

# Residuals of 5mers, Metric=SH

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 [%]

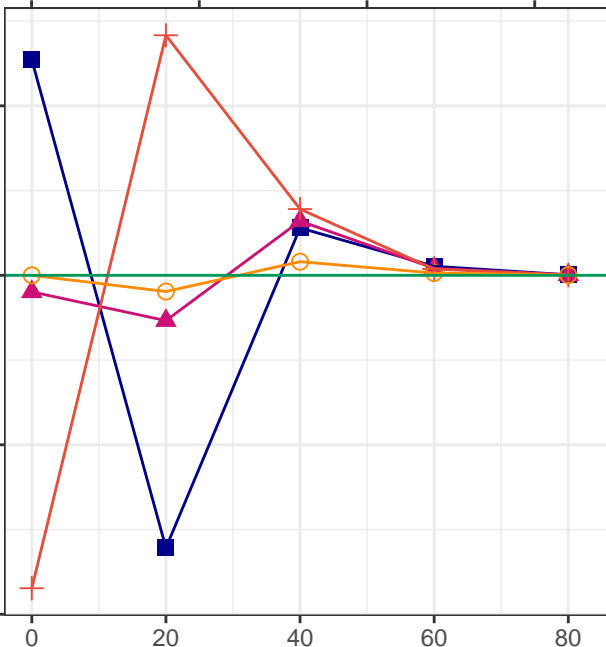
0

20

40

60

80



# Residuals of 10mers, Metric=SH

Share of maximal distance [%]

100 90 80 70 60 50

Residual [%]

0.25

0.00

-0.25

-0.50

Normalized sequence alignment score [%]

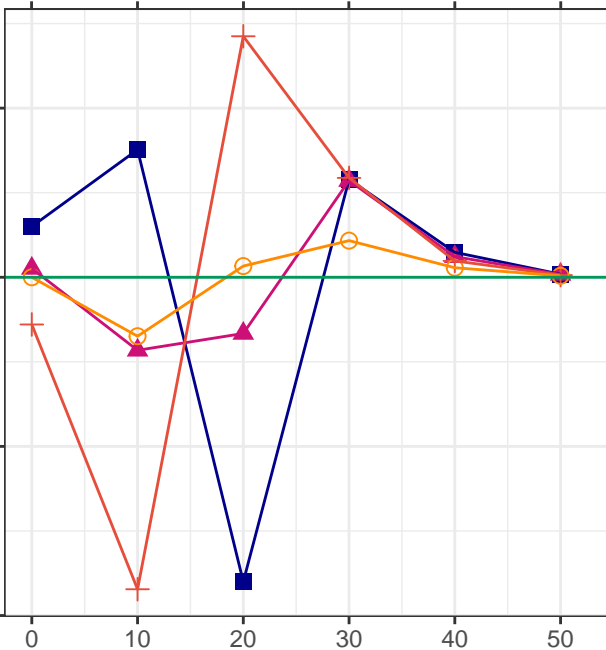
Distribution

A-model

G-model

P-model

F-model



# Residuals of 20mers, Metric=SH

Share of maximal distance [%]

90

80

70

0.5

0.0

-0.5

-1.0

10

20

30

Normalized sequence alignment score [%]

