A computational model of fast associative learning in the honeybee

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Numerous experimental studies on classical conditioning in the honeybee *Apis mellifera* have provided insights into the physiological processes of olfactory learning and memory formation. On the basis of these findings, several theoretical studies have proposed different model hypotheses for sensory processing and learning in the insect brain. However, the actual dynamics of associative learning as evident from behavior in individual animals is typically neglected. For the honeybee, recent analyses suggest that individual animals learn to associate between odor and sugar reward typically within a single trial and subsequently show a stable conditioned response during training and memory retention (Pamir et al. 2011, Learning & memory).
Here, we present a computational model approach at the spiking neuronal network level which allows us to mimic a number of different experimental protocols during classical conditioning of the proboscis extension response in the honeybee. We implement and compare different hypotheses on physiological mechanisms that support fast associative learning by evaluating their ability to reproduce both behavioral and physiological constraints as observed in experiments. The behavioral constraints of our model are defined by the learning performance of individual animals during various conditioning paradigms (e.g. absolute, differential, backward, delay, trace and massed conditioning, negative patterning). Physiological constraints comprise recordings of neuronal activity from different processing stages along the sensory-to-motor pathway.