INOH: Pathways and Ontologies

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1 Introduction

INOH[1] is a signal transduction pathway database based on manual curation. Pathways are represented in the form of a hierarchical graph called “Compound Graph”. Every pathway object such as physical-entity or biological-event is annotated by a set of bio-ontologies.

While conventional pathway data are highly structured, they use open vocabularies to name a pathway object. As this hampers data integration or mapping between data from different sources, we propose to use a set of annotation ontologies for pathway data annotation. For example, protein objects are annotated by the MoleculeRole ontology[2] and biological process objects are annotated by the Event ontology[3]. The MoleculeRole ontology captures the relations among molecule function names, generic molecule names, concrete molecule names, sequence accession numbers and complexes and their subunits. The Event Ontology manages the relation between pathways and sub-pathways and biological events of molecular, cellular and organism levels. These ontologies can be obtained from http://www.inoh.org/. Consequently, INOH provides high-quality pathway data that allow advanced ontological searches, thereby improving accuracy by extending the search range using ontological trees. Table 1 shows the list of pathways curated in the INOH project. The current INOH data release includes 1116 interactions, 1441 biological events, 7619 pysical-entities.

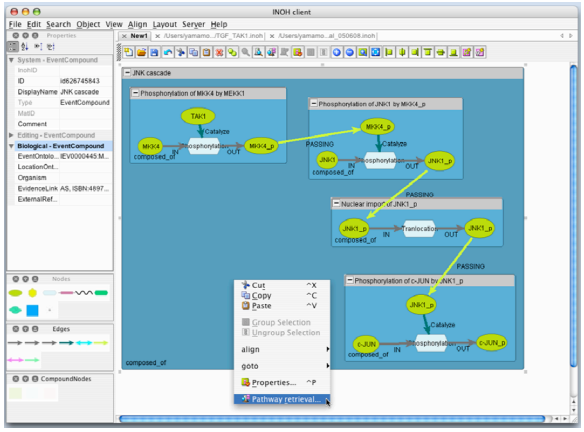

Figure 1 : INOH editing window

pathway	
Nitric oxide signaling pathway	B cell receptor signaling pathway
Glutamate receptor signaling pathway	cell cycle regulation pathway
PPAR signaling	Wnt signaling pathway
Steroid receptor signaling pathway	Notch signaling pathway
Heterotrimeric GPCR signaling pathway	HedgeHog signaling pathway
RTK signaling pathway	circadian rhythm
JAK-STAT pathway	Small GTPase mediated signaling
TGF beta signaling pathway	MAPK cascade
IL-1 signaling pathway	cAMP mediated signaling
TNFR signaling pathway	AKT signaling
Toll-like receptor signaling	PLC signaling
Insulin receptor signaling pathway	p53 signaling pathway
Integrin signaling pathway	Caspase cascade
T cell receptor signaling pathway	

Table 1: INOH pathway list

2 IOH Client

The “INOH Client” is a JAVA based platform independent graphical pathway navigation/editor tool to edit and search pathways in the INOH database. This tool provides automatic layout function of compound graph pathways. A user can search pathways, pathway objects by specifying a molecule name or a biological process name. Besides, he/she can query previous/next events, molecular variations or homologues of an event via the pathway retrieval utility (Figure 2). Downloaded pathways can be then modified and saved.

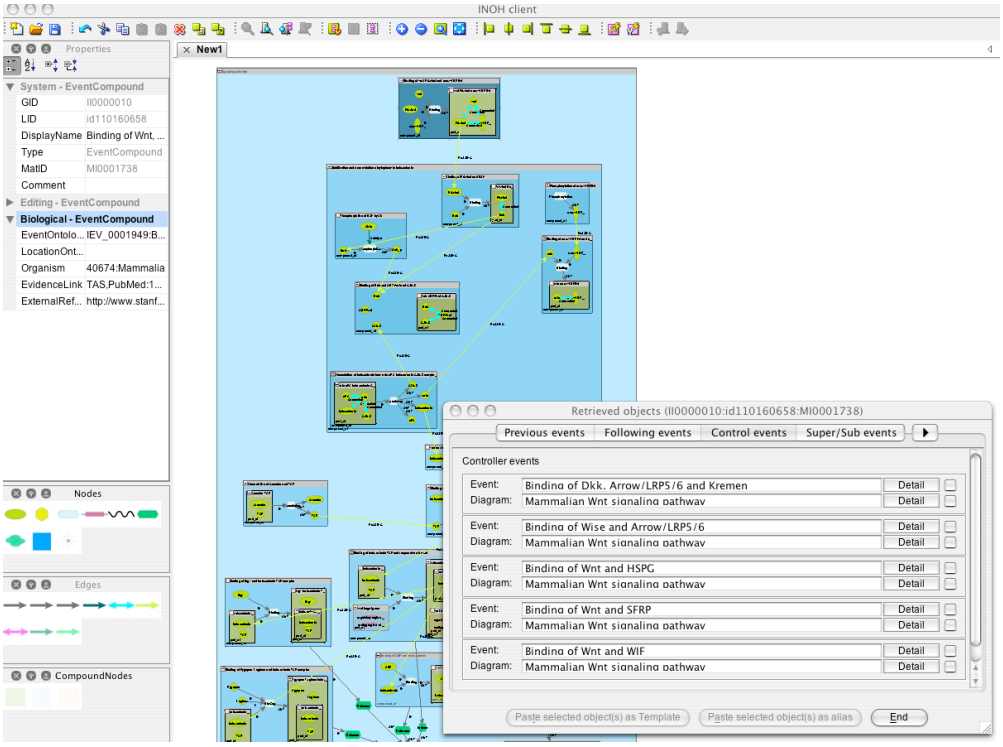

Figure 2: INOH search window

Acknowledgments

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