GRIMM - Genome rearrangement algorithms

Source genome:

1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 80 79 78 77 75 74 73 72 71 70 69 68 67 66 65 64 63 42 52 41 62 59 58 57 54 56 55 50 48 47 46 60 61 45 44 51 40 43 49 53 39 38 37 36 35 34 76 33 32 31 30 29 28 27 26 25

Destination genome:

1 2 3 4 5 6 7 8 −9 −10 −11 12 −13 −14 −15 −16 −17 18 −19 −20 21 22 23 24 −25 −26 −27 −28 −29 −30 −31 −32 −33 −34 −35 −36 −37 −38 −39 −40 41 42 −43 −44 −45 −46 −47 −48 −49 −50 51 −52 53 54 −55 −56 −57 −58 −59 60 61 −62 −63 −64 −65 −66 −67 −68

Chromosomes:

○ circular ○ linear (directed) ○ multichromosomal or undirected

Signs:

○ circular ○ linear (directed) ○ multichromosomal or undirected

○ signed ○ unsigned

□ undo □ clear form ○ Or, □ choose sample data ▼

Formatting options

Report Style: One column Two column before & after (chromosomes concatenated) (chromosomes separated) (chromosomes separated) Horizontal Show all chromosomes Vertical Only affected chromosomes Show all possible initial steps of optimal scenarios Should operations (reversal, translocation, fission, fusion) be highlighted, and when? ○ before ○ after ○ between/both ○ no highlighting ○ numeric (10) subscripts (C₁₀) ○ omit Chromosome end format: Genes should be colored according to their chromosome in which genome: Color coding: source education run | undo | clear form Click here or scroll up to enter new data or change options 106 genes Reversal Distance: 22

One optimal reversal scenario

 Step Description

 0 (Source)
 1 2 3 18 4 5

 1 Reversal
 1 2 3 18 4 5

Reversal

20 Reversal21 Reversal22 Reversal

 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 80 79 78 77 75 74 73 72

 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 80 79 78 77 75 74 73 72

 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 80 79 78 77 75 74 73 72

 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 80 79 78 77 75 74 73 72

 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 80 79 78 77 75 74 73 72

 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 80 79 78 77 75 74 73 72

9 -8 -7 -104 -105 106

8 Reversal 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 2
9 Reversal 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 2
10 Reversal 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 2
11 Reversal 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 2

 12
 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 8

 13
 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 8

 14
 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 8

 15
 Reversal
 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 8

GRIMM 2.01 by Glenn Tesler, University of California, San Diego.
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MGR 1.36 by Guillaume Bourque (now moved to McGill).
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