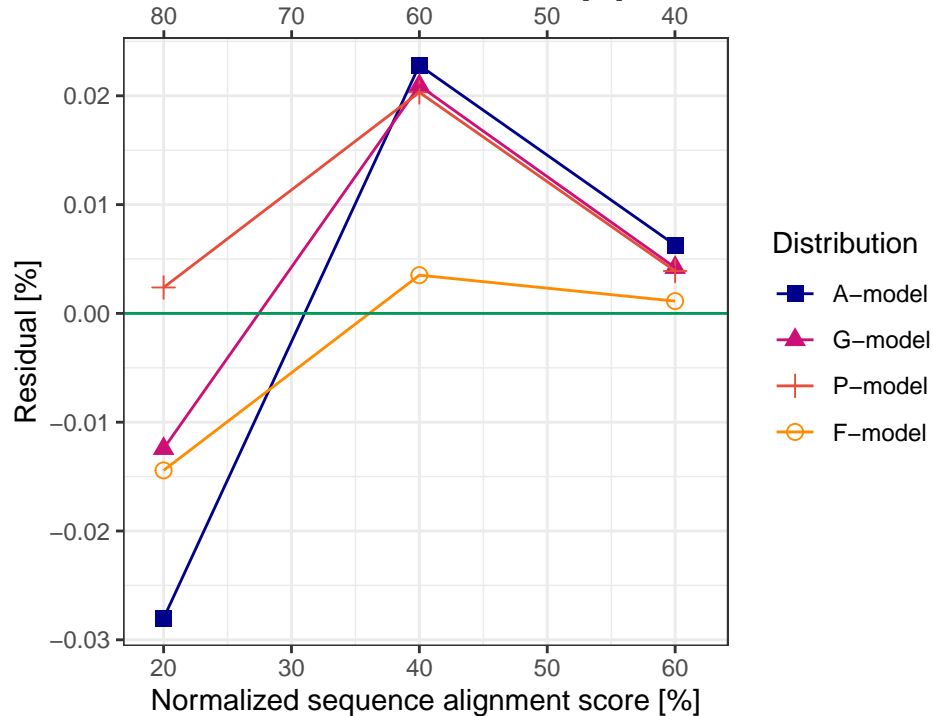


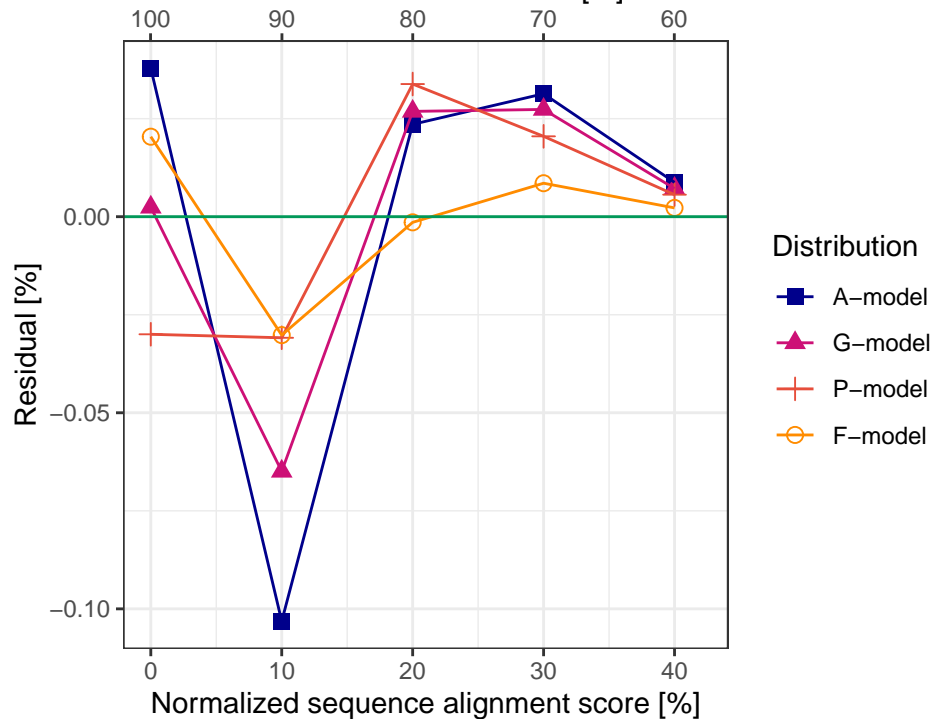
Residuals of 5mers, Metric=NWMn

