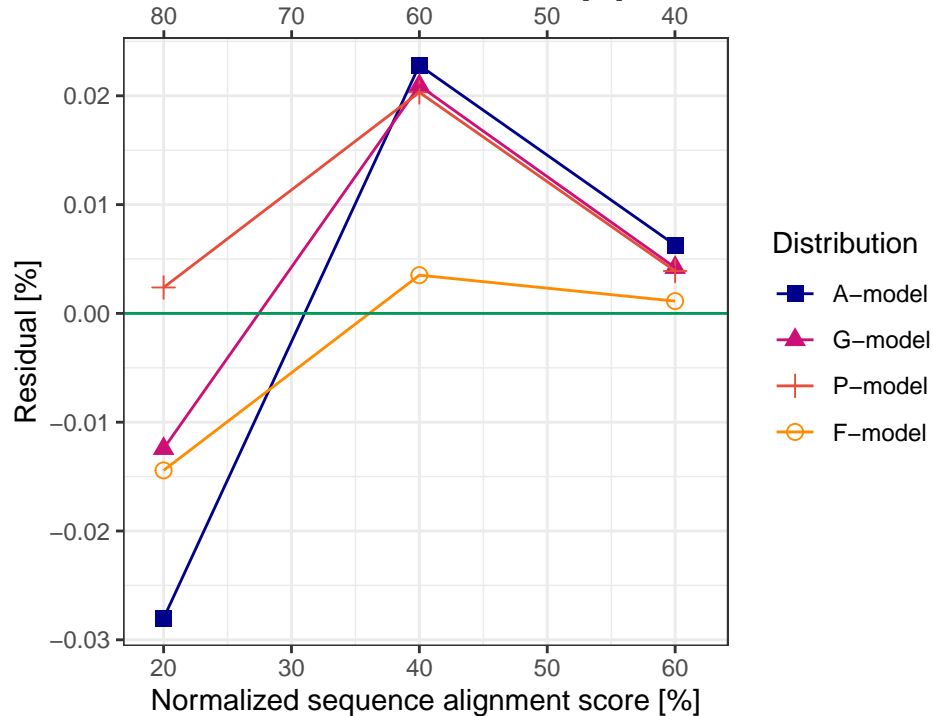


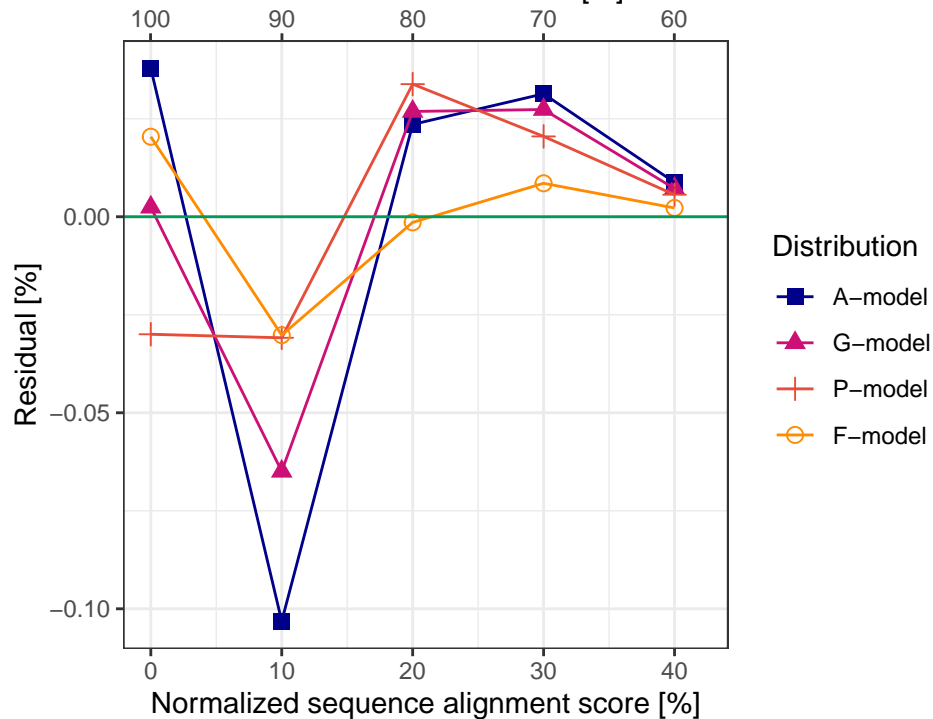
# Residuals of 5mers, Metric=HD

Share of maximal distance [%]



