An efficient manual method for aligning DNA restriction map data on very large genomic restriction maps

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Recently, low and high resolution restriction maps of the entire E. coli chromosome were constructed (1,2). This allows rapid physical mapping of genes on the chromosome. Efficient use of the high resolution restriction map awaits the availability of computerized version of the genomic map and a method for aligning restriction map data on it. Here, we describe a simple and efficient method for manually aligning such data.

The high resolution physical map of E. coli (2) contains restriction map data for 8 enzymes. The graphical representation resembles a music score, parallel lines for each enzyme with vertical bars indicating cut sites. The restriction map data of the gene to be mapped should be graphically represented on a transparent film, exactly to the same format and scale. Physical mapping of a gene simply requires sliding the transparent film over the genomic restriction map. Inspection of the superimposed restriction maps easily reveals alignment (see Figure) and hence, the location of the gene on the chromosome. Visual alignment does not require precise restriction map alignment. The advantage of this method is that it allows an approximate pattern match to be recognized, and this may handle ambiguities arising from process in data or unanticipated genetic rearrangements. Recently, this method was applied to physically mapping the skp gene (3) encoding a 17 K DNA binding protein (4).

It is not necessary to scan the entire genomic map if candidate regions have been preliminarily identified. For instance, candidate regions may be identified by localization to a NotI fragment (1) by hybridization experiments, by a simple visual search for a distinctive restriction pattern (i.e. a large EcoRI restriction fragment) or by genetic mapping data. This method could form the basis for an algorithm for computer alignment.

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