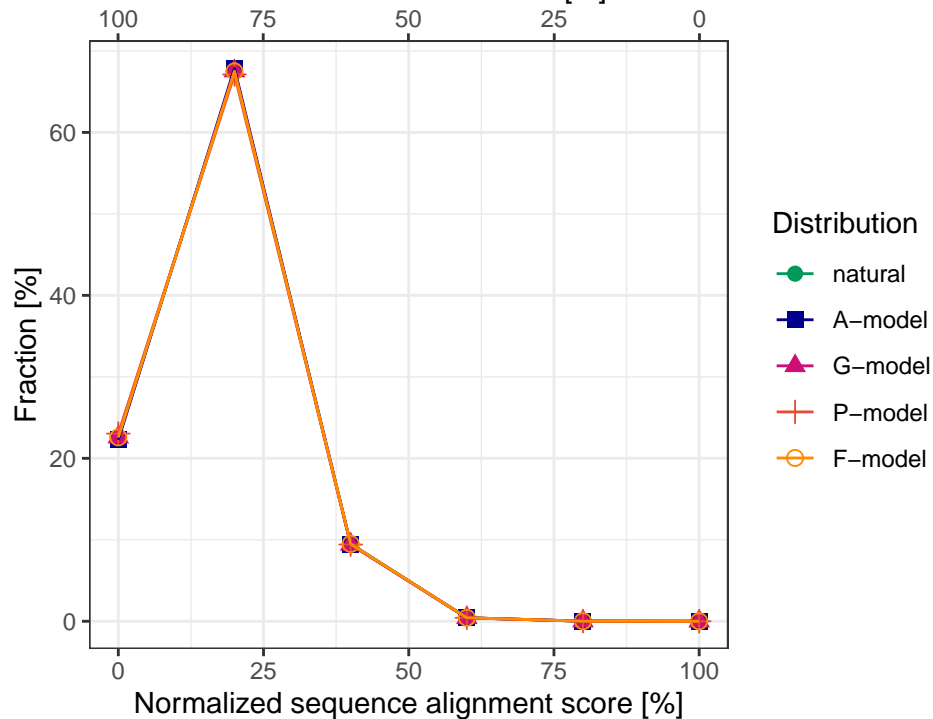


# Distance Distribution of 5mers, Metric=SH

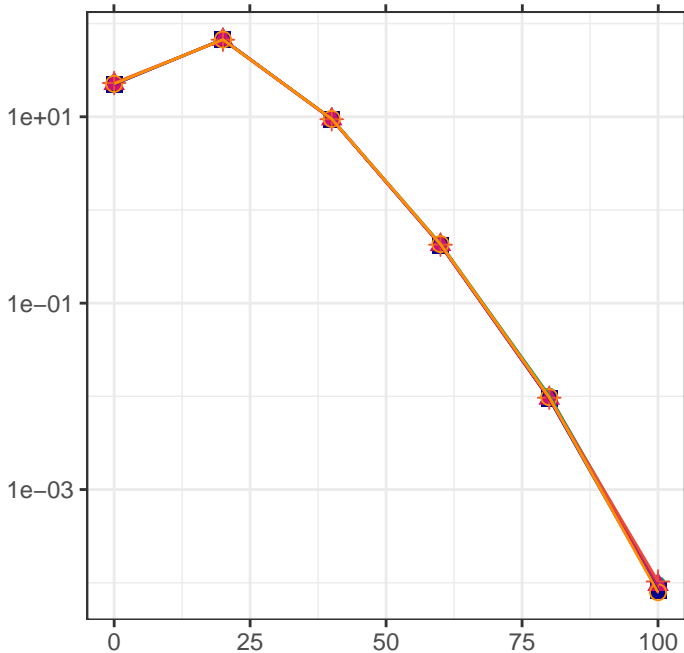
Share of maximal distance [%]



# Distance Distribution of 5mers, Metric=SH

Share of maximal distance [%]

