**Circles1.5.py**

**Installation**

Install python (2.7.10) for Windows from:

https://www.python.org/downloads/

Install latest BLAST for windows from:

ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ncbi-blast-2.2.31+-win64.exe

If you want to be able to double-click on the program to run it, you need to add python and python/scripts to the system environment variable called 'Path'.

To do this, in any File Explorer window, right click on 'Computer' and select properties > advanced > Environment variables. Select 'Path' from the list in 'System Variables' and click edit. Then copy and paste the following to the end of the line:

;C:\Python27\;C:\Python27\Scripts;

Install C++ for windows from here: http://www.microsoft.com/en-us/download/confirmation.aspx?id=44266

You will need to log out and back in or restart computer after this.

Next you need to install a Python library called 'numpy'. Open a Command Prompt window as administrator: In the Start search box, type Command... then when you see it in the list right click and select 'Run as Administrator'.

At the prompts type:

pip install numpy

then

pip install image

Finally, in order to save images, install ghostscript, download from :

https://github.com/ArtifexSoftware/ghostpdl-downloads/releases/download/gs920/gs920w64.exe

and add this line to the Path environment variable as above:

;C:\Program Files\gs\gs9.20\bin

Everything should now be ready to run circles1.1.py by double clicking it.

**Instructions**

The program uses a folder of blast results to draw a the circular similarity diagram. The blast searches should all use the same reference sequence. Nothing else should be in the folder, only the blast output files. The files can be called anything you like. The File names will be used to label the key in the diagram, minus any extension and dot.

To run blasts you should use the command format below:

blastn -task blastn -query input1.fasta -subject reference.fasta -out 5-input1.blast -max\_target\_seqs 1 -outfmt 6

or

blastp -query input1.fasta -subject reference.fasta -out 5-input1.blast -max\_target\_seqs 1 -outfmt 6

or you can use the script included to blast all fasta files in a folder against a single reference fasta:

python win\_blastfolder2.py -i C:\\input\_folder\\ -o C:\\output\_folder\\ -r reference.fasta -t blastn

Once you have a folder of blast results, you can run circles1.5.py. Set the options as required. You must enter the known size of the reference genome in base-pairs.

The 'Colour map file' input box sets the location of a list of colours to use in your circles diagram. The format is 'RGB', with each colour separated with a semicolon, e.g.

235,128,114;46,139,87;235,193,203;235,215,20;20,20,128;221,160,221

All on one line in the file, no returns.

You can use this to define colours for each ring in the same order as the rings. The sequence of rings, starting from the innermost, is the file names in alphanumeric order. If not enough or no colours are specified then the program chooses random ones. If no file is specified, then inbuilt colours are used.

The optional "Outer ring annotation file" format is simply a tab delimited text file with feature name in first column and bp coordinate (single number only, not ranges) in the second column.

The optional "Ref annotation file" format is also simply a tab delimited text file with feature name in first column and bp coordinate (single number only, not ranges) in the second column. These annotations (for the reference genome only) will appear in a separate box (and the terminal window) when you click on the image.

To close the program press return in the Command Prompt window. You can draw multiple diagrams with different settings without restarting the program. Each opens in its own window. Files 'image.eps' 'image.jpg' and 'image.tiff' are saved in the program folder for each diagram drawn, overwriting previous ones, so change the file names manually if you want to keep an image.

Clicking anywhere on the diagram will show the bp coordinate in the diagram window and the command window if there is an annotation file.

Most normal window sized diagrams will give poor resolution image files. To make a high resolution image, draw a diagram much larger than the screen size, e.g. 5000 wide x 3000 high. Whilst these large diagrams are not practical for exploring features because they will process slowly, the image.jpg file, can be used to do so. To keep image files, rename or move them after each run or they will be overwritten.