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presentation of the
fundamental
algorithms and data
structures that power
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foundations of biological sequence analysis (alignments and hidden Markov models), to classical index structures (k-mer indexes, suffix arrays and suffix trees), Burrows-Wheeler indexes, graph algorithms and a number of advanced omics applications.

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to address important
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structures that power
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the removal of protein-coding genes for minimal genome designs using 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

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

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design using models
and algorithms ...

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book that fills a gap in
the recent literature □
[on algorithms] for
bioinformatics. It
offers a sound, clear,
and rich overview of
computer science
methods for the
challenge of today's
biological sequence
analysis. I

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[recommend] it to students as well as to researchers in the field.'

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However, genome-scale experiments are costly and laborious, yielding "big data" that are conceptually and

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statistically difficult to
analyze. There is no
obvious consensus
regarding design or
analysis. Here we
discuss the relevant
technical
considerations to
generate
reproducible,
statistically sound,
and broadly useful
genome-scale data.

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