INOH Pathway Database

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1 Introduction

INOH[1, 2] is a manually curated database of signal transduction pathways and it provides pathway knowledge that resides in the scientific literature in a machine-accessible form. To make the background knowledge that biologists use to interpret pathway descriptions available to computers, every pathway component in INOH is annotated by a biological ontology. The MoleculeRole ontology[3] and the Event ontology[4] are uniquely-developed in INOH, because there is no standard ontology for pathway data annotation.

A user can view INOH pathway data as diagrams with our pathway editor “INOH client” and INOH ontology data with our ontology browser “INOH Ontology Viewer” [5]. The INOH client is a graphical pathway navigation tool to edit and search pathways in the INOH database. The INOH Ontology Viewer allows the user to search the ontology by names, synonyms, and ontology IDs of INOH, UniProt, KEGG, GO, and SO.

These ontologies and 62 signal transduction pathway diagrams (including over 1,566 interactions and 8,660 protein entities) (Table 1) are freely available at http://www.inoh.org/. INOH pathway data are downloadable in INOH XML format and BioPAX level 2 format. BioPAX format is a common exchange format developed to share biological pathway data between different databases and we are working as member of the BioPAX working group [6].

<table>
<thead>
<tr>
<th>Pathway Description</th>
<th>Annotation</th>
</tr>
</thead>
<tbody>
<tr>
<td>B cell receptor signaling</td>
<td>GPCR signaling (mitogen-activated protein kinase)</td>
</tr>
<tr>
<td>BMP2 signaling (through TAK1)</td>
<td>Growth hormone signaling (G protein-coupled receptor)</td>
</tr>
<tr>
<td>BMP2 signaling (through TGF-beta signaling MolecularVariation)</td>
<td>BMP signaling pathway</td>
</tr>
<tr>
<td>CD4 T cell receptor signaling (JNK cascade)</td>
<td>TNF signaling pathway</td>
</tr>
<tr>
<td>CD4 T cell receptor signaling (NF-kB cascade)</td>
<td>TNF signaling pathway</td>
</tr>
<tr>
<td>Drosophila IMD pathway</td>
<td>TNF signaling pathway</td>
</tr>
<tr>
<td>Drosophila Toll-like receptor signaling</td>
<td>TNF signaling pathway</td>
</tr>
<tr>
<td>EGF signaling pathway</td>
<td>TNF signaling pathway</td>
</tr>
<tr>
<td>FGF signaling pathway</td>
<td>TNF signaling pathway</td>
</tr>
<tr>
<td>GPCR signaling (cholera toxin)</td>
<td>TNF signaling pathway</td>
</tr>
<tr>
<td>GPCR signaling (G alpha q)</td>
<td>TNF signaling pathway</td>
</tr>
<tr>
<td>GPCR signaling (G alpha s, Epac and ERK)</td>
<td>TNF signaling pathway</td>
</tr>
<tr>
<td>GPCR signaling (G alpha s, PKA and ERK)</td>
<td>TNF signaling pathway</td>
</tr>
</tbody>
</table>
| Table 1. List of curated pathways

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2 INOH pathway data in BioPAX level 2 and level 3

BioPAX level 2 covers metabolic pathways, molecular interaction etc., and in addition level 3 will cover signaling pathways and gene regulation. Since INOH database deals mainly with signaling pathway data, they can be represented more correctly in level 3 than in level 2. For instance, the transcription and translation processes in INOH are mapped to the class Conversion in BioPAX level 2, but they are mapped to the new class TemplateReaction with more suitable properties in level 3. And the new class BindingFeature and ModificationFeature express molecular states in INOH in detail. BindingFeature can specify the binding domains of two entities in a complex that are bound to each other. A phosphorylated protein is mapped to the class Protein, and the property “feature” point to the class ModificationFeature whose property “modificationType” is assigned “phosphorylated”. BioPAX level 3 format is under consideration, but will be released soon.

3 New features in INOH client and INOH Ontology Viewer

Now, three new features are added to INOH client; 1) the reduced view that focused on molecular transition in the normal view (Figure 1), and these modes can be easily switched back and forth, 2) magnifier view and overhead view, 3) pathway search function that find similar pathways across organisms using hierarchical tree structure in the INOH ontology. And a user can access INOH client through INOH Ontology Viewer. By clicking the icon near the ontology term, INOH client under Java Web Start start and search the diagram contains the term.

Figure 1. INOH client normal view and reduced view

Acknowledgments

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References