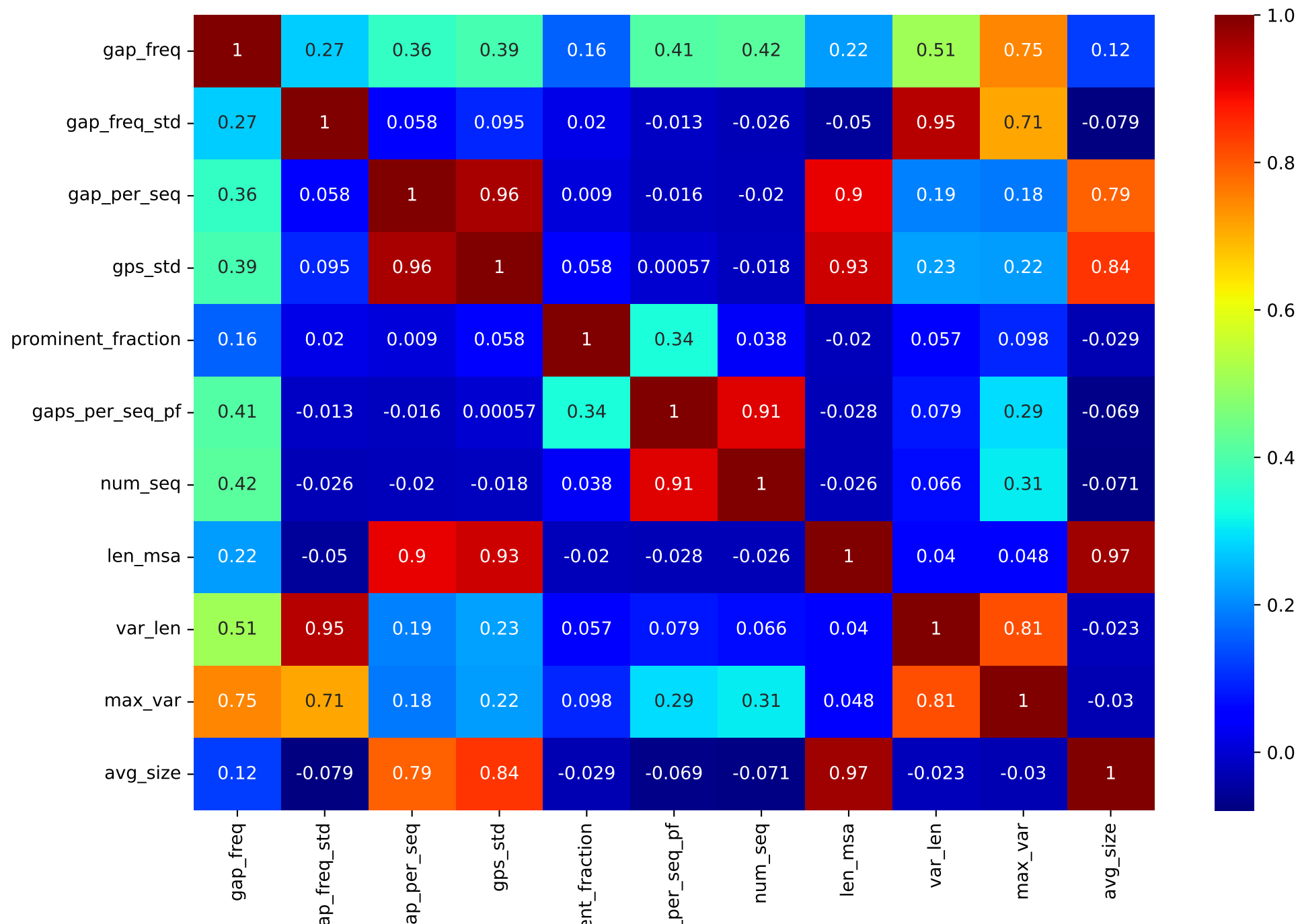
