

# Introduction to Circos

### Instructions

This tutorial is meant to be a quick introduction to the basics of Circos.

Slides are formatted to display a Circos image and its associated code sideby-side. As you click through the slides, the image and code will change and you can watch for movement and differences to determine which lines in the code change certain parts of the image. It might be helpful to click through the entire tutorial very quickly to get an overview of the Circos image, and then go back through in more detail.

For more information on each slide, you can turn the "Comments" layer on in Adobe Acrobat.

The link at the top of each slide will open Martin Krzywinski's online Circos tutorials (from which this tutorial has been adapted) for very in-depth information.

Krzywinski, M. et al. Circos: an Information Aesthetic for Comparative Genomics. Genome Res (2009) 19:1639-1645

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Data Format



### **Data Categories**

These five categories are used to enter data for all 2D data tracks. All categories except options are required.

Chromosome Name – tells Circos on which ideogram to attach the data point. This name must be the same as the one specified in the karyotype.txt file. It is a good practice to have some form of letter identifier in front of the number to allow you to identify the data at a later time.

Start Position – basepair point on the chromosome at which the data point is located.

End Position – base pair point that allows Circos to display the data with a width.

If the end position is the same as the start position, bins will be displayed as single pixel lines. For a larger width, a good starting point is to add 1,000,000 basepairs to the end position.

Value – your data for that basepair point. Circos only reads numbers in the Value column, so if you have data points with an NA value, or another kind of text entry, use Excel's Replace function to delete these entries. Here I have replaced "NA" with "0".

Option – based on the text identifier you enter here, Circos will later format your data point in whatever way you specify in a rule.

The option column can have a number of different formatting data, including color, size, glyph, and here, an identifier. You can enter any word/text you want for the option identifier, but it must be preceeded by an "id=" for Circos to read it.

Circos requires a separate data file for every plotted track, thus the repetition of chromosome name and positional information. In this tutorial there are 2 tracks, and thus two sets of data, each in their own file, are required.

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Plot 1



#### .txt Files

Once you have the data formatted in Excel, you can either: copy-paste plot data to a text editor like Notepad++ and save as a .txt file; or, put each plot's data in a separate worksheet and use the included Excel macro to save each worksheet as a .txt file. Make sure that any text that isn't data, such as column headings, has a # in front of its row (only one # is needed for the row).

Your data files should be placed inside the "data" folder within the main Circos folder. Within "data" there can be as many folders as you need to organize your files.

Circos only reads numbers in the Value column, so if you have data points with an NA value, or another kind of text entry, use Notepad++'s Replace function to delete these entries. Here I have replaced "NA" with "0".

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