

Residuals of 5mers, Metric=NWSn

Share of maximal distance [%]

80 70 60 50 40

0.02

0.01

0.00

-0.01

-0.02

-0.03

Residual [%]

20 30 40 50 60

Normalized sequence alignment score [%]

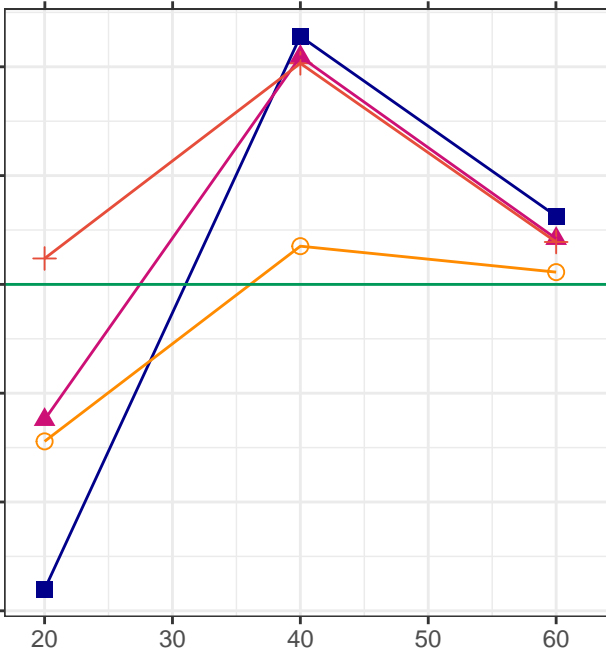
Distribution

■ A-model

▲ G-model

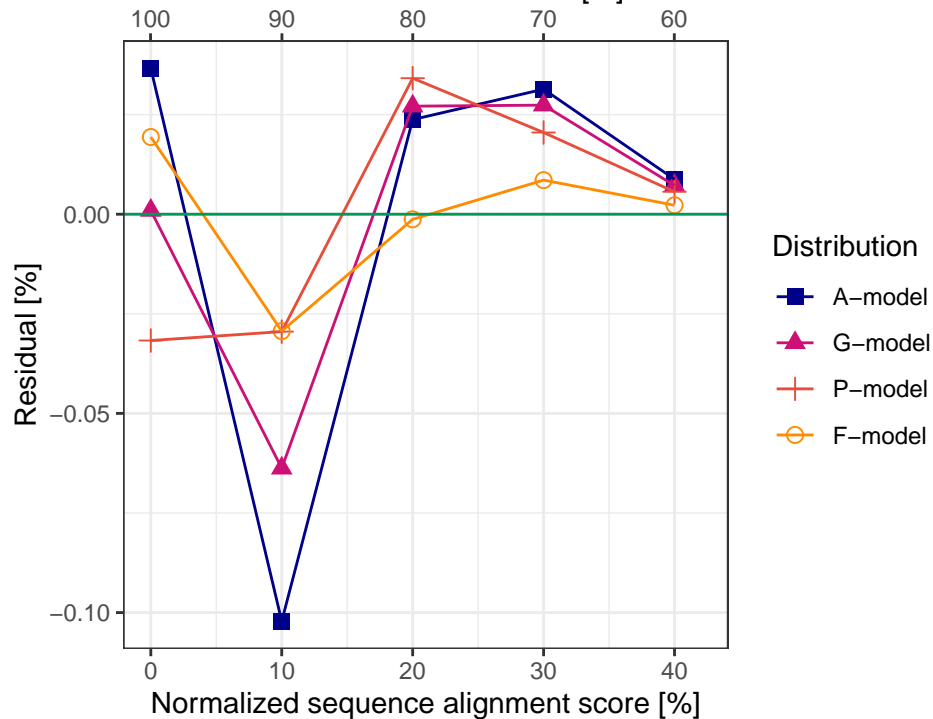
+ P-model

○ F-model



Residuals of 10mers, Metric=NWSn

Share of maximal distance [%]



Residuals of 20mers, Metric=NWSn

Share of maximal distance [%]

100

90

80

70

0.05

0.00

-0.05

-0.10

Residual [%]

0

10

20

30

Normalized sequence alignment score [%]