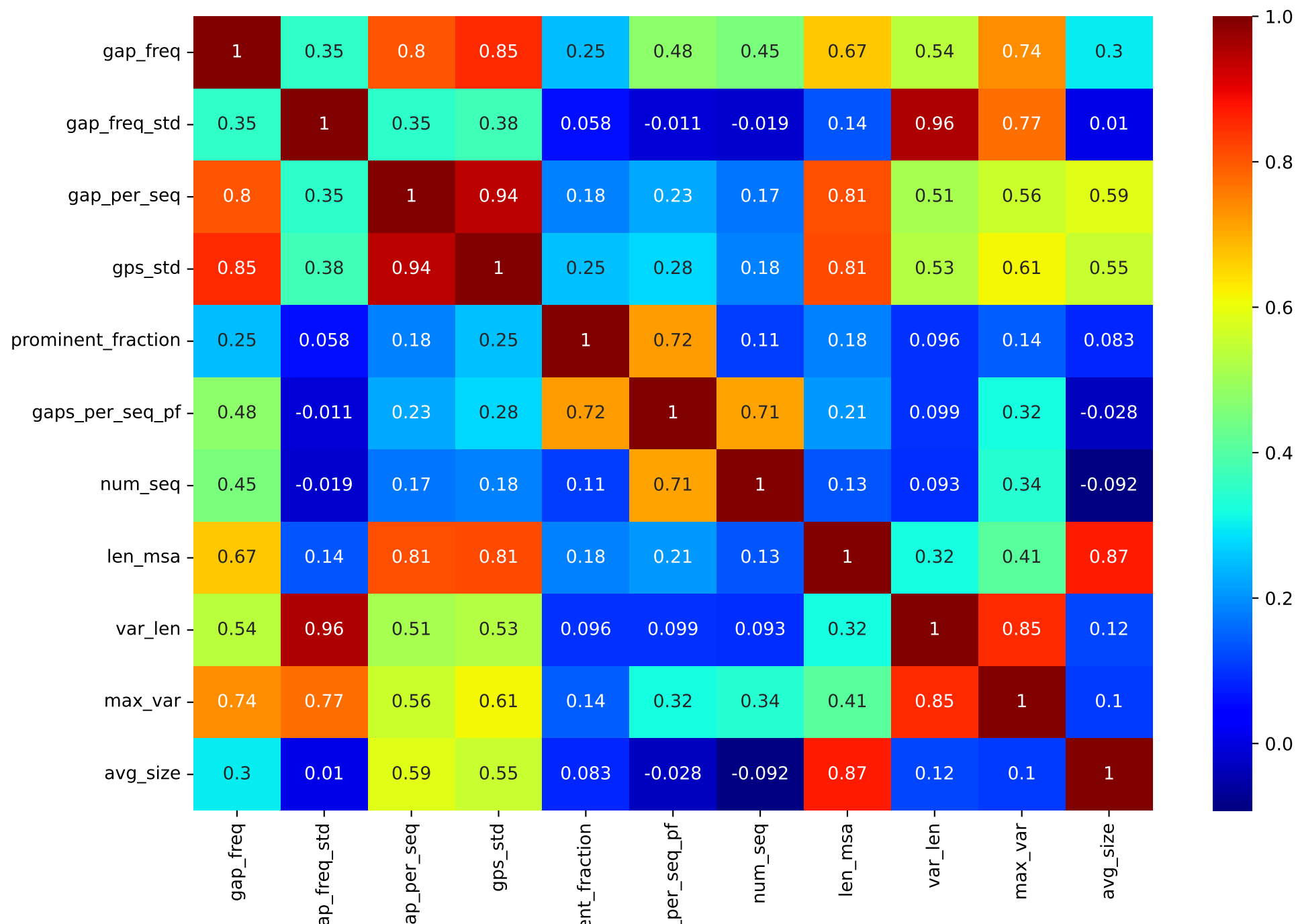


