PlasMap
by Tito Sciortino

What is it?

PlasMap is a little utility for drawing maps of plasmids. It allows you to color each segment of the plasmid in one of several colors. You can also provide a label for each segment. The output is in resolution-independent encapsulated postscript format. This format can be read by Photoshop, Preview, Acrobat, and lots of other programs.

System requirements

PlasMap is written in Perl, with a wrapper supplied by Platypus.

The Perl part means that you need to have Perl installed to run the program. Fortunately, Perl is already installed and ready to go on Macs right from the factory, so there's nothing special you need to do in that regard if you're on a Mac.

The Platypus part means that you need a Mac to run the app.

If you don't have a Mac, but you do have Perl, and if you're a tinkerer, you can find the actual Perl script (which is more-or-less platform-independent) in the PlasMap package. In addition, I've bundled the script itself (named "script.pl") with this. You might be able to just run it from a command line on whatever computer you have that has Perl installed. But to get to the script from within the app itself, on a Mac, right-click on the PlasMap icon, and from the pop-up menu select Show Package Contents. Doing that will open a folder called PlasMap.app. Inside there, go to Contents > Resources > script. You'll have to add ".pl" to that file.
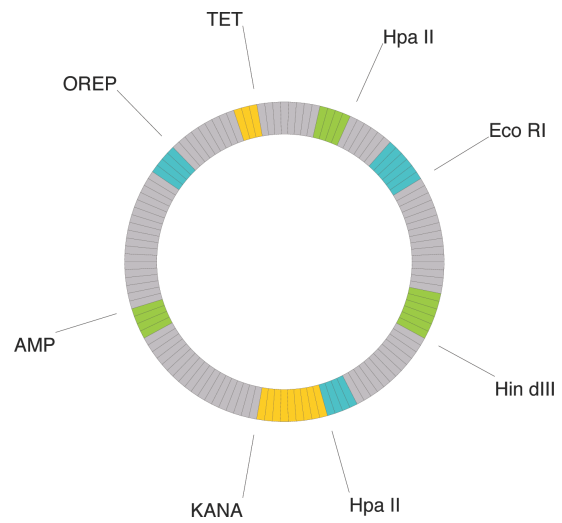
How do I install it?

Just copy it to your Mac. As long as you have Perl installed (and virtually all Macs come that way from the factory), there should be nothing else you have to do.

How do I use it?

All you have to do is drag a file containing the plasmid data onto the PlasMap icon. The output file will be saved to wherever you specify in the data file.

PlasMap should have come with a file called sample_data.txt. Make a copy of this file so that you can just modify the copy for each new plasmid you draw.

The data file

The data file is just a plain text file. In the top part of the file are the parameters that control the drawing and the file output, while the bottom part is the specific plasmid data.

In the data file, any line that starts with a pound sign (#) is a comment and is ignored by PlasMap. The lines that don't start with # are the data lines.

```
# output path
# you can set this explicitly to something like /Users/tito/Desktop/PlasMap/
# or set it to TO_DESKTOP to just save the output files to your desktop
TO_DESKTOP
```

The first data line is the **output path**. This is the location that PlasMap will save its file to. At a minimum, unless your user name on your Mac is tito, you'll need to change this. In general, it should be usable to set this to

```
/Users/[your_user_name]/Desktop/
```

Replace "[your_user_name]" with your user name on your Mac, without the square brackets. If you do this, your plasmid drawings will appear on your desktop, and from there you can later move them wherever you like. (This accomplishes the same thing as using TO_DESKTOP there.)

```
# output file name (name stem)
# you can set this to a specific name
# or set it to USE_INPUT_FILENAME
USE_INPUT_FILENAME
```

The next data line is the output file name, and in one sample file I've set it to "plasmid" (you can name it anything you like), while in the other I've set it to USE_INPUT_FILENAME. With the latter, the input file's name is used as the name stem. PlasMap automatically adds a timestamp to each file it creates, after the name stem specified here. The timestamp is formatted as yyyymmdd_hhmmss. Finally, .eps is added at the very end.

```
# outer radius (in pixels)
100

# inner radius (in pixels)
80
```

Next are the **outer** and **inner radii**. Together these allow PlasMap to draw the plasmid map with a hollow center. These are in pixels.

```
# segment label offset, inner radius (multiple of outer radius, above)
1.10

# segment label offset, outer radius (multiple of outer radius, above)
1.50
```

Following that are two more radii, the **segment label offset radii**. These are in multiples of the outer radius defined above. They control the length of the lines that point from the segment labels to the segments themselves. Usually these will have values greater than 1.00, which will put the labels outside

the plasmid in the drawing. But the values can be less than 1.00 as well, and this can be used to put labels in the interior space.

```
# image margins (in pixels)
100
```

Image margin is next. This is in pixels and provides some padding around the image.

```
# line color (in RGB: three values between 0 and 1; 0 = black, 1 = white)
0.22 0.22 0.22
```

The lines that are drawn around each wedge, and pointing from the segment labels to the segments will have the color specified in **line color**, next. This color, and the other colors defined in the data file and used by PlasMap, are a mixture of red, green, and blue and so are represented by three numbers. For each of those three component colors, 0 is the darkest version, while 1 is the brightest. So each of the three numbers defining a color must be between 0 and 1 (inclusive).

```
# line thickness (in pixels)
0.25
```

