Viewer User Guide

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Document Revisions

Date	Version Number	Document Changes
01/15/2018	1.0	Initial Release

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Table of Contents

1   Introduction to the SOLOR Viewer

The SOLOR Viewer will allow users to view specific medical terminologies (such as SNOMED and LOINC) that have been transformed into SOLOR's common model. Please note that the SOLOR Viewer does not come pre-loaded with content due to licensing restrictions. It is left to the user to ensure that the proper licenses are obtained by the user prior to importing these terminologies into the SOLOR Viewer.

The SOLOR Viewer User Guide provides an overview of the SOLOR Viewer's installation process, and the commonly used functions used to view and search content.

The SOLOR Viewer has been tested on WindowsXP and MacOS Sierra version 10.12.6. The minimum specifications for the SOLOR viewer are:

Apple:

> **Operating System:** macOS Sierra 10.12.6 or higher
>
> **Processor:** 2.6 GHz
>
> **Memory:** 8 GB

Windows:

> **Operating System:** Windows 10
>
> **Processor:** 2.6 GHz
>
> **Memory:** 8 GB

1.1 The SOLOR Viewer Overview

This section will describe the overall layout of the SOLOR Viewer. However, please note that content will need to be downloaded, imported, and transformed. Therefore, be sure to follow instructions in sections 2.3 (Download Content) and 2.4 (Import Content) prior to using the SOLOR Viewer.
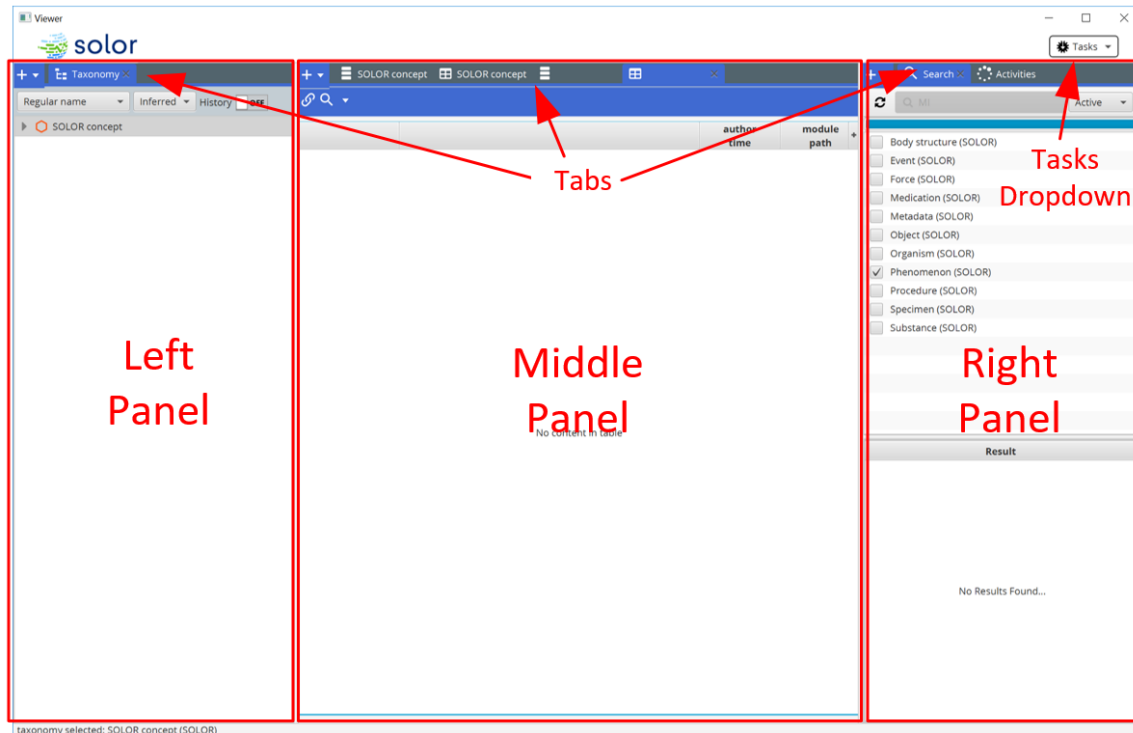
1.1.1 The SOLOR Viewer Panels

The SOLOR Viewer consists of three panes: left, middle, and right. Each panel will allow the user to display various components, which is described below.

1.1.2 View (Tabs)

By default, the left panel will automatically display the "Taxonomy" view, the middle pane will include two "Concept Details" tabs and two "Concept Details Table" tabs, which are linked to the Taxonomy and Search panels (more on this later). The right panel will display "Search" and "Activities" views.

