

Residuals of 5mers, Metric=SWSn

Share of maximal distance [%]

100

75

50

25

0.25

0.00

-0.25

-0.50

Distribution

A-model

G-model

P-model

F-model

Residual [%]

Normalized sequence alignment score [%]

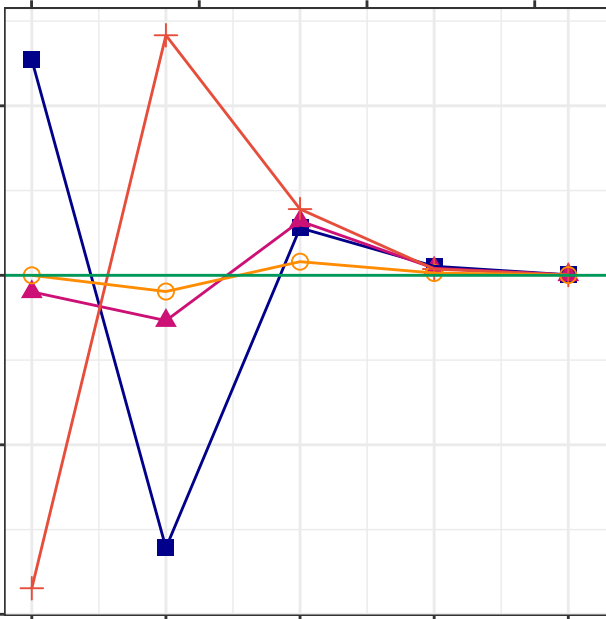
0

20

40

60

80



Residuals of 10mers, Metric=SWSn

Share of maximal distance [%]

100 90 80 70 60 50

Residual [%]

0.25

0.00

-0.25

-0.50

Normalized sequence alignment score [%]

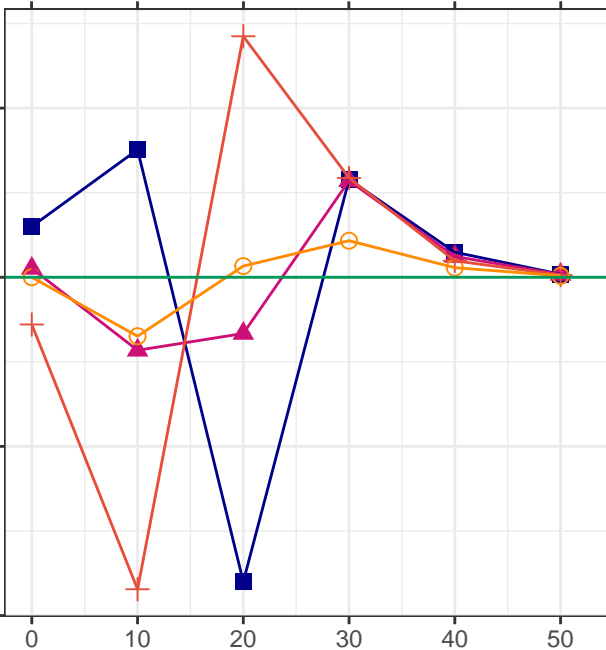
Distribution

A-model

G-model

P-model

F-model



Residuals of 20mers, Metric=SWSn

Share of maximal distance [%]

90

80

70

0.5

0.0

-0.5

-1.0

10

20

30

Normalized sequence alignment score [%]

