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Accelerated Simulation of Biological Neural Networks

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After many years of research in neuroscience, the manifestation of intelligence in spiking neurons remains a puzzle. Computational neuroscience has the potential to uncover the underlying principles but is burdened by the computational complexity of executing biological neural network simulations of sufficient size and realism.

Varying efforts have addressed the challenge of acceleration applying software as well as hardware design optimizations. Thereby a classic gap opens between the flexibility and usability of a platform versus the performance it provides.

In 2018, we had the opportunity to take a fresh look at the challenge at hand assessing existing system solutions as well as gained knowledge in the domain of neuroscience. It quickly became clear, that any platform to be successful has to combine all three aspects: the usability for neuroscientist, flexibility to accommodate new models and insights as well as sufficient computing performance to handle reasonably large networks as well as to provide insights into slow plasticity processes.

In this talk, I will review key requirements put on such a system from a neuroscience but also from an engineering perspective. Thereby a focus is put on the three key bottlenecks: communication, data access as well as numeric updates of the model equations. Next, follows a discussion on the potential of existing architectural concepts to address these. Finally, the real-world neuroAIx FPGA-cluster with its 20x speed-up is juxtaposed to its blue-print promising a 100x acceleration.

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References

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