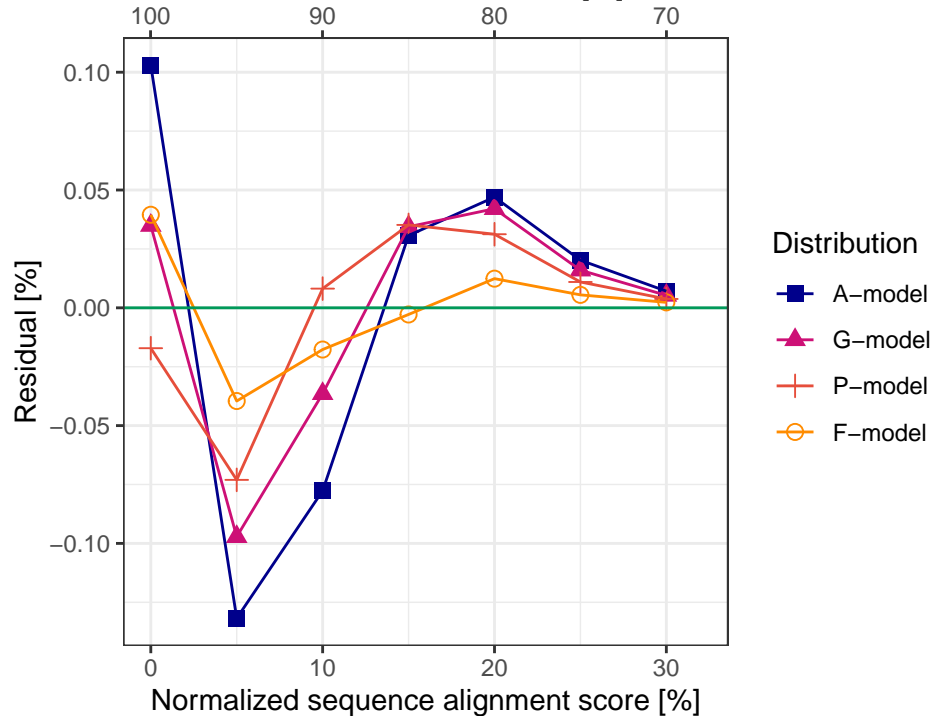
# Residuals of 10mers, Metric=HD

Share of maximal distance [%]



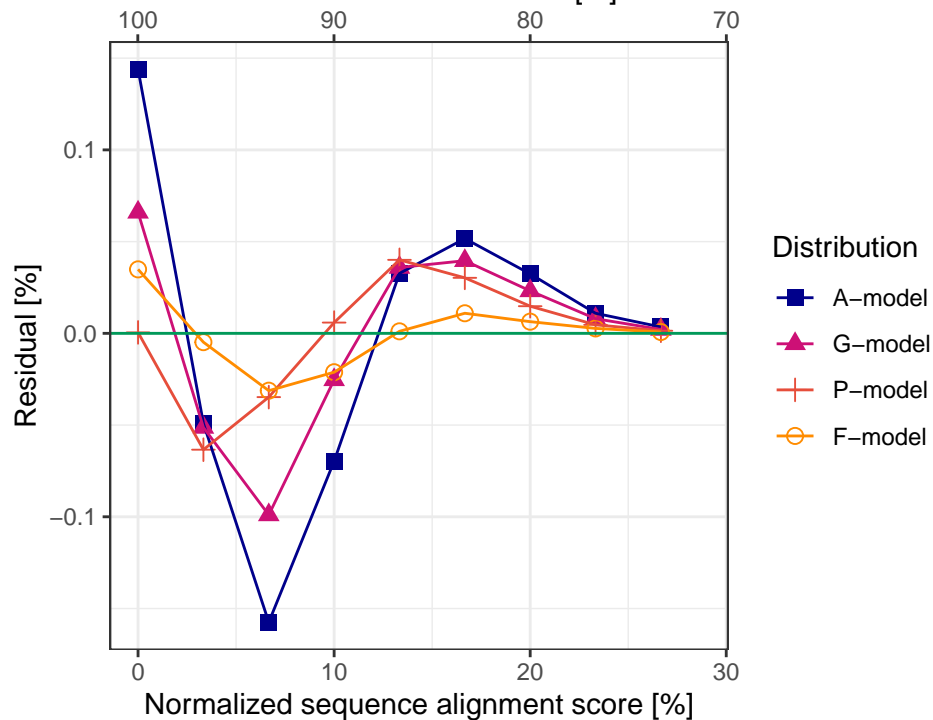
# Residuals of 20mers, Metric=HD

Share of maximal distance [%]