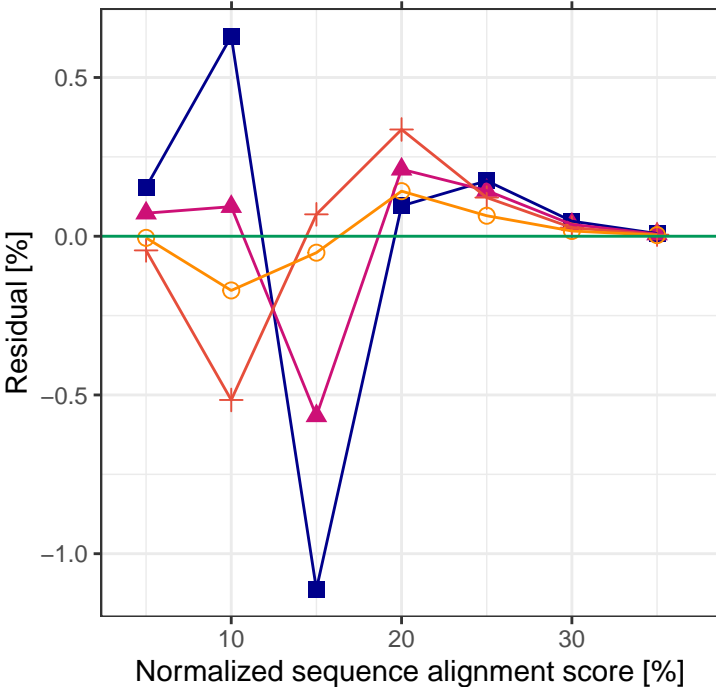
Distribution

A-model

G-model

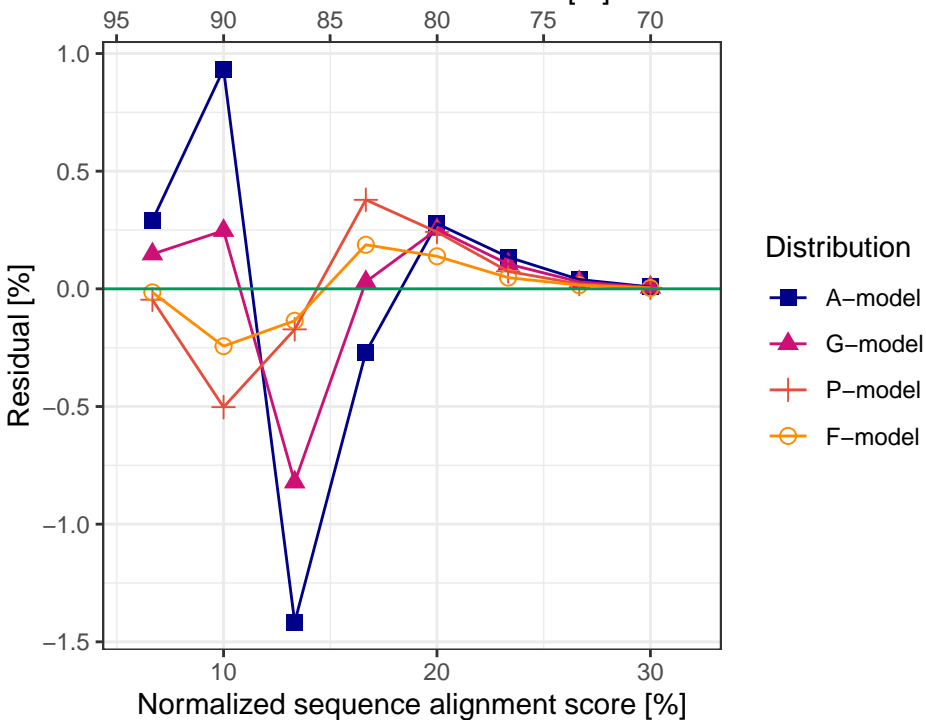
P-model

F-model



Residuals of 30mers, Metric=SWSn

Share of maximal distance [%]

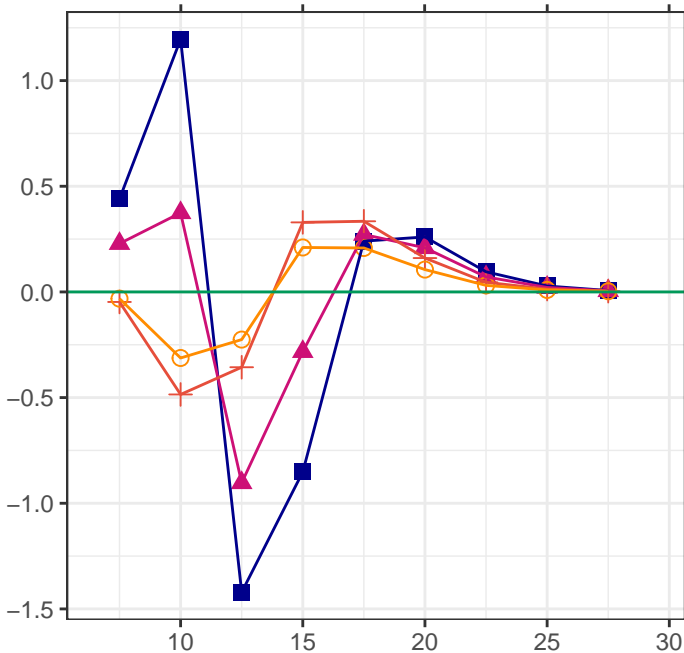


Residuals of 40mers, Metric=SWSn

Share of maximal distance [%]

90 85 80 75 70

Residual [%]



Distribution

A-model

G-model

P-model

F-model

Normalized sequence alignment score [%]

Residuals of 50mers, Metric=SWSn

Share of maximal distance [%]

95

90

85

80

75

1.5

1.0

0.5

0.0

-0.5

-1.0

Residual [%]