100 75 50 25 0



Distribution

natural

A-model

G-model

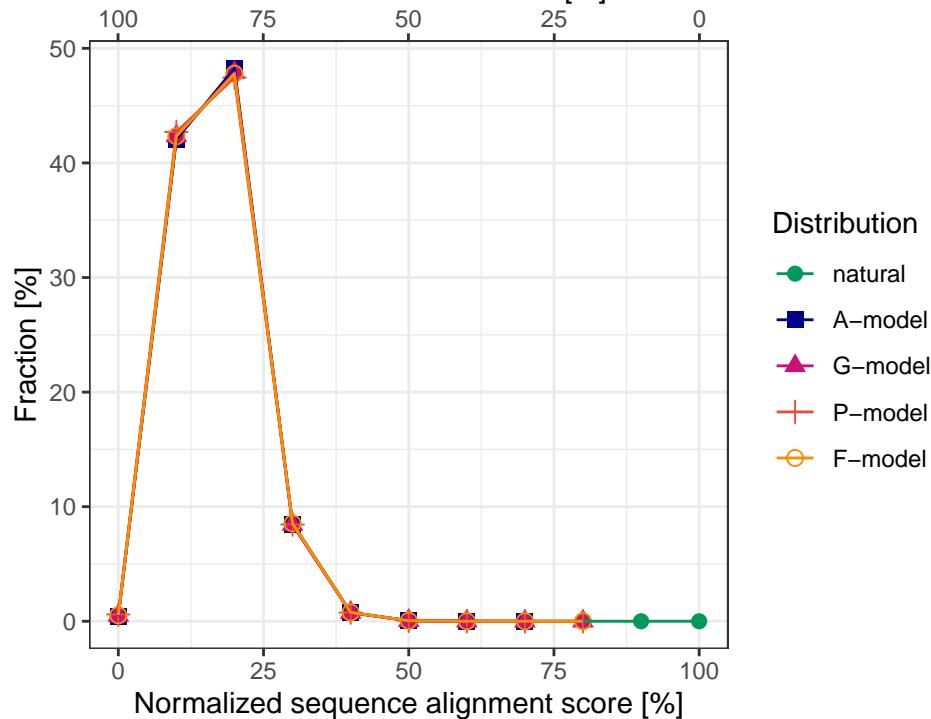
P-model

F-model

Normalized sequence alignment score [%]

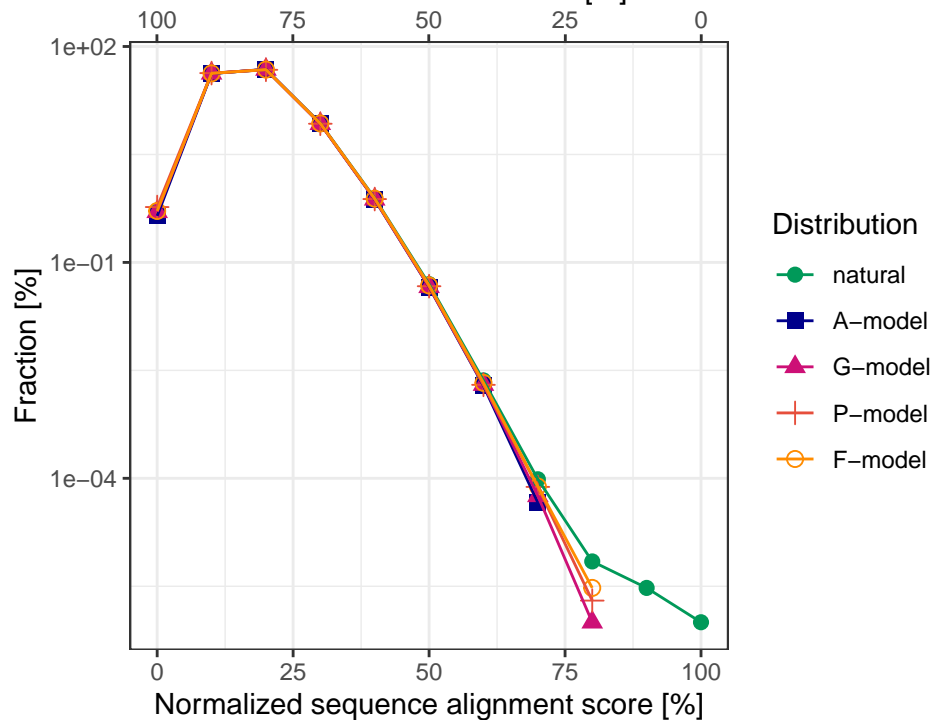
# Distance Distribution of 10mers, Metric=SH

Share of maximal distance [%]



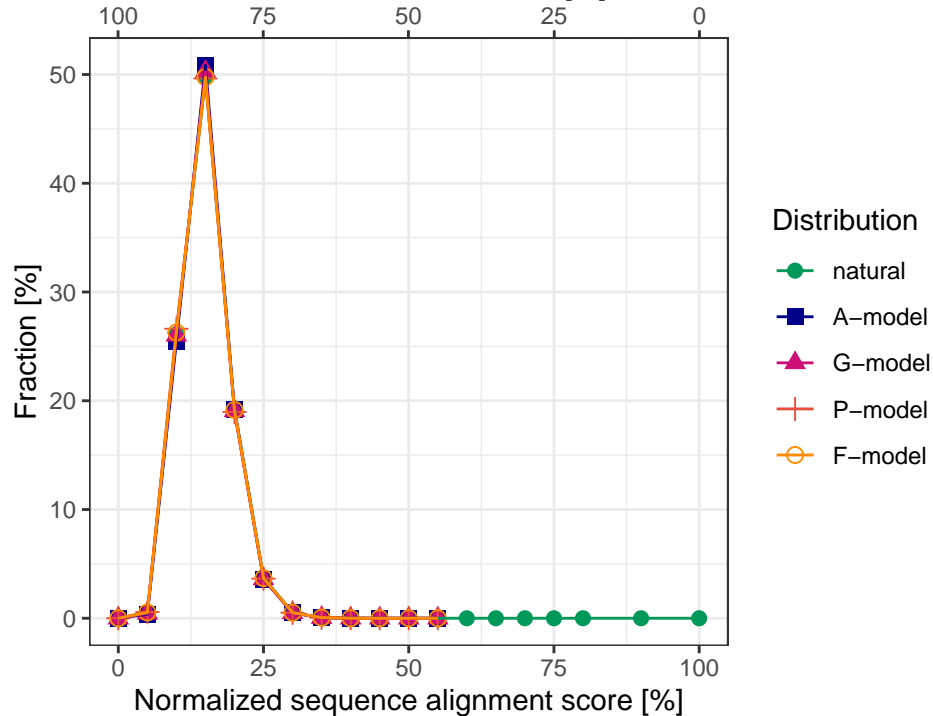
# Distance Distribution of 10mers, Metric=SH