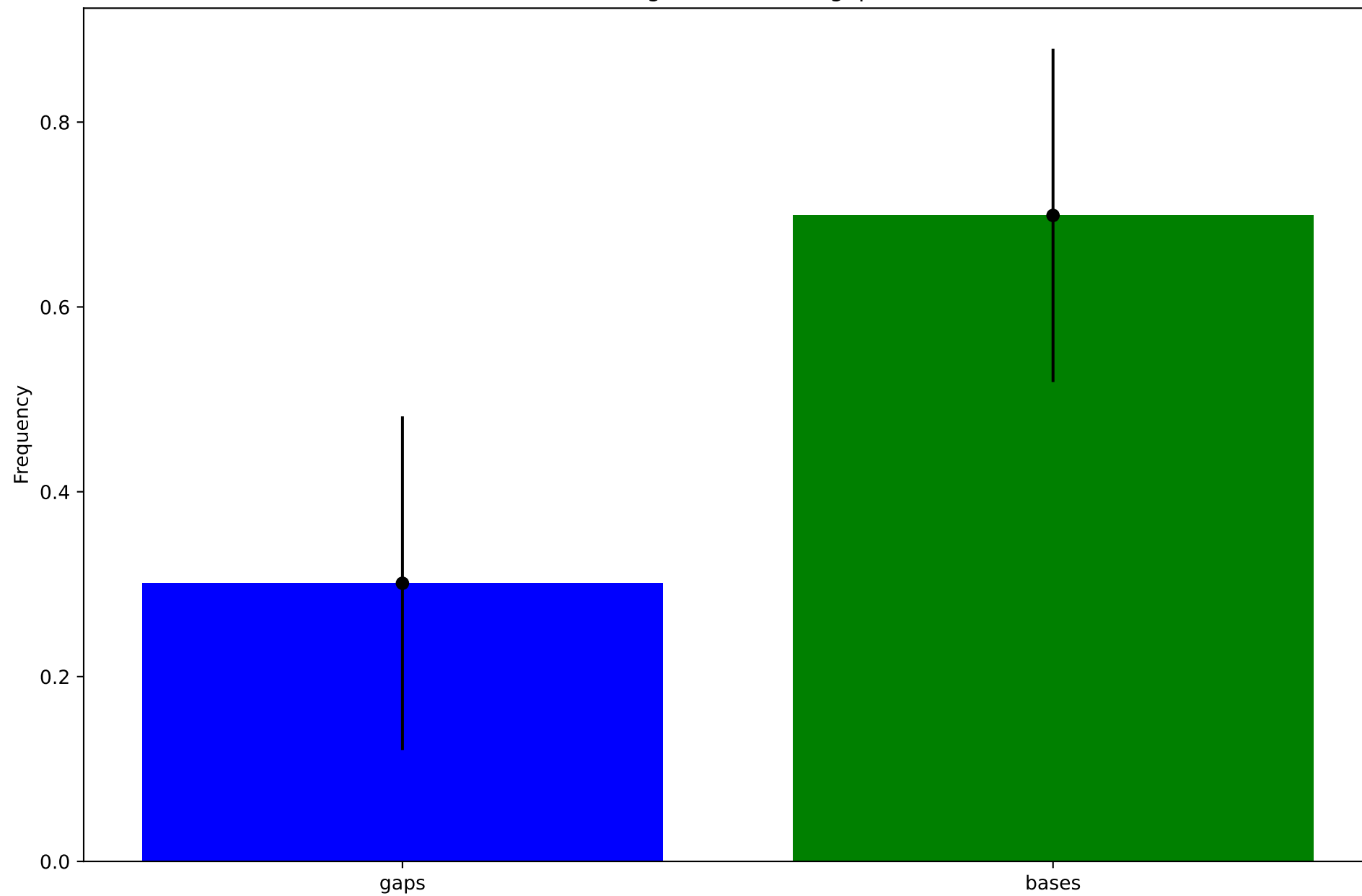
Pearson correlation (linear)