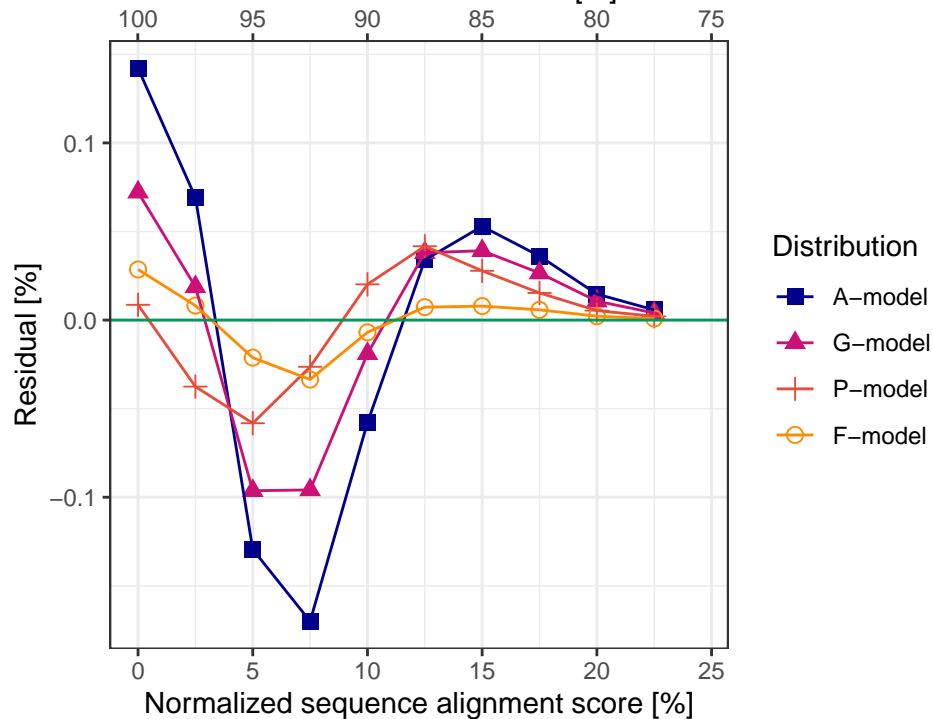
# Residuals of 30mers, Metric=HD

Share of maximal distance [%]



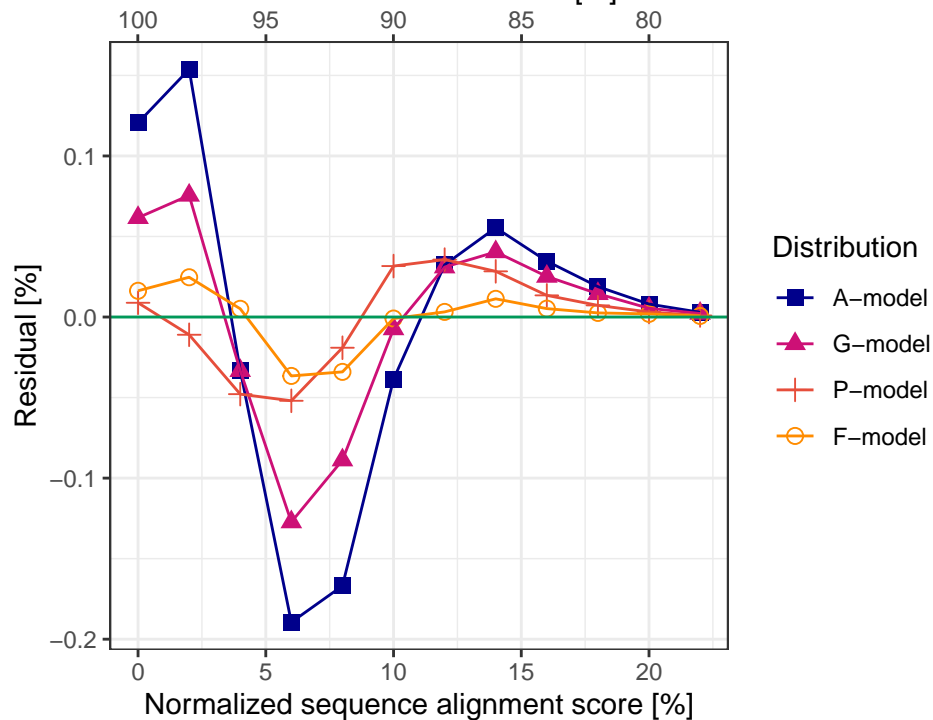
# Residuals of 40mers, Metric=HD

Share of maximal distance [%]