Line thickness refers to the thickness of the lines surrounding each wedge and the lines pointing from the labels to the segments. This is in pixels, and fractions of pixels are allowed (as in 0.25 pixels, or one-quarter of a pixel, for a very thin line).

```
# label (text) color (in RGB)
0 0 0
```

Label text color colors the segment labels, and is a set of three numbers, just like line color above.

```
# font name
Helvetica

# font size (in pixels)
12
```

Next, in **font name** and **font size**, you can specify the font to be used in writing the segment labels. Be careful to spell the name of the font correctly or you may have problems when you open the drawing later.

```
# segment color 1 (in RGB)
0.75 0.75 0.75

# segment color 2 (in RGB)
0.2 0.8 0.8

# segment color 3 (in RGB)
0.6 0.8 0.0

# segment color 4 (in RGB)
1.0 0.8 0.0

# segment colors 5-10 (in RGB)
1.0 0.6 0.8
1.0 1.0 0.6
0.8 1.0 0.8
0.8 1.0 1.0
0.6 0.8 1.0
0.8 0.6 1.0
```

Finally among the general parameters, we define ten **segment colors** to be applied to the wedges as they are drawn (and of course, segments are made up of wedges). Each color is identified in the plasmid data section in the lower part of the data file by a single number (so, we have colors `1, 2, 3, … 10`). Again, like the other colors above, these are each defined using three numbers. Only four colors are used in the examples.

After all the foregoing general parameters, a list of the **segments** follows. This will be different for each plasmid that is drawn:

```
11,1
6,2,Eco RI
4,1
2,1
4,3,Hpa II

...

9,4,KANA
4,2,Hpa II
1,1
11,1
6,3,Hin dIII
4,1
```

Each line of data in this part of the data file defines a single segment. The first item on each line is the number of wedges in the segment. I think of each wedge as representing a base pair, but it could also represent multiples of them if you find that more convenient. The second item on each line is the color number for that segment. All of the wedges making up that segment will be filled with this color. (These colors were defined above, immediately before this section of the data file.) Finally, if the segment has a label, that will be the third item on the line. Each of these things is separated by a comma.

The output file

The drawing made by PlasMap will be saved as an eps file.

One of the most flexible ways to use this file is to open it in Photoshop, where it can be converted to an editable image. Thus, you could draw additional things on the plasmid, or erase wedges or lables if you like.

Just keep in mind that when you open the eps file in Photoshop, a dialog about rasterizing the file may come up. If you are going to want to print your drawing at high resolution after editing it, be sure to set the resolution high enough for your purposes.

Of course, if you just want to print out the drawing without editing it, you should be able to do that simply by opening it in Preview, then printing.

Complete example input file

```
# Everything following the pound sign is a comment and
# is ignored by the program when this data file is read in.

# -------------------------------------------------------
#
# General parameters for drawing the plasmid map
#
# -------------------------------------------------------

# output path
# you can set this explicitly to something like /Users/tito/Desktop/PlasMap/
# or set it to TO_DESKTOP to just save the output files to your desktop
TO_DESKTOP

# output file name (name stem)
# you can set this to a specific name
# or set it to USE_INPUT_FILENAME
USE_INPUT_FILENAME

# outer radius (in pixels)
100

# inner radius (in pixels)
80

# segment label offset, inner radius (multiple of outer radius, above)
1.10

# segment label offset, outer radius (multiple of outer radius, above)
1.50

# image margins (in pixels)
100

# line color (in RGB: three values between 0 and 1; 0 = black, 1 = white)
0.22 0.22 0.22

# line thickness (in pixels)
0.25

# label (text) color (in RGB)
0       0       0

# font name
Helvetica

# font size (in pixels)
12

# segment color 1 (in RGB)
0.75 0.75 0.75

# segment color 2 (in RGB)
```

```
0.2 0.8 0.8

# segment color 3 (in RGB)
0.6 0.8 0.0

# segment color 4 (in RGB)
1.0 0.8 0.0

# segment colors 5-10 (in RGB)
1.0 0.6 0.8
1.0 1.0 0.6
0.8 1.0 0.8
0.8 1.0 1.0
0.6 0.8 1.0
0.8 0.6 1.0

# ---------------------------------------------------
#
# Segment data
# (# of wedges in segment, segment color, segment label)
#
# ---------------------------------------------------

4,1
6,2,Bam HI
4,1
6,3,Xma I
1,1
6,1
6,4,Eco RI
9,1
6,2,Hin dIII
4,1
11,1
6,3,Eco RI
4,1
2,1
4,4,Hpa II
8,1
3,2,TET
4,1
5,1
4,3,OREP
12,1
6,1
4,4,AMP
11,1
7,1
9,2,KANA
4,3,Hpa II
1,1
11,1
6,4,Hin dIII
4,1
2,1
42,5,coding
4,1
6,2,Eco RI
3,1
6,3,Hin dIII
2,1
6,4,Xma I
7,1
```