

W10-03

## METHODOLOGY OF MAPPING IN INTEGRATIVE MOLECULAR BIOLOGY

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Psychiatric illnesses remain of unclear etiopathogenesis and a variety of them can coexist, partly mimicking each other while contributing to and distorting symptomatic expressions. To understand the processes involved, it is necessary to unravel signalling pathways, complex interaction networks and metabolic alterations involving a plethora of anatomical components. Hence, whatever the nature of the alterations convincingly detected, these must be associated with their most-likely cellular contexts to then have a chance to reverse engineer the events that could have given rise to the observed alterations and predict their most plausible functional consequences. This requires the utilisation of analytical approaches collectively known as “Systems Biology”.

Systems biology explores how parts of biological entities function and interact to give rise to the behaviour of the system as a whole. But having said that, what can we actually do?

Two broad approaches to systems biology currently exist: the frequently followed mathematical (Bayesian) procedures and the more rarely encountered heuristic approaches.

Heuristic modelling plays the role of an architect (defines the nature, the structure, the functionalities and the contextual constraints of a process) while mathematical modelling plays the role of an engineer (reveals the dynamics and robustness of this process while defining the set of parameters sufficient to give rise to similar or very different phenotypes).

This talk will explain, through concrete examples, the approaches whereby one can harness heuristic frameworks to produce multi-level models of complex neurobiological processes that can then be independently tested and biologically validated or refuted.