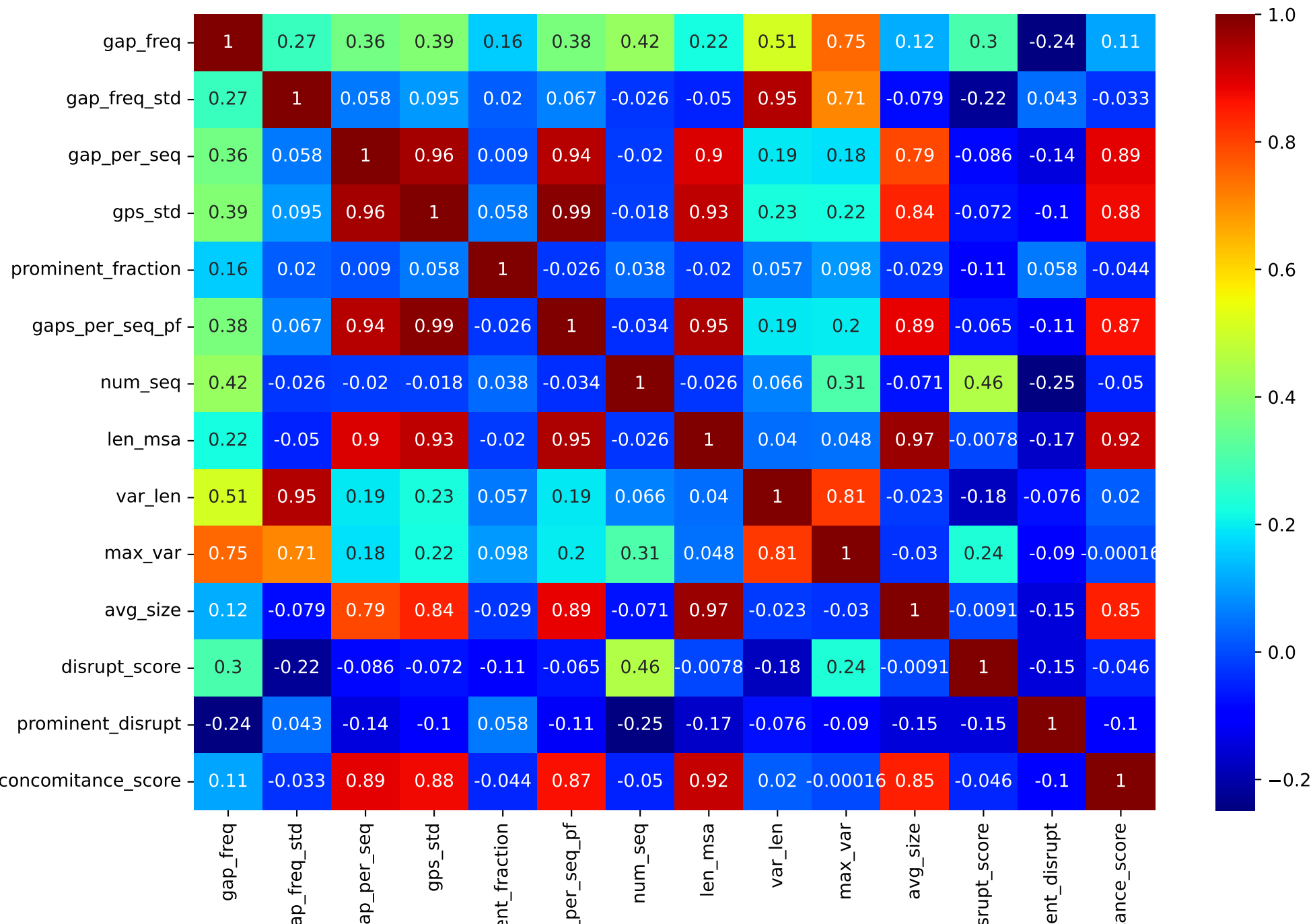
