

# 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 biportal 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