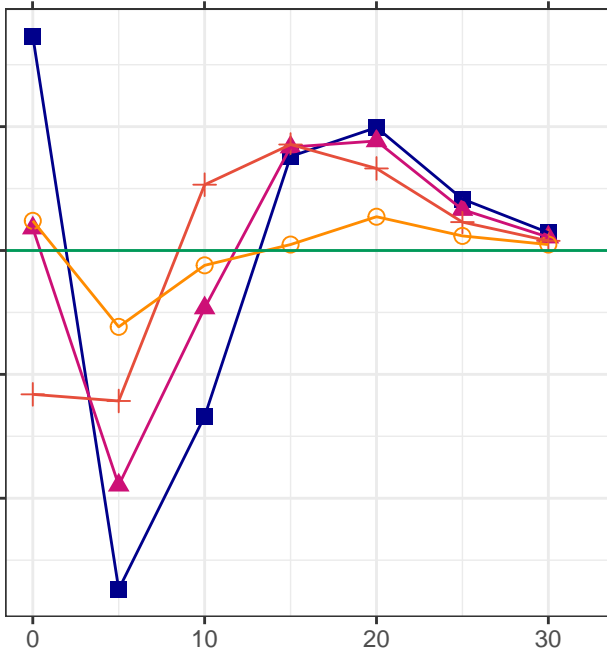
Distribution

A-model

G-model

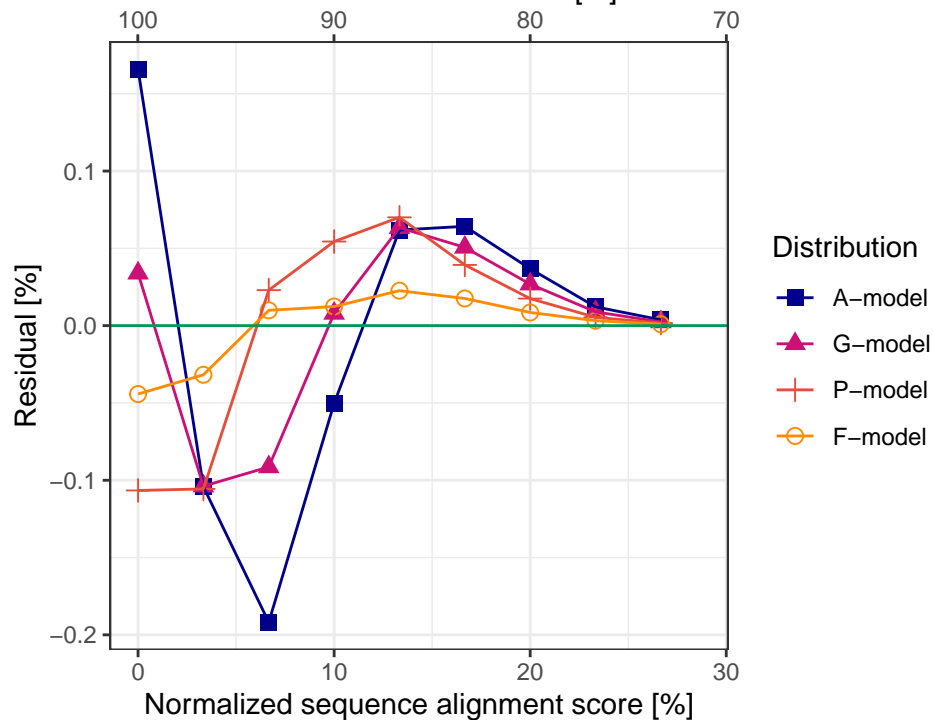
P-model

F-model



Residuals of 30mers, Metric=NWSn

Share of maximal distance [%]

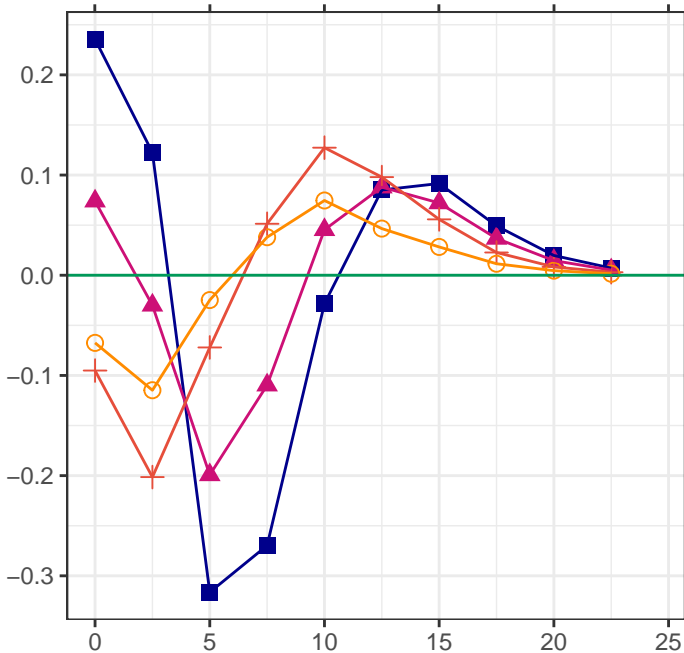


Residuals of 40mers, Metric=NWSn

Share of maximal distance [%]

