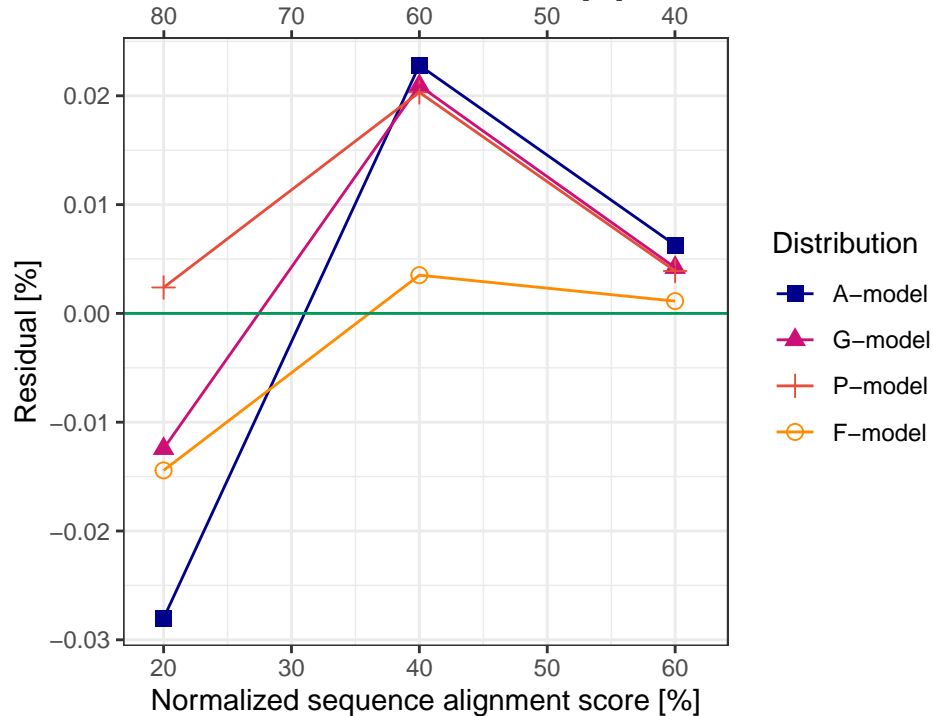


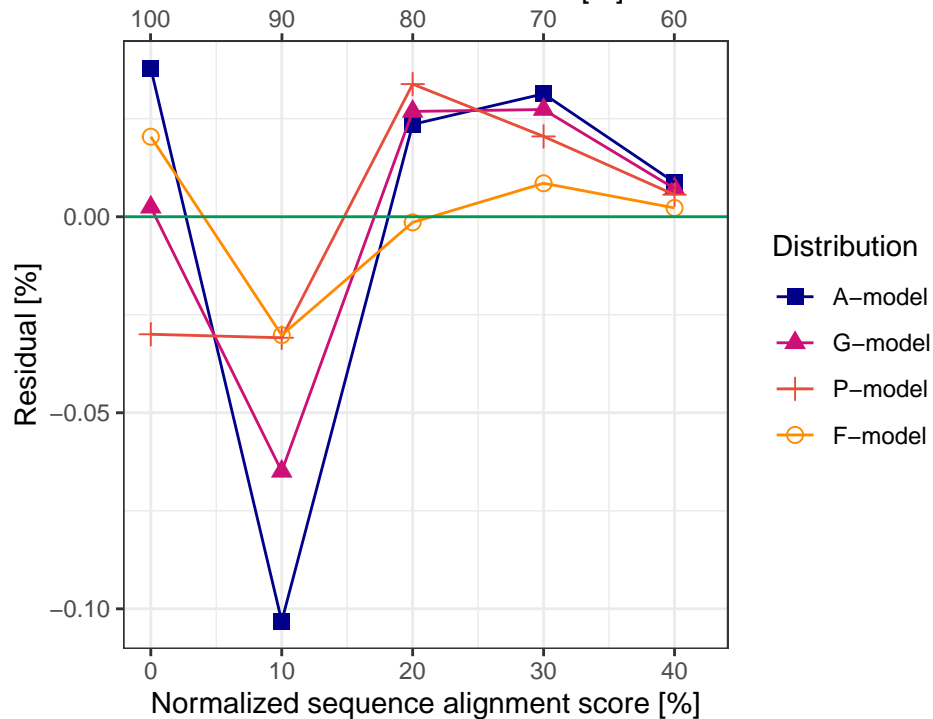
Residuals of 5mers, Metric=NWLn

