# CONCLUSIONS

After having created each genomic data and analyzing its entropy, we discovered that for each motif, depending on its size, whether it was 6 or 8, the Shannon entropy had a maximum value depending on the case (for the case with 6 bases, the highest value entropy is 1.92 and in the case with 8 bases it is 2) so what we did was take a value prior to this and based on this filter, eliminating all the motifs that were repeated the most and that had lower entropy than the maximum entropy, thus achieving keep all the data with the highest entropy

The choice of non-arbitrary values was made with the help of the same entropy calculator that we did in the code using the second highest entropy value.

**Marlon Yecid Riveros Guio**