Share of maximal distance [%]



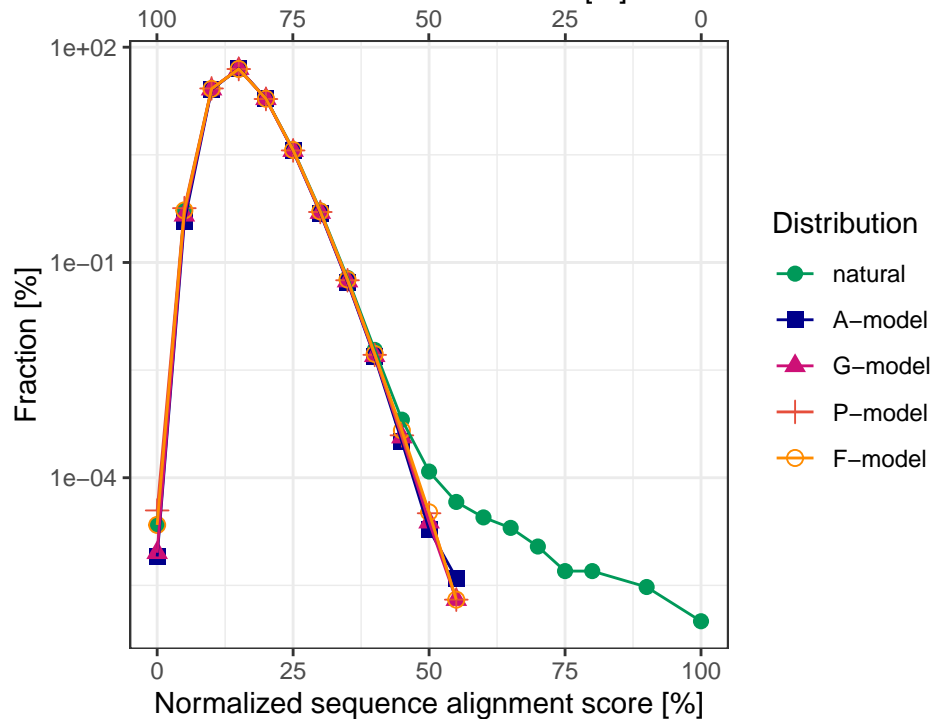
# Distance Distribution of 20mers, Metric=SH

Share of maximal distance [%]



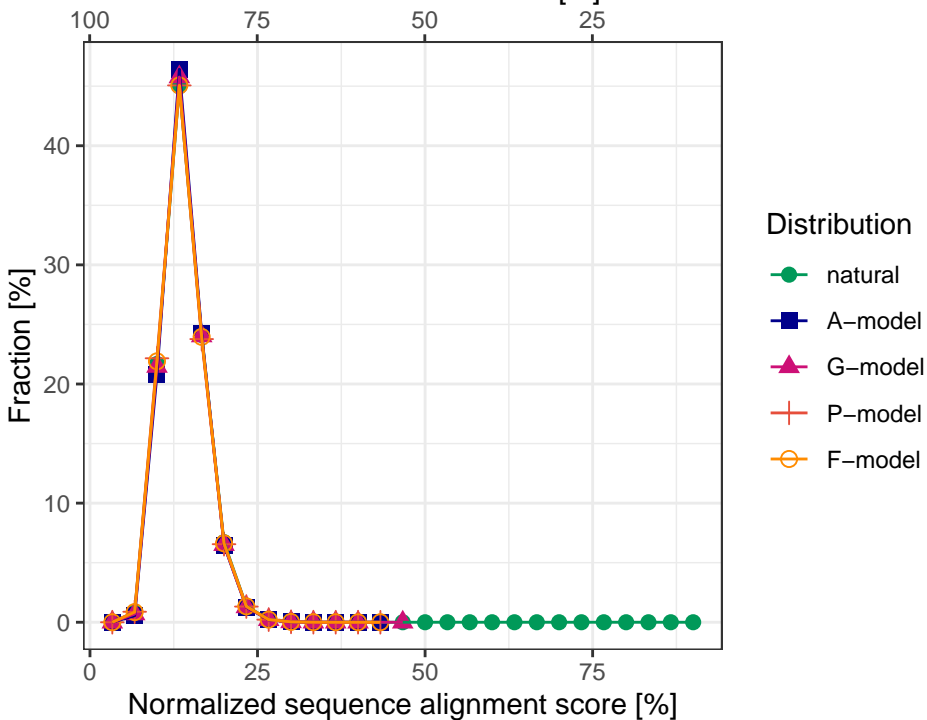
# Distance Distribution of 20mers, Metric=SH

Share of maximal distance [%]



