

Circos and ClicOs: an introduction to circular graphs

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The following is a guide for making informative circular graphs. Before you dig in, check out the great examples [online](#) for inspiration.

[Circos](#) is a very powerful tool, but it has a LOT of documentation and can be overwhelming. [ClicOs](#) is an interactive online tool which takes care of the nitty gritty configuration bits. I've included templates of a simple plot highlighting connections between the age of onset and disease severity of PCDH19 epilepsy patients. You'll need the test files (karyotype.txt and data.txt) and screenshots below to generate the figure. I recommend that you go through this, then play around with the karyotype and data files to see how that affects different parameters, then try some of your own data.

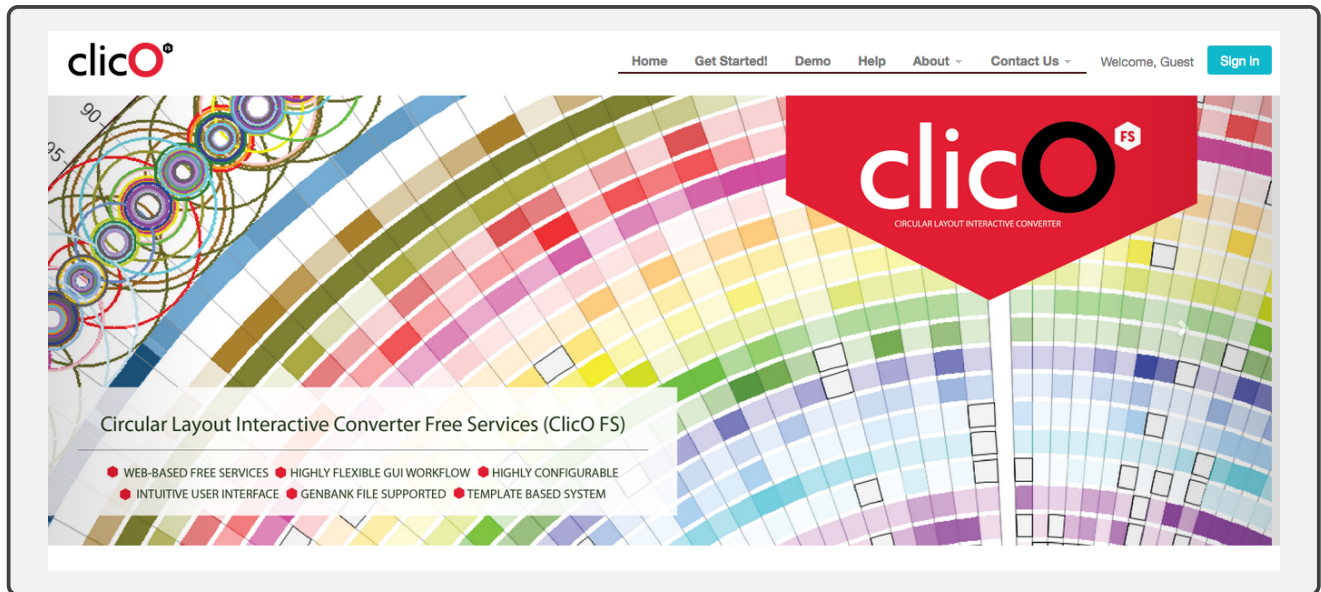
“The best way to learn a system is to break it” - said someone probably.

Protocol requirements

- A computer, internet connection, and desire for pretty plots.
- Two input files (provided):
 - karyotype.txt
 - data.txt

