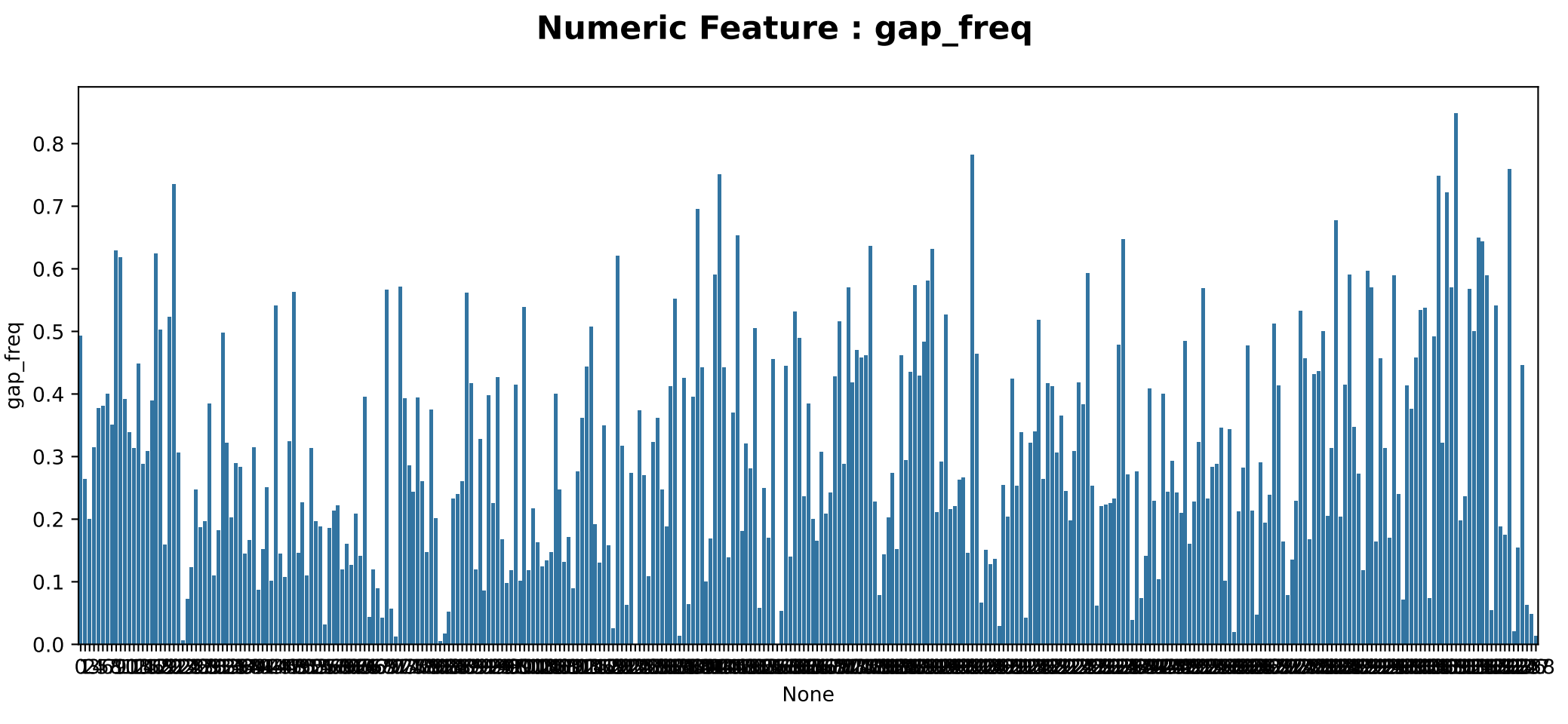
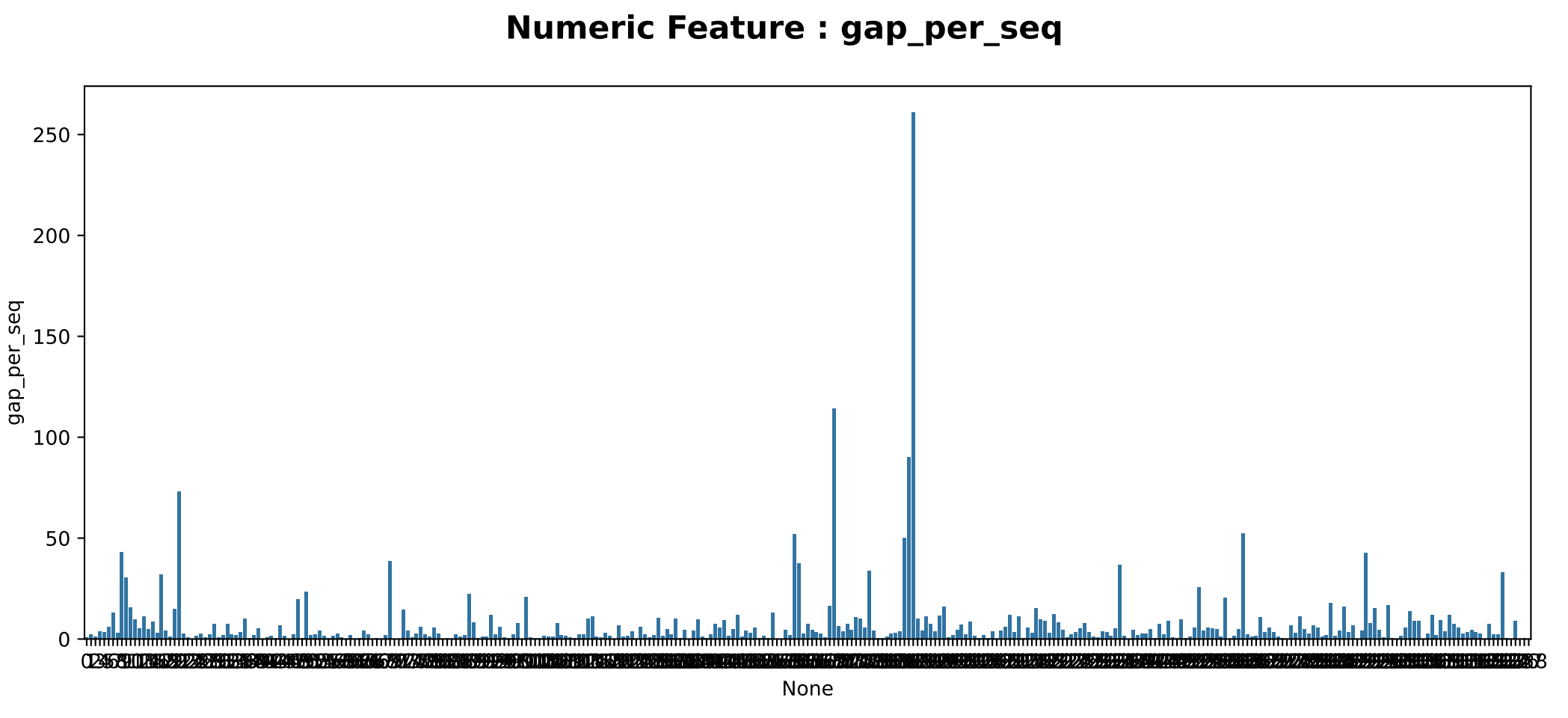
