The University of York   Department of Computer Science

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Parallel Programming Tools for Exploring Immune System Development

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Abstract

More powerful computers are paving the way for realistic simulations of previously underexplored biological systems. As advancements in computing tend increasingly towards parallelism and distributed systems, these ever more complex simulations must take full advantage of this change in order to be computed in a reasonable time. In this project, we will explore some of the current technologies for doing so and develop new tools for the future.

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1 Introduction

1.1 Project Overview

This project has been carried out with regard to the set of ethical guidelines set out by the University of York. This project does not involve human participants, so guidelines on informed consent and confidentiality will be met. The simulation of the biological model is for the purpose of developing understanding of applying GPGPU methods to an agent based model. It will not be used to publish results, in its current form and does not simulate a biological process.

1.2 Ethics

Lorem ipsum dolor

1.3 Report Structure

Lorem ipsum dolor.

2 Literature Review

Simulation becoming more and more prevalent: tools need developing to allow less technical users to create these sims easier and run faster...[1] Original PPSim[2] Kieran Machine Learning Custom Code?[3] model based -> FlameGPU[4]

Flame is a start..

3 The Experiment

3.1 The Domain Model

3.2 The Platform Model

4 Results and Evaluation

4.1 Findings

4.2 Conclusion

4.3 Further Work

Bibliography

[1]   D. Noble, 'The rise of computational biology', *Nature Reviews Molecular Cell Biology*, vol. 3, pp. 459–463, 2002. DOI: 10.1038/nrm810.

[2]   K. J. Alden, 'Simulation and statistical techniques to explore lymphoid tissue organogenesis', PhD thesis, University of York, Heslington, York, 2012.

[3]   P. Drew, 'Parallel programming tools for exploring immune system development', Master's thesis, University of York, Heslington, York, 2017.

[4]   P. Richmond, D. Walker, S. Coakley and D. Romano, 'High performance cellular level agent-based simulation with flame for the gpu', *Briefings in Bioinformatics*, vol. 11, no. 3, pp. 334–347, 2010. DOI: 10.1093/bib/bbp073.

5 Appendix

5.1 Simulation Parameters

5.2 Cell Data Structures