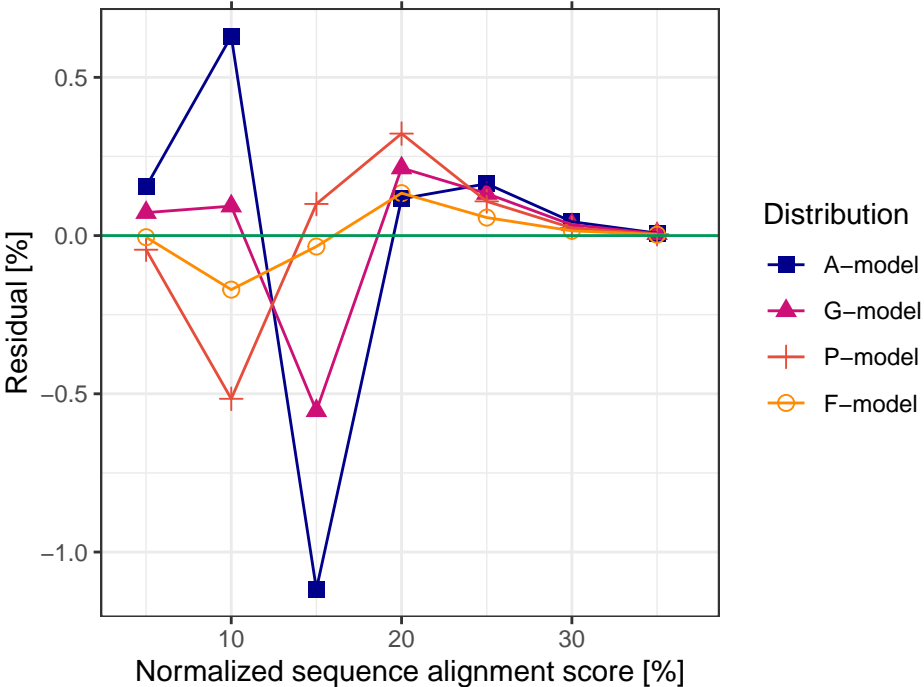
Distribution

A-model

G-model

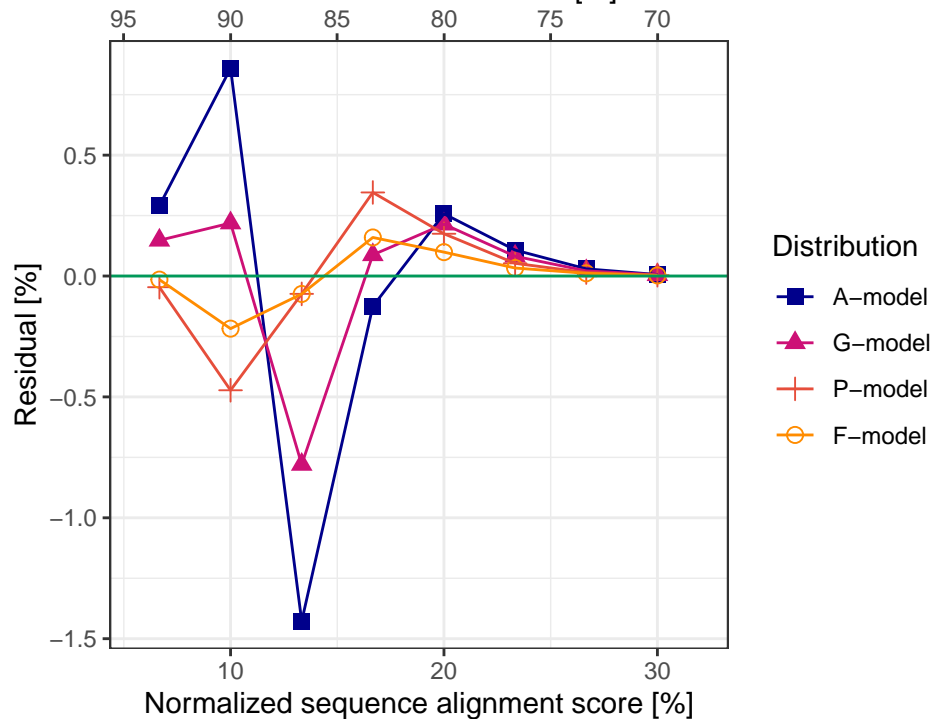
P-model

F-model



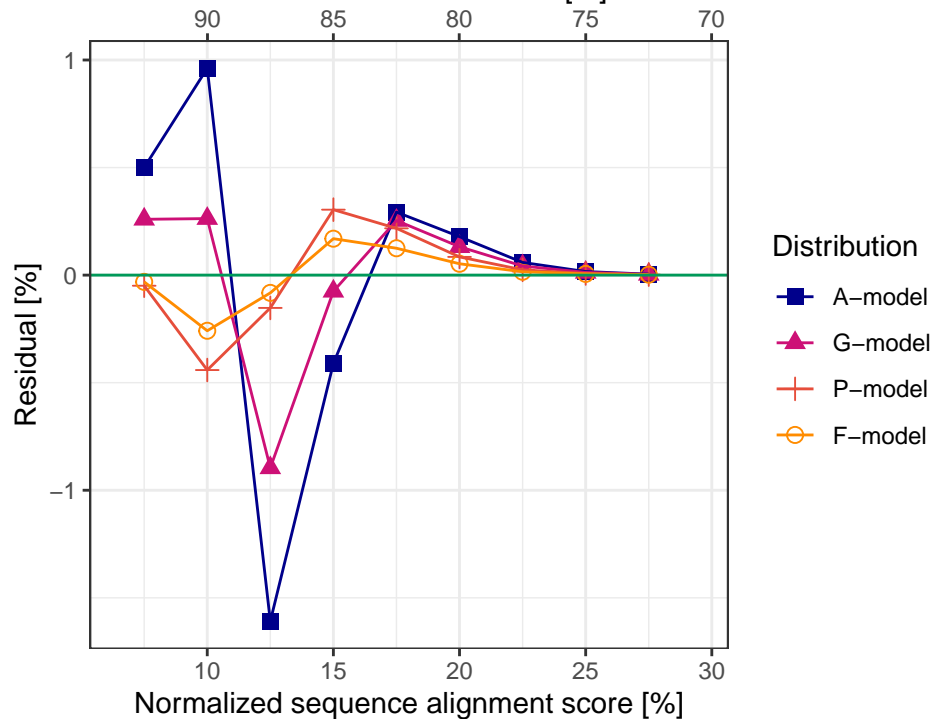