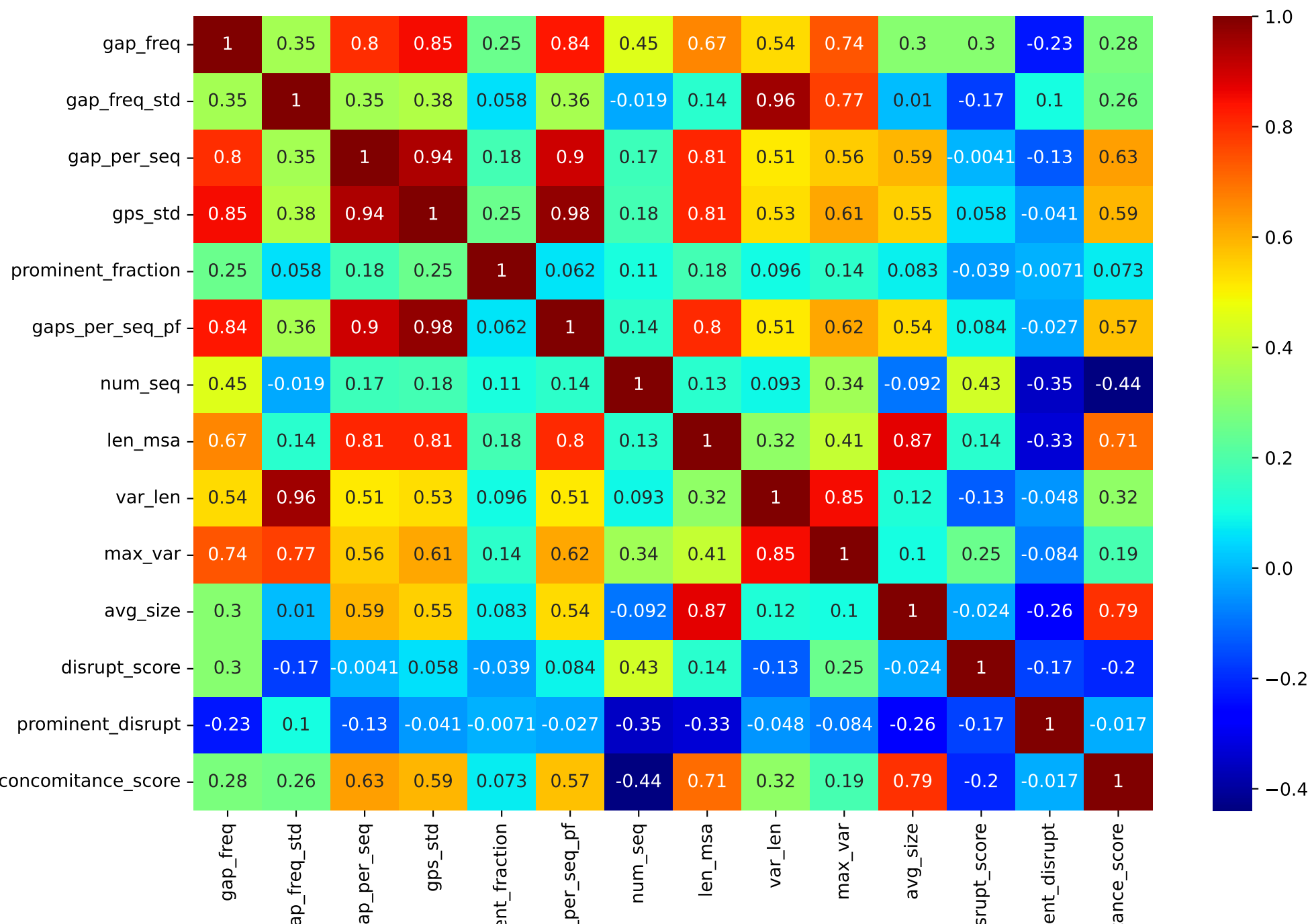