Share of maximal distance [%]



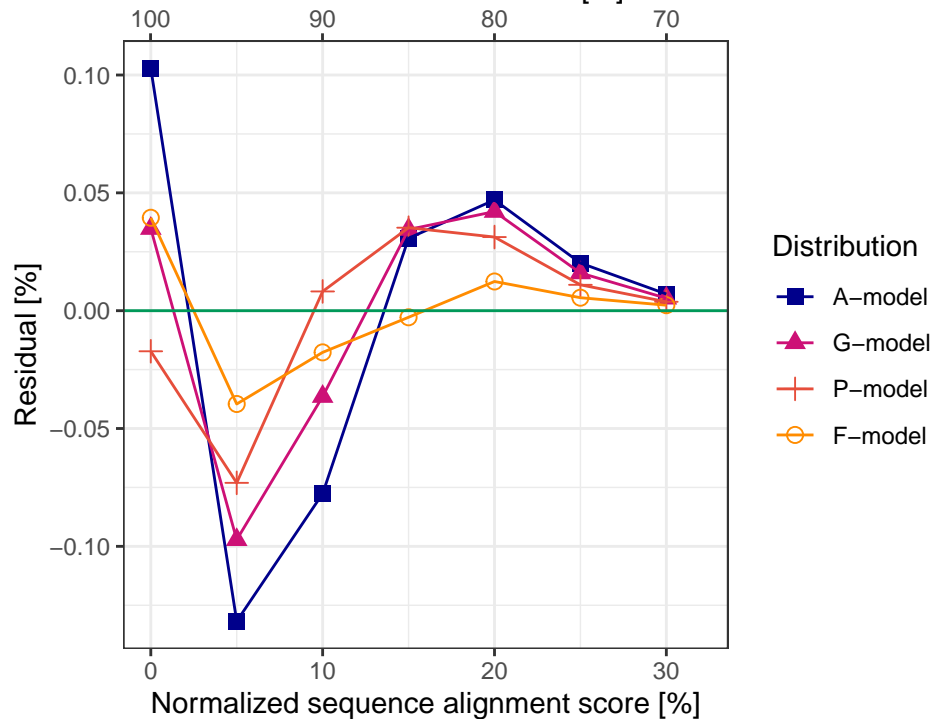
Residuals of 10mers, Metric=NWLn

Share of maximal distance [%]