Share of maximal distance [%]



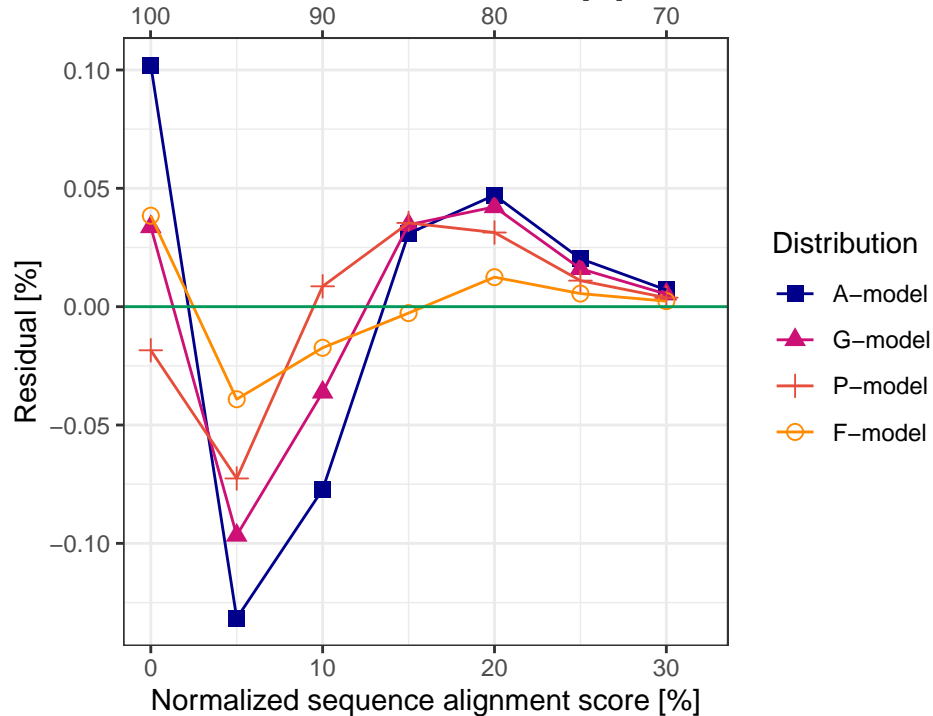
Residuals of 10mers, Metric=NWMn

Share of maximal distance [%]



