NCBO Extraction tool version 1.1

i2b2 Sponsored Project - Extraction Tool 1.1

The i2b2 Hive software is composed of core modules called 'cells' that create a system to allow the use of patient data for research. These cells communicate through web services and use i2b2 standard XML messages to transfer ontology-related metadata. To date, a subset of ICD-9 has been provided with the i2b2 demo software package. There has been a need in the community for access to a complete ICD-9 ontology as well as other clinical-based ontologies.

NCBO hosts a repository of biomedical ontologies. These ontologies are stored in formats that are not understood by i2b2. A tool has been developed to not only extract these ontologies via bioportal REST services, but to transform them into a format that is understood by the i2b2 ONT cell.

New Features

Users can specify an optional time-out parameter in the Extraction step.

The default NCBO REST timeout is set to 300 seconds. Users may now set the timeout to a setting of their choice.

Users can specify a single root node in the Process step.

Often the data extracted from NCBO will have several root nodes. If desired, users can specify a single root node name for the final table.

Tooltip generation has been redesigned and now allows multi-line tooltips.

Tutorials

NCBO_Extraction_Overview Step by step example of how metadata trees are created and configured using the NCBO Extraction tool.

NCBO_Extraction_Users_Guide_1-1 Users Guide for version 1.1 of the NCBO Extraction tool

Release 1.1 Software

NCBO Extraction Tool 1.1 package Software package for version 1.1 of the command-line based NCBO metadata extraction tool