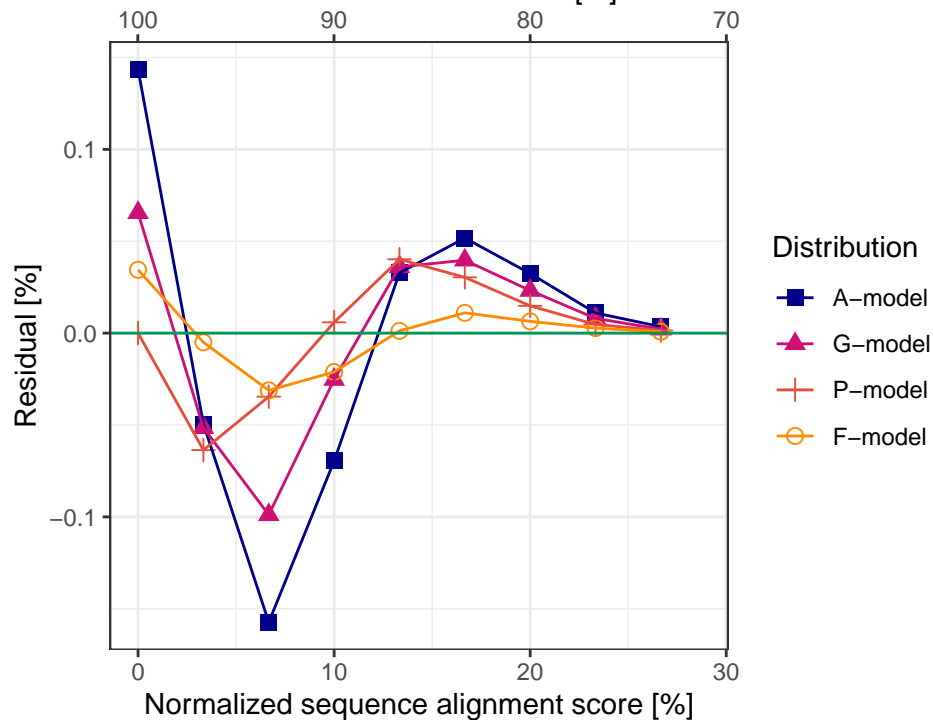
Residuals of 20mers, Metric=NWLn

Share of maximal distance [%]



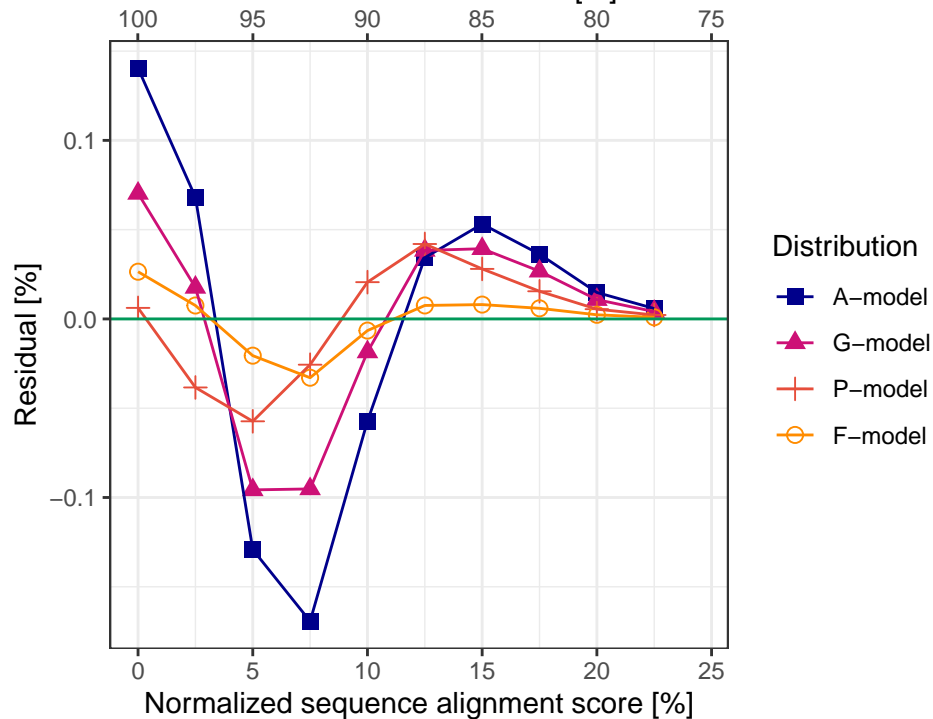
Residuals of 30mers, Metric=NWLn

Share of maximal distance [%]