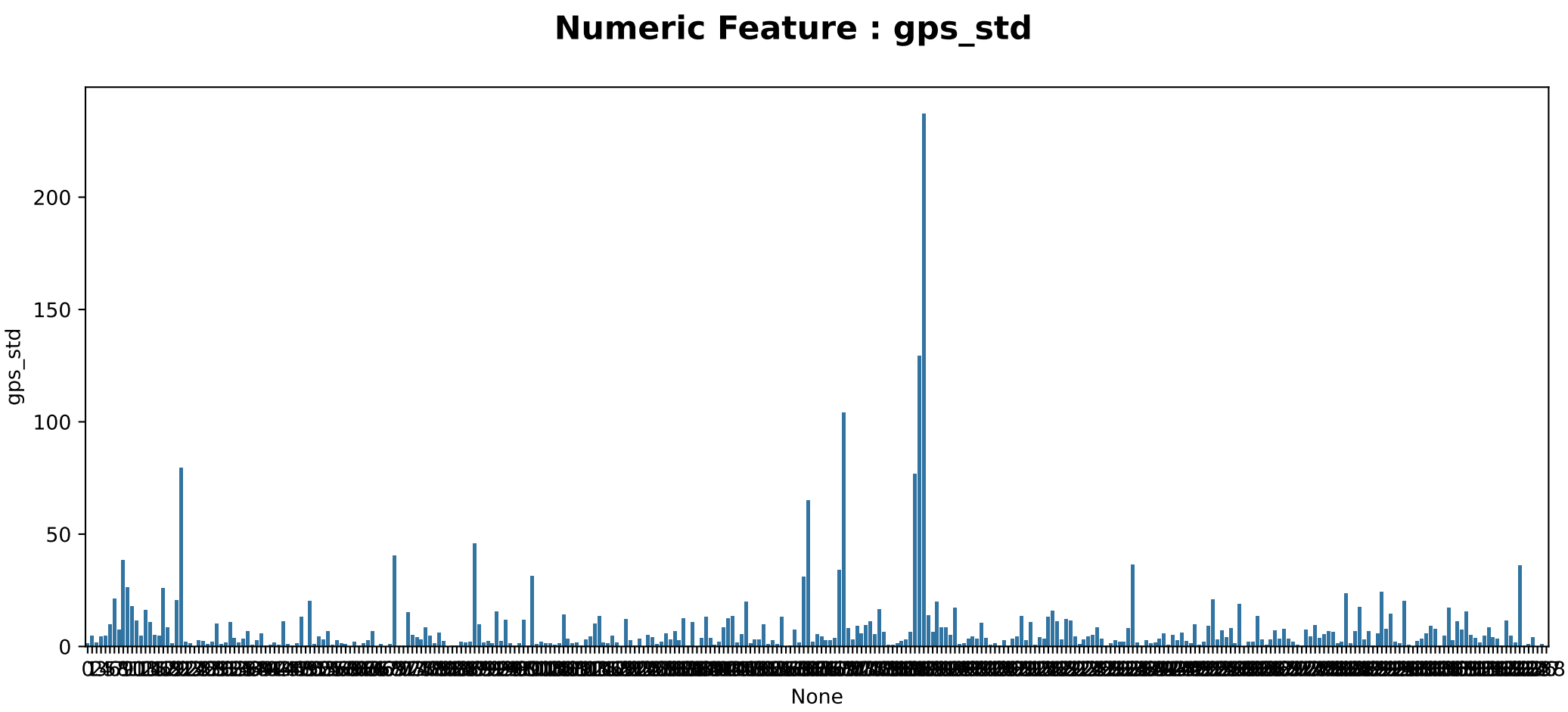
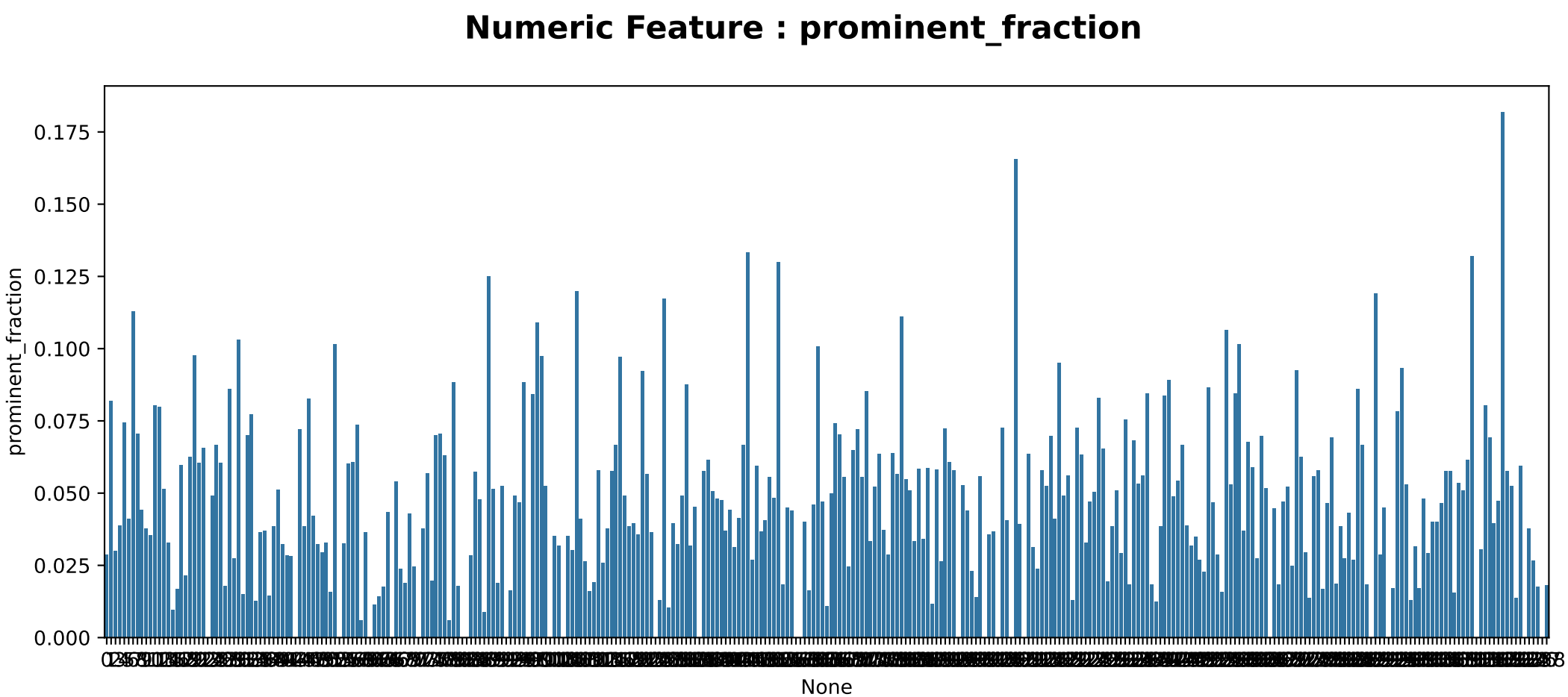
