$S \leftarrow \text{divide all of the DNA sequences in the input database into } \alpha\text{-patterns}$

$\sigma_l' \leftarrow \text{construct an index of } 4^\alpha \text{ entries with the } \alpha\text{-patterns in } S \text{ as index keys}$

\text{if the number of available processors } > 1 \text{ then}

$L \leftarrow \text{generate a processing order list of all of the entries in } \sigma_l'$ by the PEL heuristic

\text{else}

$L \leftarrow \text{construct a processing order list of all of the entries in } \sigma_l'$ in an arbitrary order

\text{end if}

\text{for an entry } E \text{ in } L \text{ do}

assign an available processor to handle $E$

$K_P \leftarrow \text{the entry key of } E$

\text{for a candidate pattern } P \text{ in } E \text{ do}

\text{for an entry } E' \text{ whose key is } (\alpha, \beta)\text{-mismatched to } K_P \text{ do}

\text{compare } P \text{ to all of the patterns in } E'

\text{if } P \text{ is } (l', d')\text{-mismatched to any of the compared patterns then}

\text{discard } P

\text{end if}

\text{end for}

\text{end for}

\text{end for}

mark the remaining candidate patterns as the signatures of $(l', d')$