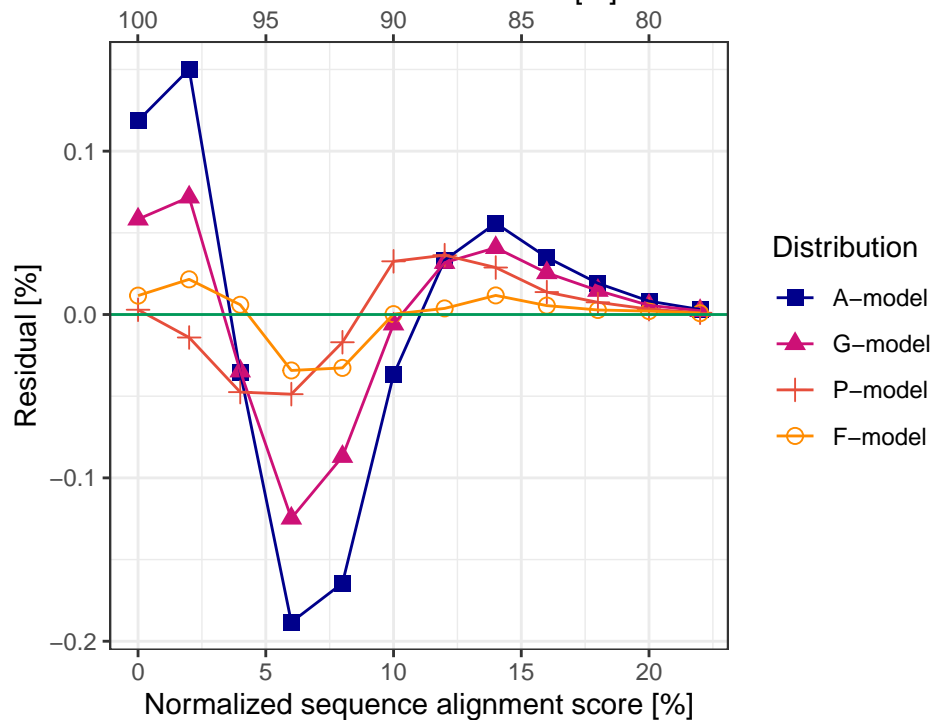
Residuals of 40mers, Metric=NWLn

Share of maximal distance [%]



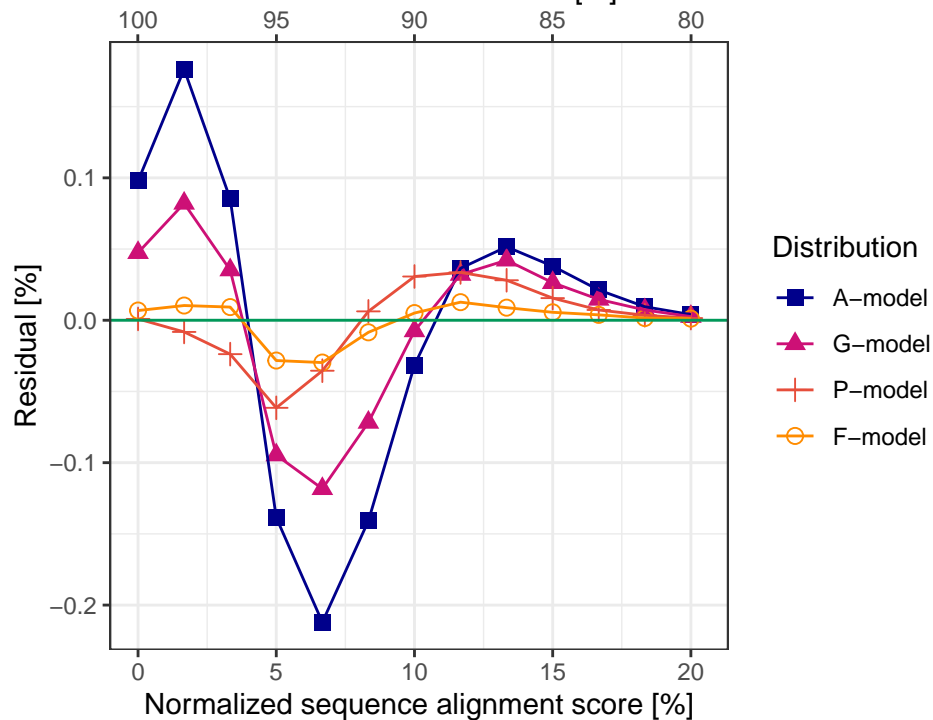
Residuals of 50mers, Metric=NWLn

Share of maximal distance [%]



