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.”