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Conférence Générale

16h30 – 17h15

Computational significance of differentiating CA1 from CA3

The CA3 and CA1 fields of the mammalian hippocampus are strikingly different in their network architecture: massively recurrent the former, essentially feed-forward the latter. The functional significance of this structural differentiation is not clear, in that neural activity in the two fields shows qualitatively similar features, and computational models generally succeed in mimicking hippocampal functions even when equipped with the architecture of CA3 alone. To assess the possibility that the functional advantage of the differentiation may be merely quantitative, I have proposed a simulation approach that quantitatively compares the performance of a differentiated with a uniform network model, both comprised of the same number of units and connections. The approach has been initially applied to test the hypothesis that the specific contribution of CA1 is in storing associations across time, but simulations demonstrated a very small quantitative advantage of the differentiation in that case.
Recent experiments in the Moser lab in Trondheim have discovered instead a striking functional difference between CA3 and CA1 activity patterns: multiple environments with overlapping features are represented by distinct ensembles in CA3, whereas ensembles in CA1 show a correspondingly graded overlap (Leutgeb et al, Science 2004). These rat recordings indicate that CA3 sets up a new, arbitrarily assigned representation to any distinguishable environment, whereas CA1, although able to access the CA3 representation when needed, by default tends to reflect the non-orthogonalized entorhinal inputs.
Given that the necessity of the CA1 stage is logically not apparent, we have extended the simulation approach to again assess the quantitative effect of the differentiation per se, decoupled from the predictable advantage of merely adding more computing resources to an existing CA3 network model.

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