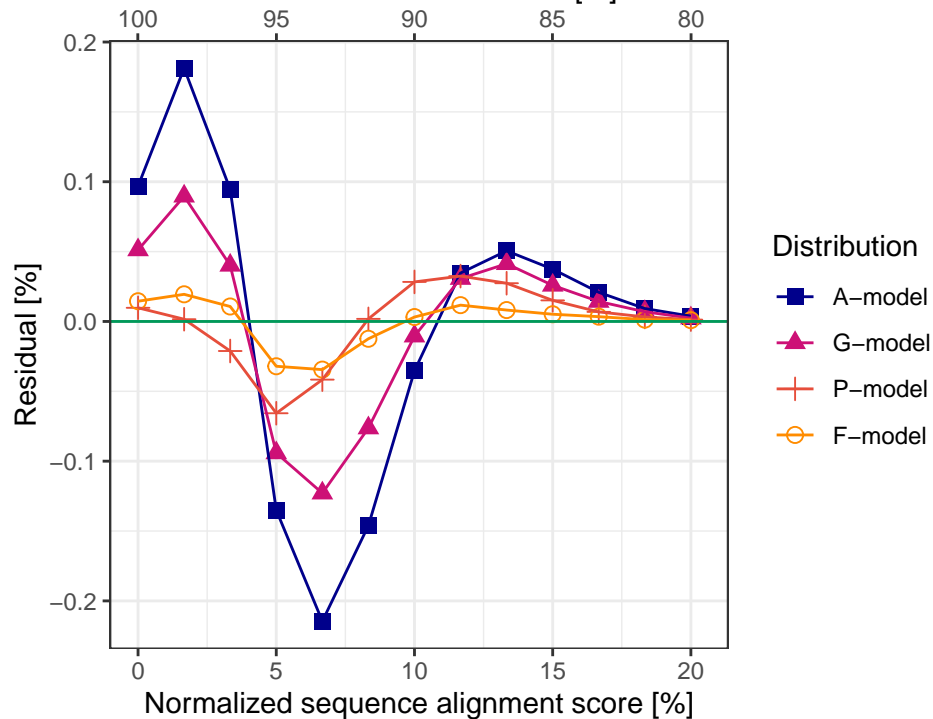
# Residuals of 50mers, Metric=HD

Share of maximal distance [%]



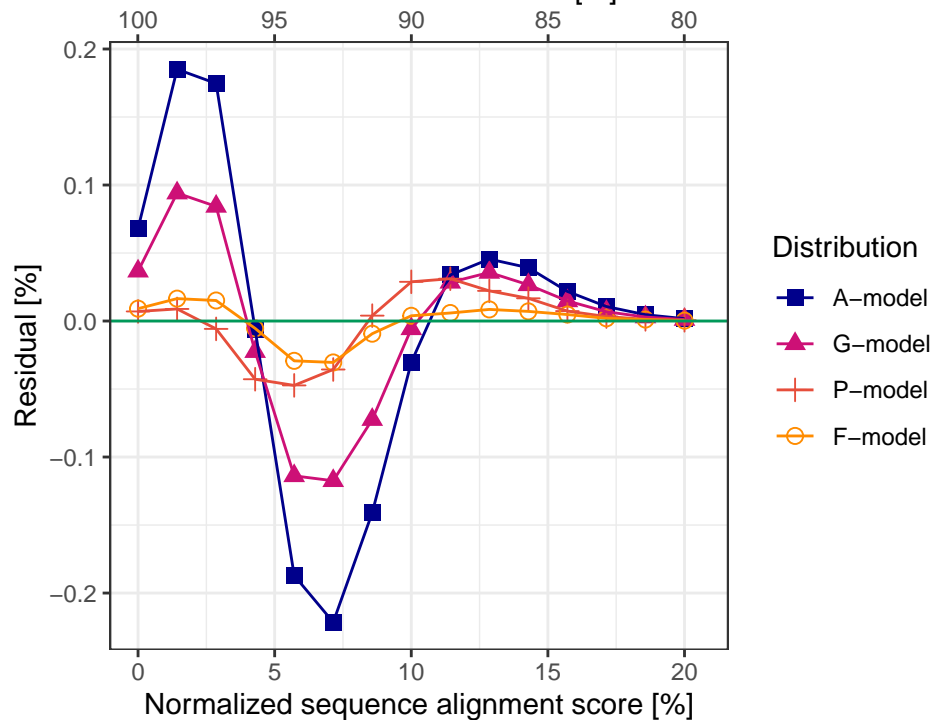
# Residuals of 60mers, Metric=HD

Share of maximal distance [%]



