

#### 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 popping up on the plots).
4. Locate `"Figure_1_RFMSE.pdf"`. This is panel a (left).
5. Locate `"Figure_1_rpart.pdf"`. This is panel b (right).
6. Locate `"Figure_1_Random_forest.svg"` in the folder. `"RFMSE.pdf"` and `"rpart.pdf"` combined in inkscape as one figure, respectively.
7. Locate `"Figure_1_RFMSE_a_data.csv"` in `Figure_1_Random_forest` folder. This is the data that makes up `"Figure_1_RFMSE.pdf"`. First row is reserved for the title of the column, and the first column is reserved for the title of the variables selected. Column names referring to `"Permutation_ {trial number}"` is the MSE% of the permutation, and column names designated as `"MSE%_mean"` and `"MSE%_std"` is the arithmetic average and standard deviation of the permutations. Row names refer to the variable tested `"Alpha, Particle_type, Zeta_potential, Mucus_source, and Dominant_mucin"` is anomalous exponent, particle type, zeta potential, mucus source and dominant mucin, respectively.

#### Output(s):

1. Locate `Figure_1_Random_forest.pdf`. This is the source pdf that combines `"Figure_1_RFMSE.pdf"` and `"Figure_1_rpart.pdf"`.