**Project Assignment 3: data in qiime2**

McKeeley Stansberry- ANSC 516

Take a screenshot of the quality scores.

Graphical user interface, application

Description automatically generated

What values will you choose for the next step of trim and trunc? Is this long enough to allow for overlap to allow for sequence merging?

I will choose the values

--p-trim-left 0 **\**

--p-trunc-len 200 **\**

For the next step of trim and trunc.

I choose these numbers because the quality score is high at the begin and

begins to drop off at around 200 as the quality score starts to go down each time and where both forward and reserve reads at the 25th percentile of the Q value are above 20.

This is long enough to allow for overlap to allow for sequence merging

because both the forward and reserve reads remain at good quality values at these parameters.