# Residuals of 30mers, Metric=SH

Share of maximal distance [%]



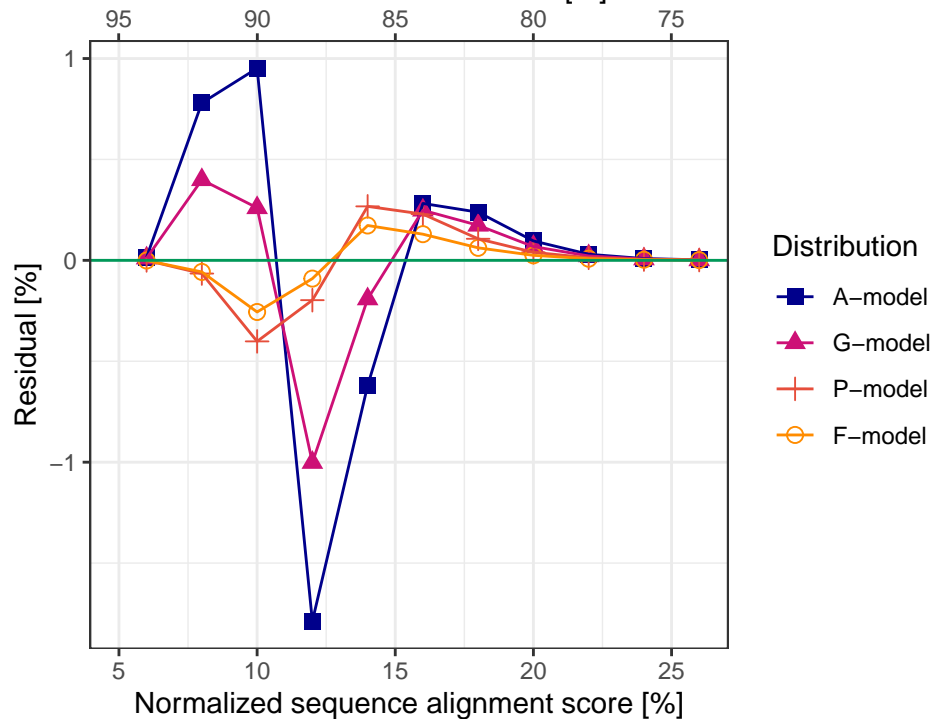
# Residuals of 40mers, Metric=SH

Share of maximal distance [%]



