

GRIMM - Genome rearrangement algorithms

Multiple genome form

Source genome:

1231845610310210110099989796959493929190212223248079787775747372717069686766656463425241625958575456555048474660614544514043495339383736353476333231302928272625

Destination genome:

12318456103102101100999897969594939291-28-29-30-31-32-33-76-34-35-36-37-38-39-53-49-43-40-51-44-45-61-60-46-47-48-50-55-56-54-57-58-59-62-41-52-42-63-64-65-66-67-68-69-70-71

Chromosomes:

☒circular☐linear (directed)☐multichromosomal or undirected

Signs:

☒signed☐unsigned

runundo

clear form

Or, 

choose sample data

Formatting options

Report Style:

One line per genome (chromosomes concatenated)

☒Horizontal☐Vertical

One column (chromosomes separated)

☐Yes

Two column before & after (chromosomes separated)

☐Show all chromosomes☐Only affected chromosomes

Show all possible initial steps of optimal scenarios☐

Highlighting style:

Should operations (reversal, translocation, fission, fusion) be highlighted, and when?

☐before☐after☒between/both☐no highlighting

☐numeric (10)☒subscripts (C<sub>10</sub>)☐omit

Chromosome end format:

Color coding:

Genes should be colored according to their chromosome in which genome:

☐source☒destination

runundo

clear form

[Click here or scroll up to enter new data or change options.](#)

106 genes    Reversal Distance: 1

One optimal reversal scenario

Step	Description	
0	(Source)	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 81 82 83 84 85 86 87 88 89 20 19 17 16 15 14 13 12 11 10 9 105 104 7 8 106
1	Reversal (Destination)	1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 -28 -29 -30 -31 -32 -33 -76 -34 -35 -36 -37 -38 -39 -53 -49 -43 -40 -51 -44 -45 -61 -60 -46 -47 -48 -50 -55 -56 -54 -57 -58 -59 -62 -41 -52 -42 -63 -64 -65 -66 -67 -68 -69 -70 -71 -72 -73 -74 -75 -77 -78 -79 -80 -24 -23 -22 -21 -90 27 26 25 81 82 83 84 85 86 87 88 89 20 19 17 16 15 14 13 12 11 10 9 105 104 7 8 106

GRIMM 2.01 by Glenn Tesler, University of California, San Diego.  
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Contains code from [GRAPPA](#), © 2000-2001, The University of New Mexico and The University of Texas at Austin.

MGR 1.36 by Guillaume Bourque (now moved to McGill).  
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