Set up

1. Go to **ClicO** (codoncloud.com:3000)

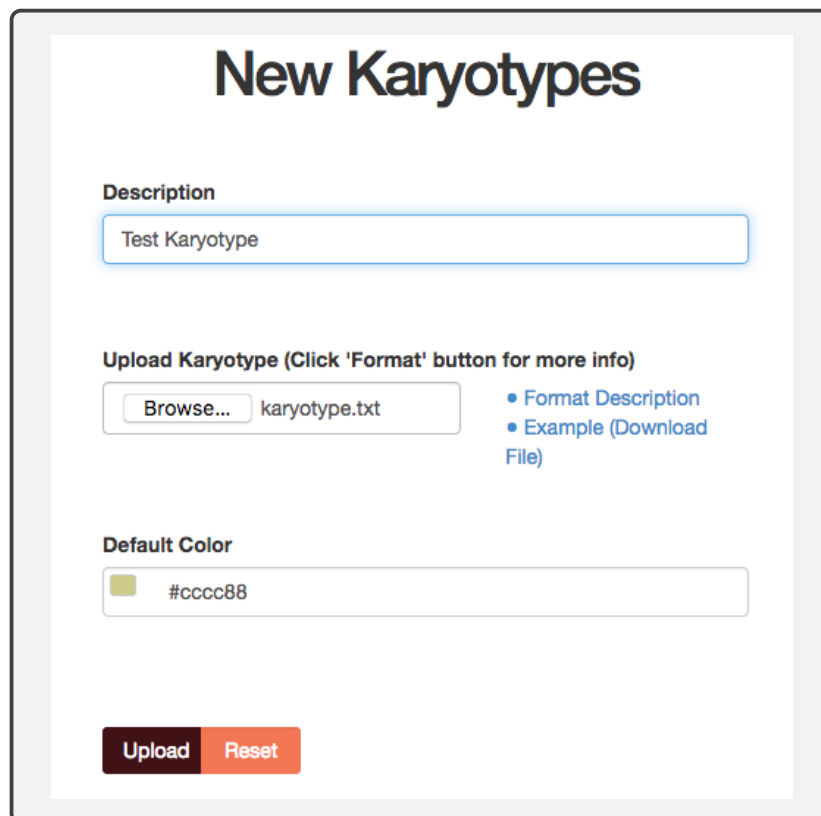


2. Click 'Get Started!'
3. Select 'Blank Template'
4. Click 'Go'
5. Enter in the details requested (Name of Project -> Captcha -> click 'Start')

The screenshot shows a web form titled 'Enter a name for project'. It has a text input field containing the text 'yo'. Below this is a 'Captcha' section with a box containing the text 'CTGOI'. Below the captcha box is a text input field with the placeholder text 'Enter the image v:'. Below this is a text input field with the placeholder text 'Enter captcha'. At the bottom of the form is a large teal button labeled 'Start'.