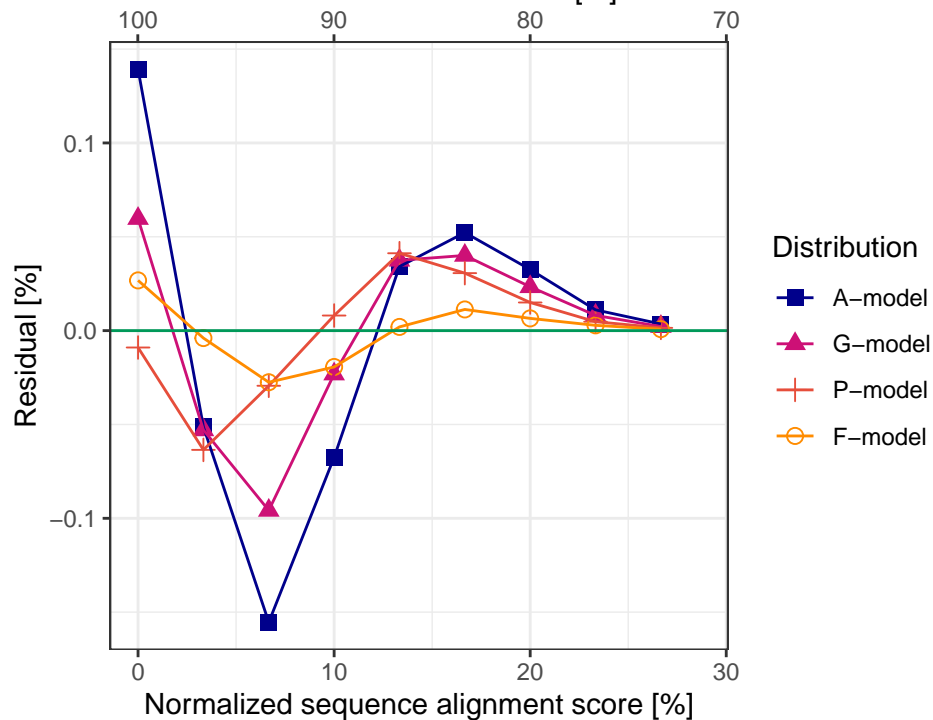
Residuals of 20mers, Metric=NWMn

Share of maximal distance [%]



Residuals of 30mers, Metric=NWMn

Share of maximal distance [%]



Residuals of 40mers, Metric=NWMn

Share of maximal distance [%]

100 95 90 85 80 75

Residual [%]

0.1

0.0

-0.1

Normalized sequence alignment score [%]

