



A GPU Reaction Diffusion Soil-Microbial Model

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Parallelised algorithms are frequent in bioinformatics as a consequence of the close link to informatics – however in the field of soil science and ecology they are less prevalent. A current challenge in soil ecology is to link habitat structure to microbial dynamics. Soil science is therefore entering the ‘big data’ paradigm as a consequence of integrating data pertinent to the physical soil environment obtained via imaging and theoretical models describing growth and development of microbial dynamics permitting accurate analyses of spatio-temporal properties of different soil microenvironments. The microenvironment is often captured by 3D imaging (CT tomography) which yields large datasets and when used in computational studies the physical sizes of the samples that are amenable to computation are less than 1 cm³. Today’s commodity graphics cards are programmable and possess a data parallel architecture that in many cases is capable of out-performing the CPU in terms of computational rates. The programmable aspect is achieved via a low-level parallel programming language (CUDA, OpenCL and DirectX). We ported a Soil-Microbial Model onto the GPU using the DirectX Compute API. We noted a significant computational speed up as well as an increase in the physical size that can be simulated. Some of the drawbacks of such an approach were concerned with numerical precision and the steep learning curve associated with GPGPU technologies.