Distribution

■ A-model

▲ G-model

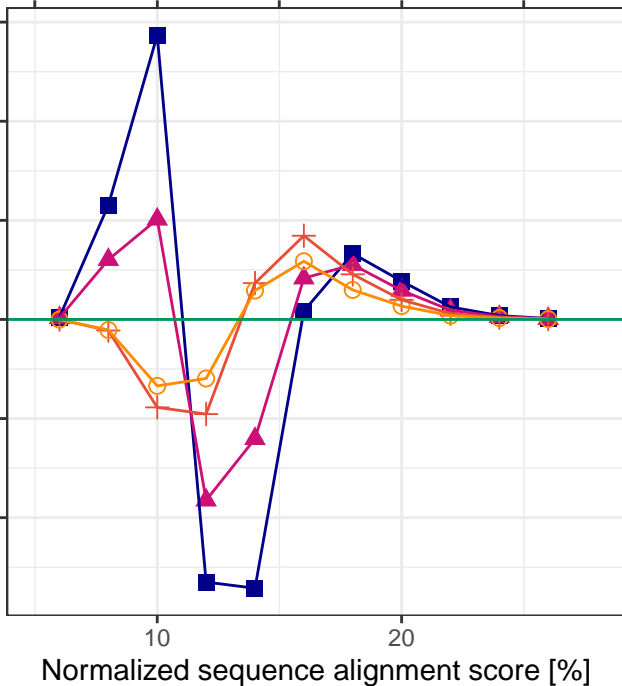
+ P-model

○ F-model

10

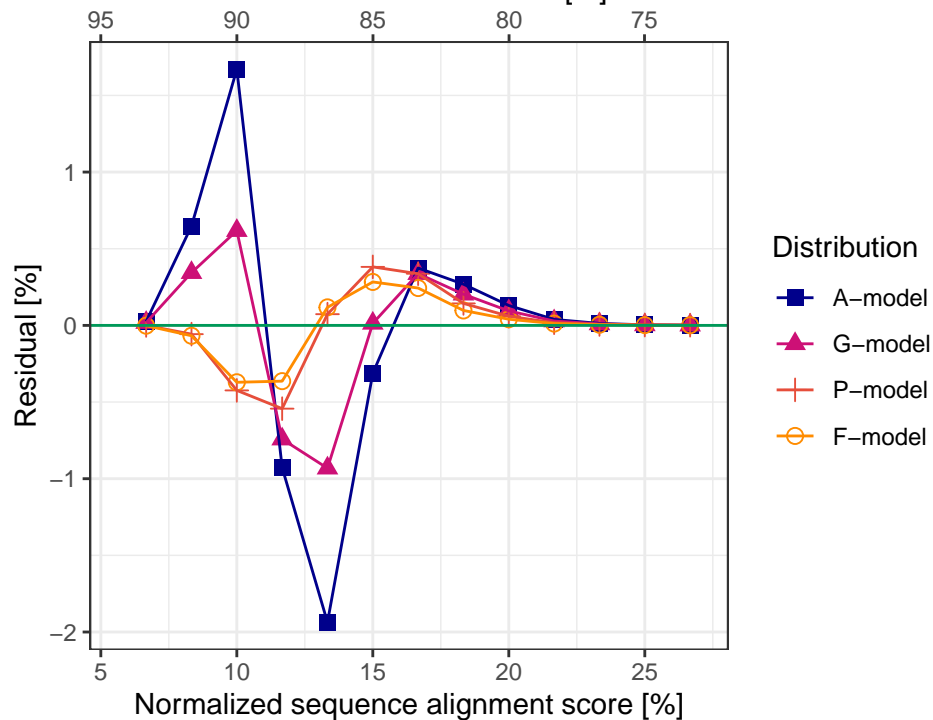
20

Normalized sequence alignment score [%]



Residuals of 60mers, Metric=SWSn

Share of maximal distance [%]



Residuals of 70mers, Metric=SWSn

Share of maximal distance [%]

90

85

80

75

Residual [%]

1

0

-1

-2

Normalized sequence alignment score [%]