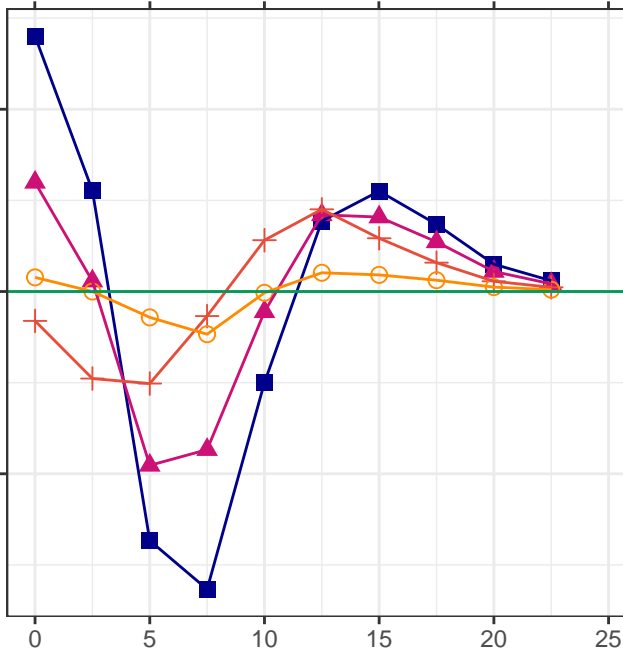
Distribution

■ A-model

▲ G-model

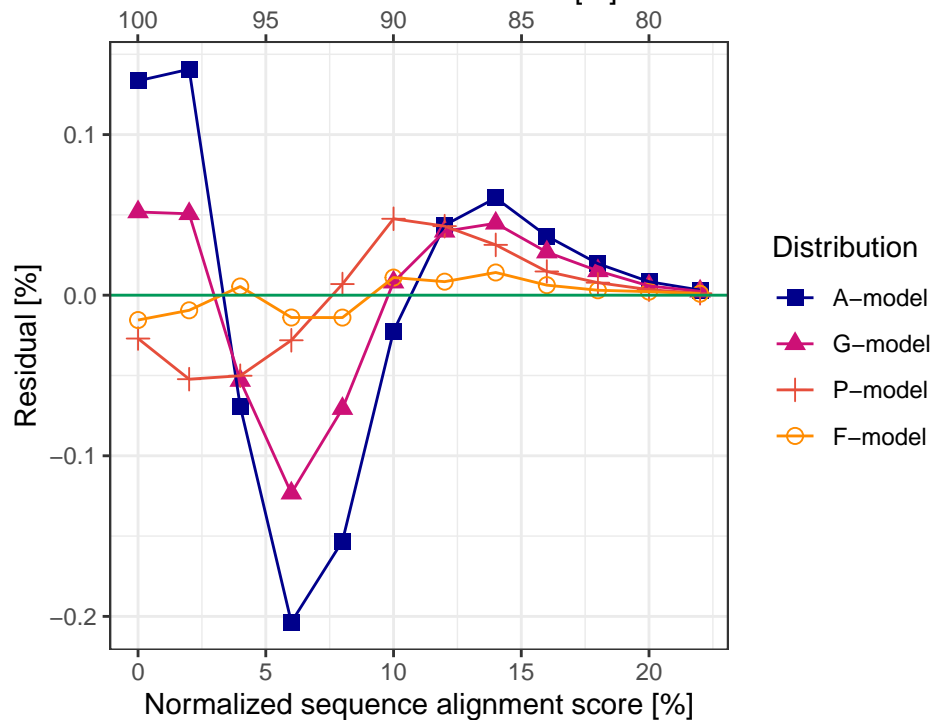
+ P-model

○ F-model



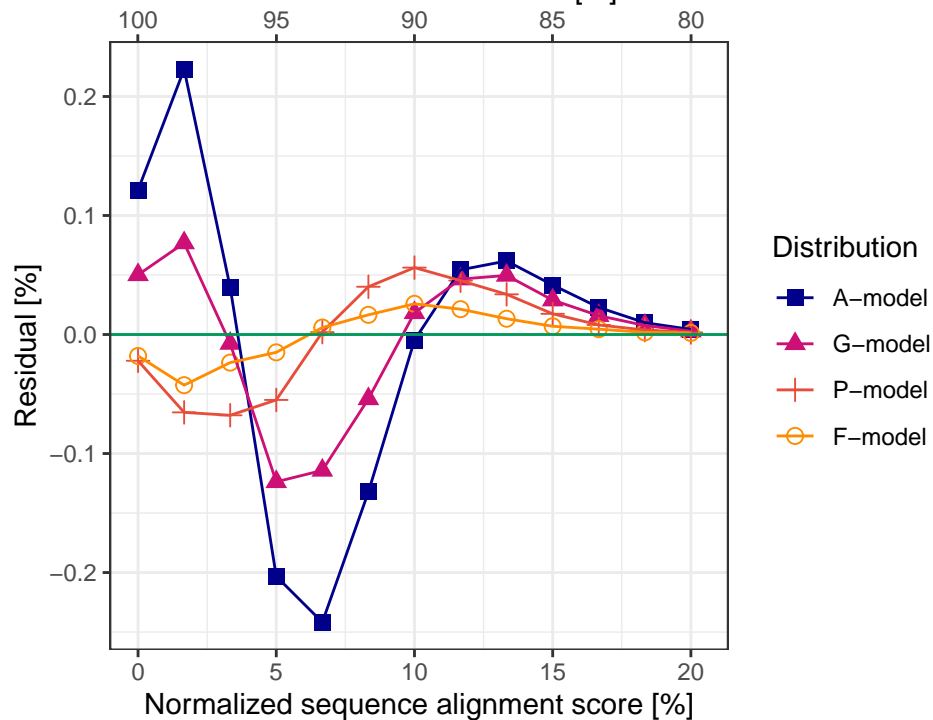
Residuals of 50mers, Metric=NWMn

Share of maximal distance [%]