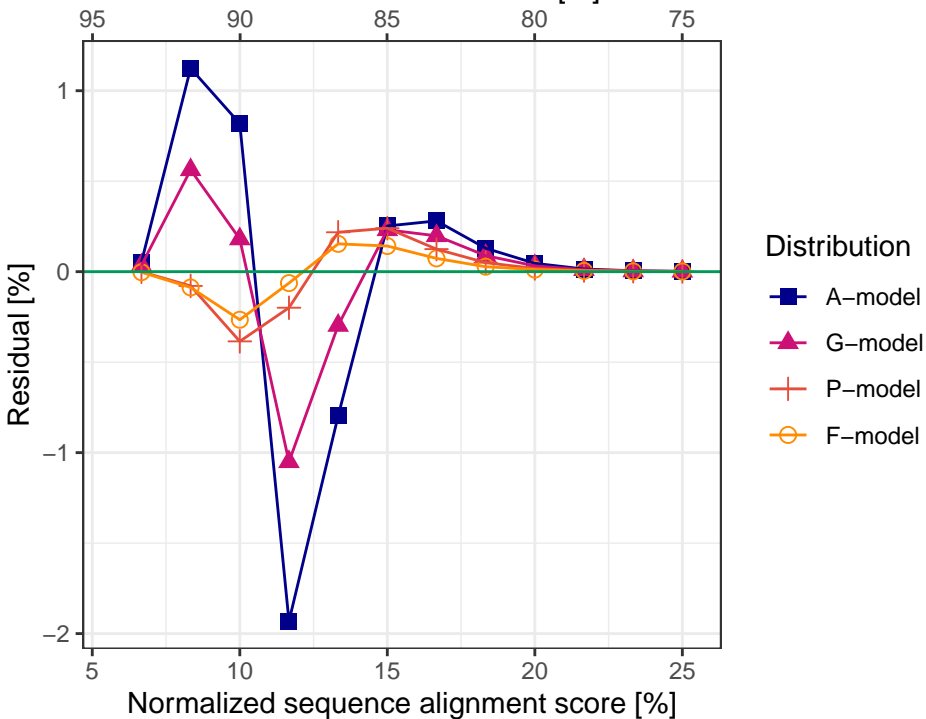
# Residuals of 50mers, Metric=SH

Share of maximal distance [%]



# Residuals of 60mers, Metric=SH

Share of maximal distance [%]



# Residuals of 70mers, Metric=SH

Share of maximal distance [%]

90

85

80

Residual [%]

1

0

-1

-2

10

15

20

Normalized sequence alignment score [%]

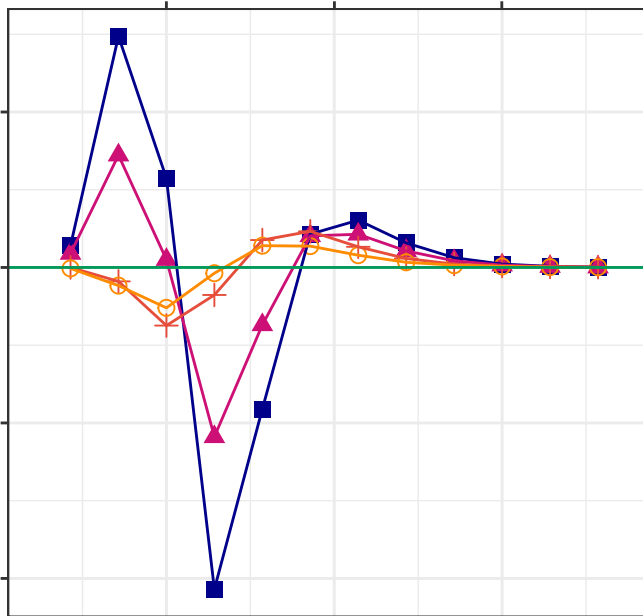
Distribution

A-model

G-model

P-model

F-model





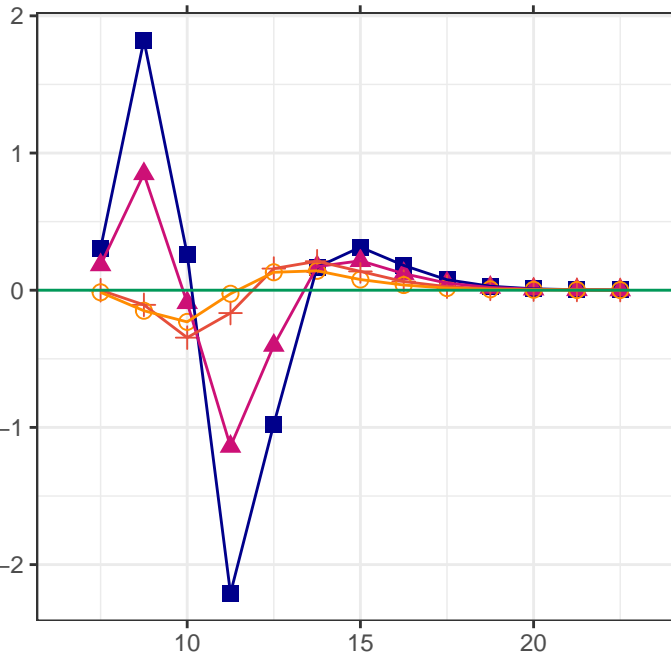
# Residuals of 80mers, Metric=SH

Share of maximal distance [%]