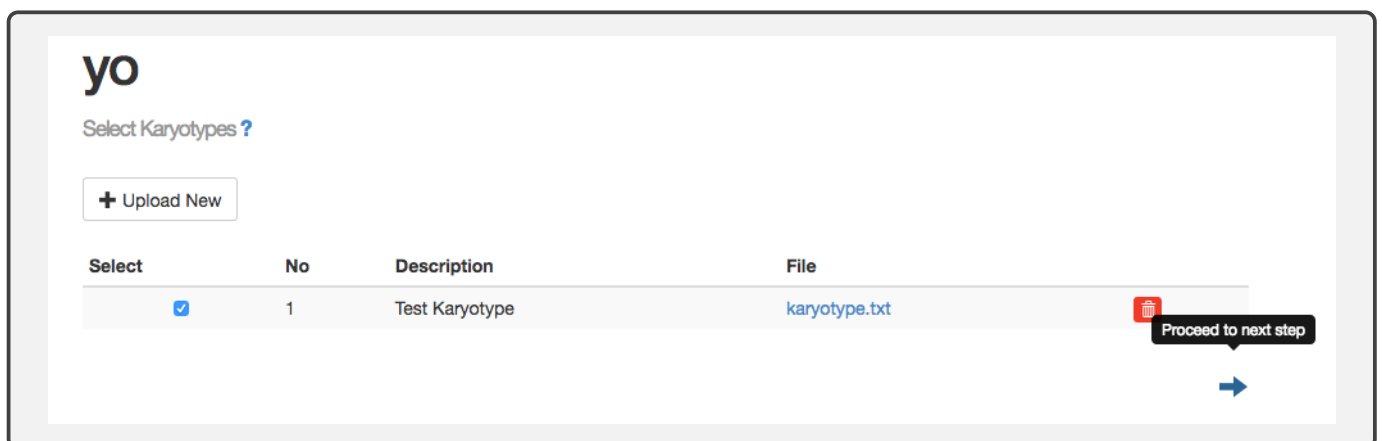
Karyotypes

1. Click '+ Upload New'
2. Add a name under 'Description' and upload **karyotype.txt**
3. Leave the default colour as is (we're overriding it anyway)
4. Click 'Upload'



The screenshot shows a form titled "New Karyotypes". It has three main sections: "Description" with a text input field containing "Test Karyotype"; "Upload Karyotype (Click 'Format' button for more info)" with a "Browse..." button, the filename "karyotype.txt", and two links: "Format Description" and "Example (Download File)"; and "Default Color" with a color picker showing "#cccc88". At the bottom are "Upload" and "Reset" buttons.

5. Select the karyotype file you have just uploaded and proceed to the next step



The screenshot shows the "yo" interface. At the top is the "yo" logo and a link "Select Karyotypes?". Below is a "+ Upload New" button. A table lists the uploaded karyotype:

Select	No	Description	File
<input checked="" type="checkbox"/>	1	Test Karyotype	karyotype.txt

At the bottom right, there is a red trash icon and a button labeled "Proceed to next step" with a blue arrow pointing right.

6. Click 'Preview' to have a look at the uploaded karyotype. This will be the backbone for your circos plot. You'll see that everything has automatically been filled in (e.g. each "chr" or band, label, length and colour).

Karyotype Settings ?

← →

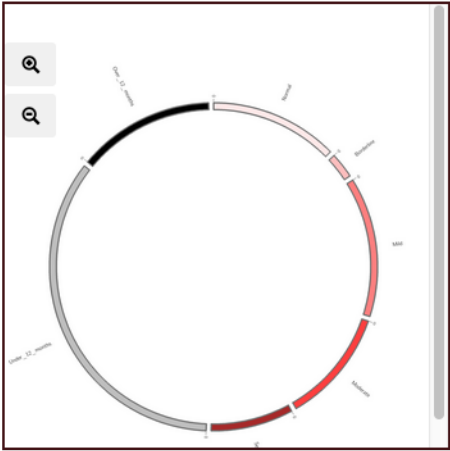
Save Reset Preview

Test Karyotype

Select color scheme.. Apply & Save

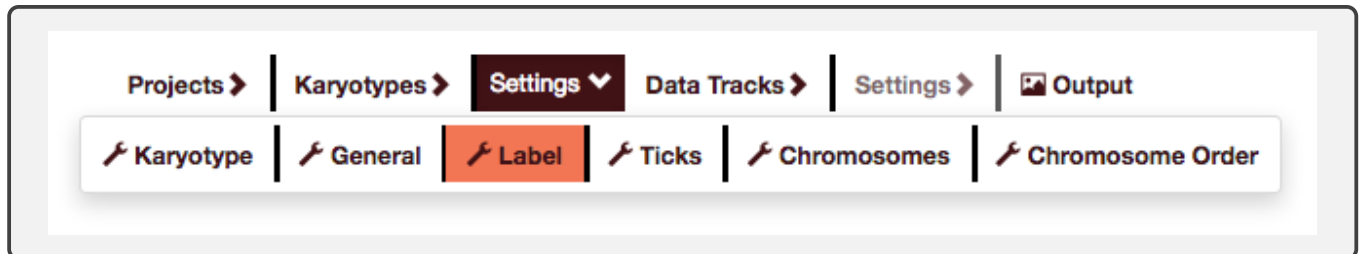
Chr ID	Label	Length	Color
Normal	Normal	45	<div></div> #ffeaea
Borderline	Borderline	9	<div></div> #ffbfbf
Mild	Mild	49	<div></div> #ff8080
Moderate	Moderate	40	<div></div> #ff4040
Severe	Severe	29	<div></div> #a62a2a
Under_12_months	Under_12_mont	124	<div></div> #c0c0c0
Over_12_months	Over_12_month	48	<div></div> #000000

