

SUPPLEMENTAL MATERIAL 5

for the paper “Quality estimation of multiple sequence alignments by Bayesian hypothesis testing”

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Table 1. Methods for the statistical estimation of short ungapped alignments and their running time (L-length of alignment, M-size of the lattice).

Method	Running time
NC-naïve method (Hertz and Stormo, 1999)	$O(L^2M^2)$
LD method (Hertz and Stormo, 1999)	$O(LM\log(LM))$
sFFT (Keich, 2005)	$O(LM\log(LM))$
csFFT (Nagarajan, et al., 2005)	$O(\sqrt{LM} \log(\sqrt{LM}))$

References

- Hertz, G.Z. and Stormo, G.D. (1999) Identifying DNA and protein patterns with statistically significant alignments of multiple sequences, *Bioinformatics*, **15**, 563-577.
- Keich, U. (2005) sFFT: a faster accurate computation of the p-value of the entropy score, *J Comput Biol*, **12**, 416-430.
- Nagarajan, N., Jones, N. and Keich, U. (2005) Computing the P-value of the information content from an alignment of multiple sequences, *Bioinformatics*, **21 Suppl 1**, i311-318.