90

85

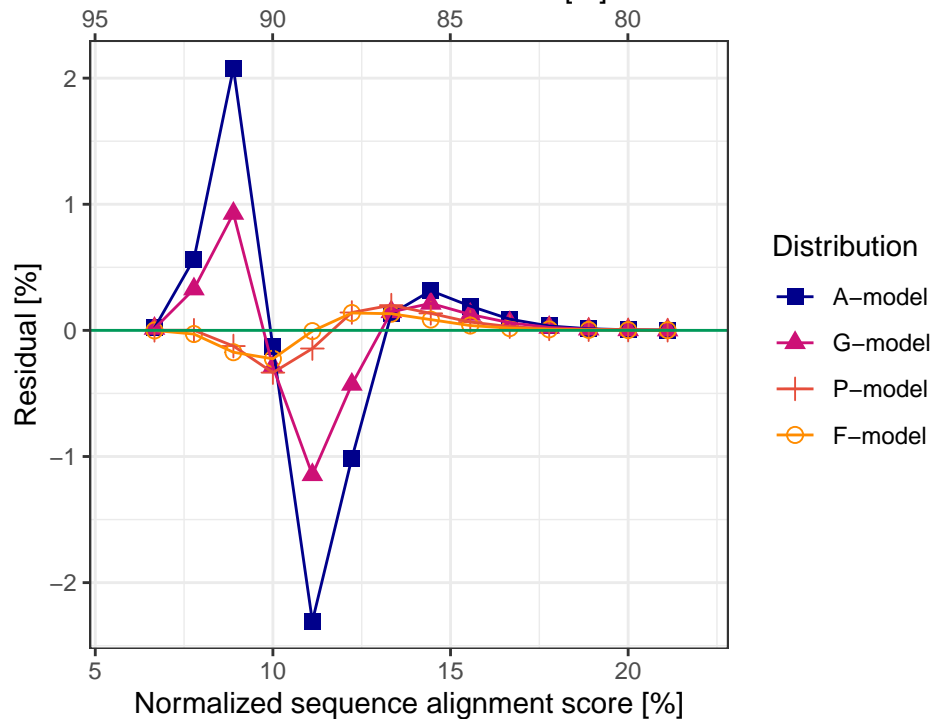
80



Normalized sequence alignment score [%]

# Residuals of 90mers, Metric=SH

Share of maximal distance [%]



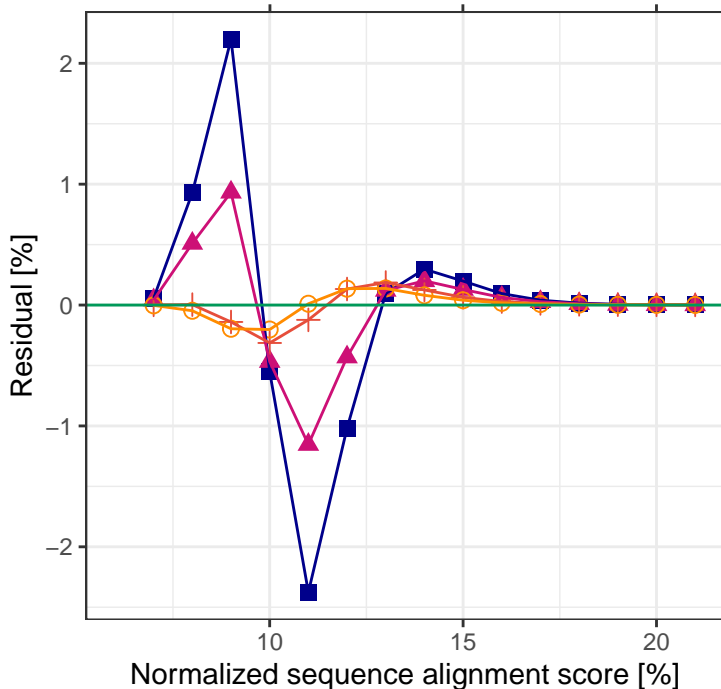
# Residuals of 100mers, Metric=SH

Share of maximal distance [%]

90

85

80



Distribution

- A-model
- G-model
- P-model
- F-model