

In our red blood cell simulation, at any time step there is a computation stage involving a series of matrix-matrix multiplications. Let  $p$  denote the independent size variable,  $N$  the number of RBC's, and let  $A^i (i = 0, \dots, p)$ ,  $B$ , and  $C$  denote the matrices involved. Matrices  $A^i$  are fixed, while the matrix  $B$  is the position of RBC's that changes between time steps. Letting  $M := 2p(p+1)$ , then we have  $A^i \in \mathbb{R}^{M \times M}$ ,  $B, C \in \mathbb{R}^{M \times N}$ . The pseudocode for that portion of the code would be

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for  $i = 0$  to  $p$  do
  for  $j = 0$  to  $2p - 1$  do
     $A^{i,j} \leftarrow$  permute  $A^i$  {The permutation formula is given below}
     $C \leftarrow A^{i,j} B$ 
    //Perform some processing on C
  end for
end for

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The permutation step mentioned in the pseudocode involves exchanging columns of  $A^i$ . For any fixed  $j$  ( $j = 0, \dots, 2p - 1$ ) it is defined as

$$A^{i,j}(n, m) = A^i \left( n, \left\lfloor \frac{m}{2p} \right\rfloor + m \bmod 2p - j \right),$$

where we used Matlab's notation for indexing. It is understood that  $m \bmod 2p - j$  is to be positive and between 0 and  $2p - 1$ . When negative it is shifted by  $2p$ .