Function “findRxcuiByld”

RxNorm SOAP API

findRxcuiByld( idType, id, allSourcesFlag )

Search for an identifier from another vocabulary and return the RxCUIs of any concepts which have an RxNorm term as a synonym or have that identifier as an attribute.

Input:

idType - the identifier type. See the getIdTypes example for the valid types. This parameter defines the types:

<table>
<thead>
<tr>
<th>idType</th>
<th>Example Id</th>
<th>Details</th>
</tr>
</thead>
<tbody>
<tr>
<td>AMPID</td>
<td>2050</td>
<td>the Gold Standard Drug Identifier from Gold Standard Drug Database (SAB:GS)</td>
</tr>
<tr>
<td>ANDA</td>
<td>ANDA007581</td>
<td>the FDA Abbreviated New Drug Application identifier</td>
</tr>
<tr>
<td>ATC</td>
<td>M02AA01</td>
<td>the Anatomical Therapeutic Chemical (ATC) identifier</td>
</tr>
<tr>
<td>GCN_SEQNO</td>
<td>009172</td>
<td>the Generic Code Sequence Number from First Databank Inc (SAB:NDDF)</td>
</tr>
<tr>
<td>GFC</td>
<td>108077</td>
<td>the Generic Formula Code (GFC) from Micromedex RED BOOK (SAB:MMX)</td>
</tr>
</tbody>
</table>
| GPCR         | 44550      | the first five characters of the Generic Product Packaging Code from Master Drug Data Bank (SAB:MRDB) Multi-dose divisions of Watson Healthcare Lister Hill National Center for Biomedical Communications
Function “findRxcuiById”

- **Input 1**: 
  - Types: function, workflow_element
  - Same Individual As
  - Different Individuals
- **Input 2**: 
  - has_input2 ID
  - has_input3 flag
  - has_output RXCUI
  - has_input id_string
  - has_input flag
  - has_input1 id_string
  - has_input ID
  - provided_by RxNorm_API
- **Input 3**: 
  - Negative object property assertions
  - Negative data property assertions
- **Source**: 
  - Provided by RxNorm_API
- **Output**: 
  - Provided by RxNorm_API
Function “getRelatedByType”

RxNorm SOAP API

getRelatedByType( rxcui, type-list )

Get the related RxNorm identifiers of an RxNorm concept specified one or more term types. See default paths for the paths traveled to get concepts for each term type.

Input:

rxcui - the RxNorm identifier

type-list - an array of one or more RxNorm term types. Valid RxNorm term types are list in the getTermTypes example.

Output:

an array of RxNorm concept group structures. An RxNorm concept group structure has the following fields:
• Type - the RxNorm term type
• Array of RxNorm concept structures. See getRxConceptProperties for the description of the RxNorm concept structure.

Example:
Function “getRelatedByType”

input 1

input 2

output
Rules of interoperability

❖ Main rule – If the input of B matches the output of A, then A is potentially interoperable with B

❖ Additional rules
  • Interoperability between generic IDs and specific IDs in the input or output of functions

❖ Example
  • A: `rxnorm:findRxcuiById` has_output RxCUI
  • B: `rxnorm:getRelatedByType` has_input RxCUI
  • input of B matches the output of A
    => `rxnorm:getRelatedByType` interoperable_with `rxnorm:findRxcuiById`
findRxcuiById → getRelatedByType
The OWL ontology supports the interoperability rules

Interoperability relations inferred from the rules support the determination of interoperability for a given pair of functions

The ontology and the interoperability relations drive

- The validation of workflows
- The graphical interface for creating workflows
  - Only allowable functions are proposed in the menu
Production rules (SWRL)

If the input of c matches the output of a
Then c interoperable with a (i.e., c can follow a)
Implementation

- Rules applied through a reasoner in Protégé
  - HermIT
- Inferred properties added to the knowledge base
  - Interoperable_with properties
Properties before/after applying rules

Property assertions: findRx cuisByld

Object property assertions
- has_input2 ID
- has_input3 flag
- has_output RXCUI
- has_input id_string
- has_input flag
- has_input1 id_string
- has_input ID
- provided_by RxNorm API

Data property assertions

Negative object property assertions

Interoperable with getUNII
Interoperable with getQuantity
Interoperable with getRxTermDisplayName
Interoperable with getSplSetId
Interoperable with findConceptsById
Interoperable with has_input3 flag
Interoperable with getAllProperties
Interoperable with getRxConceptProperties
Interoperable with getRelatedByRelationship
Interoperable with getRx cuiStatus
Interoperable with getNDCs
Interoperable with getRelatedByType
has_output RXCUI
RxMix demo

Olivier Bodenreider
“Real-life” use case

- Find all the NDC codes for a given allergy class (e.g., barbiturates)
  - Input: [NDF-RT] Barbiturates (N0000008016)
  - Output: [RxNorm] list of NDC codes

- Complex workflow

```
findConceptsByName getRel.ConceptsByRev.Role findRxcuiById getRelatedByType getNDCs
```