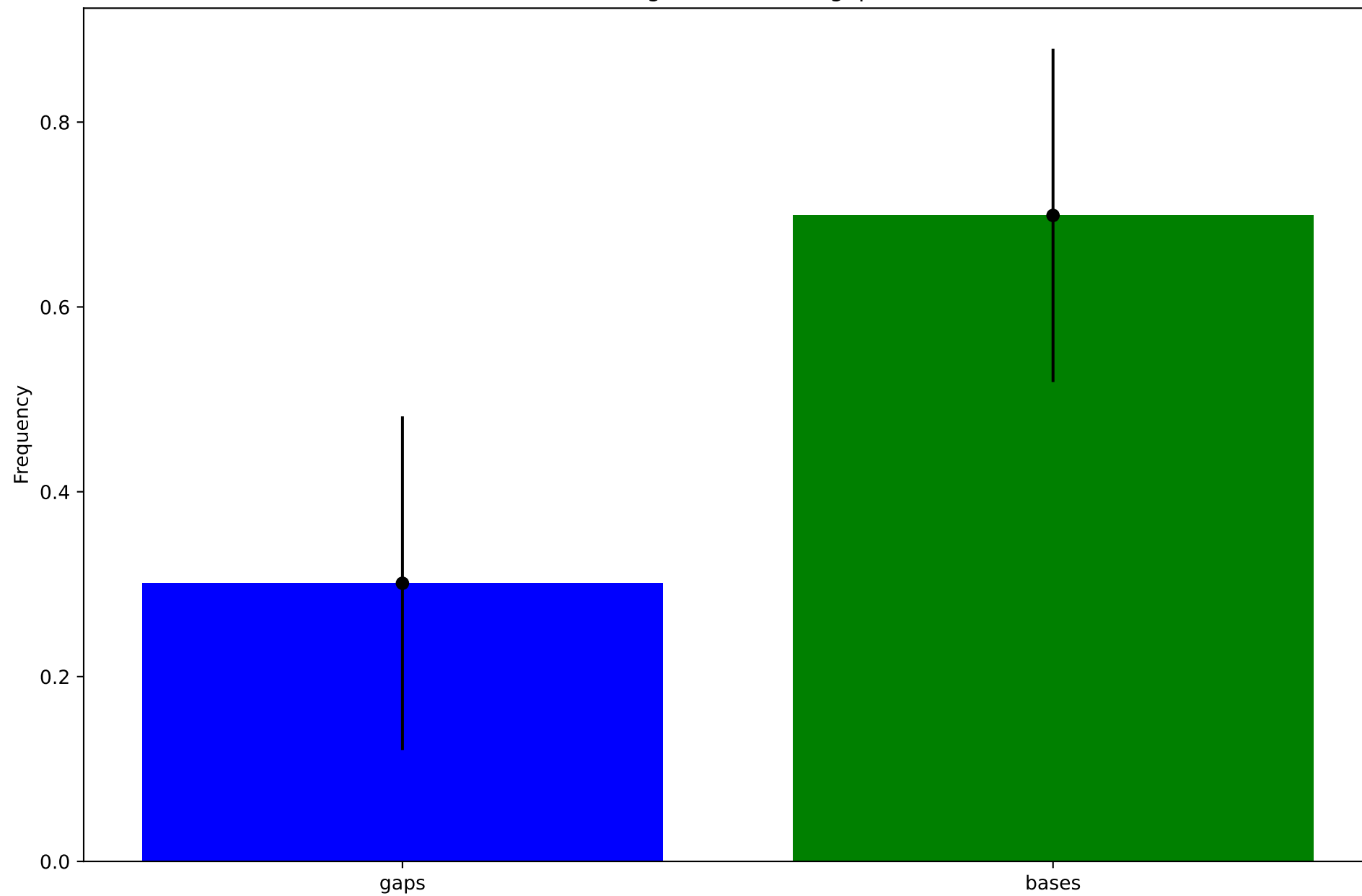
Pearson correlation (linear)



