DIFFUSION KURTOSIS IMAGING: MONTE CARLO SIMULATION OF DIFFUSION PROCESSES USING CROWDPROCESS

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KEYWORDS: *Diffusion kurtosis imaging, Simulation of diffusion processes, Distributed computing.*

ABSTRACT: Being sensitive to the heterogeneity of biological tissues, Diffusion Kurtosis imaging (DKI) quantifies the non-gaussianity of water diffusion [1]. The sensitivity of the diffusion kurtosis model in varying microstructural environments can be studied by using Monte-Carlo (MC) simulations [2], which being computationally expensive, can be better applied using parallel computing.

For the purpose of demonstrating the advantages of simulating diffusion processes in distributed computing, in this study, we focused only on the correlation between diffusion kurtosis (K) and the intracellular volume fraction (V). A comparison is made between processing in a common laptop CPU, and in CrowdProcess, a new method of distributed computing [3]. A MC diffusion simulation was implemented in *nodejs*, based on the methods used by C-Y Lee et al. [2] and using an Intel i3-4010U processor (experiment 1). The intracellular volume fraction was varied between 0.1 and 0.8 in 14 steps, and cell configurations were designed randomly using a gamma distribution of the cell radii, with a mean of 10 um and a standard deviation of 7 um. In our study 1,000,000 random walkers performed a walk of 0.0263 s. Intracellular and extracellular diffusion coefficients were set to $1.0x10^{-3}$ mm^2/s and $2.5x10^{-3}$ mm^2/s, respectively. The membrane permeability was set to 0.01 mm/s. The same experiment was performed 10,000 times simultaneously in CrowdProcess with 1,000 random walkers, but corresponding to a 10-fold increase in the total number of random walkers (experiment 2).

The results for each value of V were then averaged. Fig 1A and 1B show the generated cell configurations corresponding to V values of 0.1 and 0.8, respectively. Fig. 1C and 1D show that in both experiments the expected results were obtained: a negative correlation between the mean diffusion coefficient D and V; and regarding K a positive correlation with V is observed for $V<0.65$, a maximum for K at $V=0.65$ and a negative correlation for $V>0.65$. Whilst the first experiment took 45 minutes to run, the second took only 18 seconds (150x faster) and had more sensitivity to the heterogeneity of cell environments, which explains why the kurtosis curve in the second experiment was 'smoother'.

CrowdProcess has proved to be extremely fast compared to the traditional method, bringing higher precision without the time-consuming cost. In the future we want to apply this method to study the correlation between K and other microstructural parameters with different coefficients of intracellular and extracellular diffusion. With the generalization of this kind of approach we expect research in this area to become increasingly improved.

Acknowledgements: This study was financed by Fundação para a Ciência e Tecnologia (FCT) under the grant PTDC/SAU-ENB/120718/2010. The authors thank the technical support from João Menano and colleagues from CrowdProcess.

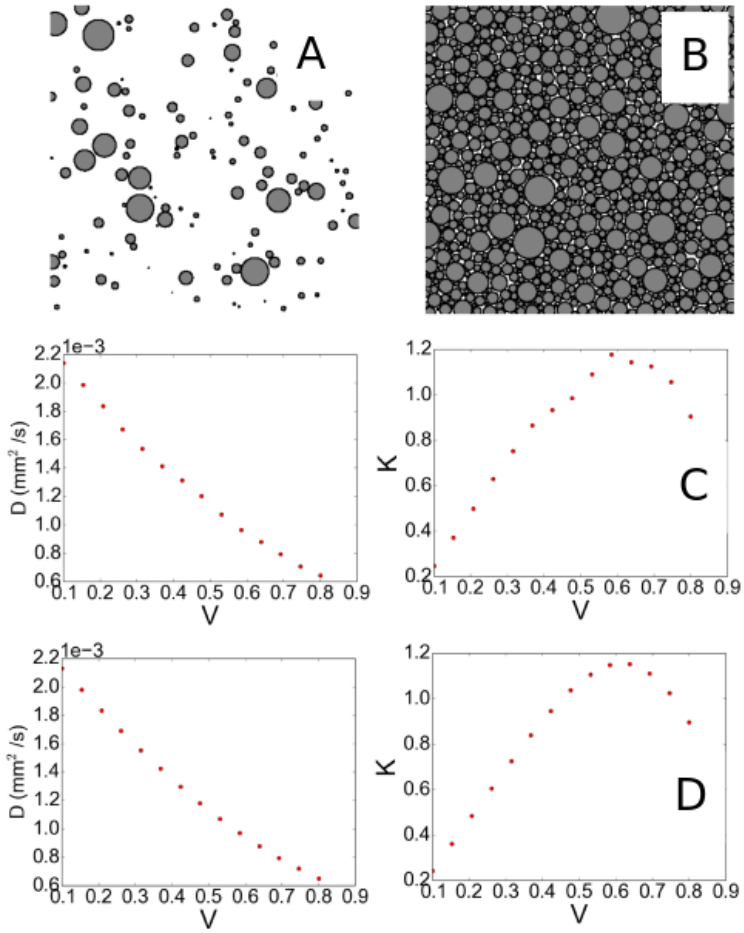

Fig. 1 A, B: Cell configurations corresponding to V values of 0.1 and 0.8, respectively. C: Results for experiment 1. D: Results for experiment 2.

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