**Executable Knowledge: the KAMI project**

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The study of cellular signalling pathways and their deregulation in disease states is a large and extremely complex task. Indeed, these systems involve many parts and processes but are studied piecewise and their literatures and data are consequently fragmented, distributed and sometimes---at least apparently---inconsistent. This makes it extremely difficult to build significant explanatory models with the result that effects in these systems that are brought about by many interacting factors are poorly understood.

The rule-based approach to modelling, exemplified by the Kappa and BNGL languages, has shown some promise for the representation of the highly combinatorial systems typically found in signalling where many of the proteins are composed of multiple binding domains, capable of simultaneous interactions, and/or peptide motifs controlled by post-translational modifications. However, the rule-based approach requires highly detailed information about the precise conditions for each and every interaction which is rarely available from any one single source. Rather, these conditions must be painstakingly inferred and curated, by hand, from information contained in many papers and/or databases---each of which contains only part of the story.

We introduce KAMI, a new rule-based meta-modelling tool attuned to the representation of cellular signalling networks, which allows for the flexible representation of knowledge at various levels of granularity. In particular, it allows us to deal with information which has either too little, or too much, detail with respect to Kappa (or BNGL). Our approach provides a basis for the gradual aggregation of fragmented biological knowledge extracted from the literature which can serve as a resource in its own right -- but from which we can also define an automated translation into executable Kappa models which can be further subjected to simulation and other analyses.