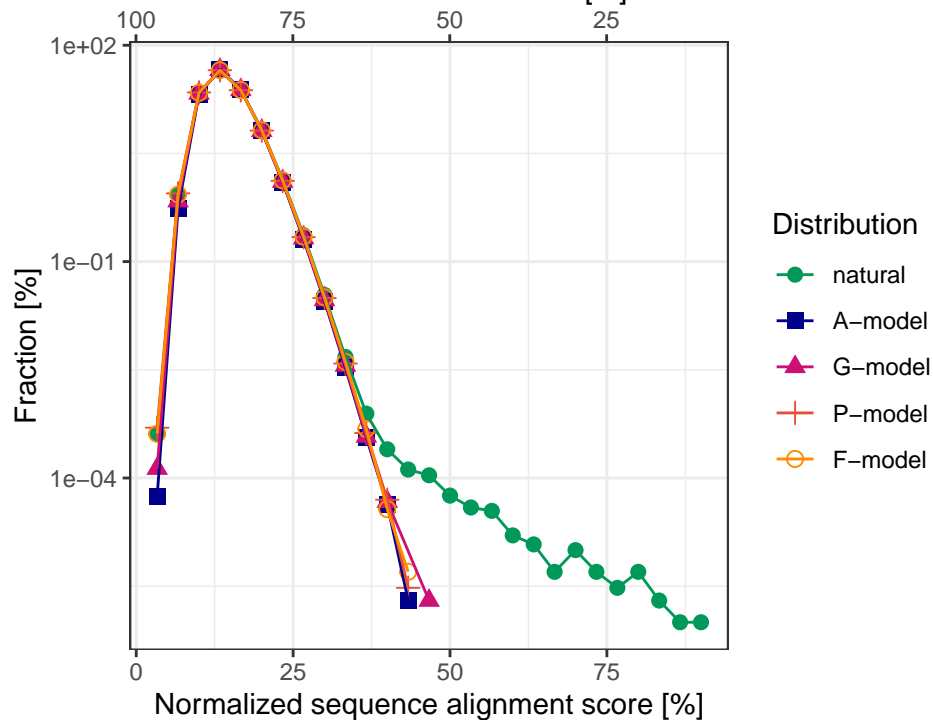
# Distance Distribution of 30mers, Metric=SH

Share of maximal distance [%]



# Distance Distribution of 30mers, Metric=SH

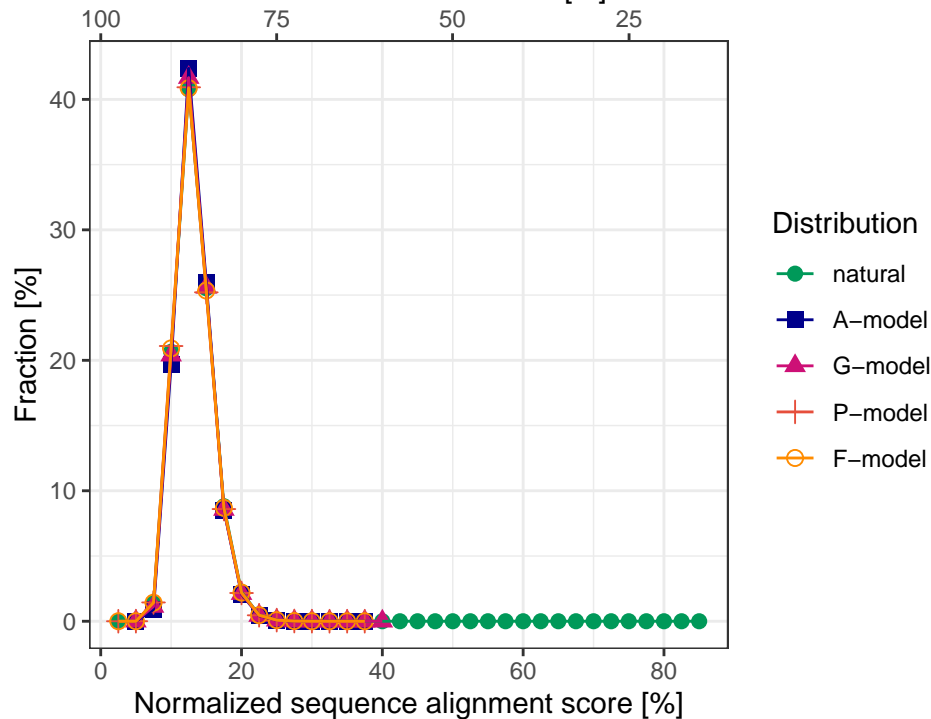
Share of maximal distance [%]





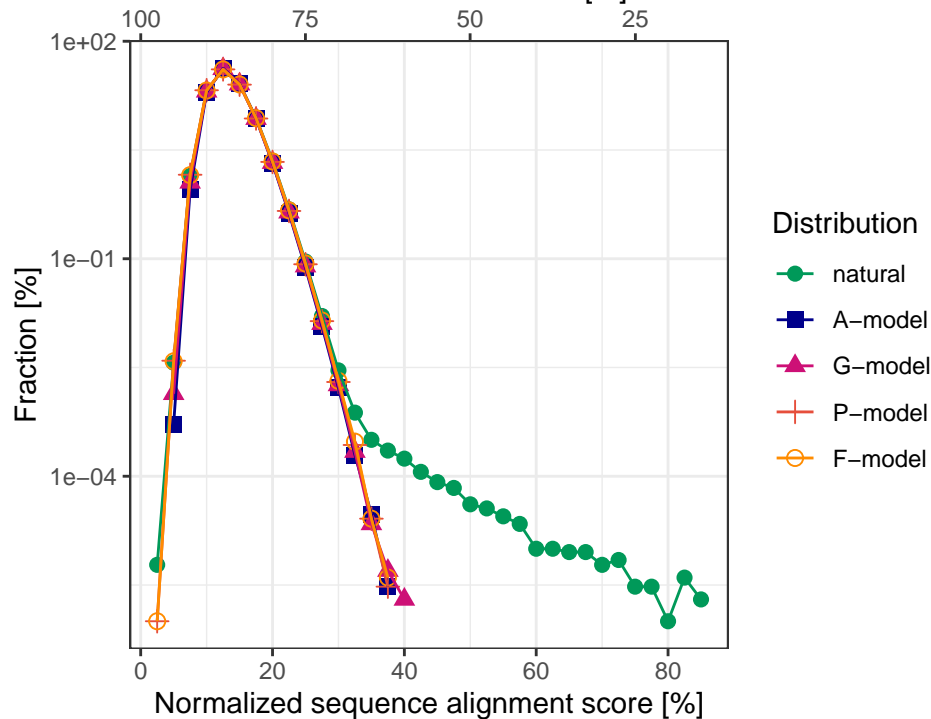
# Distance Distribution of 40mers, Metric=SH