Spearman correlation (non linear)

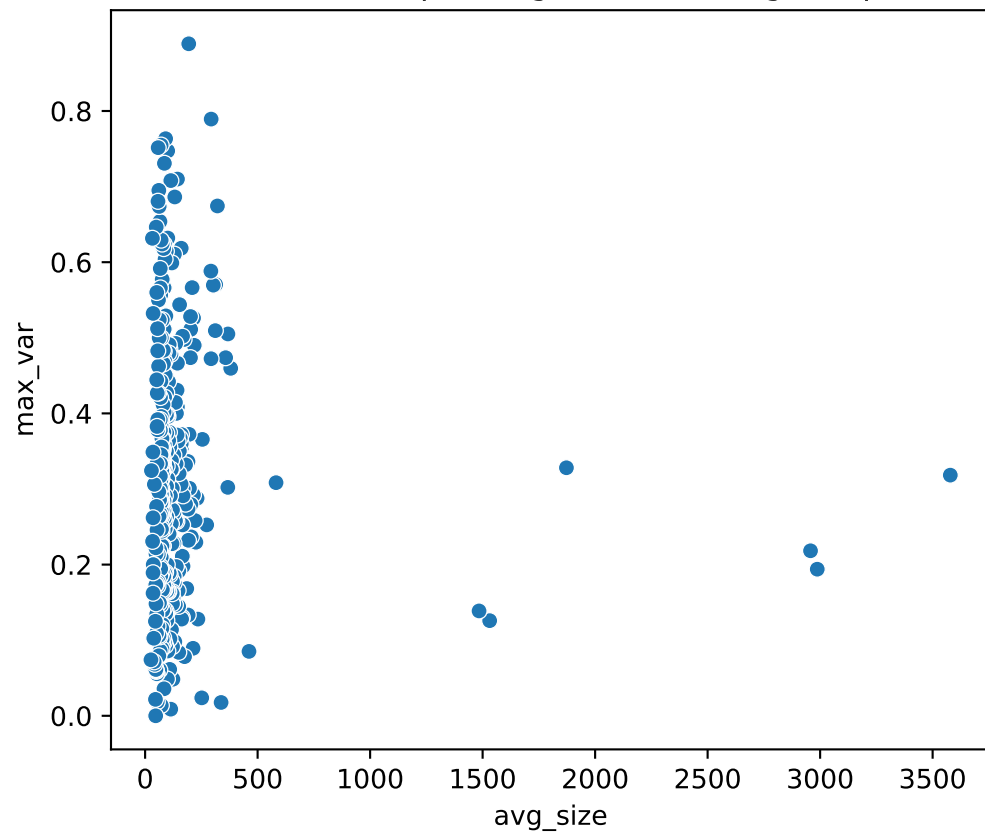


Rfam Seed alignment overall gap fraction

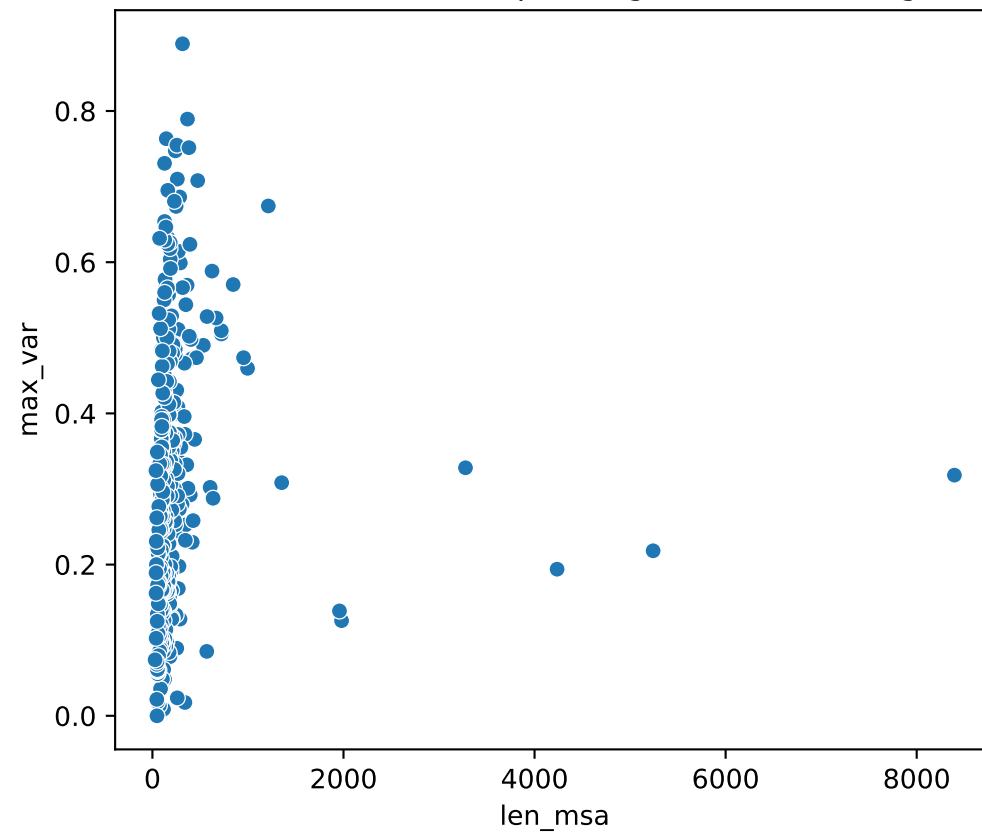


Maximum variation in gaps' number per sequence depending on MSA's and sequence average size

