

INOH: A Pathway Database of Biological Events

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1 Introduction

INOH[1] is a pathway database of model organisms including human, mouse, rat and others. In INOH, the term pathway refers to higher order functional knowledge such as relationships among multiple bio-molecules that constitute signal transduction pathways or biological events in general. As most part of this knowledge resides in the scientific literature, the database focuses on encoding text based knowledge into a machine-processable form. The system contains a number of unique features to encode this type of knowledge. Biological terms such as protein names typically represent abstract, conceptual molecules that are used for unspecified organisms. Biologists interpret the name as a specific instance of protein using background knowledge. For example, the term "MAP-kinase" indicates ERK1 of a human, JNK1 of a mouse, p38alpha of a rat, etc. To encode background knowledge, the INOH database provides a set of bio-ontologies such as "Molecule Role Ontology", "Biological Event Ontology". Each of these ontologies annotates a certain class of objects appearing in each pathway and sub-pathway. These annotations render computers capable of computing pathway knowledge.

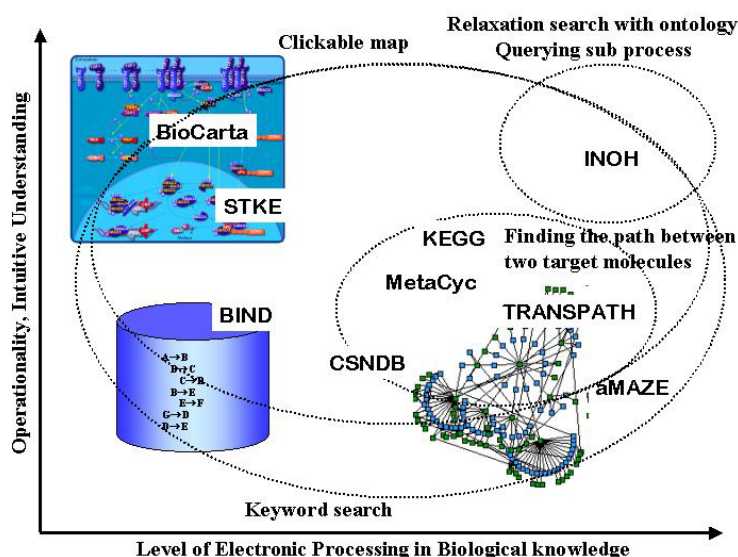


Figure 1: Position Chart of INOH and other Pathway Databases

2 Contents and Systems

2.1 Ontology

The MoleculeRole ontology[2] captures the relations among (1) molecule function names (e.g. protein serine / threonine kinase) (2) abstract molecule names (e.g. R-smad), (3)concrete molecule names (e.g. Smad2 of human), (4) sequence accession numbers and (5) complexes and their subunits.

The Biological Event Ontology manages the relation between pathways and sub-pathways and biological events of molecular, cellular and organism levels. This Ontology root has two subclasses “Environmental event” and “Biological Event”. “Environmental event” includes subclasses such as “Treatment” and “Medium”. “Biological Event” has three subclasses, “Molecular event”, “Cellular event”, and “Organism event”.

2.2 The INOH Applications

In order to process pathways annotated with rigid classification systems of many biological concepts related to signal transduction knowledge in the literature, we use a compound graph expression [3]. The “INOH Curation Tool” is a graphical pathway navigation tool to edit and search pathways or ontologies in the INOH database (Figure 2). This tool provides automatic layouting of compound graph pathways.

INOH ontology can be accessed through the web application, called Ontology Viewer[4]. Ontology Viewer allows the user to search the ontology by names, synonyms, and ontology IDs (Figure 3).

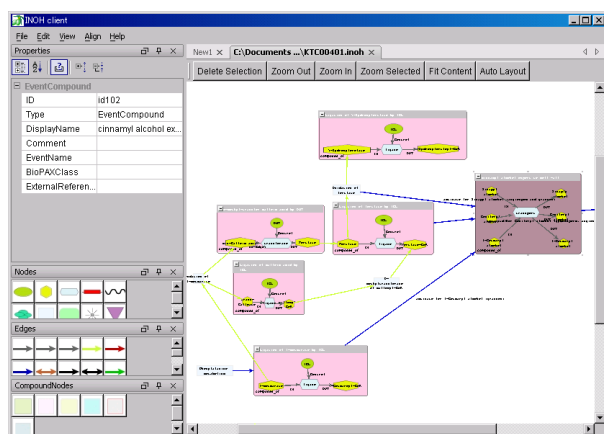


Figure 2: The INOH Curation Tool

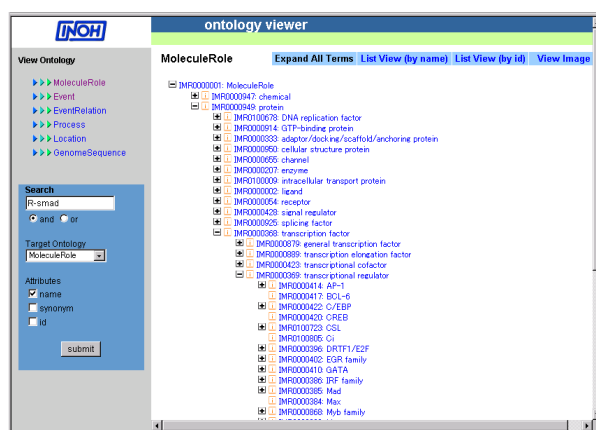


Figure 3: The Ontology Viewer

Acknowledgments

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References

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