← →



Settings

This section shows you how to tweak general settings like border colour, radius, thickness of your karyotype bands, label settings, tick settings, and so on. **It is very important to ‘Preview’ and ‘Save’ your changes as you go, or you will lose all changes.** At any time, you can go back or skip ahead to different settings options using the Settings menu at the top of the page.



1. First, we have general settings. Click ‘Preview’ every time you make a change to see what it does. Once you’re happy with the changes, click ‘Save’ and go on.

I’ve changed the following:

(a) **1 chromosome unit (u) represents 1: b (1 base)**

- i. This will add ticks at each “base”, or in our case, for each individual.

(b) **Border thickness: 5**

- i. This reduces the thickness of the line around each band.

(c) **Border color: #120f0f**

- i. This changes the color of the border line to black.

General Settings ?

←

→

Save

Reset

Preview

yo

Title

yo

Title position

top

Show Ideogram?

Yes

Show Fill?

Yes

1 chromosome unit (u) represents 1 :

b (1 base)

Radius (eg: 0.8)

0.8

r

Thickness (eg: 50p)

50p

Angle offset (eg: -90)

-90

°

Spacing (eg: 0.005r)

0.005r

Border thickness (eg: 10)

5

p

Border color

#120f0f

2. Next, we have label settings. This controls your band labels. As before, make changes, 'Preview' your changes, then 'Save' once you're happy with them.

I've changed:

(a) **Parallel Label:** Yes

The screenshot displays the 'Label Settings' window. At the top left is the title 'Label Settings ?' with a back arrow. Below it are three buttons: 'Save' (dark teal), 'Reset' (light teal), and 'Preview' (orange). A small 'yo' label is positioned below the buttons. The 'Settings' section contains three main controls: a 'Show Label?' toggle set to 'Yes', a 'Radius (eg: 1.1r)' input field with '1.1r', a 'Size (eg: 30)' input field with '30' and a unit selector set to 'p', and a 'Parallel Label?' toggle set to 'Yes'. At the bottom is a 'Case' dropdown menu set to 'default'. To the right of the settings is a preview window showing a curved band with labels 'Normal' and 'Borderline' and numerical values '0' and '1'.

3. For tick settings, I've changed:

(a) **Label multiplier: 1e-0**

- i. This is the multiplier for the labels shown in the output. E.g. if we were drawing a genome and had position 20,000,000, we could set the multiplier to 1e-6 and then the label would be shown as 20. While this function is useful for genomes, we don't need it in this case. Setting it to 1e-0 will make each label appear as the real number.

(b) **Major Ticks Label spacing: 5u**

- i. Add a major tick at every 5 individuals.

(c) **Minor Ticks Label spacing: 1u**

- i. Add a minor tick at every 1 individual.

Ticks Settings ?

←→

SaveResetPreview

yo

Show Ticks?
☒ Yes

Label multiplier (eg: 1e-6)

Label Decimals

Major Ticks ?

Show Label?
☒ Yes

Label spacing (eg: 25u)

Label size (eg: 25)

Prefix

Suffix

Minor Ticks ?

Show Label?
☐ No

Spacing (eg: 5u)

8

4. Finally, the chromosome settings are used to control which bands you want to appear and in what order. This can be useful if you want to have say Figure 1a as the whole genome, then Figure 1b as a close-up view of a particular chromosome. In our case, I left everything as default.

Chromosomes Settings ?

← →

Save Reset Preview

Test Karyotype

Chromosome ID	Show ?	Reverse ?	Scale	Radius
	<input type="checkbox"/> Select All	<input type="checkbox"/> Select All		
Normal	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1.0	1.0 r
Borderline	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1.0	1.0 r
Mild	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1.0	1.0 r
Moderate	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1.0	1.0 r
Severe	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1.0	1.0 r
Under_12_months	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1.0	1.0 r
Over_12_months	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1.0	1.0 r

← →

Chromosomes Ordering ?