Spearman correlation (non linear)

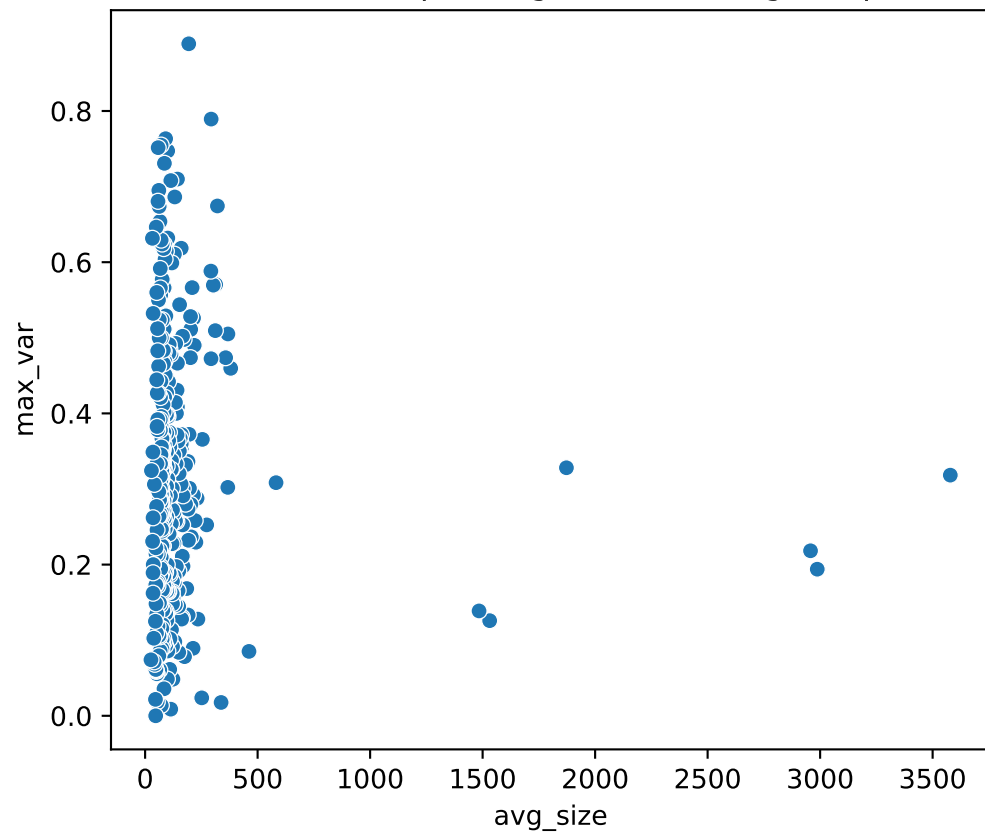


Rfam Seed alignment overall gap fraction

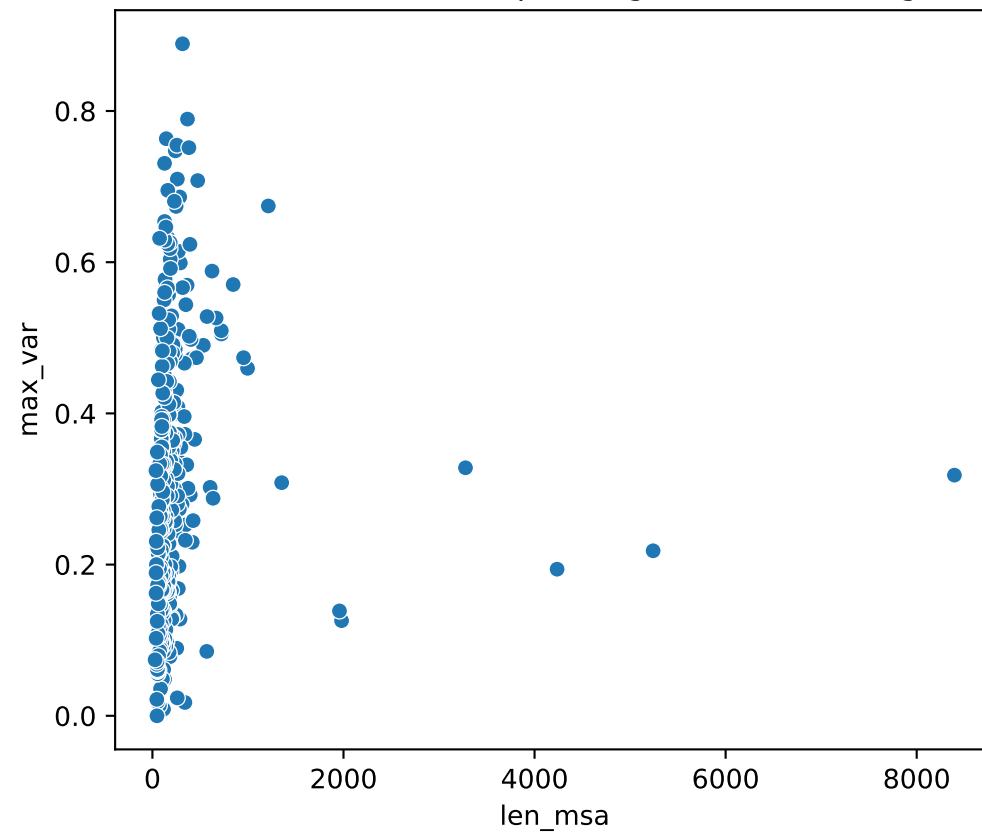


Maximum variation in gaps' number per sequence depending on MSA's and sequence average size