100 95 90 85 80 75

Residual [%]



Distribution

A-model

G-model

P-model

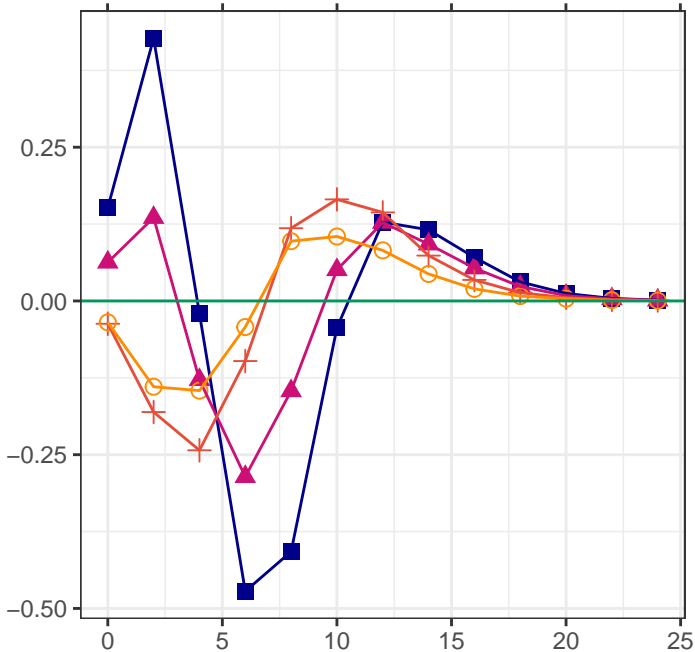
F-model

Residuals of 50mers, Metric=NWSn

Share of maximal distance [%]

100 95 90 85 80 75

Residual [%]



Distribution

■ A-model

▲ G-model

+ P-model

○ F-model

Normalized sequence alignment score [%]

Residuals of 60mers, Metric=NWSn

Share of maximal distance [%]

100

95

90

85

80

0.4

0.0

-0.4

-0.8

Distribution

A-model

G-model

P-model

F-model

Residual [%]

Normalized sequence alignment score [%]

0

5

10

15

20

0

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10

15

20

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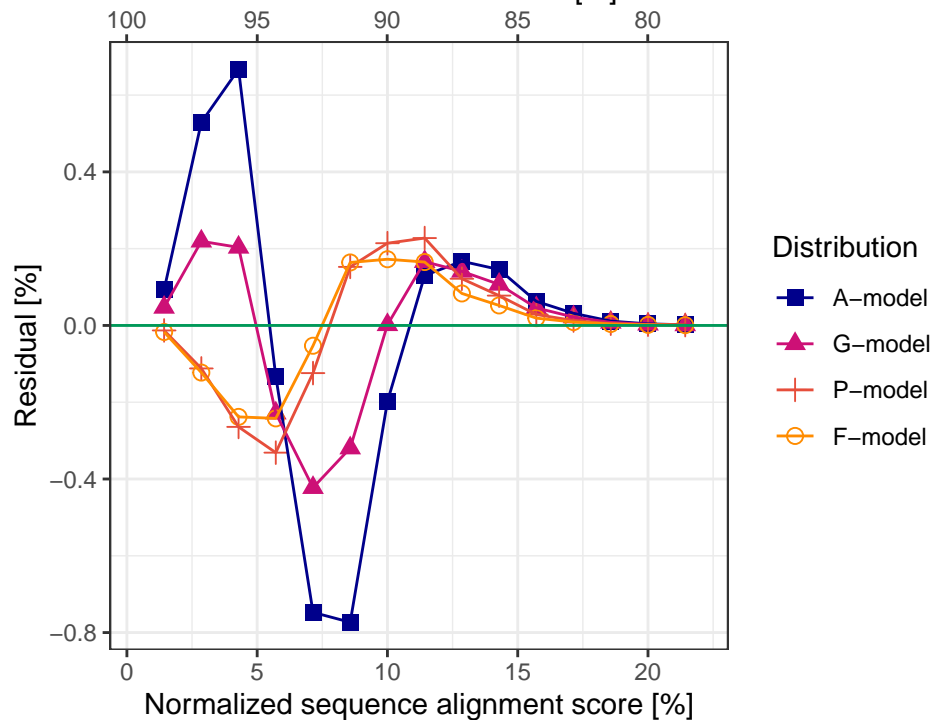
5