Additional views can be added to any panel by clicking on the icon, and the selected panel will be added as an additional tab.

The view types are:

- Activities: Displays the status of processes that are in progress, such as importing and transforming content

- Assemblage: Displays a collection, such as members in a refset

- Concept Details: Displays the associated details of the concept

- Concept Details Table: Displays the associated data points of the concept in a table format

- Search: Allows users to perform full-text searches (based on Lucene)

- Taxonomy: Enables browsing of content in a hierarchical view, and allows the user to navigate in a "top-down" fashion from broad concepts down to granular concepts

1.1.3 Linking a Panel to a View Type

For "Concept Details," "Concept Details Table," and "Assemblage" views, they can be linked to Search, Taxonomy, or remain Unlinked. Default tabs of the middle pane will have "Concept Details" and "Concept Details Table" tabs linked to Taxonomy, and "Concept Details" and "Concept Details Table" tabs linked to Search.

Any new "Concept Details," "Concept Details Table," or "Assemblage" tabs will default to Unlinked. When linked, the tabs will display the information associated with the selected view. For example, "Concept Details" tab linked to Taxonomy will display items when a concept is clicked in the Taxonomy view, while tabs linked to Search will display selected search result items.

To change the linkage, click on the "Concept Details," "Concept Details Table," or Assemblage" tabs, and a ribbon with a drop-down arrow will be displayed:
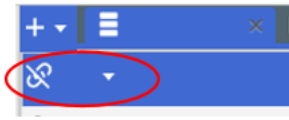
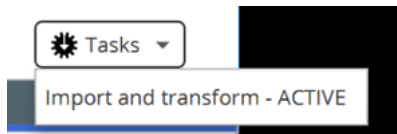Clicking on the drop-down arrow will show the views for "Concept Details," "Concept Details Table," and "Assemblage" tabs to link to:
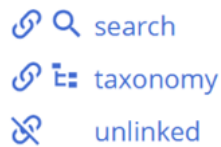
1.1.4 Tasks

The "Tasks" button is located at the upper right-hand corner of the application. When clicked, a drop-down menu will appear:

The currently available tasks are:

- Import and transform: Imports and transforms most recent version of the concept into SOLOR

2 Setup

2.1 Download and Install the SOLOR Viewer

1. Visit http://solor.io to get latest release of the SOLOR Viewer.

2. For Window users, download the.exe file. For Mac users, download the .dmg file.

⚠️ Mac users: If the user receives a messaging stating that the "'SOLOR Viewer Installer App' cannot be opened because it is from an unidentified developer," go to System Preferences' Security & Privacy tab, and click the "Open Anyway" button next to the message "SOLOR Viewer Installer.app."

⚠️ Reinstalling the Viewer: If this is a re-installation, please make sure to move or have copies of the downloaded terminology files previously moved into data\to-import folder. Failure to do so may require the user to find or re-download the terminology files. If the folder is not empty, please delete the entire folder before re-installing the SOLOR Viewer.