Maximum variation depending on the average sequence size

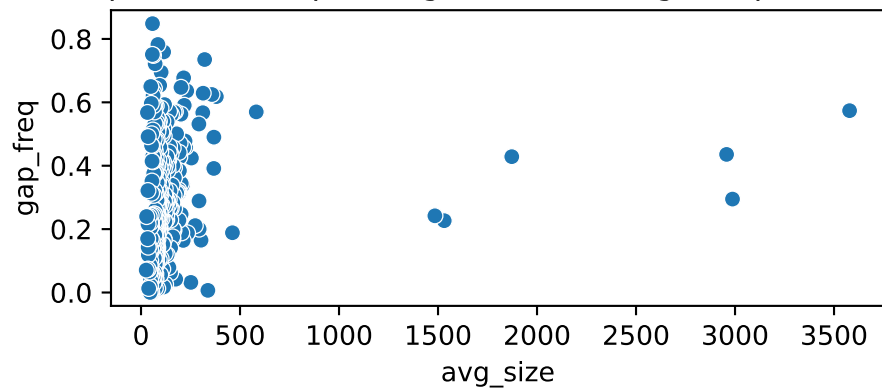


Maximum variation depending on the MSA length

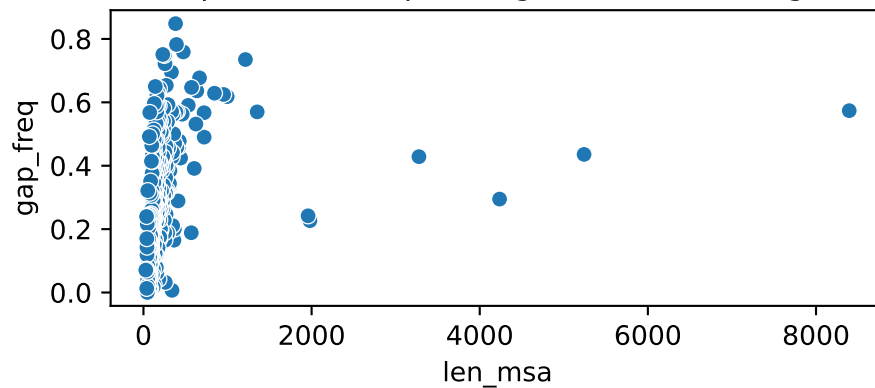


Correlation of gap frequency with sequences and MSA size depending on MSA's and sequence average size

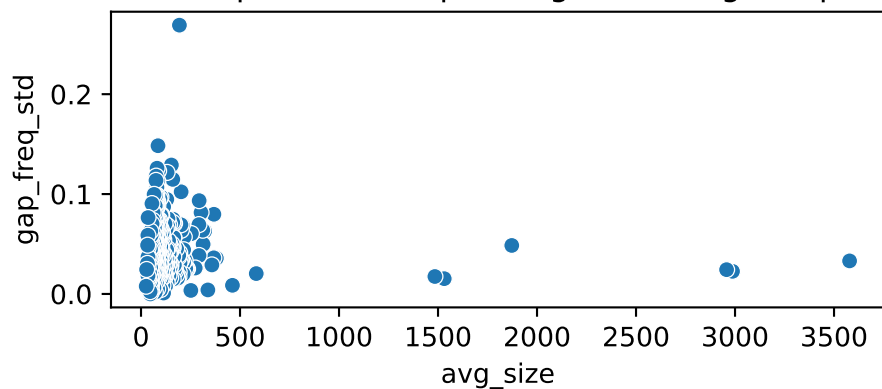
Gap fraction depending on the average sequence size