10

15

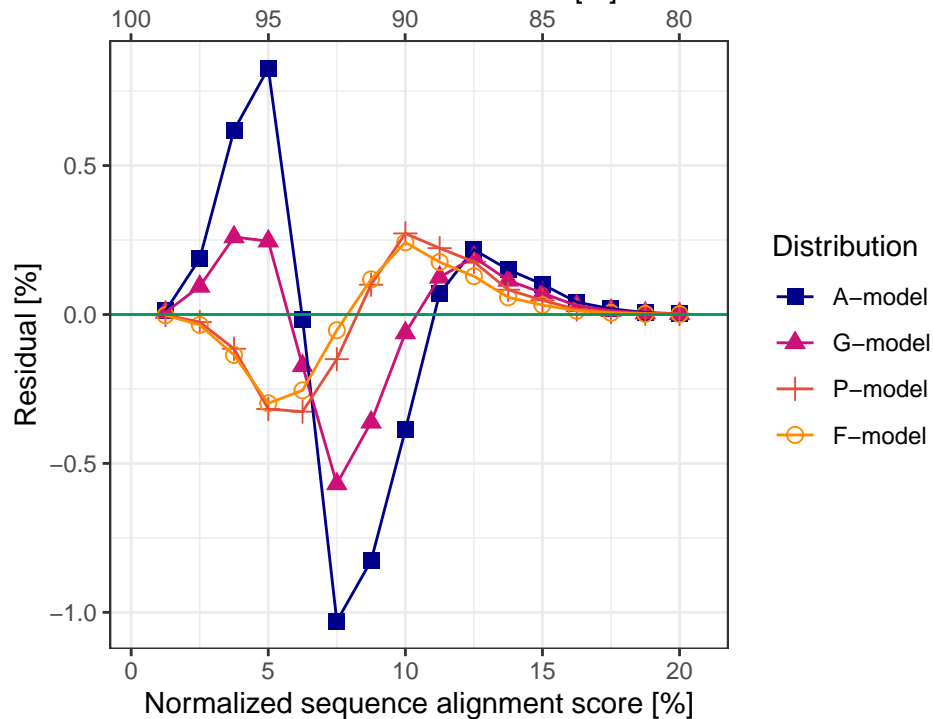
Residuals of 70mers, Metric=NWSn

Share of maximal distance [%]



Residuals of 80mers, Metric=NWSn

Share of maximal distance [%]



Residuals of 90mers, Metric=NWSn

Share of maximal distance [%]

95

90

85

80

0.5

0.0

-0.5

-1.0

Distribution

A-model

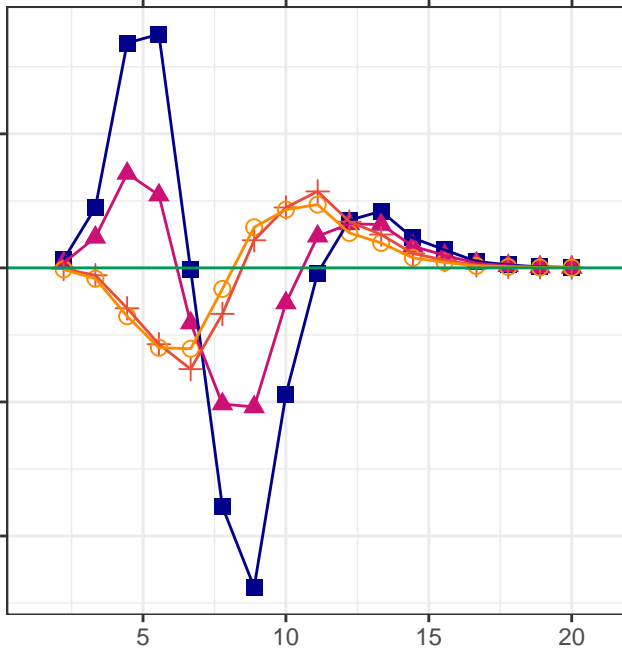
G-model

P-model

F-model

Residual [%]

Normalized sequence alignment score [%]



Residuals of 100mers, Metric=NWSn

Share of maximal distance [%]

95

90

85

80

Residual [%]

1.0

0.5

0.0

-0.5

-1.0

Distribution

A-model

G-model

P-model

F-model

Normalized sequence alignment score [%]

5

10

15

20

