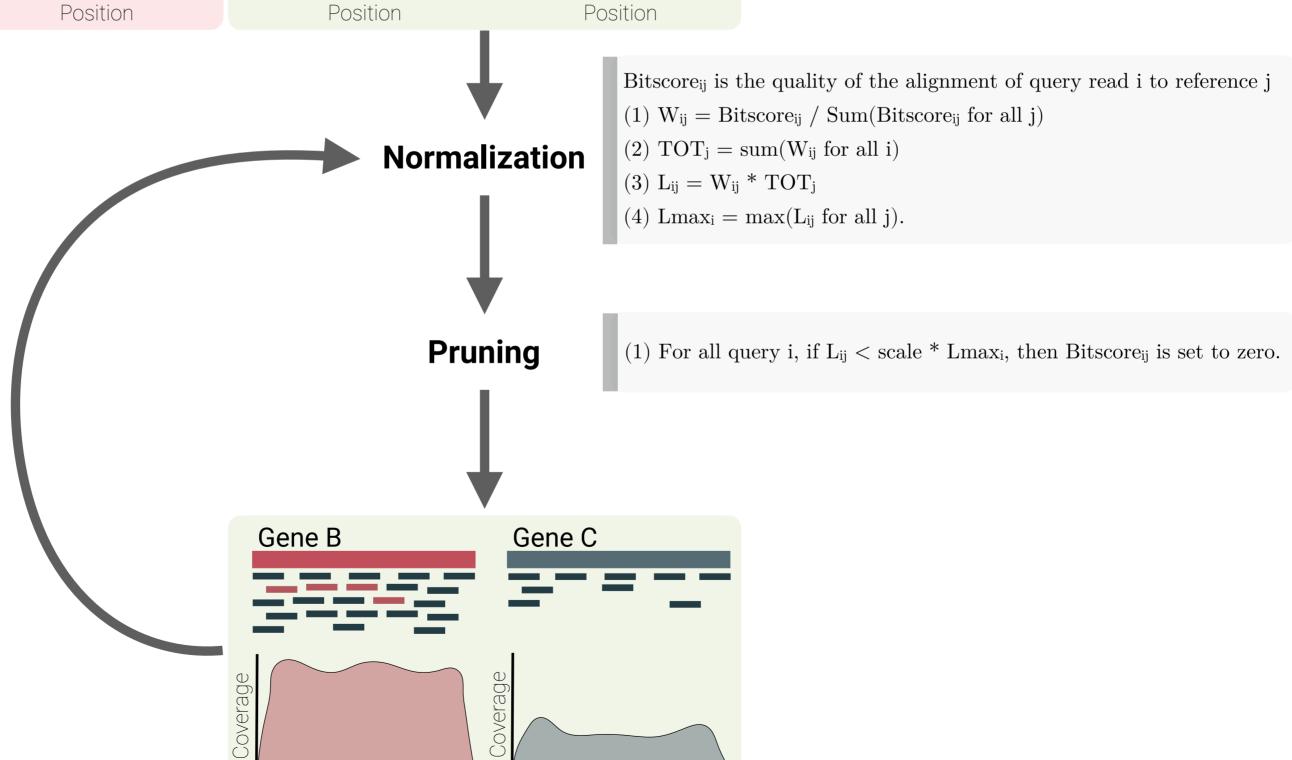In silico benchmarking of metagenomic tools for coding sequence detection reveals the limits of sensitivity and precision

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Bitscore$_{ij}$ is the quality of the alignment of query read i to reference j

(1) $W_{ij} = Bitscore_{ij} / Sum(Bitscore_{ij}$ for all j)

(2) $TOT_j = sum(W_{ij}$ for all i)

(3) $L_{ij} = W_{ij} * TOT_j$

(4) $Lmax_i = max(L_{ij}$ for all j).

(1) For all query i, if $L_{ij} < scale * Lmax_i$, then $Bitscore_{ij}$ is set to zero.