Using Dot Plots for Comparative Genomic Analyses: Learning Activity Assessment



## Assignment description

Now that you know how dotplots work, it’s time to create one to answer one of your own research questions. In this assessment, you are tasked with formulating a hypothesis which you can investigate by the construction of appropriate dotplots.

You may approach this task by reviewing the literature that describes the cluster, host, or morphology of your desired phage and consider how your phage may be similar to other phages. For example, if you have a myoviridae phage, you might be interested in other clusters of myoviridae phage that are similar to your phage, and you can demonstrate this similarity using a dotplot. Or perhaps you’re curious about which other clusters from your phage’s host might have similarity to your own. The possibilities are endless - all you have to do is decide what you want to compare.

You may also wish to review the Smith, et al., reference for ideas on how to proceed with your analysis. For example, you may decide to carry out whole genome comparisons using the dotplot tool, or you may, like Smith, et al., decide to focus on a single gene. What types of genes may be good candidates for sorting phages into specific clusters? What types of genes would not be good candidates, and why?

Before you complete your work, have a classmate peer review your work. Decide if/how to incorporate your classmate’s suggestions into your project before turning in your work to your instructor.

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## Planning Your Dotplot

The question about phage genomics that I plan to answer using a dotplot is: \_\_\_\_\_\_

My hypothesis is: \_\_\_\_\_\_\_ (*what do you expect to see on your dotplot, and why? Provide a rationale based on PhagesDB and/or a scientific paper.*)

The type of data I will be using as input is: \_\_\_\_\_ (*whole-genome or single-gene sequences? nucleotide or amino acid?*)

These are the names of the phages I’m planning to compare (*along with other information relevant to my question like host, cluster, etc*): \_\_\_\_\_\_\_\_\_\_\_\_

## Creating your Dotplot

Follow the instructions in the Dotplot Learning Activity Instructions to create a dotplot.

Annotate your dotplot as in the Annotating Dotplots presentation.

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## Dotplot Results

Insert an image of your completed dotplot below. Don’t forget to annotate it so we can see which phages are where!

What were your results? What is the answer to your research question above?

Are your results what you were expecting? Why or why not?

Knowing how diverse phages are, what limitations can you think of when it comes to interpreting this plot? How could you address them in the future?