Share of maximal distance [%]



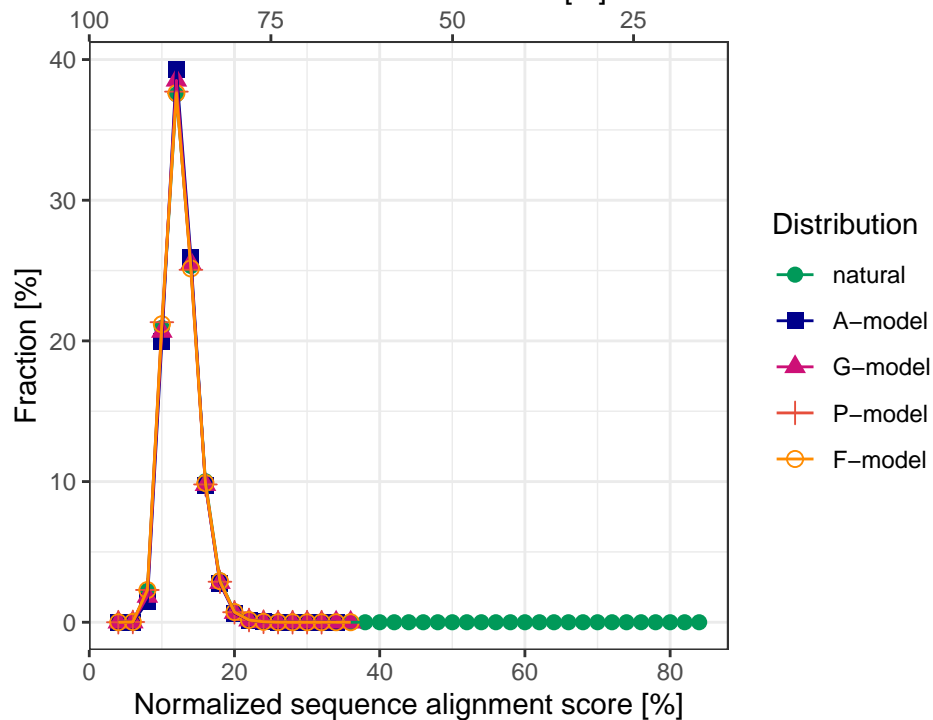
# Distance Distribution of 40mers, Metric=SH

Share of maximal distance [%]



# Distance Distribution of 50mers, Metric=SH

Share of maximal distance [%]



# Distance Distribution of 50mers, Metric=SH

Share of maximal distance [%]

100

75

50

25

1e+01

1e-01

1e-03

1e-05

Fraction [%]

0

20

40

60

80

Normalized sequence alignment score [%]