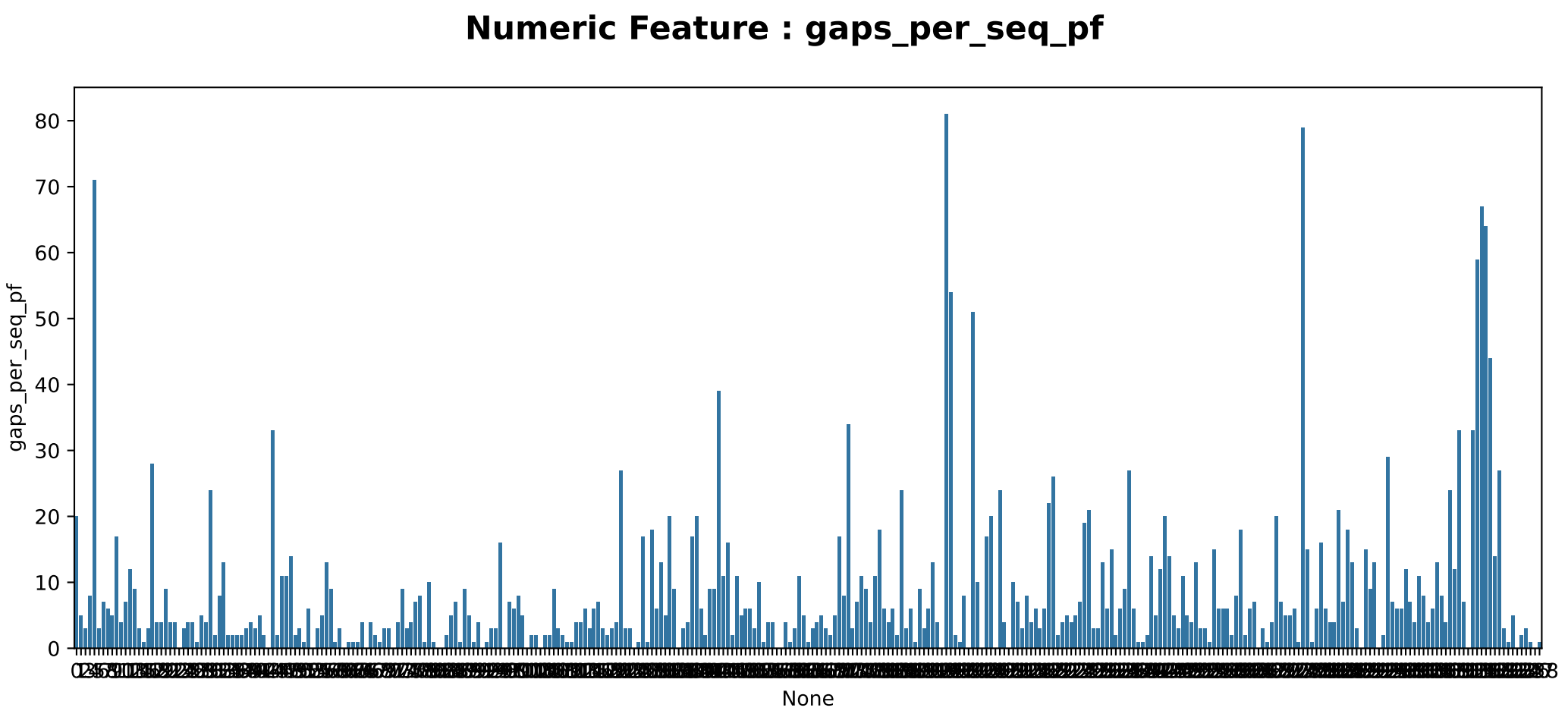
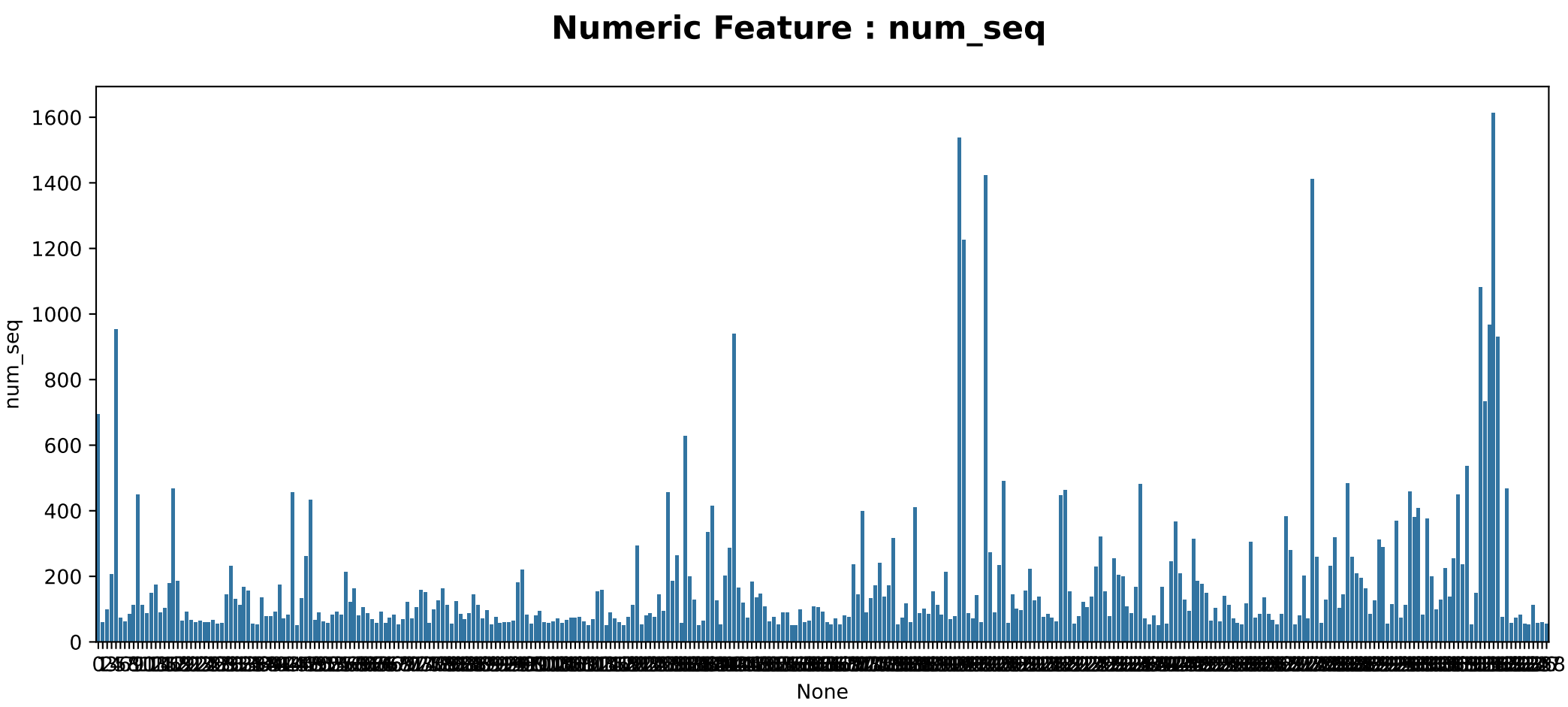

