Instructions:

- 1. Download common core8.csv and Mucus Code.R from Codes and data folder.
- 2. Download all the packages listed in Rstudio package list from Codes and data folder.
- Run Mucus_Code.R in the same directory as common_core8.csv (This code was found to have
 issues with some computers running Windows OS, specifically with points not popping up on the
 plots).
- 4. In the "Table_S3_linear_analysis" folder, locate "Table_S3_linear_analysis.txt" file. Download file. This is a text file containing information of the simple linear regress, Spearman's test and Pearson's test for Effective diffusion versus diameter less than 100 nm, effective diffusion versus negative zeta potential, effective diffusion versus positive zeta potential, effective diffusion versus anomalous exponent, anomalous exponent versus diameter less than 100 nm, anomalous exponent versus negative zeta potential, and anomalous exponent versus positive zeta potential.
- 5. In the 'Table_S3_linear_analysis" folder, locate csv files "Table_S3_'{a-g}'.csv". Download them to your local directory. The first row of all the files are headers. The label a-g refers to the row of the linear analysis in the order: Effective diffusion versus diameter less than 100 nm, effective diffusion versus negative zeta potential, effective diffusion versus positive zeta potential, effective diffusion versus anomalous exponent, anomalous exponent versus diameter less than 100 nm, anomalous exponent versus negative zeta potential, and anomalous exponent versus positive zeta potential. None of the data files contains logarithmic values. These files contain the data points that make up the linear analysis for "Table S3".