Distribution

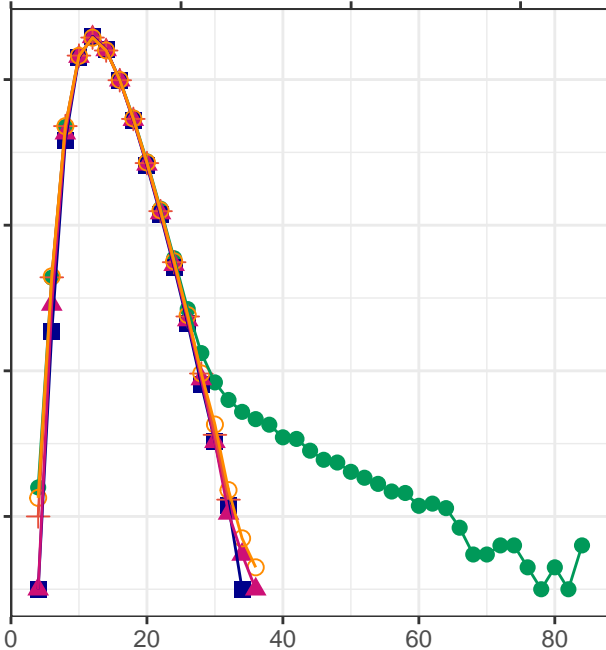
● natural

■ A-model

▲ G-model

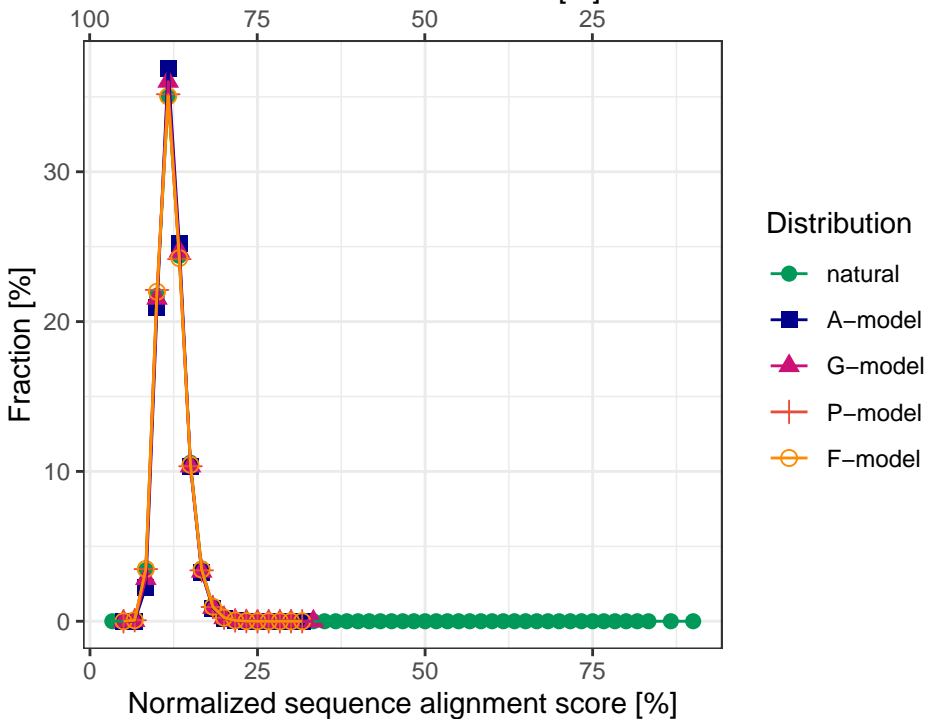
+ P-model

○ F-model



# Distance Distribution of 60mers, Metric=SH

Share of maximal distance [%]



# Distance Distribution of 60mers, Metric=SH

Share of maximal distance [%]

100

75

50

25

1e+01

1e-01

1e-03

1e-05

Fraction [%]

0

25

50

75

Normalized sequence alignment score [%]

Distribution

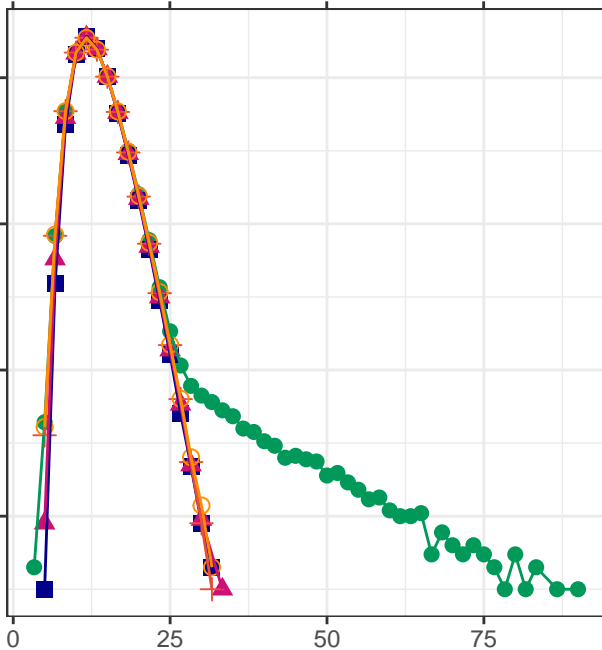
—●— natural

—■— A-model

—▲— G-model

—+— P-model

—○— F-model



# Distance Distribution of 70mers, Metric=SH

Share of maximal distance [%]

100

75

50

25

30

20

10

0

Distribution

—●— natural

—■— A-model

—▲— G-model

—+— P-model

—○— F-model

Fraction [%]

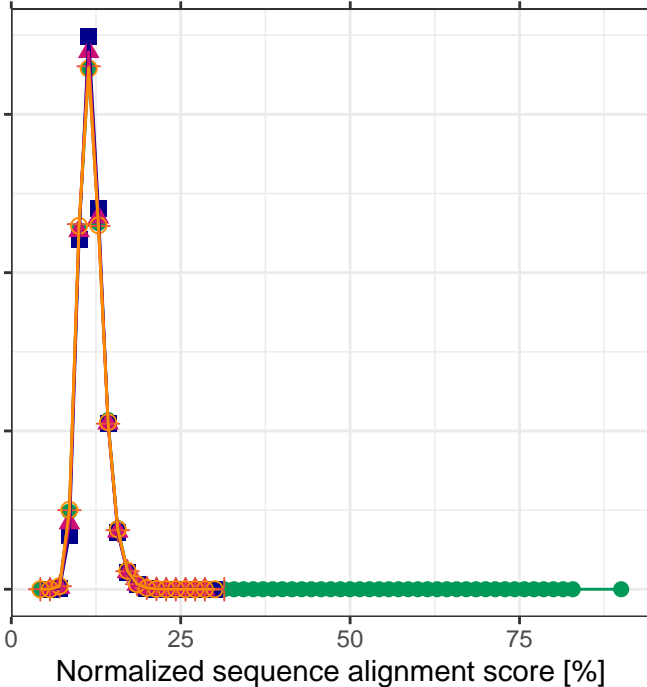
0

25

50

75

Normalized sequence alignment score [%]



