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Algorithm

6.1.3 Myers'

bitparallel

algorithm 6.2

Longest common

subsequence

6.2.1 Sparse

dynamic

programming 6.3

Approximate

string matching

6.4 Biological

sequence

alignment 6.4.1

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Global alignment

6.4.2 Local

alignment 6.4.3

Overlap

alignment 6.4.4

Affine gap

scores 6.4.5 The

invariant

technique 6.5

Gene alignment

6.6 Multiple

alignment 6.6.1

Scoring ...

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design is
complicated by
scale; if you
consider the
removal of
protein-coding
genes for
minimal genome
designs using

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brute force and no assumptions, the number of possible genome-scale designs with *M. genitalium*'s 525 genes is 2^{525} . This is infeasible in vivo;

laboratories can only follow a small number of

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- High-quality computational models can investigate many more research avenues and model contextual essentiality, assuming that cellular interactions are ...

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genome design
using models and
algorithms ...*

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researchers in
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scale
sequencing
experiments are
costly and
laborious,
yielding "big

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data" that are conceptually and statistically difficult to analyze. There is no obvious consensus regarding design or analysis. Here we discuss the relevant technical considerations to generate

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reproducible,
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sound, and
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