Maximum variation depending on the average sequence size

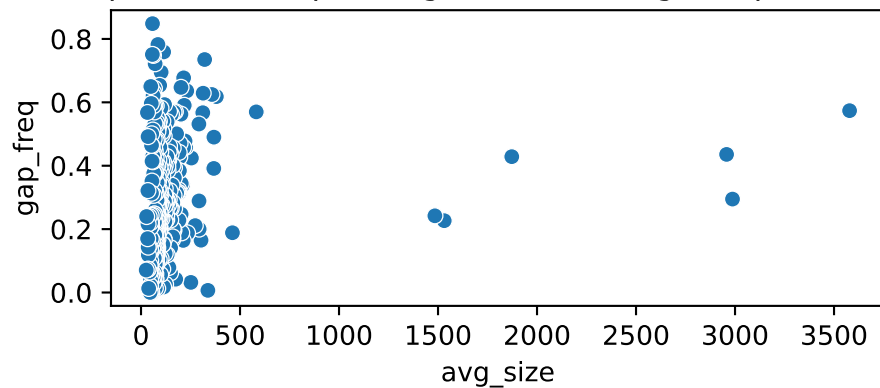


Maximum variation depending on the MSA length

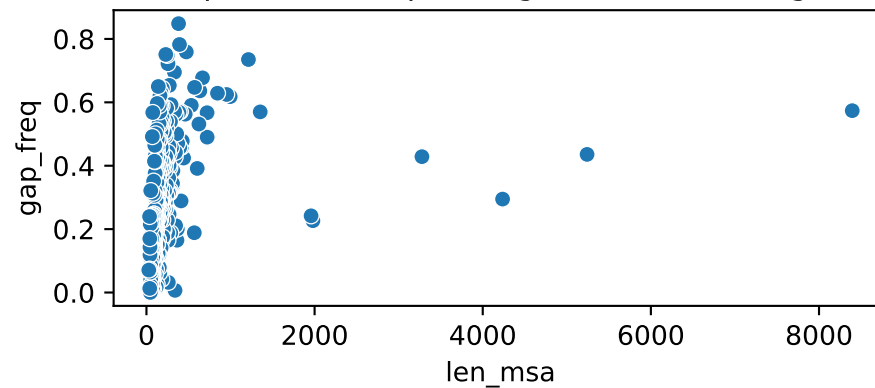


Correlation of gap frequency with sequences and MSA size depending on MSA's and sequence average size

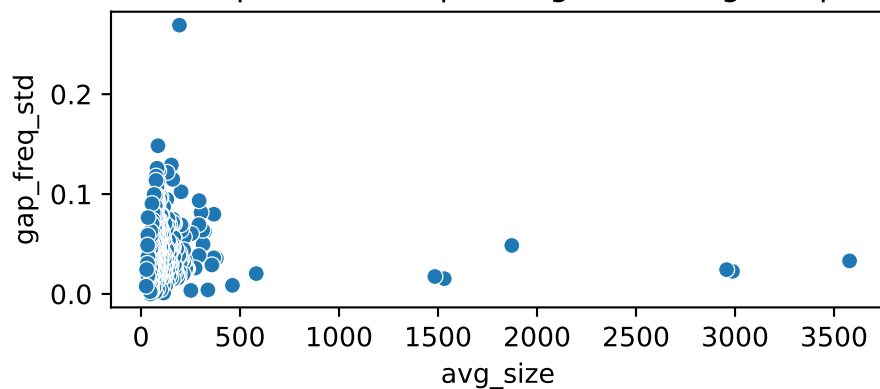
Gap fraction depending on the average sequence size



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