← →

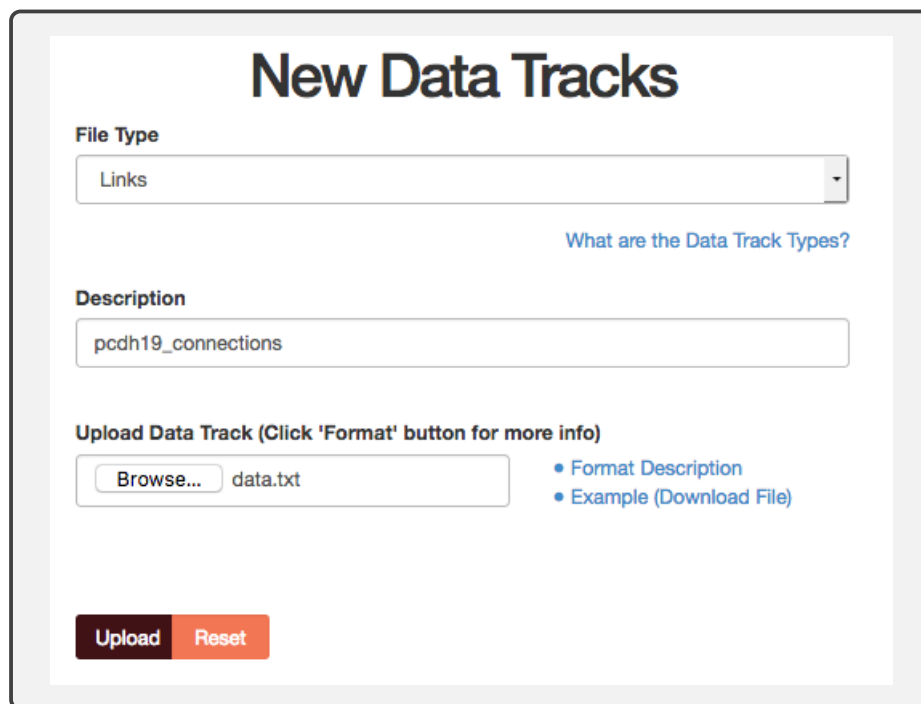
Save Reset Preview

Normal Borderline Mild Moderate Severe Under_12_months Over_12_months

← →

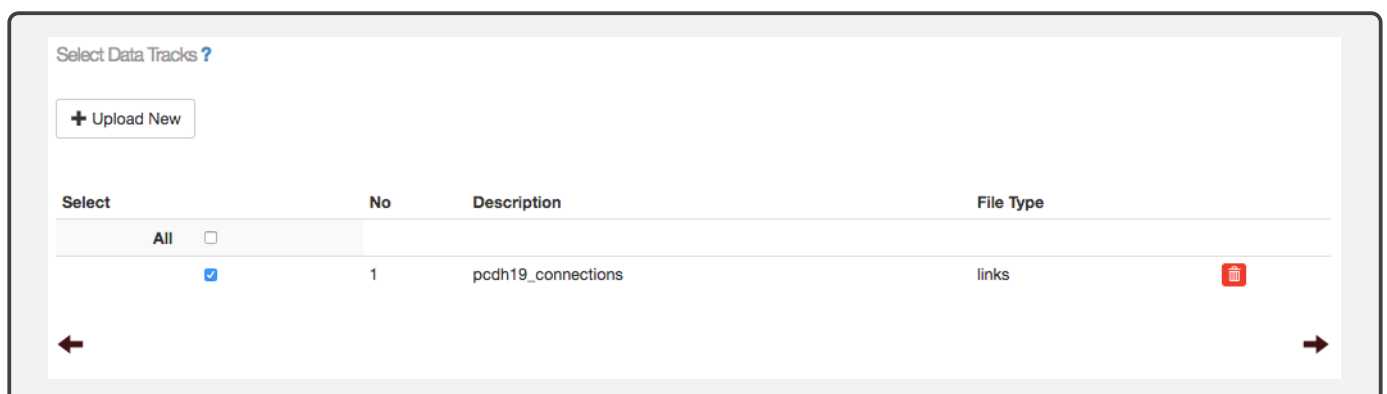
Data Tracks

1. Click ‘+ Upload New’
2. Select File Type: Links (for this example, we’ll be drawing connections between different bands)
3. Add a description of your dataset (preferably something meaningful to you)
4. Add the **data.txt** file
5. Click ‘Upload’




The screenshot shows a form titled "New Data Tracks". It has a "File Type" dropdown menu set to "Links". Below it is a link to "What are the Data Track Types?". The "Description" field contains the text "pcdh19_connections". Under the heading "Upload Data Track (Click 'Format' button for more info)", there is a "Browse..." button followed by the filename "data.txt". To the right of this are two links: "Format Description" and "Example (Download File)". At the bottom are two buttons: "Upload" (dark red) and "Reset" (orange).

6. Select (i.e. tick) your data set and continue.