# Residuals of 70mers, Metric=HD

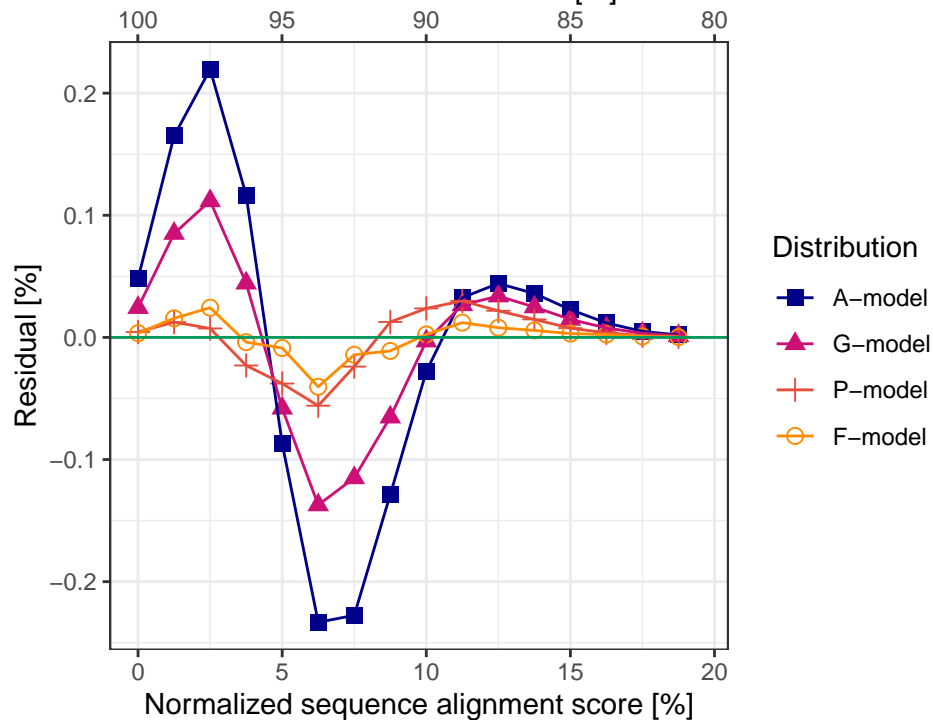
Share of maximal distance [%]





# Residuals of 80mers, Metric=HD

Share of maximal distance [%]



# Residuals of 90mers, Metric=HD

Share of maximal distance [%]

100

95

90

85

0.2

0.1

0.0

-0.1

-0.2

Distribution

A-model

G-model

P-model

F-model

Residual [%]

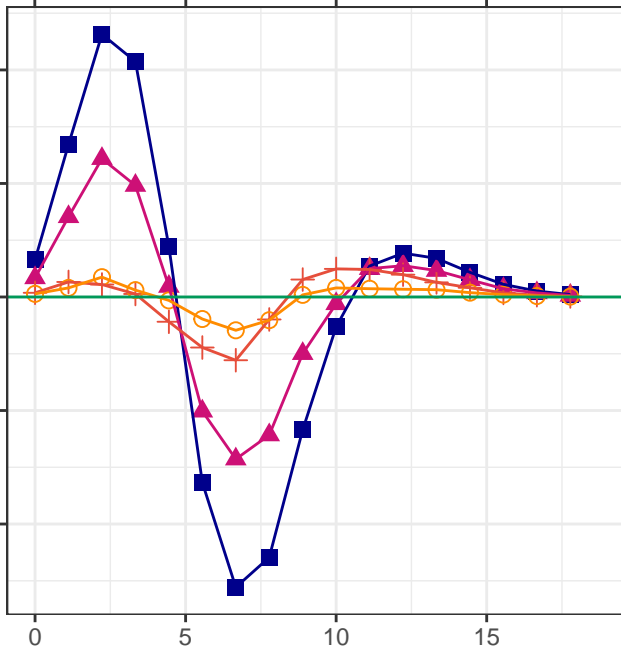
Normalized sequence alignment score [%]

0

5

10

15



# Residuals of 100mers, Metric=HD

Share of maximal distance [%]

100

95

90

85

0.2

0.1

0.0

-0.1

-0.2

-0.3

Distribution

■ A-model

▲ G-model

+ P-model

○ F-model

Normalized sequence alignment score [%]

0

5

10

15

Residual [%]