***Analysis plan for Loess – Fungal textures***

First step is to make an **explorative analysis** of the data to identify common and diverging trends among the 4 fungal strains and among the food considered. Could batch, sequencing center or any other parameter affect the measurements? To answer these questions:

* Table of sample size of textural measures / variables per growth condition / Missing values for the four strains
* Table of sample size of textural measures variables per food type (fish, meat and other food types)
* Boxplots of textural measures / variables per growth condition (for 4 fungal species)
* Boxplots of textural measures / variables per food type (for all available food samples)
* Investigate whether batch, sequencing center or others can have any effect (perhaps using different shapes for different batches?)

To find out if any of the strains exhibits a **profile similar to any food**, and to identify which measurements of features can explain the similarity or differences between the profiles:

* Join the data of all measurements at all conditions for all strains and food in one matrix (investigate whether some measurements need to be dropped due to missing data)
* Standard-normalize the data (by substracting the mean and divide by sd)
* Running a principal component analysis PCA to find out if any of the strains exhibits a similar behaviour (and therefore a similar texture) to meat, fish or other food samples.
* Which conditions are driving the similarity or difference between groups of samples? Extract drivers and how much variance do they explain (R2) from the PCA
* With Euclidian distances compare the distances between the strains and each food (perhaps group all types of meat and all types of fish) in boxplots.

With the **strain sequenced data** try to identify proteins, BGCs or toxins. To that end:

* Gene calling on fungal strains genomes
* Mapping with funcscan (nf-core pipeline) to Biosynthetic gene clusters (BGCs), antibiotic resistance genes (ARGs) and AMP (Antimicrobial peptides)
* Mapping with EggNoGG-mapper to many functional databases (KEGG pathways, COGs, PFam, EC, CaZY, etc…)