CELL PROLIFERATION STUDY: A NEW COMPUTATIONAL MODEL SOLVED BY THE SPH METHOD

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Introduction

When cell damage occurs cells tend to proliferate in order to replace the damaged ones [3, 4]. During this process, cells grow and divide into two new genetically identical cells [1, 2]. This is a well-organized process that is still not entirely understood due to its complexity. In the last years, computational models have started to be applied in the study of cell proliferation since they offer attractive advantages for biomedical research. Among them, less time and cost expenditure can be highlighted [5]. To solve these models, numerical methods are usually proposed and several examples can be found in the literature. The Smoothed Particle Hydrodynamics (SPH) method is a discrete meshless method and one of the most commonly used [6]. In this work, a new 3D non-linear algorithm to simulate cell proliferation was developed. The SPH and the Navier-Stokes equations were used and both the growth and division of single and multiple cells was considered. The viability of the algorithm was tested and further calibrated. Analyses of volume growth and evolution of the diameter, volume and form of the clusters were done.

Methods

The SPH discretizes the problem domain without pre-connected particles. Using these particles, an integral representation is obtained to find the approximation functions and to approximate the field function. With these functions and with the Navier-Stokes equations, particle approximation is done [6].

To initiate the algorithm, initial input data is needed. From this, particle discretization is done and three types of particles are created (cell, extracellular matrix and boundary). One cell is placed in the middle of the domain, and after that, for all particles, the initial velocity, internal pressure and acceleration are calculated. When all this is achieved, the cell starts to grow and divides when its initial volume doubles. The division creates a new particle/cell in the domain that also grows and divides, repeating the previous process. Throughout the iterations, the new positions of the particles are updated resorting to the kernel functions obtained in each one.

Results

For this work, 20 simulations were done in order to verify the reproducibility and viability of the algorithm. In all of them, 7 cell divisions were considered, as well as the evolution of the volume along the iterations, from the first individual cell to the last division. Also, as the number of cells increased, the total form, volume and diameter of the cluster of cells was considered and compared between all simulations since a random parameter was defined in the algorithm. When one cell was analysed, a linear volume growth was obtained until the cell doubled its initial volume. At this point, the division occurred. The simulations started with one cell and then an exponential growth in the number of cells along the division was visible. With the evolution of the number of cells, different clusters were formed but, in all simulations, the results were quite similar in terms of form, diameter and volume.

Discussion

In this work, the process of cell proliferation for a single cell and for groups of cells was simulated with the created algorithm. However, it is important to stress that the development of the algorithm is still in the beginning. Thus, several improvements can be done in future work in order to improve it and obtain more realistic simulations. In spite of that, even in the initial phase, the results were quite satisfactory. All simulations generated coherent results between them and followed what is described in the literature. This suggests that, in the future, this algorithm can be an efficient numerical tool to simulate the process of cell proliferation.

References

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