# Distance Distribution of 70mers, Metric=SH

Share of maximal distance [%]

100

75

50

25

1e+01

1e-01

1e-03

1e-05

Fraction [%]

0

25

50

75

Normalized sequence alignment score [%]

Distribution

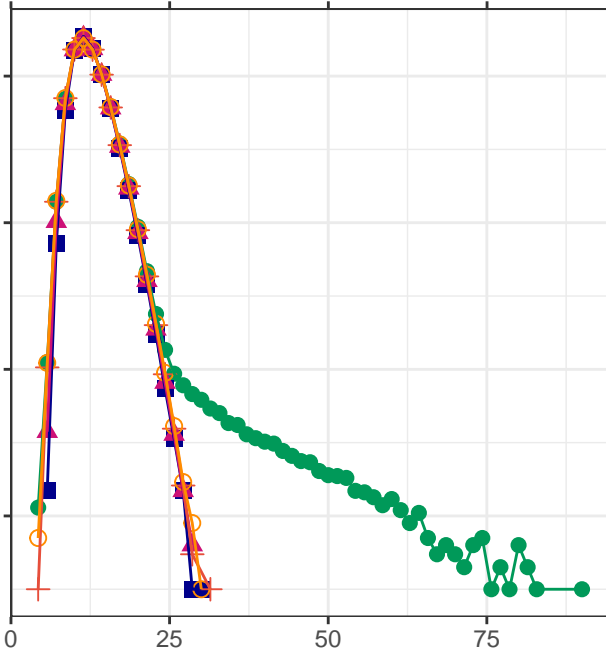
—●— natural

—■— A-model

—▲— G-model

—+— P-model

—○— F-model





# Distance Distribution of 80mers, Metric=SH

Share of maximal distance [%]

100 75 50 25

30

20

10

0

Distribution

—●— natural

—■— A-model

—▲— G-model

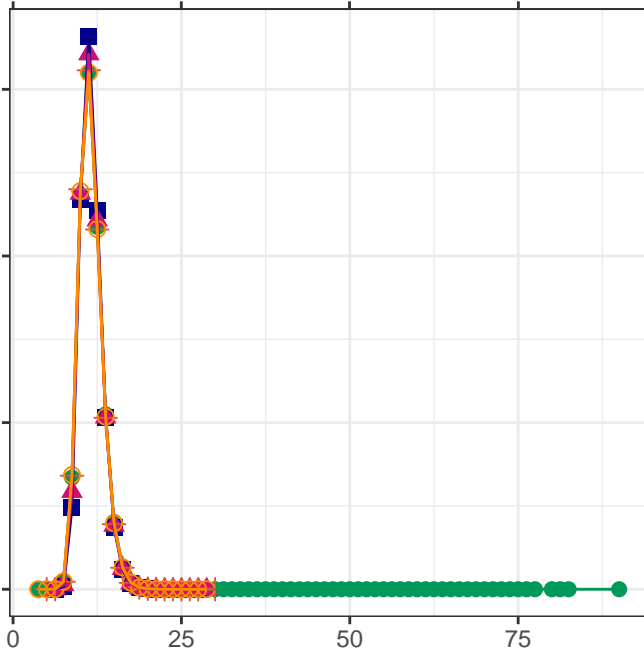
—+— P-model

—○— F-model

Fraction [%]

0 25 50 75

Normalized sequence alignment score [%]



# Distance Distribution of 80mers, Metric=SH

Share of maximal distance [%]

100

75

50

25

1e+01

1e-01

1e-03

1e-05

Distribution

—●— natural

—■— A-model

—▲— G-model

—+— P-model

—○— F-model

Fraction [%]

0

25

50

75

Normalized sequence alignment score [%]

0

25

50

75

0

25

50

75

# Distance Distribution of 90mers, Metric=SH

Share of maximal distance [%]

100 75 50 25

30

Fraction [%]

20

10

0

0 25 50 75

Normalized sequence alignment score [%]