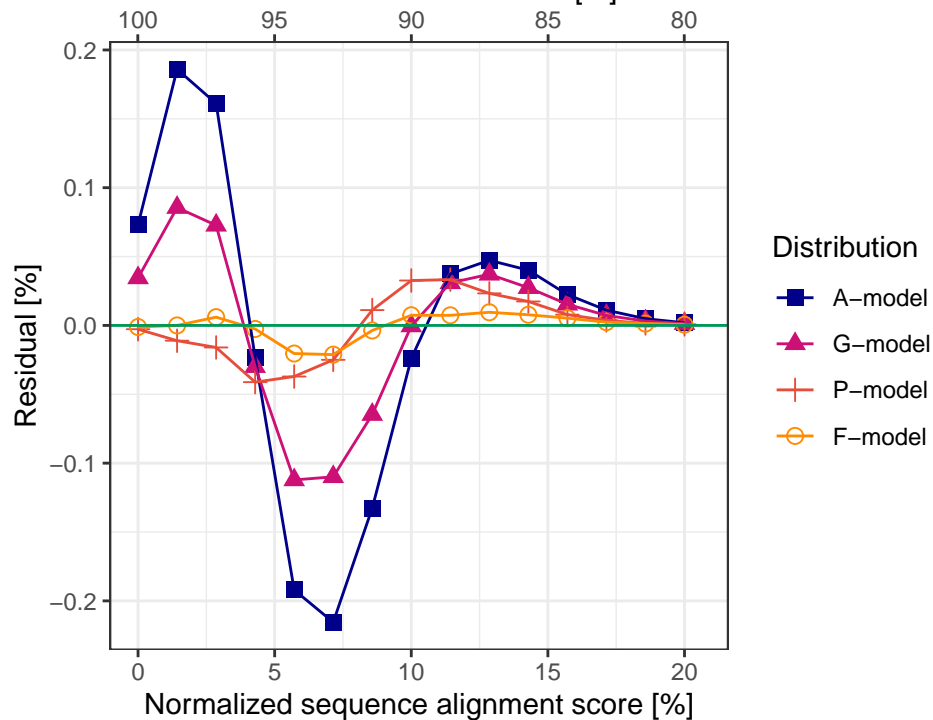
Residuals of 60mers, Metric=NWLn

Share of maximal distance [%]



