

Computational principles of biological memory

Memories are stored and retained through complex, coupled processes operating on multiple timescales. To understand the computational principles behind these intricate networks of interactions, we construct a broad class of synaptic models that efficiently harness biological complexity to preserve numerous memories by protecting them against the adverse effects of overwriting. The memory capacity scales almost linearly with the number of synapses, which is a substantial improvement over the square root scaling of previous models. This was achieved by combining multiple dynamical processes that initially store memories in fast variables and then progressively transfer them to slower variables. Notably, the interactions between fast and slow variables are bidirectional. The proposed models are robust to parameter perturbations and can explain several properties of biological memory, including delayed expression of synaptic modifications, metaplasticity, and spacing effects. Work done in collaboration with M.K. Benna.