Distribution

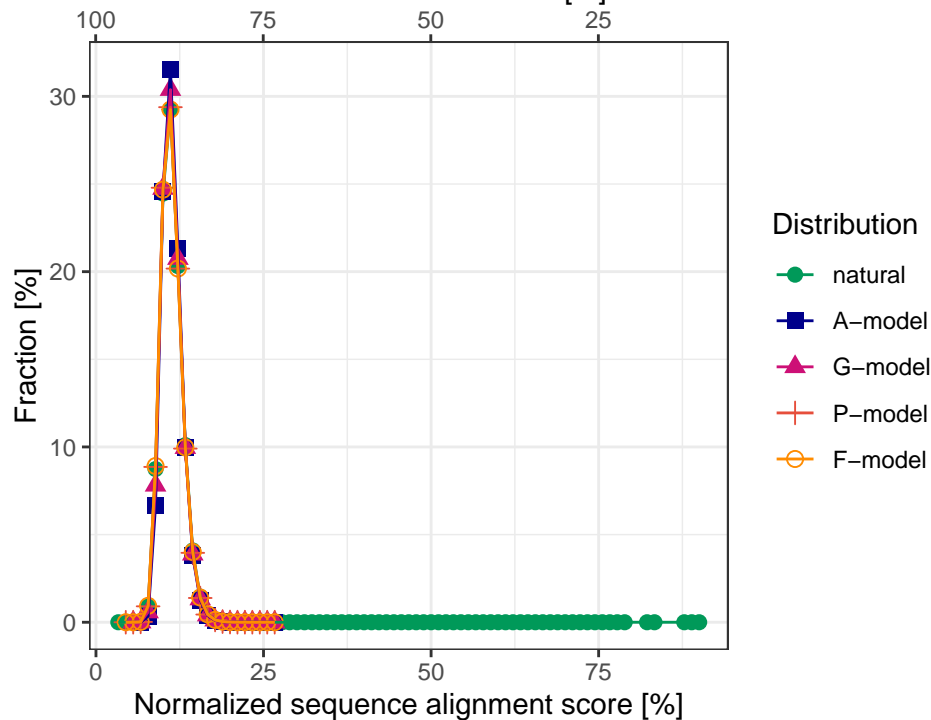
—●— natural

—■— A-model

—▲— G-model

—+— P-model

—○— F-model



# Distance Distribution of 90mers, Metric=SH

Share of maximal distance [%]

100

75

50

25

1e+01

1e-01

1e-03

1e-05

Fraction [%]

0

25

50

75

Normalized sequence alignment score [%]

Distribution

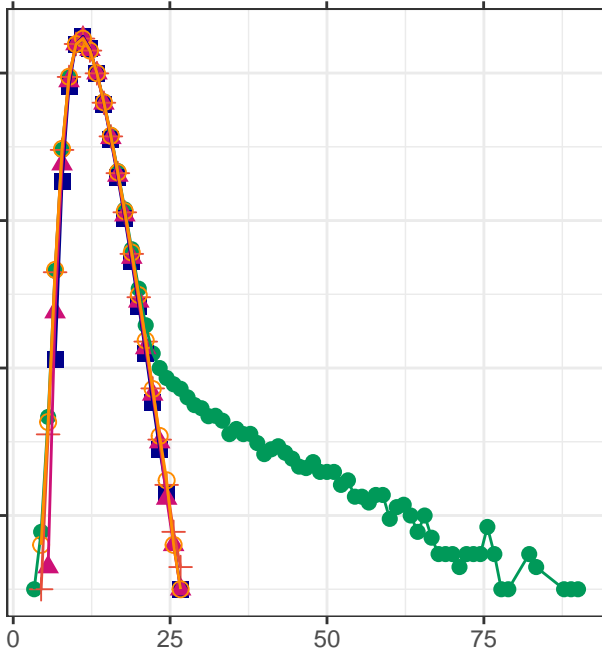
—●— natural

—■— A-model

—▲— G-model

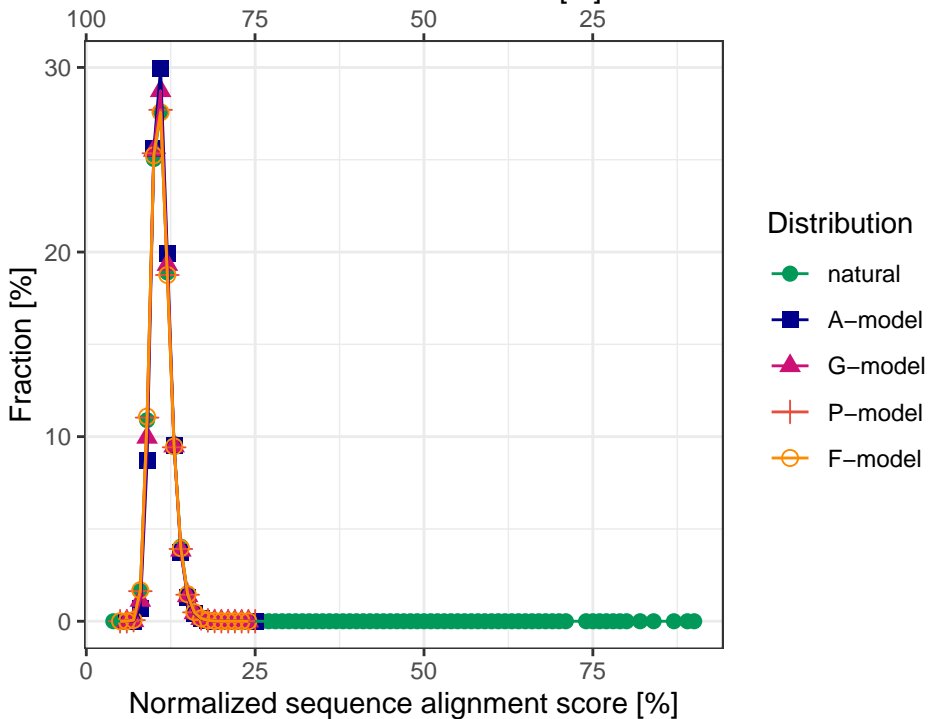
—+— P-model

—○— F-model



# Distance Distribution of 100mers, Metric=SH

Share of maximal distance [%]



# Distance Distribution of 100mers, Metric=SH

Share of maximal distance [%]

100

75

50

25

1e+01

1e-01

1e-03

1e-05

Fraction [%]

0

25

50

75

Normalized sequence alignment score [%]

Distribution

—●— natural

—■— A-model

—▲— G-model

—+— P-model

—○— F-model