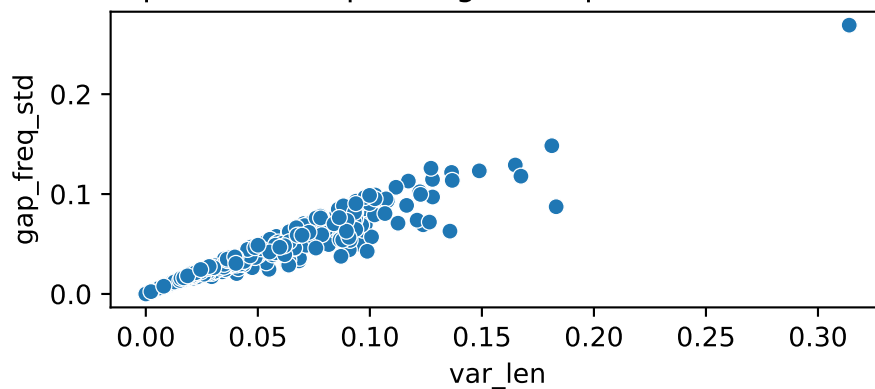
Gap fraction depending on the MSA length



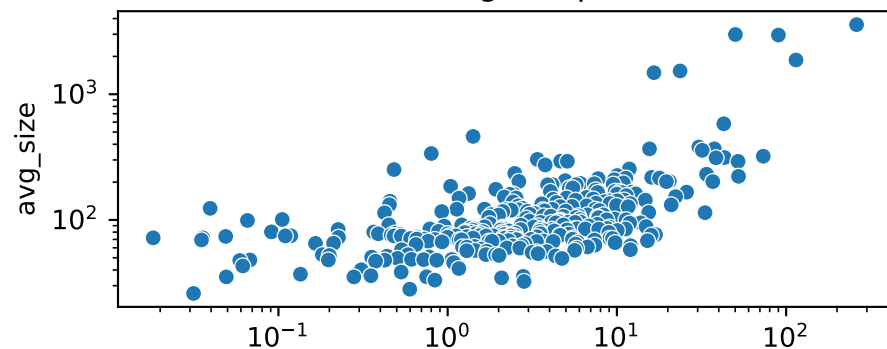
Variation of Gap fraction depending on average sequence size



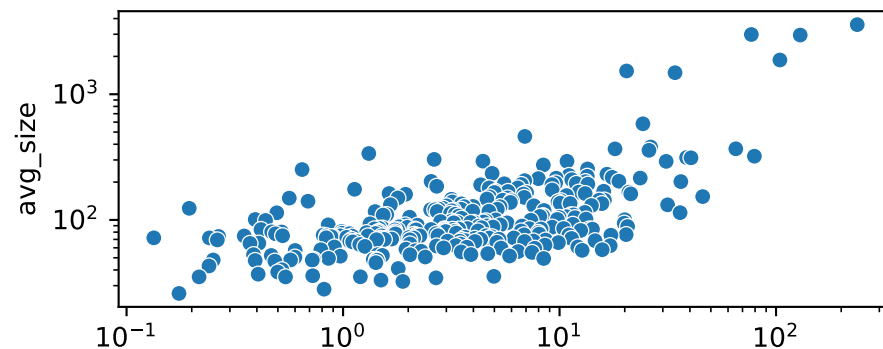
Variation of Gap fraction depending on sequences size standard deviation



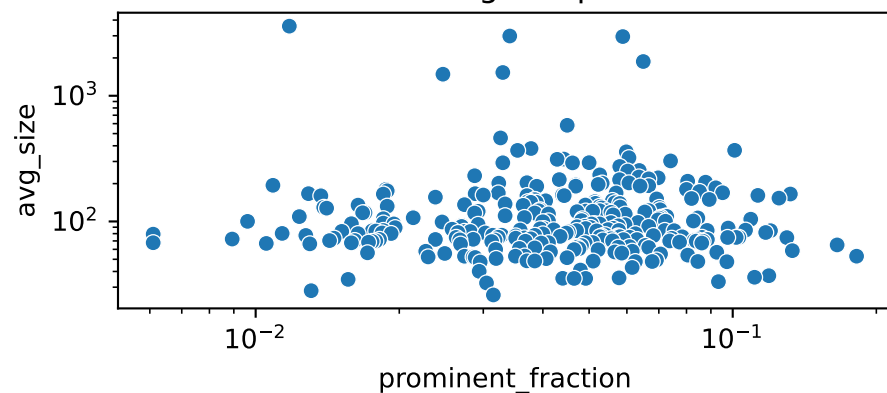
Correlation between the number of gaps created by a sequence in a MSA and the average sequence size