The screenshot shows a table titled "Select Data Tracks ?". At the top left is a button "+ Upload New". The table has four columns: "Select", "No", "Description", and "File Type".

Select	No	Description	File Type
All <input type="checkbox"/>			
<input checked="" type="checkbox"/>	1	pcdh19_connections	links 

At the bottom of the table are two arrows: a left-pointing arrow on the left and a right-pointing arrow on the right.

7. There's only one page of data track settings. I like to specify everything in the **data.txt** file so that I don't need to change these settings manually. Note that anything you put in **data.txt** will override these manual settings. Click 'Preview' to check that everything looks as expected.

Data Tracks Settings ?

←

SaveResetPreview

pcdh19_connections

Links

Radius (eg: 0.5r)

0.95r

Bezier radius (eg: 0.0)

0r

Color

■

#ff451c

Alpha value (eg: 0.67)

0.67

Thickness (eg: 2)

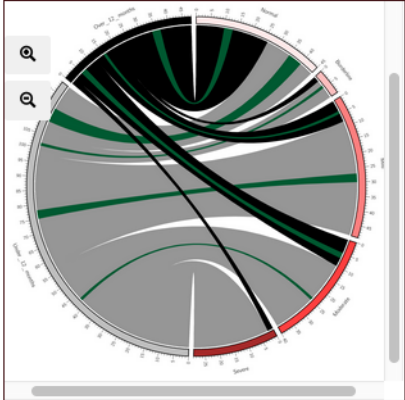
2p

Record limit

Ribbon?

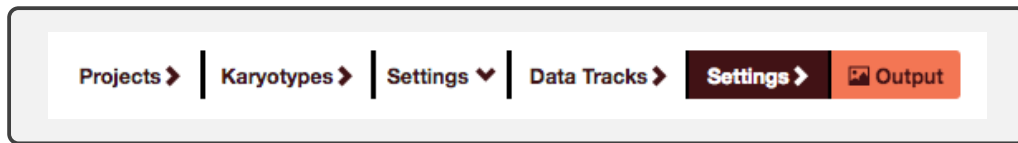
No

[Advanced: Input Custom Rules](#)



Output

To see your finished masterpiece, click ‘Output’.



