Simulation with 1.5M cores enable near real-time electrophysiological heart models

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Tissue-level models of cardiac electrophysiology are reaction-diffusion systems that require the solution of partial differential equations. The reaction component arises from the excitable cardiac cells that depolarize on each heartbeat. The cardiac cells are described by state variables and non-linear ordinary differential equations that simulate ionic channels and exchangers, cellular signaling and track ion concentrations. The diffusion component arises from electrical propagation from cell to cell via gap junctions. Diffusion is computed with the standard monodomain formalism and includes anisotropic conduction that results from the fiber structure of the heart (conduction is faster in the direction versus transverse to fibers). Single cell cardiac models have been developed since the 1960s, but simulation of tissues with large numbers of cells only became feasible in the 1990s with the advent of multiprocessor computers. While computing capabilities have increased tremendously since then, simulation of whole hearts at cellular spatial resolution remains a challenge to the field with execution rates that are thousands of times slower than real time. To further the state of the art, IBM Research and Lawrence Livermore National Laboratory collaborated to develop a highly optimized code to take advantage of Sequoia, a 96 rack Blue Gene/Q installation comprising 1,572,864 cores, with a combined peak speed of 20 PFLOP/s. A heart model with 370 M cells with near cellular spatial resolution can now be simulated in only 3.3 sec, over 1200x faster than previously possible. The talk will discuss how the code was optimized to make best use of the hardware at different levels of parallelism. As one example, the 16 cores in each computational node were divided between reaction and diffusion tasks. Sample results will be shown for scientific studies that were enabled by the newly develop capabilities.