Numeric Feature : gap_freq
gap_freq
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
None

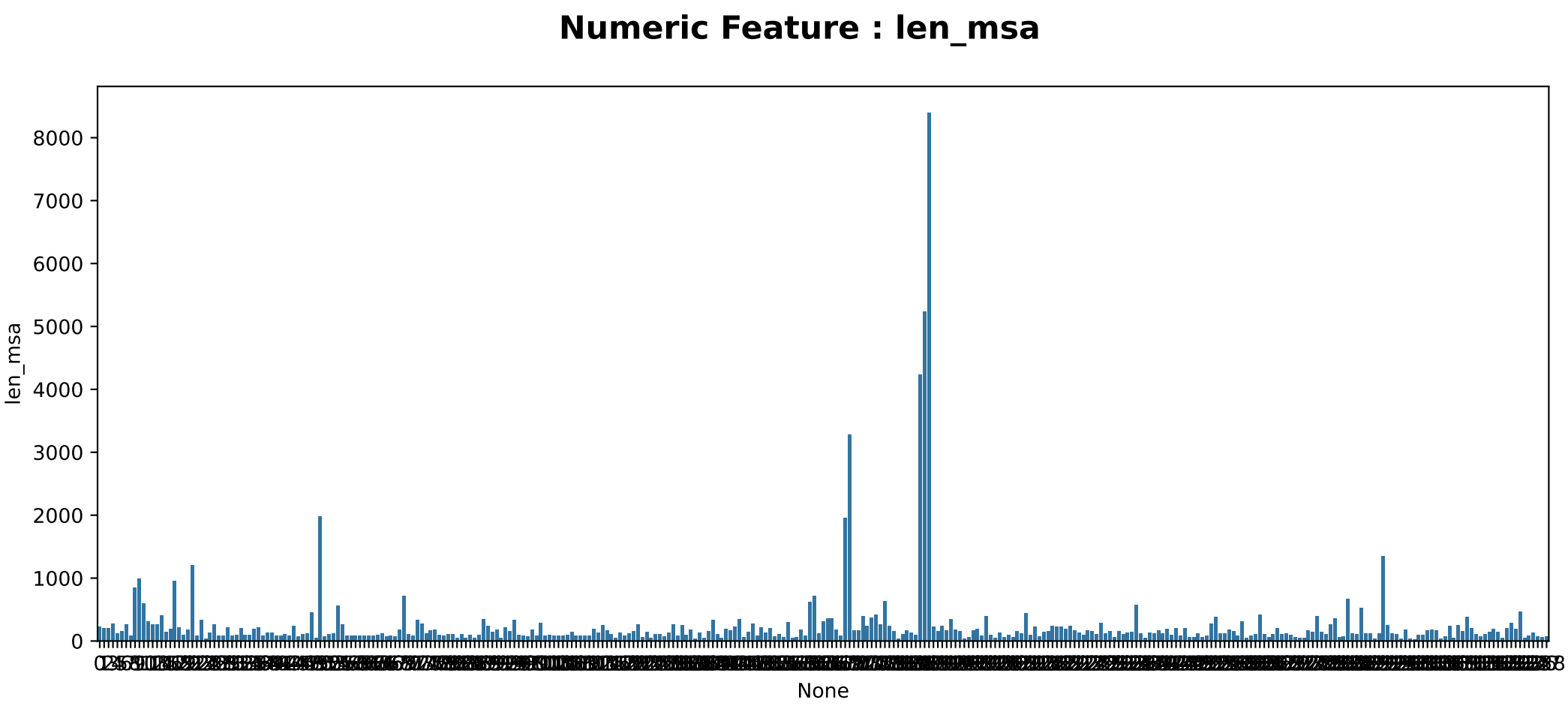

Numeric Feature : gap_per_seq
gap_per_seq
250
200
150
100
50
0
None

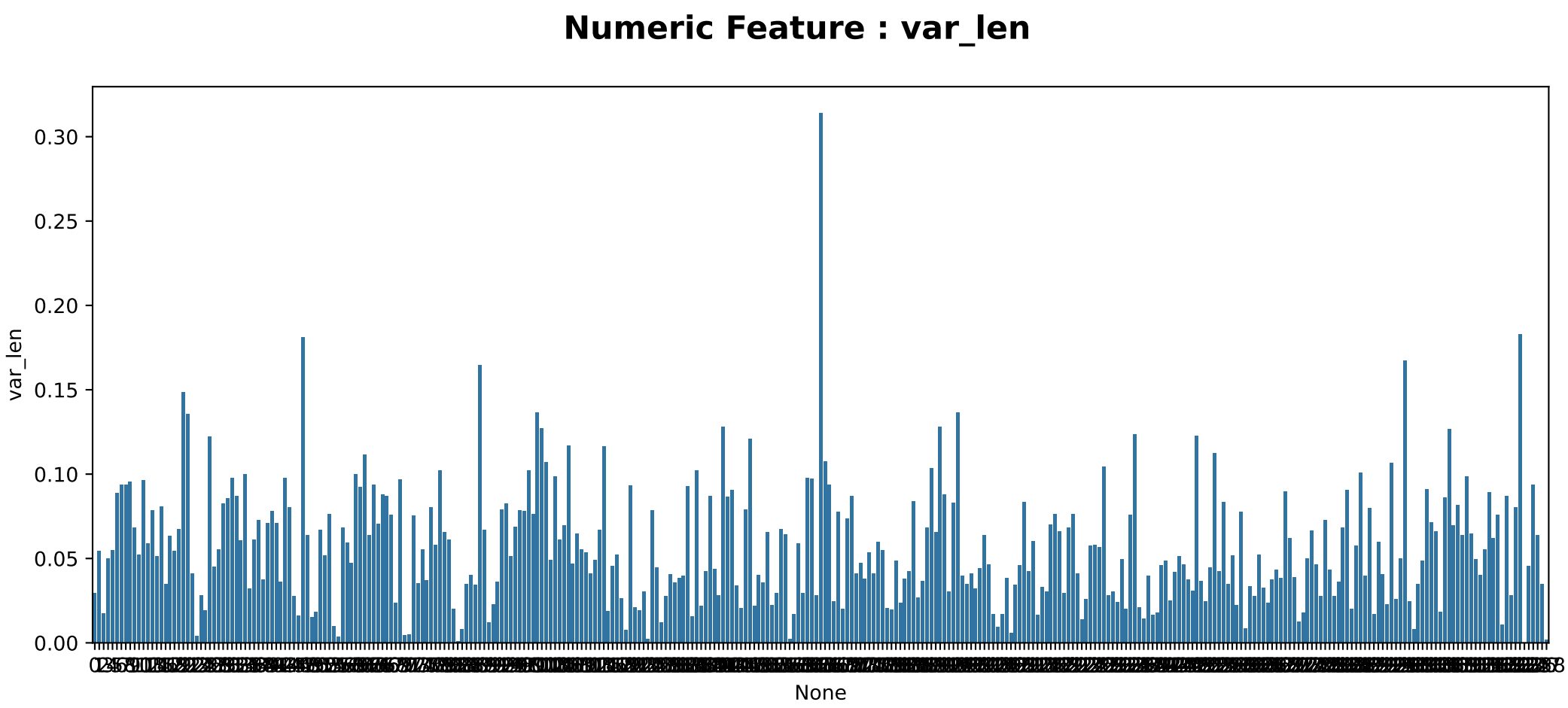

Numeric Feature : gps_std
gps_std
0
50
100
150
200
None

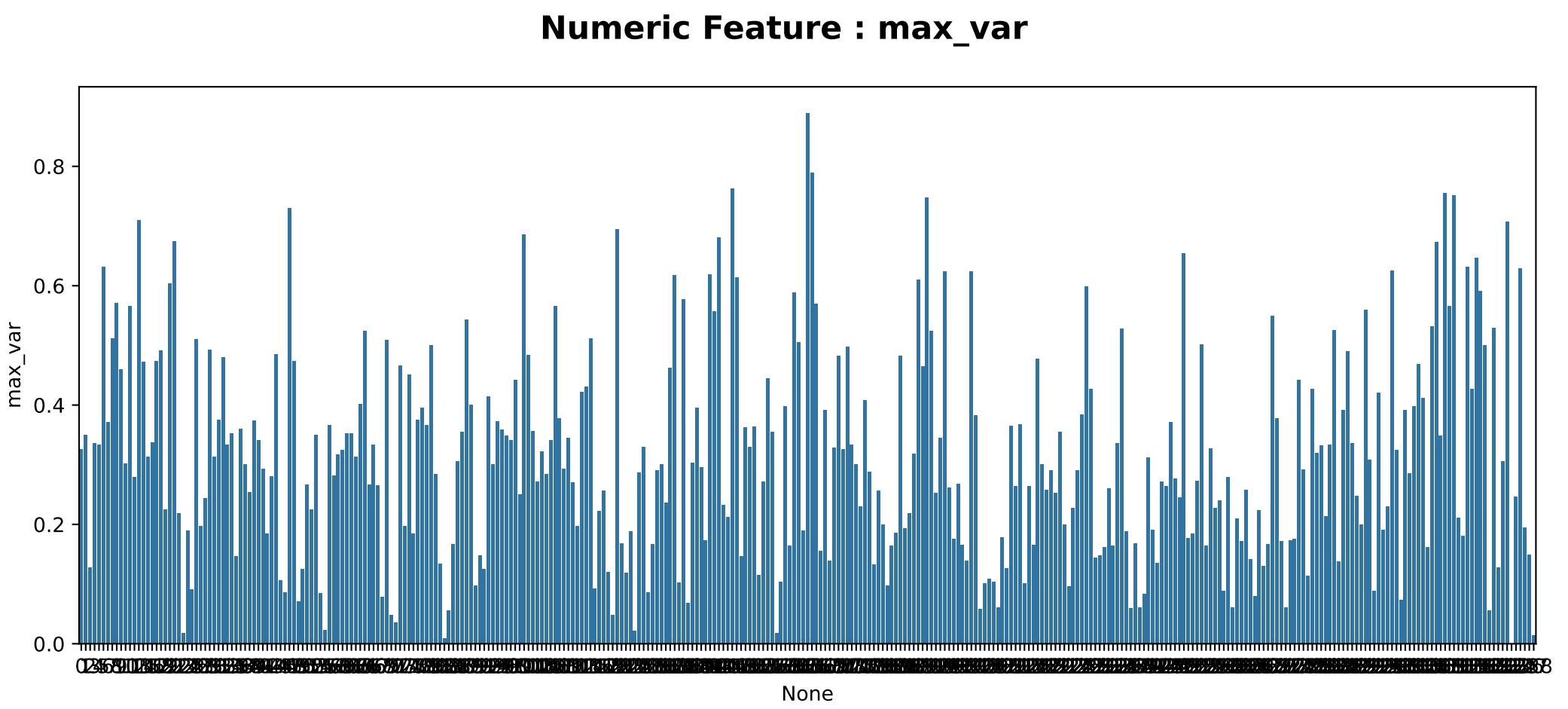

Numeric Feature : prominent_fraction
prominent_fraction
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
None