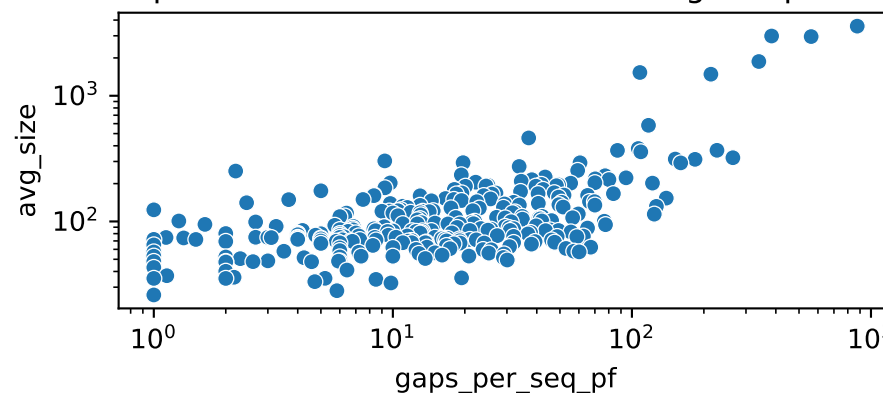
Correlation of the standard deviation



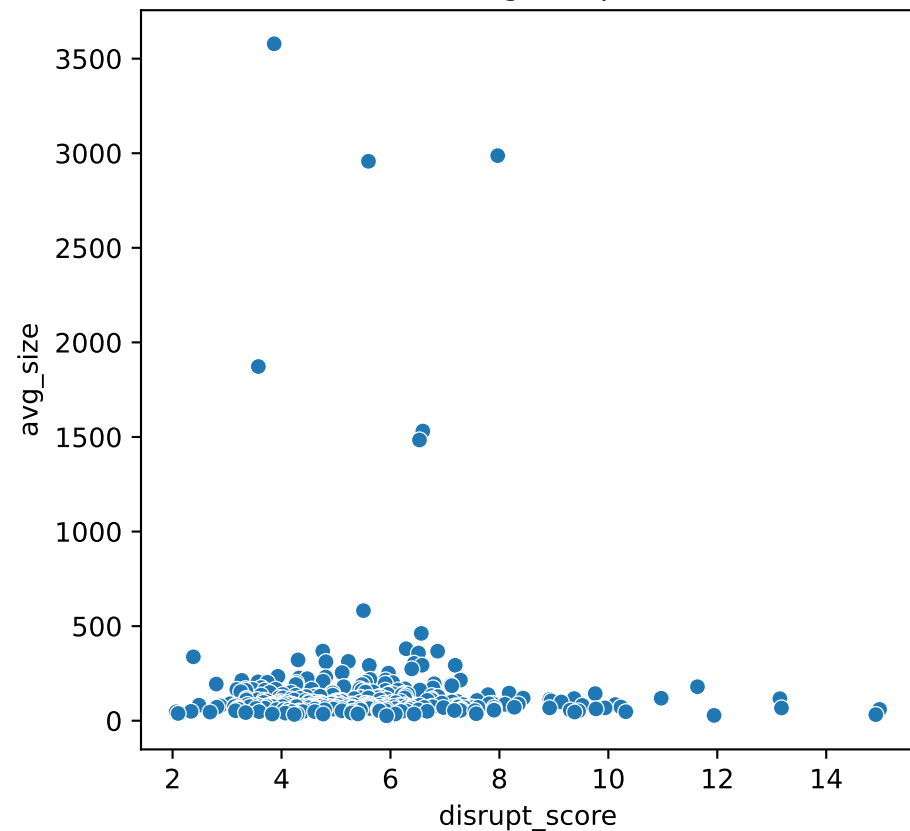
Correlation between the size of a prominent fraction and the average sequence size



Correlation between the number of gaps created by the sequences of the prominent fraction and the average sequence size



Correlation between a family disruption score
and the average sequence size



Correlation between a family disruption score
and the gaps creation in the sequences prominent fraction