<table>
<thead>
<tr>
<th>name</th>
<th>NDF-RT ID (chem. ingr.)</th>
<th>NDF-RT ID (drug/ingr.)</th>
<th>RxNorm ID (ingredient)</th>
<th>RxNorm ID (SCD/SBD)</th>
<th>NDC code</th>
</tr>
</thead>
<tbody>
<tr>
<td>Barbiturates</td>
<td>N0000008016</td>
<td>N0000005827</td>
<td>719</td>
<td>201628</td>
<td>42998030301</td>
</tr>
<tr>
<td></td>
<td>Barbiturates</td>
<td>Amobarbital</td>
<td>Amobarbital</td>
<td>Amytal Sodium</td>
<td>[…]</td>
</tr>
</tbody>
</table>
<pre><code>                      |                         | […]                   |                        | 100 MG/ML Injectable Solution | […]      |
</code></pre>

[http://mor.nlm.nih.gov/RxMix/]
RxMix is an interface for building applications that allows users to combine functions of the RxNorm, RxTerms, NDF-RT, and RxImageAccess APIs. It allows users to run either interactively or in batch mode.

Sample RxMix configurations

- Find drug interaction brands for Morphine (RXCUI = 7052)
- Find allergy drugs for Proton Pump Inhibitors (NUI = N0000000147)

APIs

- RxNorm
- NDF-RT
- RxTerms
- RxImageAccess

References

<table>
<thead>
<tr>
<th>TAG</th>
<th>DEFINITION</th>
</tr>
</thead>
<tbody>
<tr>
<td>acqDate</td>
<td>The physical sample acquisition date</td>
</tr>
<tr>
<td>allSourcesFlag</td>
<td>0=only return an RXCUI if it contains an RXNORM vocabulary term. 1=return any RXCUI which has a match</td>
</tr>
<tr>
<td>AMPID</td>
<td>The Gold Standard Drug Identifier from Gold Standard Drug Database (SABGS)</td>
</tr>
<tr>
<td>ANDA</td>
<td>The FDA Abbreviated New Drug Application identifier</td>
</tr>
<tr>
<td>association_type</td>
<td>Values: Heading_Mapped_To, Ingredient_1, Ingredient_2, Product_Component</td>
</tr>
<tr>
<td>classId</td>
<td>The source identifier of the drug class.</td>
</tr>
</tbody>
</table>
name → NDF-RT ID (chem. ingr.) → NDF-RT ID (drug/ingr.) → RxNorm ID (ingredient) → RxNorm ID (SCD/SBD) → NDC code
Complete workflow
Add input and run (interactively)

**Basic Instructions**
1. BUILD workflow using Select Function, then Add to Workflow (or select a button in LOAD section to load a workflow)
2. Enter INPUT value for interactive mode (or input file name for batch mode)
3. Select OUTPUT fields and output format
4. EXECUTE by pressing Run/Submit button

**Output Format**
- TABLE
- XML
- JSON
- TEXT

**Input**
- name: barbiturates
Over 1000 NDCs retrieved

<table>
<thead>
<tr>
<th>NDC</th>
</tr>
</thead>
<tbody>
<tr>
<td>00179003680</td>
</tr>
<tr>
<td>13925015816</td>
</tr>
<tr>
<td>21695035116</td>
</tr>
<tr>
<td>21695050416</td>
</tr>
<tr>
<td>21695097016</td>
</tr>
<tr>
<td>33358004604</td>
</tr>
<tr>
<td>42192052016</td>
</tr>
<tr>
<td>5295927403</td>
</tr>
<tr>
<td>5295927406</td>
</tr>
<tr>
<td>5295927430</td>
</tr>
<tr>
<td>54868208700</td>
</tr>
<tr>
<td>54868208701</td>
</tr>
<tr>
<td>55045132409</td>
</tr>
<tr>
<td>63629135602</td>
</tr>
<tr>
<td>63874072412</td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td>00143114010</td>
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<tr>
<td>00143114051</td>
</tr>
<tr>
<td>00440718320</td>
</tr>
<tr>
<td>10544057220</td>
</tr>
<tr>
<td>10544057230</td>
</tr>
<tr>
<td>13338000060</td>
</tr>
<tr>
<td>16590029030</td>
</tr>
<tr>
<td>21695099010</td>
</tr>
</tbody>
</table>
Script of the demo

- RxMix overview
  - documentation is integrated
- Objective:
  - Find all the NDC codes for a given allergy class (e.g., barbiturates)
- Build a workflow
  - [at first, all functions are available]
  1) NDF-RT: findConceptsByName
     - select INGREDIENT_KIND
     - [show output in mouse over]
     - [show that only the functions compatible with the output are listed]
  2) NDF-RT: getRelatedConceptsByReverseRole
     - role_type = has_ingredient
     - transitive = 1
     - [show access to the documentation]
     - [show that the parameter passed between functions is listed]
     - [cross over to RxNorm]
  3) RxNorm: findRxciuByld
     - [NUI is already preselected -- only element from the output to match the input]
  4) RxNorm: getRelatedByType
     - click SCD
     - ctrl-click SBD
  5) RxNorm: getNDCs
- [look at the complete workflow]
- Input value: barbiturates
- Execute workflow: Run
  - takes about 10 seconds
- Output
  - over 1000 NDCs
- Can save the workflow for reuse
- Can run any workflow on a list of input values (batch mode)
- Library of workflows
  - Find the National Drug Codes (NDCs) for clinical drugs of an ingredient
  - fairly close to what we did