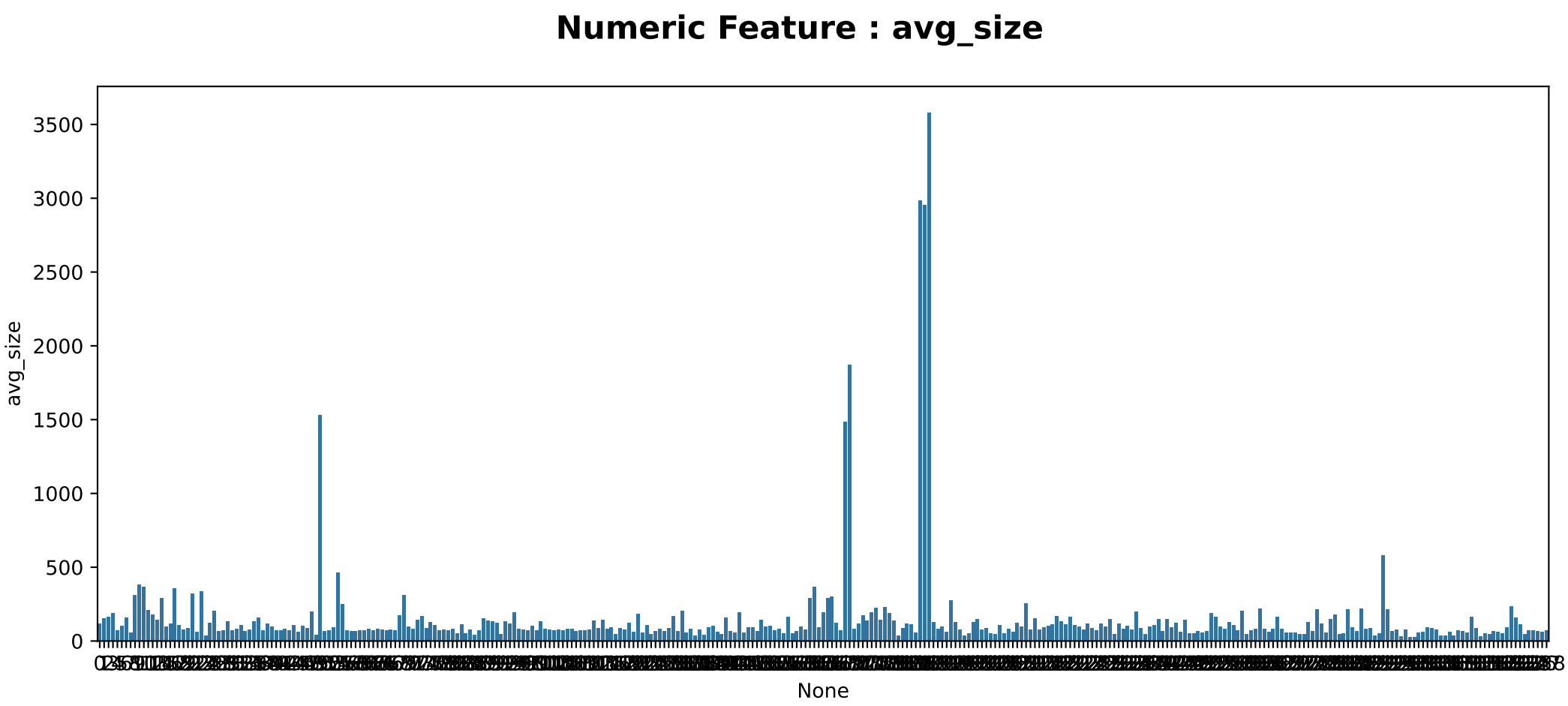

Numeric Feature : gaps_per_seq_pf
gaps_per_seq_pf
0
10
20
30
40
50
60
70
80
None

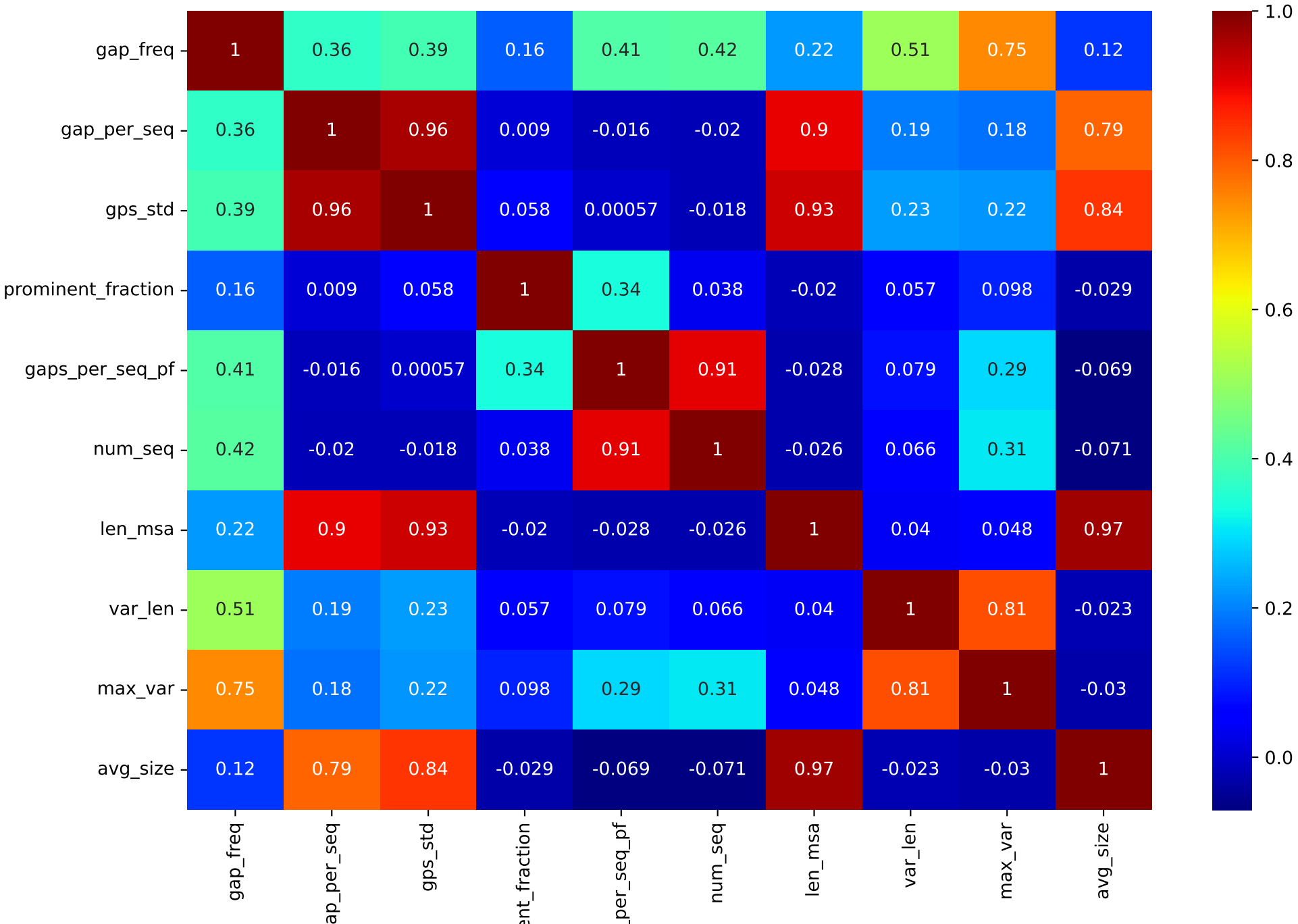

Numeric Feature : num_seq
num_seq
0
200
400
600
800
1000
1200
1400
1600
None

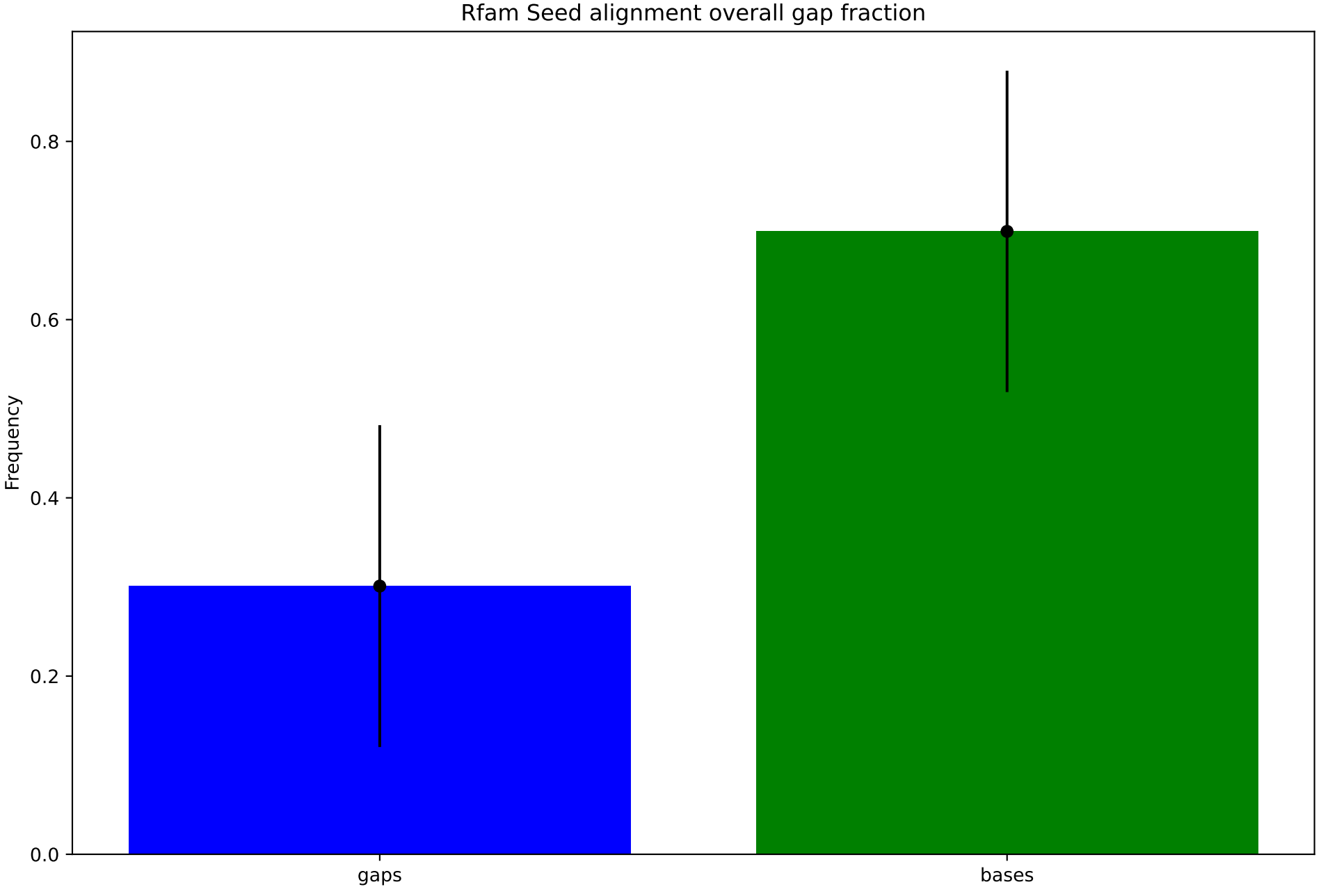

Numeric Feature : len_msa
len_msa
8000
7000
6000
5000
4000
3000
2000
1000
0
None

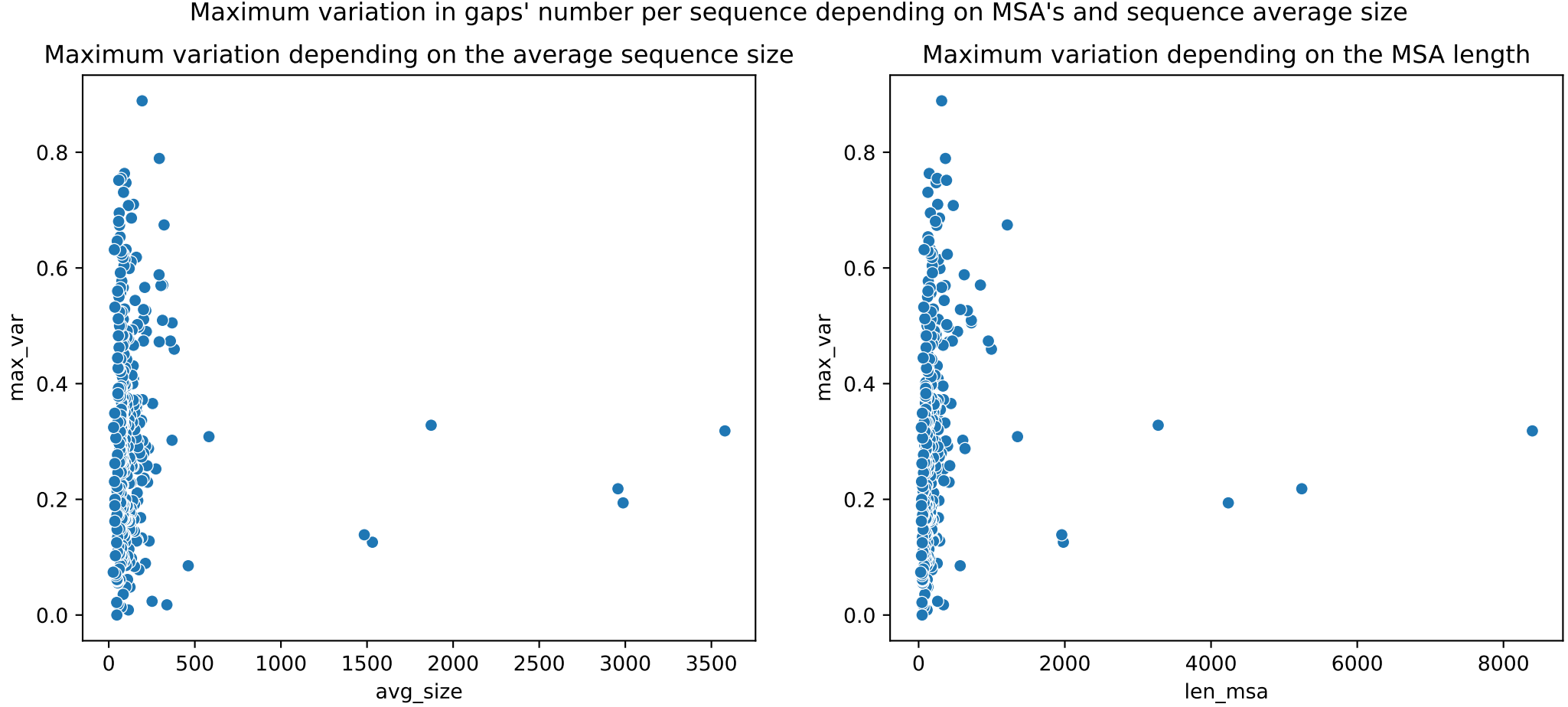

Numeric Feature : var_len
var_len
0.00
0.05
0.10
0.15
0.20
0.25
0.30
None

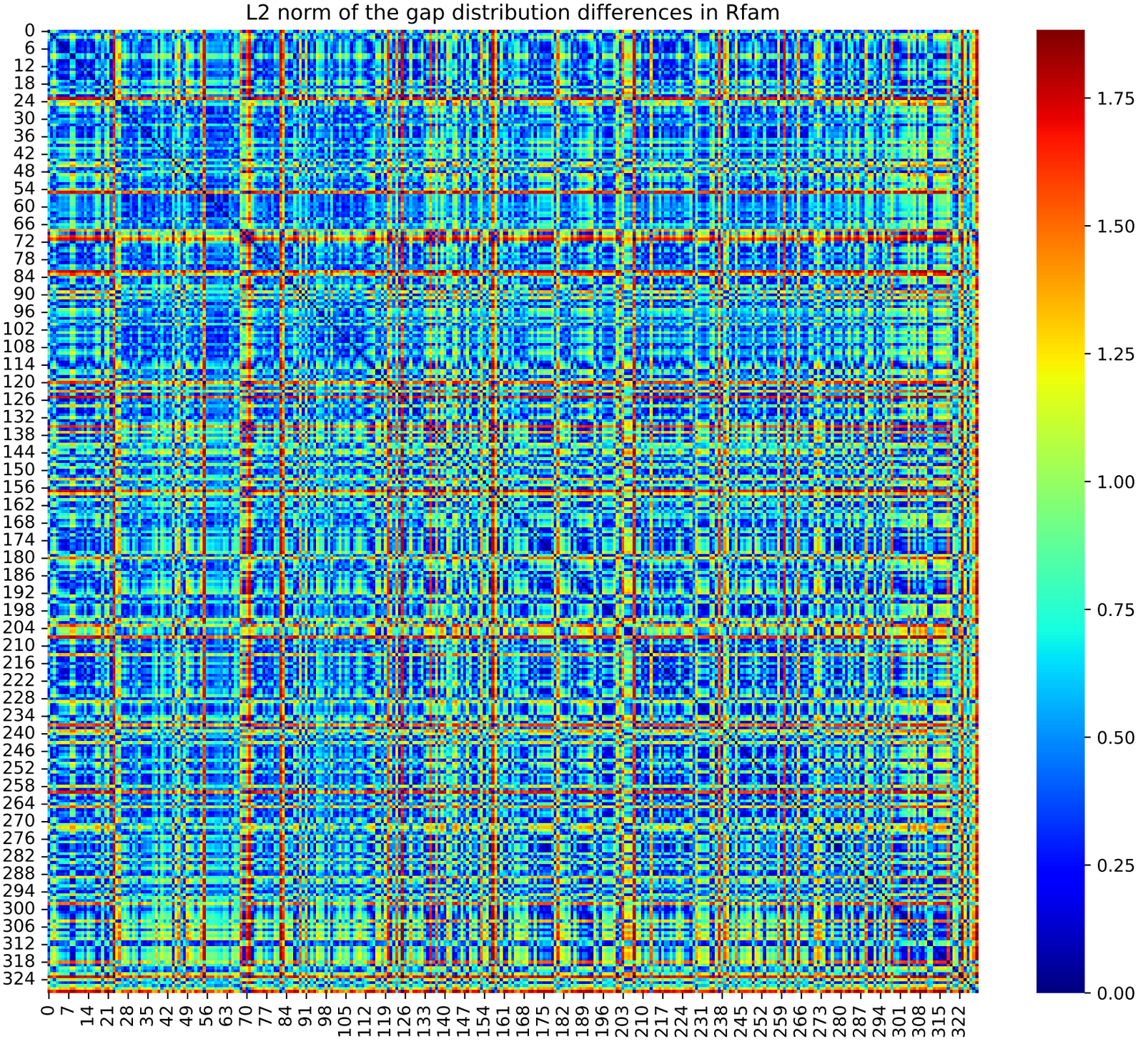

Numeric Feature : max_var
max_var
0.0
0.2
0.4
0.6
0.8
None

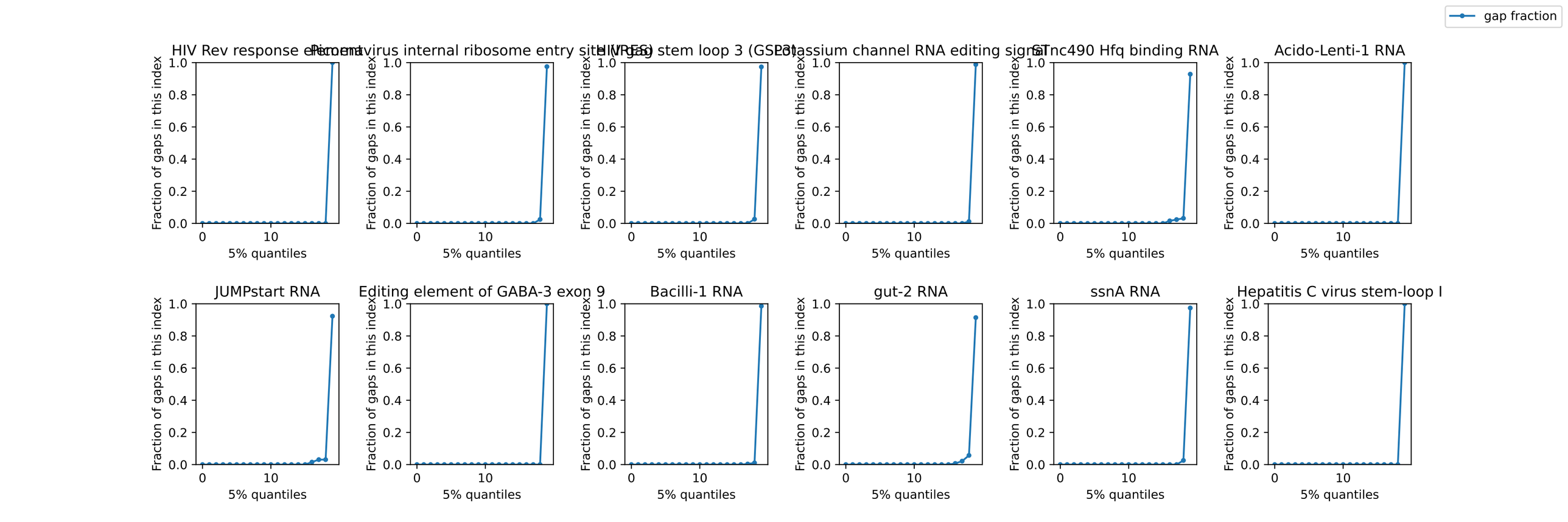

Numeric Feature : avg_size
avg_size
3500
3000
2500
2000
1500
1000
500
0
None

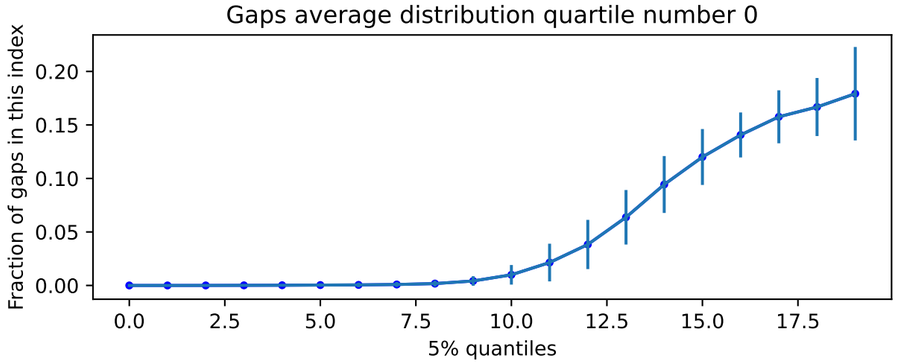

gap_freq
gap_per_seq
gps_std
prominent_fraction
gaps_per_seq_pf
num_seq
len_msa
var_len
max_var
avg_size