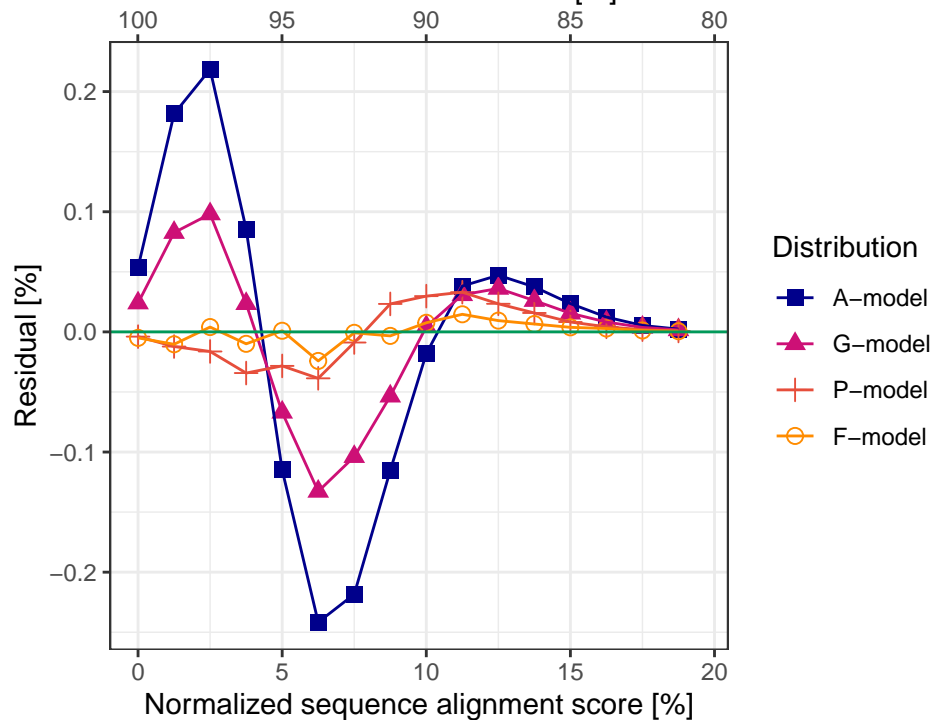
Residuals of 70mers, Metric=NWLn

Share of maximal distance [%]



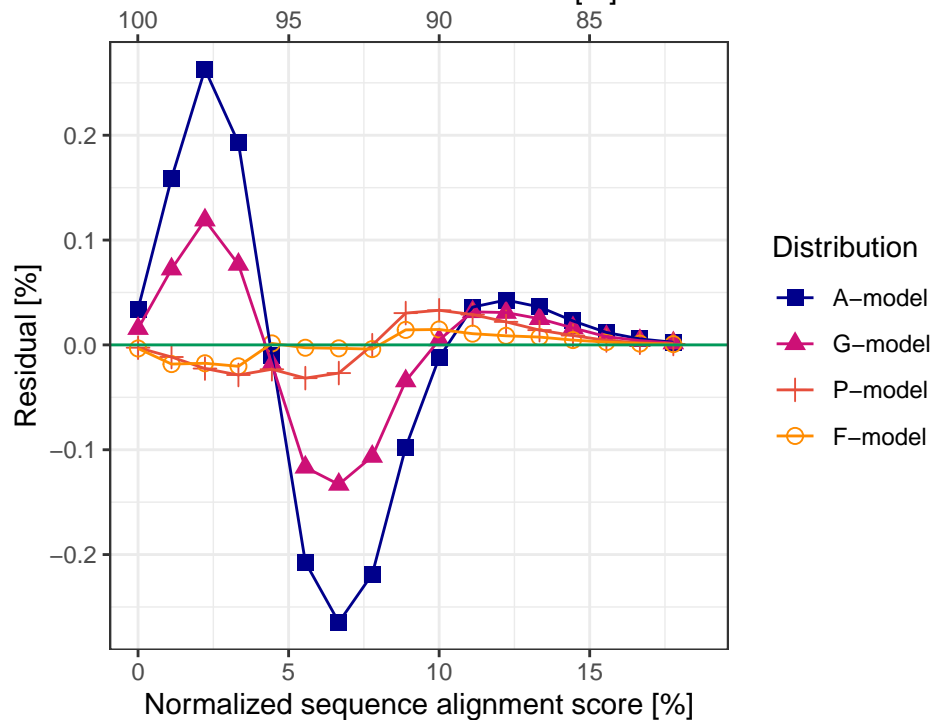
Residuals of 80mers, Metric=NWLn

Share of maximal distance [%]



Residuals of 90mers, Metric=NWLn

Share of maximal distance [%]



Residuals of 100mers, Metric=NWLn

Share of maximal distance [%]

100

95

90

85

0.2

0.0

-0.2

Distribution

■ A-model

▲ G-model

+ P-model

○ F-model

Residual [%]

Normalized sequence alignment score [%]

0

5

10

15