3. Locate the downloaded file, and double click on the icon.

4. Click on 'Run.'
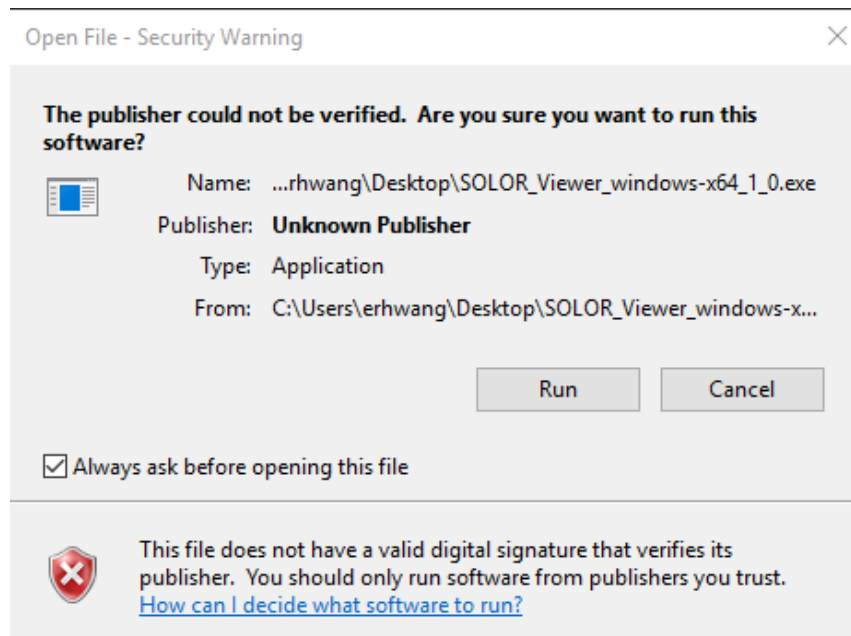
5. After installation preparation, the Setup Wizard will be seen. Click on 'Next.'
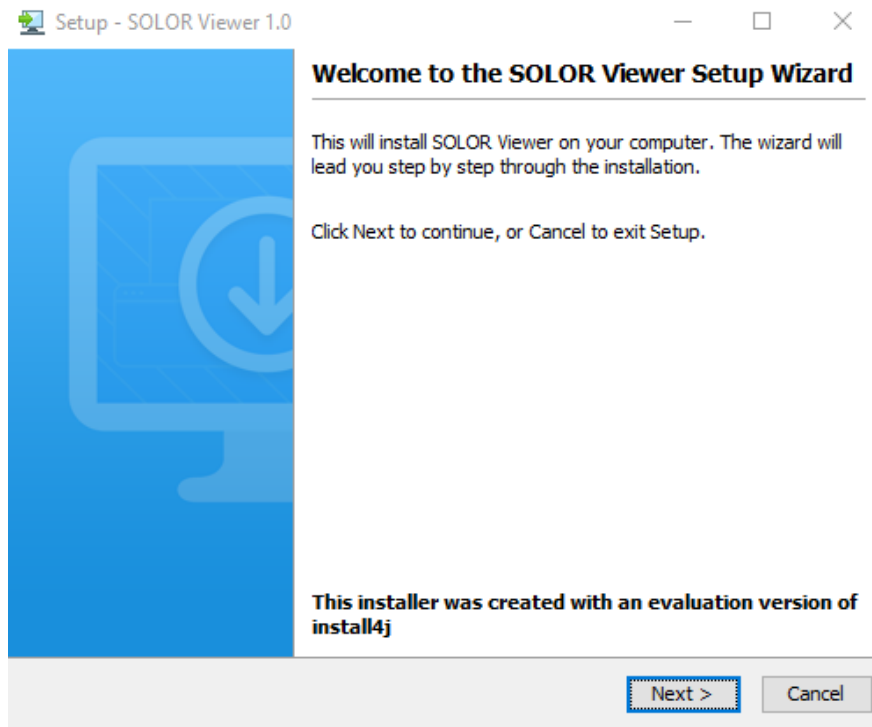
6. Select the desired location for the SOLOR Viewer, or accept the default folder, and click on 'Next.

⚠️ **Windows Default installation folder:** The SOLOR Viewer will create a folder under "C:\Program Files". It is recommended to install outside of this default folder, e.g. Documents.

7. Click on 'Finish' when the installation process completes.

8. Navigate to the installed folder for SOLOR Viewer.

9. Double click on "SOLOR Viewer" (Windows: SOLOR Viewer.exe; Mac: SOLOR Viewer.app) to launch SOLOR Viewer.

⚠️ **Note**: It may take a few minutes for the application to start.

2.2   Download Content

Prior to using SOLOR Viewer, users will need to ensure at a minimum that SNOMED and LOINC are available. The following sections describe the steps to: obtain the appropriate licenses and download instructions for the content files to be imported. As additional content is made available, instructions will be added to include the new content files.

⚠️   **Zip File Format**: SOLOR Viewer will expect the downloaded .zip file. Please make sure that the user's system does not automatically unzip the downloaded files.

> **Safari Mac users** will need to go to Preferences (in Safari) and under General tab, uncheck the option Open "safe" files after downloading to prevent the files from automatically being unzipped.

2.2.1   Download SNOMED CT

Downloading and usage of SNOMED CT files require a license. To obtain a license, the user must register with National Library of Medicine (NLM) – License for Use of the UMLS Metathesaurs (https://uts.nlm.nih.gov/license.html). If the user already has a UMLS license, please proceed to 2.2.1.2. Otherwise, please follow instructions under 2.2.1.1 to obtain a UMLS license.

2.2.1.1   Obtaining a UMLS license

1. Visit UMLS Metathesaurus License website (https://uts.nlm.nih.gov/license.html).
2. After reading and accepting the agreement, the user will be asked to fill out and submit a UMLS License Request Form.
3. Once the request has been submitted, an email will be sent to the user's registered email account[1].

2.2.1.2   Download SNOMED CT

2.2.1.2.1   SNOMED CT International Edition

1. After obtaining the required affiliate license, visit NLM's SNOMED CT International Edition download site (https://www.nlm.nih.gov/healthit/snomedct/international.html), and navigate to the "Current International Edition Releases" section.

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[1] It may take up to 3 days for the NLM to complete the registration process, and the email will expire after 15 business days.