10

15

20

25

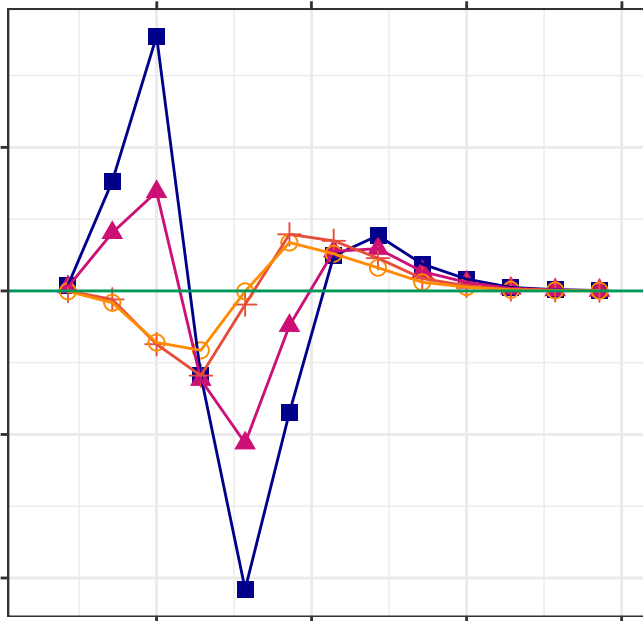
Distribution

A-model

G-model

P-model

F-model



Residuals of 80mers, Metric=SWSn

Share of maximal distance [%]

90

85

80

75

2

1

0

-1

-2

Residual [%]

Distribution

A-model

G-model

P-model

F-model

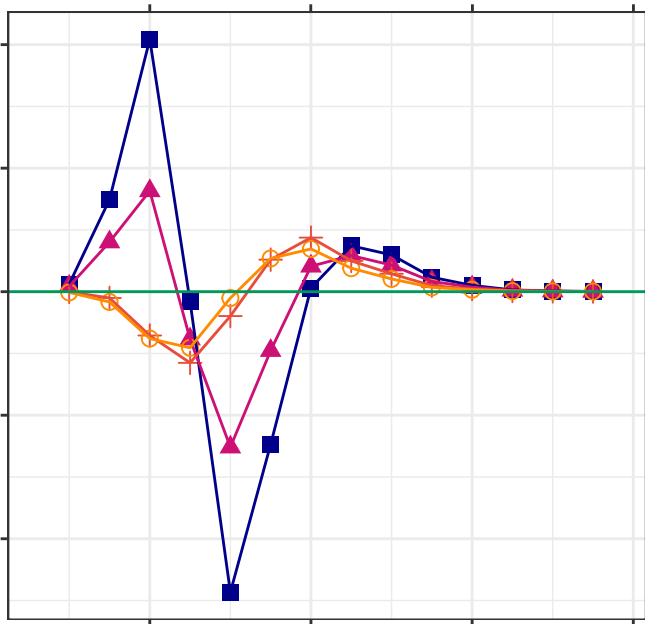
Normalized sequence alignment score [%]

10

15

20

25



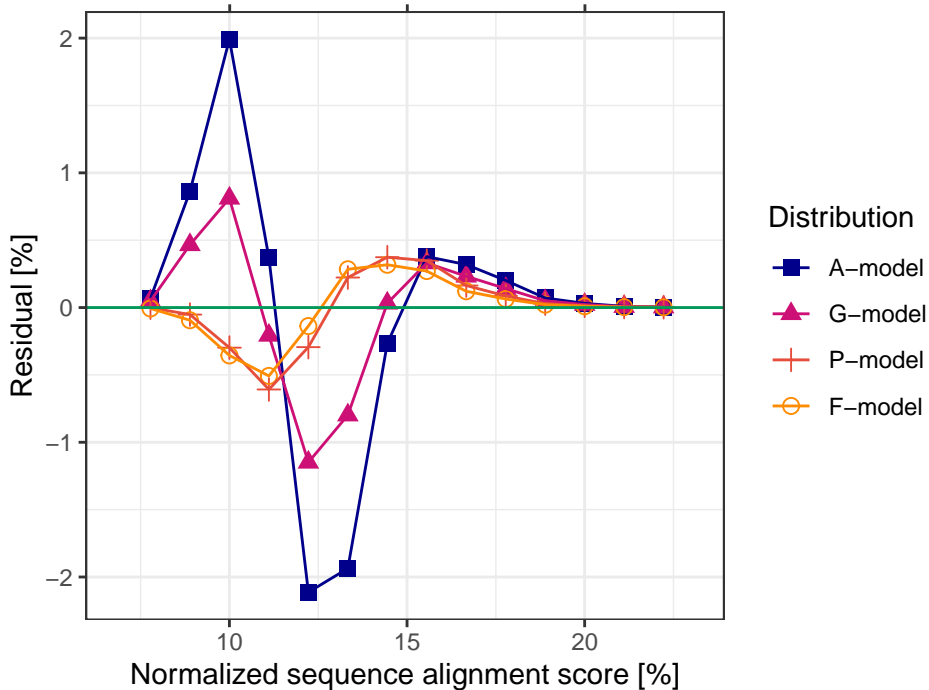
Residuals of 90mers, Metric=SWSn

Share of maximal distance [%]

90

85

80



Residuals of 100mers, Metric=SWSn

Share of maximal distance [%]

90

85

80

