

/******ASSUMPTION*****

Query sequence length $\rightarrow qlen$, aligned to 8 bytes and padded with dummy residues;
Subject sequence length $\rightarrow dblen$, aligned to 8 bytes and padded with dummy residues;

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for ($i = 1; i \leq qlen; i += 8$) {

 Initialize all the relevant variables;

 for ($j = 1; j \leq dblen; j += 4$) {

 Load the packed 4 residues between j and $j + 3$ from texture memory to shared memory;

 for ($k = 0; k < 4; k++$) {

 Get the $(j + k)$ -th residue of the subject sequence from shared memory;

 Load H and E values of the cell $(i - 1, j + k)$ from global memory;

 Load substitution scores for cells from i to $i + 3$ from the query profile;

 Compute the H , E and F values of the cells from $(i, j + k)$ to $(i + 3, j + k)$;
 and calculate the maximum score;

 Load substitution scores for cells from $i + 4$ to $i + 7$ from the query profile;

 Compute the H , E and F values of the cells from $(i + 4, j + k)$ to $(i + 7, j + k)$;
 and calculate the maximum score;

 Save H and E values of the cell $(i + 7, j + k)$ from global memory;

 }

}

}