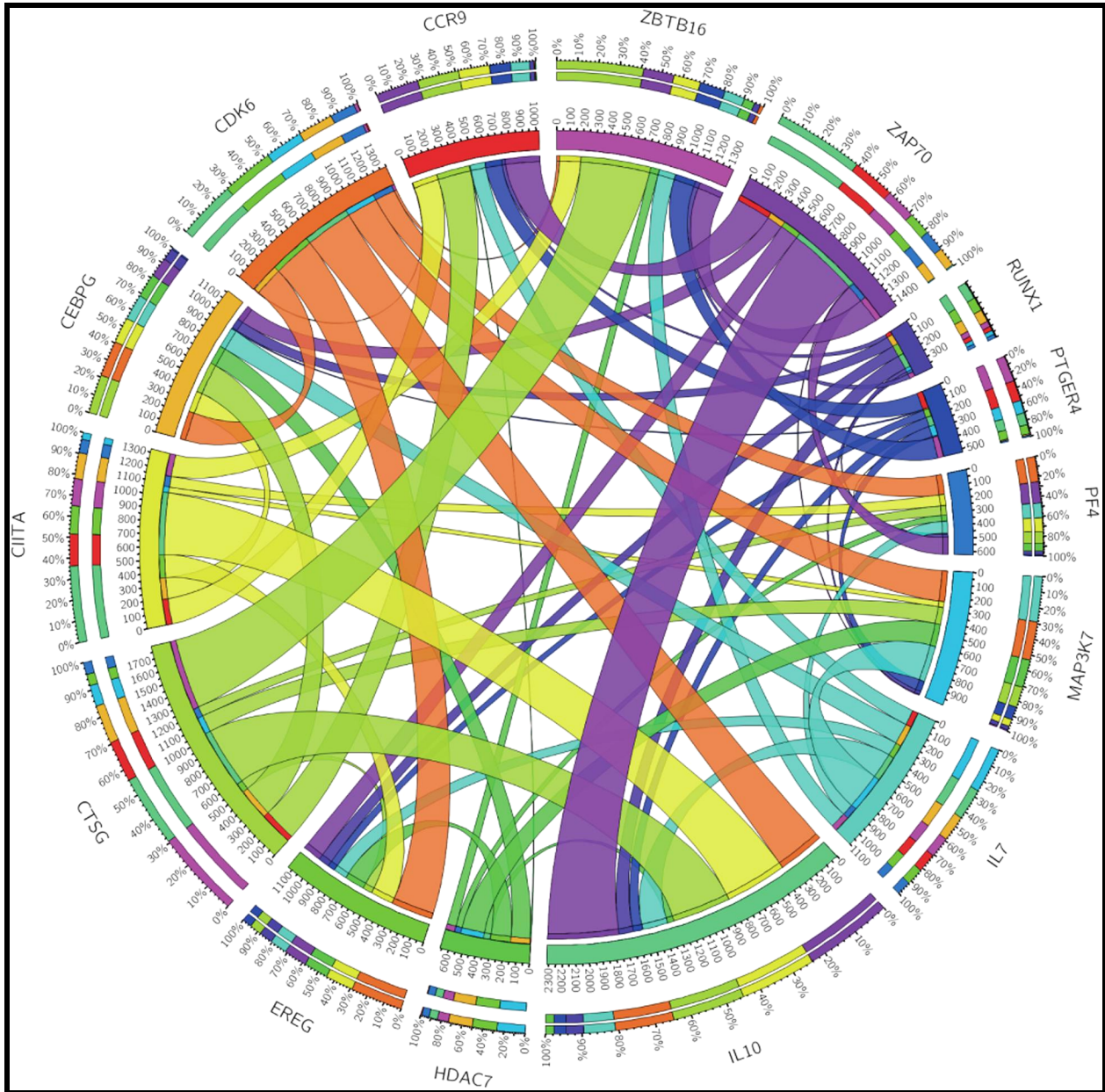
Figure 1. Circos plot showing the correlation among 15 immune genes in bladder cancer. Figure taken from Chen *et al*. 2020 (1).

In the human body, every product comes after several interactions. The molecular-level interactions and the cellular level interactions are very complex. The investigation of these interactions produces huge, complex, and complicated data. The data when not expressed makes it hard to convey. Circos plot is one such illustration that depicts the interactions and relationships that give clear insights. Circos is software that helps in originating publication-quality images and makes the work easier for scientists to illustrate their data. Though Circos is developed for sketching the genomic data, one can leverage it to interpret the data that subsist correlations. Circos plot is easy to understand, flexible, and can produce the plot with the plain-text configuration files. There are 20 different types in circos plot: glyph, highlight with depth control, scatter, paired-location, ribbon, histogram, tile, highlight with auto depth, text with auto arrange, heat map, high-density text, high-density glyph, multi-type composite, variable scale control, fine geometry control, flexible text and element placement, transparent ribbons, stacked histogram, connectors, and tick rings.

The circos plot specified in Figure 1 of this commentary is a ribbon-type circos plot. This commentary is about an original research article that was published recently in the year 2020 in frontiers in genetics by Chen *et al*. This article shows the bioinformatics analysis of the bladder cancer prognostic immune gene markers. Each gene is depicted with one specific color and the width of the ribbon that is getting connected to the other gene shows their interaction levels. The investigation of fifteen immune genes concerning the signaling pathways and cellular responses was illustrated in this circos plot (see Fig.1). The quantification of 24 immune cells was done using the single-sample gene set enrichment analysis method which is related to the tumor immune microenvironment. This circos plot is showing the correlations of the 15 immune genes that are found to be the markers for the bladder cancer prognosis. The data in the paper may help in improvising immunotherapy for treating bladder cancer. For one who knows how to look at the circos plot, understanding the correlations of the genes is easy; not only the genes but the correlations and interactions of various biomolecules like proteins, metabolites as well.

References

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2. http://circos.ca/.

How to cite this article?
Aggunna, M. and Yedidi, R.S. (2021). *TCABSE-J*, Vol. 1, Issue 2:33-34. Epub: Oct15th, 2021.

Conflict of interest: The author declares no conflict of interest.