The graphic in this repository – given as both a JPEG image and a PDF – was created in the R programming language using *levelplot* function from the "lattice" library. In making this choice, I relied on the recommendation in the assignment instructions that said that I "***...may find it most instructive to create the chart from scratch using a graphics API of your choice.***" I am already familiar with the graphics capability of Python and R, which are two of the programming languages most closely associated with data science. I am more familiar with the rich graphics capability of R, so I chose that for this assignment.

A cursory examination of the table provided for the minimum inhibitory concentration (MIC) values shows that it is a relation of two sets of nominal variables. The first variable is the antibiotic type, and this is given along the horizontal axis of the table. The second nominal variable is the bacteria type, and it is given along the vertical axis of the table. The intersection of these two relations is a quantitative variable with a fixed reference. A somewhat unrelated column of the relation is the "gram staining" column. The intersection in the association of antibiotic and bacteria is a binary assertion: positive or negative.

To construct an effective visual representation of these data using R, I examined the descriptions available to me at the website entitled "*The R Graph Gallery*" (https://www.r-graph-gallery.com/). The website allows its user to drill down to a particular type of visualization from a library, with types organized based on the level of abstraction. The two types that best seemed to fit these data were "heatmap," and "correlogram." Of the two, "heatmap" looked more promising. A heatmap is described thusly:

> "A **heat map** (or **heatmap**) is a graphical representation of data where the individual values contained in a matrix are represented as colors. It is a bit like looking at a data table from above. It is really useful to display a general view of numerical data, not to extract a specific data point." (https://www.r-graph-gallery.com/heatmap/)

In short, this looks like a good fit for the data. Of the available examples, I chose *levelmap* as the most promising. The *levelmap* allows the observer to quickly determine the magnitude of a value from the antibiotic/bacteria matrix using a color **value**, and the color-coded scale for the magnitude of the value is given immediately to the right of the map. The values are automatically bucketed to a specific hue. One shortcoming of this approach is that the ability to distinguish small differences within the bucketed hues are lost. However, this is made up for by the ease with which the observer is able to distinguish between differences of magnitude. For example, one can see with the bright red encoding that penicillin is a relatively ineffective antibiotic for six types of bacteria, and is only marginally effective for one other.

The effective encoding of gram-staining (positive or negative) had no example code in the aforementioned library, so I was forced to ad-lib. It might have been possible to create another column in the *levelmap* for this information. However this additionally column would have been logically unrelated to the values provided in the other columns, both by color and by the type of data encoded. I noted that since gram-staining is a binary value associated with bacteria type, it can be color encoded with the label color along the vertical axis. Since gram-staining is associated with a dark blue, I chose that as the font color for bacteria with that positive characteristic, and I also made the font bold. For bacteria with negative gram-staining characteristic, I left the font black and unbolded. I noted the proper interpretation of the font in the labeling of the vertical axis.