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. In your Rstudio workspace, locate "Core_Mucus". Call built-in Rstudio functions min() and max() on the "Diffusion_constant" column in"Core_Mucus" in the console. Here is a demonstration: min(Core_Mucus$Diffusion_constant). This is the range (minimum, maximum) of effective diffusion at one second. If there are difficulties in viewing the result of the function call View() in the console to display output. Here is a demonstration: View(min(Core_Mucus$Diffusion_constant)).

5. In your Rstudio workspace, locate "alphapoints". Call built-in Rstudio functions min() and max() on the "alpha" column in"alphapoints" in the console. This is the range (minimum, maximum) of anomalous exponent. If there are difficulties in viewing the result of the function call View() in the console to display output.

6. In your Rstudio workspace, locate "Core_Mucus". Call built-in Rstudio functions min() and max() on the "Diameter" column in"Core_Mucus" in the console. This is the range (minimum, maximum) of particle diameter. If there are difficulties in viewing the result of the function call View() in the console to display output.

7. In your Rstudio workspace, locate "Core_Mucus". Call built-in Rstudio functions min() and max() while calling na.omit on the "Zeta" column in"Core_Mucus" in the console. Here is a demonstration: min(na.omit(Core_Mucus)). This is the range (minimum, maximum) of zeta potential. If there are difficulties in viewing the result of the function call View() in the console to display output.

8. In your Rstudio workspace, locate "Core_Mucus". Call built-in Rstudio functions min() and max() on the "Temperature" column in"Core_Mucus" in the console. This is the range (minimum, maximum) of Temperature. If there are difficulties in viewing the result of the function call View() in the console to display output.

9. In your Rstudio workspace, locate "Core_Mucus". Call built-in Rstudio functions min() and max() while calling na.omit on the "Temperature" column in"Core_Mucus" in the console. See Step 7 for demonstration on how to call na.omit(). This is the range (minimum, maximum) of pH levels. If there are difficulties in viewing the result of the function call View() in the console to display output.

10. In your Rstudio workspace, locate "Mucus_Core". Call the built-in Rstudio function unique() on the "Mucus_Source" column in"Mucus_Core" in the console. Here is a demonstration on how to call it: unique(Mucus_Core$Mucus_Source). This is the list of tissues where mucus comes from. If there are difficulties in viewing the result of the function call View() in the console to display output.

11. In your Rstudio workspace, locate "Core_Mucus". Call the built-in Rstudio function unique() on the "Dominant_Mucin" column in"Mucus_Core" in the console. This is the list of tissues where mucus comes from. If there are difficulties in viewing the result of the function call View() in the console to display output.