1 0.36 0.39 0.16 0.41 0.42 0.22 0.51 0.75 0.12
0.36 1 0.96 0.009 -0.016 -0.02 0.9 0.19 0.18 0.79
0.39 0.96 1 0.058 0.00057 -0.018 0.93 0.23 0.22 0.84
0.16 0.009 0.058 1 0.34 0.038 -0.02 0.057 0.098 -0.029
0.41 -0.016 0.00057 0.34 1 0.91 -0.028 0.079 0.29 -0.069
0.42 -0.02 -0.018 0.038 0.91 1 -0.026 0.066 0.31 -0.071
0.22 0.9 0.93 -0.02 -0.028 -0.026 1 0.04 0.048 0.97
0.51 0.19 0.23 0.057 0.079 0.066 0.04 1 0.81 -0.023
0.75 0.18 0.22 0.098 0.29 0.31 0.048 0.81 1 -0.03
0.12 0.79 0.84 -0.029 -0.069 -0.071 0.97 -0.023 -0.03 1
1.0
0.8
0.6
0.4
0.2
0.0

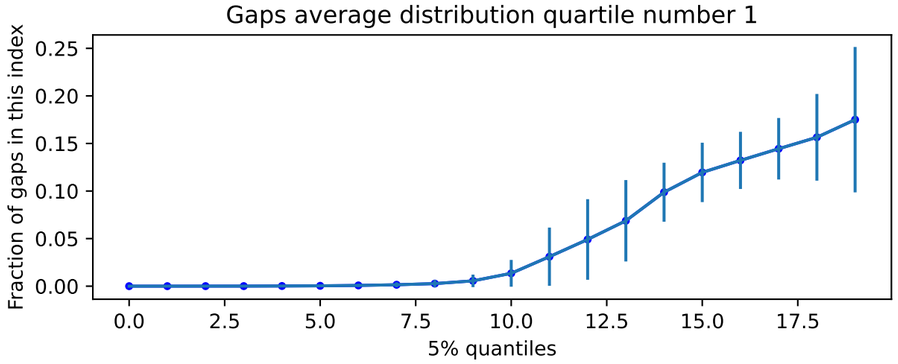

Rfam Seed alignment overall gap fraction
Frequency
0.0
0.2
0.4
0.6
0.8
gaps
bases

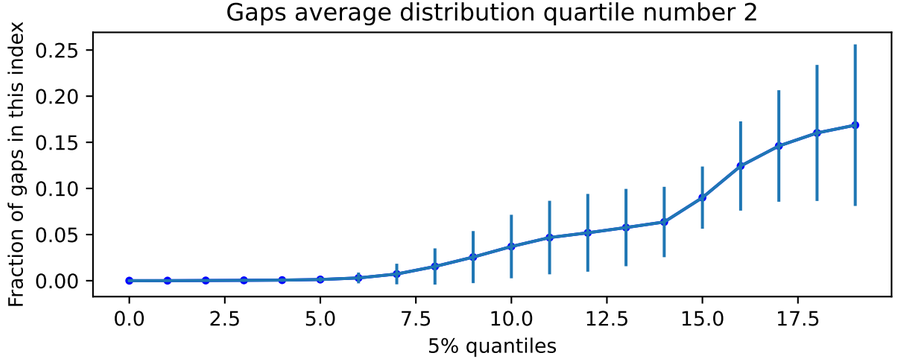

Maximum variation in gaps' number per sequence depending on MSA's and sequence average size
Maximum variation depending on the average sequence size
max_var
avg_size
0.0