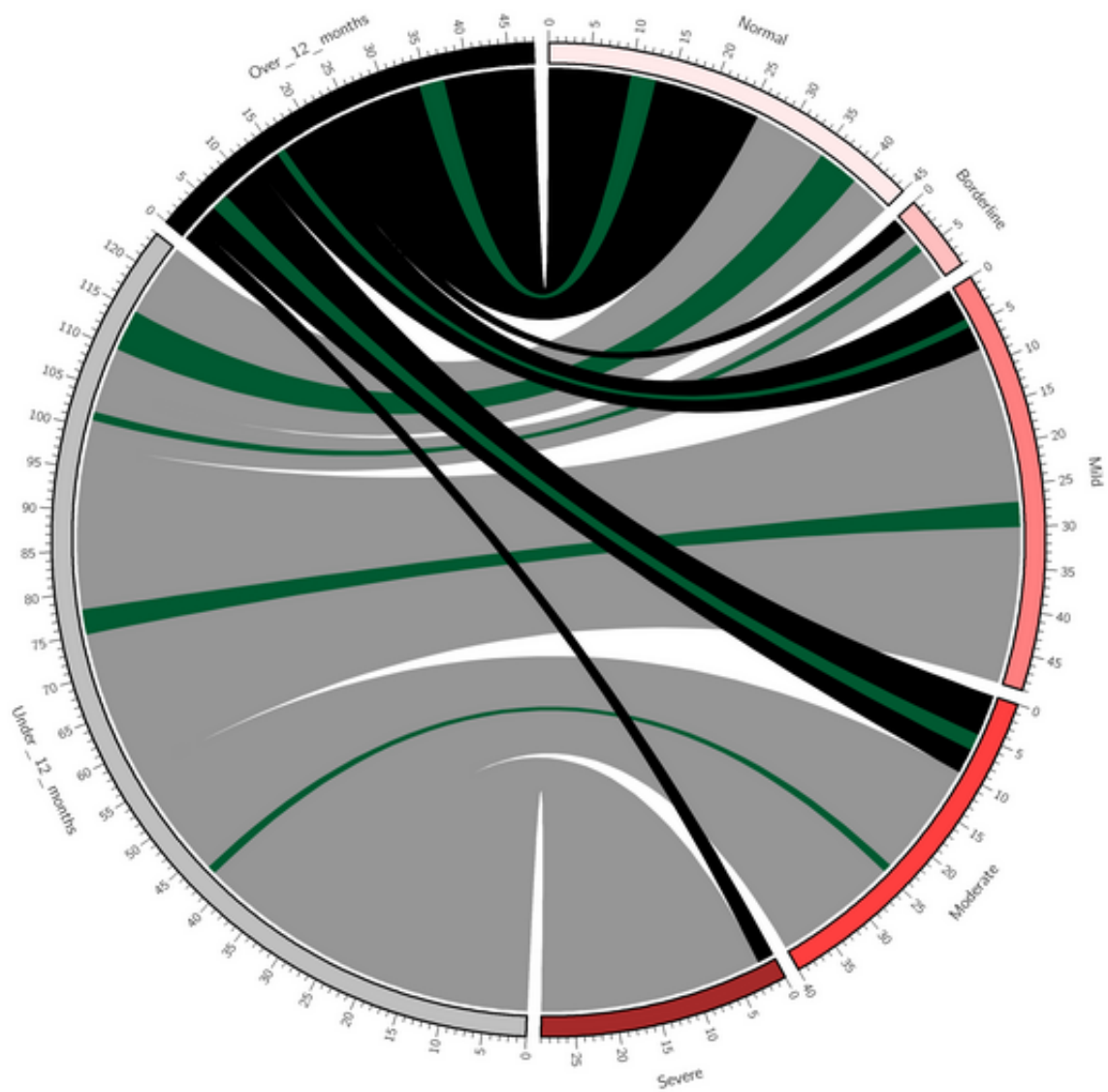
It may take a while to load - you're probably due for a tea break now anyway.



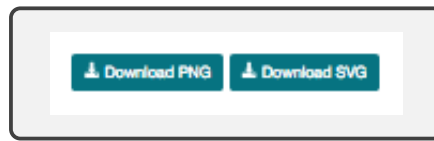
And voilà!

Circos Output

yo



The two buttons in the top right let you download your output figure as a PNG or SVG file.



And at the very bottom, you can also download the whole package of circos configuration files, if you want to make further changes directly using the command line circos package.



And there you go! Try it out and let me know how you go. I'll upload more templates soon...