*Audience:*

The audience of the visualization is Doctors and Lab practitioners who need to know the Minimum Inhibitory Concentration (MIC) of the antibiotic during (not after) the process of determining the bacteria in hand.

*Rationale*:

1. I briefly went through the procedure involved in diagnosis of bacteria. First step is Gram staining the bacteria. It’s quite fast and cheap to get Gram results as positive or negative. So, it will be beneficial if the data is visualized in two separate graphics according to Gram Stain as one wouldn’t need to go though all 16 bacteria. Moreover it tells a story, which I noticed and would like to tell while I was playing with data. It intentionally and correctly shows that Neomycin is an effective antibiotic for Gram-negative bacteria and Penicillin (in most cases) or Neomycin (for other cases) can be good choice for Gram-positive bacteria.
2. The data is arranged from lower concentration needed to higher concentration needed. As with lower MIC I wanted to represent more powerfulness or effectiveness of the antibiotic, it made sense to arrange it in that order. For example, the graphic shows Neomycin as a powerful antibiotic for Gram-negative bacteria, showing ‘capturing’ all the space and inhibiting the bacterial growth. To show the ‘capturing’ I used spider chart instead of something else.
3. The color of the text showing Gram strain is in purple for positive and in pink/red for negative as the color of bacteria after gram staining. This is can help is quick recognition.
4. As the MIC data is not linear. I applied the following formula to transform the data so that it can tell the above mentioned stories and can be fitted into the space.

Y= -1\*(-4+log(X))

It maps the values as:

0.001 to 7

0.01 to 6

0.1 to 5

1 to 4

10 to 3

100 to 2

1000 to 1

The log(base 10) is used to linearize the data. -4 helps in having all the data on one side of the axis. Then the whole -1 takes it to the positive domain. The mapping also made it easier for the graphic toolkit to represent using levels 1 to 7.

I also tried using external database of shape of the bacteria (as this is usually the next step after Gram staining) to get some patterns, but couldn’t in the specified time constrain. I think using the shape data can be the next step in improving this visualization, and might give it a tree-like structure. Bacteria can have a Coccii or a baccaii shape or others, independent of the gram