`Dotlet`: a Java applet for sequence comparisons using the dot matrix method

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Abstract

`Dotlet` is a Java applet that allows the user to compare two biomolecular sequences by producing diagonal plots using the dot matrix method[1]. Although similar programs already exist, they are limited to a few operating systems or components of software packages; moreover they often have a command-line interface. By contrast, our teaching needs required a stand-alone, GUI-based program that could be run on any platform. The closest match to these needs is Sonnhammer *et al.*'s `dotter`[2], but to our knowledge it runs under XWindow only. Like `dotter` by which it was inspired, `dotlet` is fully interactive, mouse- and menu-driven, and runs in any web browser that supports Java. It features protein, nucleic acid, and mixed comparisons; several built-in substitution matrices; and a range of scoring window sizes. Sequence similarities are represented by shades of grey on a scale that can be tuned in real time. A cursor allows the examination of local alignments of the sequences at the residue level. The scores of all points in the plot are presented as a frequency histogram, which helps in the tuning of the grey scale.

References

[1] A J Gibbs and G A McIntyre. The diagram, a method for comparing sequences. *European Journal of Biochemistry*, 16:1–11, 1970.

[2] E L L Sonnhammer and Richard Durbin. A dot-matrix program with dynamic threshold control suited for genomic dna and protein sequence analysis. *Gene*, 167(2):GC1–10, 1995.