Viral and Bacterial Data Analysis

31 folders/samples

* Viral Data Thresholds
  + 25% genome found
  + 35% genome found
  + 50% genome found
* Bacterial Data Thresholds (depending on Quantity)
  + 100 cells
  + 200 cells
  + Others
* Filter data based on thresholds
* Pair viral and bacterial data coming from same sample
* Create matrix of sample based on presence/absence
* Compile all sample matrices into one matrix showing edge weight
* Convert matrix into edge list
* Put edge list into Cytoscape and produce network
* Number of networks created based on threshold combos