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EVALUATION AND BENCHMARKING OF A NEW SCAFFOLDING METHODOLOGY

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BIOINFORMATICS AND GENOMICS MASTER

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Overview

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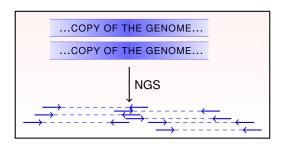
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"The Contig Scaffolding Problem is to order and orientate the given contigs in a manner that is consistent with as many mate-pairs as possible".

Hudson et al. 2002

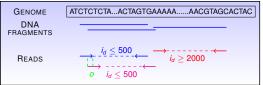
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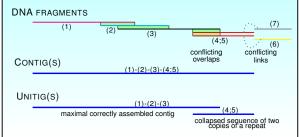
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Genome is fragmented, extremities are sequenced (\mapsto reads) . . .



... reads are assembled though high-confidence overlappings into contigs or unitigs.



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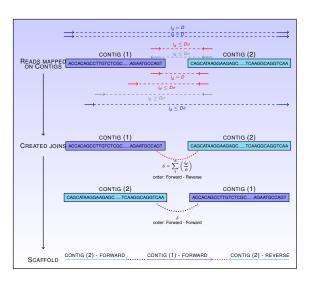
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- uses unitigs instead of contigs to better compute unitig coverage
- uses unitig coverages to duplicated regions
- several models exist, their common point is that for each unitig occurence they create a node
- ... and for each unitig orientation, a different node is yet again created

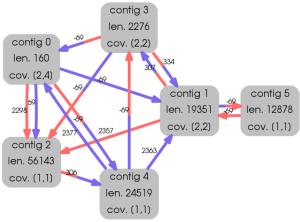
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RAW INPUT DATA OF AGROSTIS STOLONIFERA



Input data of agrostis.txt (1 contig, 1 node)

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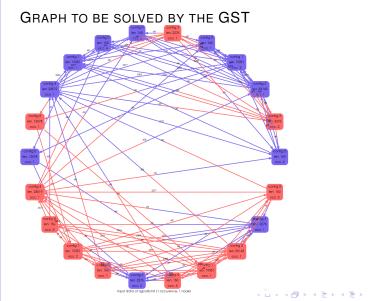
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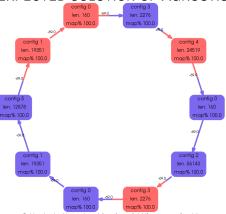
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EXPECTED SOLUTION OF AGROSTIS STOLONIFERA



Golden standard / mapping solution of agrostis.txt (1 occurence, 1 node)

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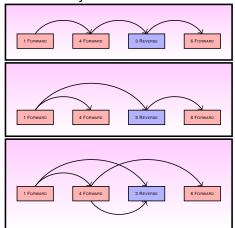
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What would you do in these situations?



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- a script to visualize input data and GST solutions: graph_generator.py
- a script to inspect the features of the modeled input graph: graph_inspector.py
- a script to automatically detect correctly solved instances: graph_comparator.py

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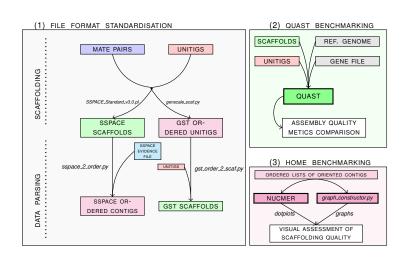
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- Genomes with big repeated regions were solved a lot better than SSPACE
- Small repeats are very challenging to assemble because too many conflicting links exists and GST can not take a decision or is too slow

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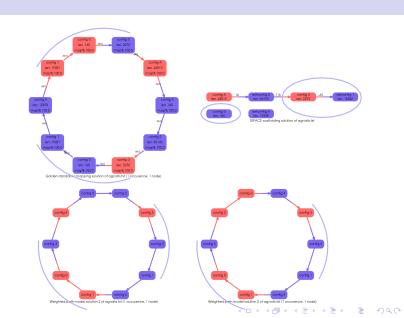
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Scaffolding solutions example: Agrostis



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- Find strategies which solve more challenging data (flow model)
- Scaffold bacterial data
- Test the GST with real data

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Thanks!

The End