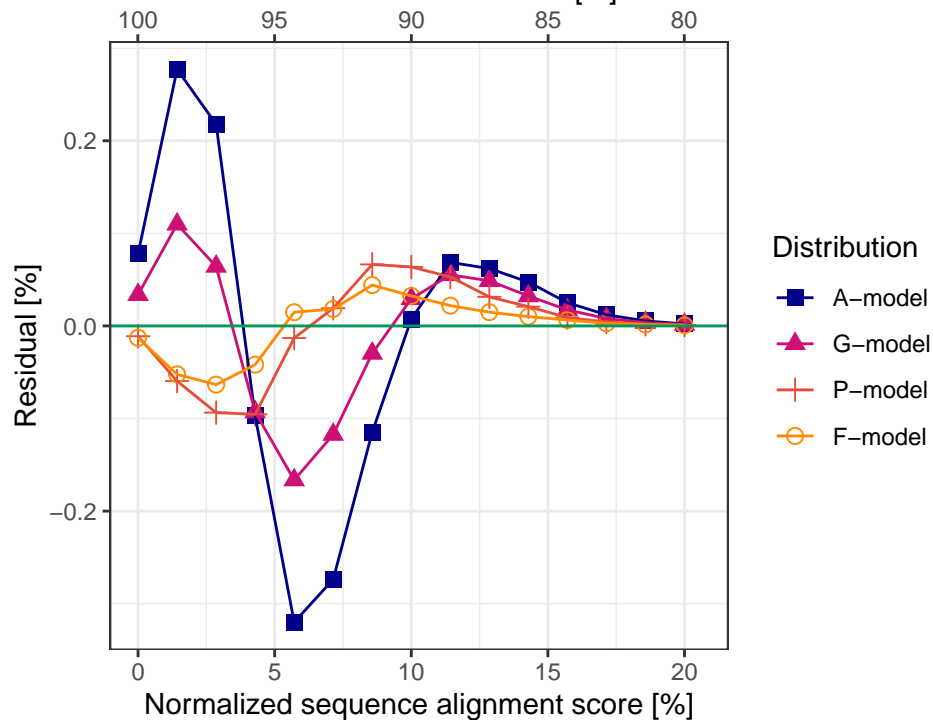
Residuals of 60mers, Metric=NWMn

Share of maximal distance [%]



Residuals of 70mers, Metric=NWMn

Share of maximal distance [%]



Residuals of 80mers, Metric=NWMn

Share of maximal distance [%]

100 95 90 85 80

Residual [%]

0.25

0.00

-0.25

0 5 10 15 20

Normalized sequence alignment score [%]

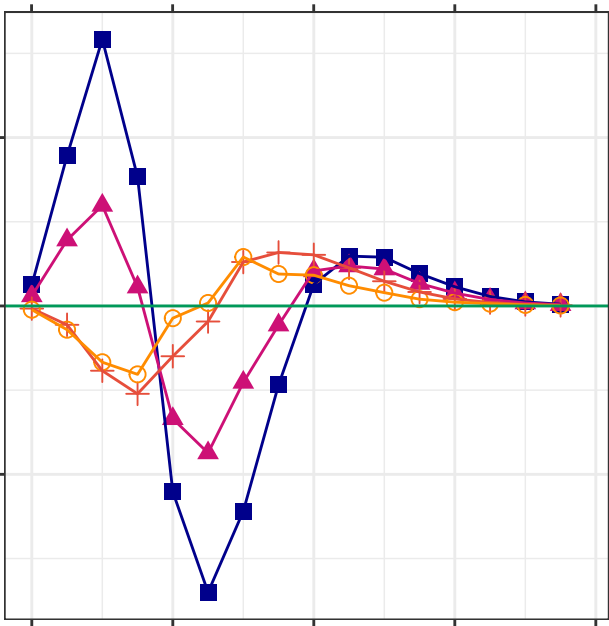
Distribution

A-model

G-model

P-model

F-model



Residuals of 90mers, Metric=NWMn

Share of maximal distance [%]

100

95

90

85

0.3

0.0

-0.3

-0.6

Distribution

A-model

G-model

P-model

F-model

Residual [%]

Normalized sequence alignment score [%]

0

5

10

15

Residuals of 100mers, Metric=NWMn

Share of maximal distance [%]

