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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 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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Genome-scale design is complicated by scale; if you consider 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 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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