0.2
0.4
0.6
0.8
0
500
1000
1500
2000
2500
3000
3500
Maximum variation depending on the MSA length
max_var
len_msa
0.0
0.2
0.4
0.6
0.8
0
2000
4000
6000
8000

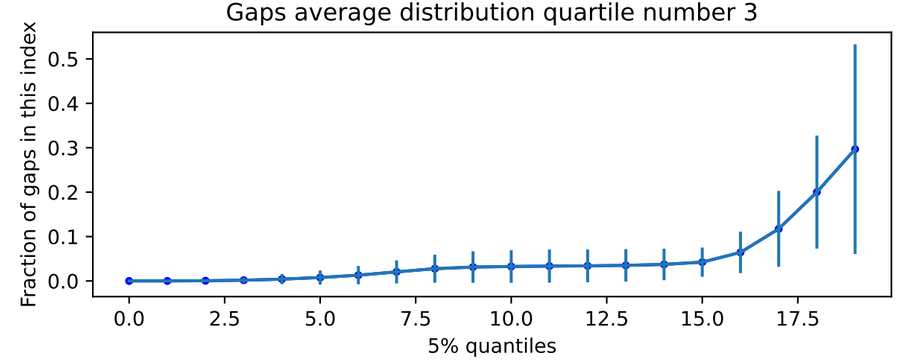

L2 norm of the gap distribution differences in Rfam
0
6
12
18
24
30
36
42
48
54
60
66
72
78
84
90
96
102
108
114
120
126
132
138
144
150
156
162
168
174
180
186
192
198
204
210
216
222
228
234
240
246
252
258
264
270
276
282
288
294
300
306
312
318
324
0
7
14
21
28
35
42
49
56
63
70
77
84
91
98
105
112
119
126
133
140
147
154
161
168
175
182
189
196
203
210
217
224
231
238
245
252
259
266
273
280
287
294
301
308
315
322
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00


gap fraction
HIV Rev response element
Picornavirus internal ribosome entry site (IRES)
HIV gag stem loop 3 (GSL3)
Potassium channel RNA editing signal
STnc490 Hfq binding RNA
Acido-Lenti-1 RNA
JUMPstart RNA
Editing element of GABA-3 exon 9
Bacilli-1 RNA
gut-2 RNA
ssnA RNA
Hepatitis C virus stem-loop I
Fraction of gaps in this index
5% quantiles
0.0
0.2
0.4
0.6
0.8
1.0
0
10


Gaps average distribution quartile number 0
Fraction of gaps in this index
0.00
0.05
0.10
0.15
0.20
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
5% quantiles


Gaps average distribution quartile number 1
Fraction of gaps in this index
0.00
0.05
0.10
0.15
0.20
0.25
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
5% quantiles


Gaps average distribution quartile number 2
Fraction of gaps in this index
0.00
0.05
0.10
0.15
0.20
0.25
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
5% quantiles


Gaps average distribution quartile number 3
Fraction of gaps in this index
0.0
0.1
0.2
0.3
0.4
0.5
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
5% quantiles