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A dictionary for genomes

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With sequence information in hand, the search for regulatory sites in promoters can be done by computers rather than cloning. But the primary tools for analysis, [multiple-alignment algorithms](#), can only handle a small amount of sequence data. In the August 29 [Proceedings of the National Academy of Sciences](#), Bussemaker *et al.* introduce an alternative algorithm that they dub 'MobyDick' (*Proc Nat Acad Sci USA* 2000, **97**: 10096-10100). MobyDick treats DNA sequence as text in which all the words have been run together. It attempts to build a dictionary of 'words' by first finding over-represented pairs of letters. Letter frequency is used to determine the probability that the pairs exist thanks to chance, and this helps determine how larger fragments continue to be built. Bussemaker *et al.* test their algorithm on a space-less version of the first ten chapters of the novel *Moby Dick*, then attack a list of all of the upstream regions in the yeast genome. For yeast, approximately 500 dictionary entries fall above a plausible significance level, including 114 of the 443 [experimentally confirmed](#) sites, and good matches to approximately half of the motifs found in previous analyses of [co-regulated genes](#), the [cell cycle](#), and [sporulation](#).

References

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