Transcript: Mapping NDC, RXCUI, and Drug Names in the RxNorm Files

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Welcome. This is a quick guide on how to get a National Drug Code, or NDC-RXCUI-Drug Name map using the RxNorm data files.

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First, I'll review the RxNorm data files. Then, I'll walk through a database query to get an NDC-RXCUIdrug name crosswalk from the RXNSAT and RXNCONSO files in the RxNorm data set.

The assumptions are: you know how to download the RxNorm files; and you are familiar with using relational databases and Structured Query Language (also known as 'S','Q','L' or sequel).

Let's review the RxNorm data files. RxNorm data files can be downloaded from the RxNorm Files page. As a reminder, you need a UMLS license account to download the full releases.

["https://uts.nlm.nih.gov/uts" appears on the screen]

The current Prescribable Subset does not require a license.

More information about the files is in the RxNorm Technical Documentation. An RxNorm full monthly release includes nine pipe-delimited text files. The files are meant to be loaded into a relational database management system and queried.

A National Drug Code, also called NDC, is found in the RXNSAT file. NDC values are in the Attribute Value (or ATV) column where the Attribute Name field equals 'NDC'. Therefore, the Attribute Name (or ATN) field needs to be specified to filter for NDCs.

Drug names are in the RXNCONSO file, specifically in the STR column.

Both RXNSAT & RXNCONSO contain various identifiers, such as RxNorm Concept Unique Identifiers (or RXCUIs), RxNorm Atom Unique Identifiers (or RXAUIs), and Codes from data sources. The RXNSAT and RXNCONSO files can be joined using an RXCUI, RXAUI, or Code identifier.

That's the end of the RxNorm files overview. We'll now review a database query example using a database tool called SQL Developer.

Here is a SQL query example to obtain a map of NDC-RXCUI-Drug Name information joined on RXAUIs in a relational database.

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SELECT rs.atv as ndc, rs.rxcui, rc.str FROM rxnsat rs, rxnconso rc WHERE rs.atn = 'NDC' AND rs.rxaui = rc.rxaui AND rc.sab = 'RXNORM' AND rc.tty in ('SCD','SBD','GPCK','BPCK') ORDER BY rc.str;] Here are the results. The first column has NDCs, the second has the RXCUIs, and finally the drug names are in the String column.

Let's review the query syntax in more detail. I'll start with the FROM clause since we're joining two data files. RXNSAT is designated as rs and RXNCONSO is designated as rc.

Then, using the SELECT statement, the values we want to retrieve are specified. The file location of the values we want, and any column name changes are also included.

For example, 'rs.atv as ndc' retrieves NDCs from the Attribute Value (or ATV) column in the RXNSAT file that is designated as rs. The column name is also changed from ATV to 'ndc'.

Next, the WHERE clause permits data to be filtered using specified conditions. In this query, we filtered the results to display NDC values by specifying the Attribute Name to equal 'NDC'.

The operator AND provides additional conditions for filtering data. The first AND statement joins the two files RXNSAT and RXNCONSO using RXAUI values. The remaining AND statements filter the results to display strings in the RXNORM source vocabulary where term type (or TTY for short) equals SCD, SBD, GPCK, or BPCK. These four TTYs are used to represent dispensable products in RxNorm that have associated NDCs.

Using the ORDER BY clause, the results are sorted by string. That's the end of the SQL query example.

In summary, RxNorm files are meant to be loaded into a relational database management system and queried.

NDCs are in the RXNSAT file in the Attribute Value (or ATV) column when the Attribute Name (or ATN) field equals 'NDC'. Drug names are in the RXNCONSO file in the String (STR) column.

RXNSAT and RXNCONSO can be joined using an identifier, such as RXCUI, RXAUI, or CODE to get a mapping of NDC-RXCUI-Drug Names.

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For more information about the RxNorm data, see the RxNorm Technical Documentation, such as: Appendix 5 – RxNorm Term Types; Section 12. Data Files; and Section 14.2 Sample Database Queries.

Thank you for watching.

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