

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.
3. 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 showing in plots).
4. Locate `Figure_S3_Dominant_Mucin.pdf`.
5. In folder `Particle_type`, locate `Figure_S3_Dominant_Mucin.svg`. Add number of data points in inkscape.
6. From the folder locate `Figure_S3_Dominant_Mucin`, locate `Figure_S3_Dominant_mucin_'(a-f)_'_data.csv`. These are data files that make up panel **a-f** of `Figure_S3_Dominant_Mucin.pdf`.
First row is the header. Each data file a-f contains information on their respective panel: Effective diffusion, anomalous exponent, Size, Charge, Temperature, and pH, respectively. Columns refer to dominant mucin gene: `"MUC2"` is MUC2 gene, `"MUC5AC"` is MUC5AC gene, and `"MUC5B"` is MUC5B gene.

Output(s):

`Figure_S3_Dominant_Mucin.pdf` is a pdf of box plots effective diffusion, anomalous exponent, particle size, charge, temperature and pH based on dominant mucin gene. Variables were ordered based on the medium of diffusion.