Biocuration and rule-based modelling of protein interaction networks in KAMI.

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KAMI, the Knowledge Aggregator and Model Instantiator, is a software for biocuration and modelling of molecular interaction networks. It provides a knowledge representation to unambiguously express the details of biomolecular interactions. This representation can be built either programmatically or graphically via the KamiStudio interface. To assist users in curating their biological knowledge, KAMI is organised in two distinct layers: a network and a set of individual interactions called nuggets. Once a new nugget is built, it can be automatically aggregated to the network. The software then performs a series of tests to ensure consistency including duplicate search, biological database grounding and semantic checking. This greatly facilitates biocuration as users do not need to have the complete network in mind to add new data. Furthermore, interaction networks represented in KAMI can be directly converted to rule-based models in the Kappa language for simulation and analysis. In this talk, we will present the use of KAMI through a model of tyrosine phosphorylation involved in cell signaling. This example is well suited to showcase the advantages of the rule-based strategy. In particular, we will demonstrate the use of causality analysis to discover pathways in the model that were not explicitly input by the user.