2. Under the latest version (Version: Month Year), click on "Download RF2 Files Now!" This leads to the UMLS Terminology Services Login Page.

3. Logging in with the credentials created in "Obtaining a License for SNOMED CT" will automatically start the download process.

4. Once the download is complete, locate the file and move the file to [Destination folder/directory from installation step]\SOLOR Viewer\data\to-import.
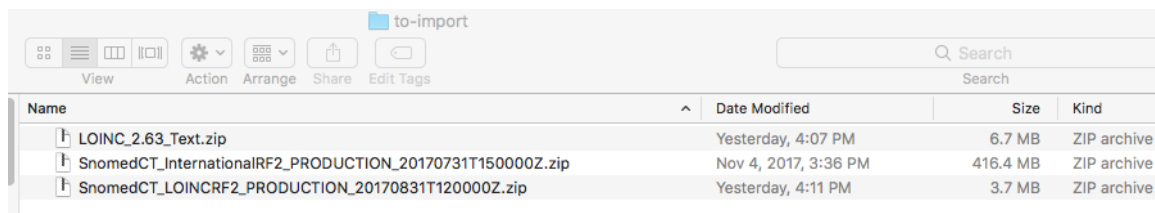
2.2.2 Download LOINC

2.2.2.1 Registration

Create a LOINC User Account (https://loinc.org/join/)[2]

2.2.2.2 File Download
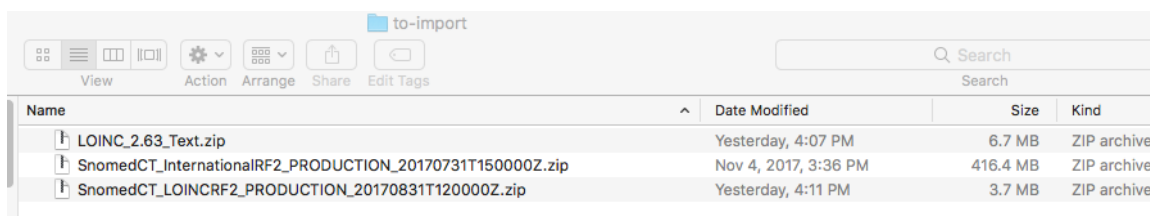
1. Visit LOINC download site (https://loinc.org/downloads/loinc/).

2. Select "LOINC Table File (CSV)."

3. Read through the "Copyright Notice and License" agreement, and accept the terms to download the file.

4. Once the download is complete, locate the file and move the file to [Destination folder/directory from installation step]\SOLOR Viewer\data\to-import.
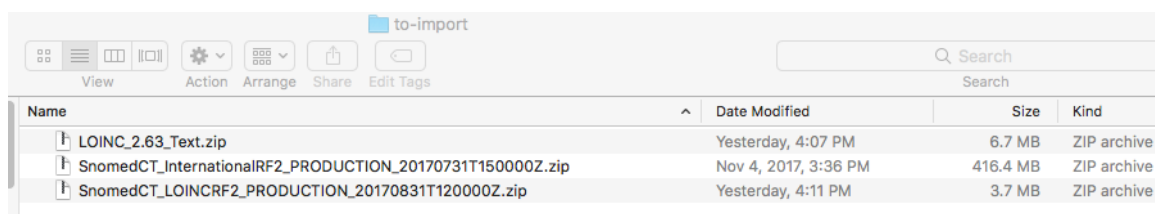

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[2] This is a one step process, and the user will be able to download LOINC files instantly.

2.2.3 Download LOINC/SNOMED CT Collaboration Files

1. Visit SNOMED CT – LOINC page (https://loinc.org/collaboration/snomed-international/), and use credentials created in LOINC Registration to login to the LOINC website.
2. Scroll down to the link or icon to download "LOINC/SNOMED CT Expression Association and Map Sets File - Production release (RF2 Format)."
3. Read through the "Copyright Notice and License" agreement, and accept the terms to download the file.
4. Once the download is complete, locate the file and move the file to [Destination folder/directory from installation step]\SOLOR Viewer\data\to-import.

2.3   Importing Content

⚠️ **Before Importing**: Before starting the process of importing content within the SOLOR Viewer, ensure that all the desired licensed downloaded files from above are moved into [Destination folder/director from installation step]\SOLOR Viewer\data\to-import].

⚠️ **Naming of Zip Files**: To ensure that files are correctly imported, double check that the files follow the naming conventions listed below:

Terminology	File Name & Size
SNOMED CT International	SnomedCT_InternationalRF2_PRODUCTION_20170731T150000Z.zip
SNOMED LOINC Collaboration	SnomedCT_LOINCRF2_PRODUCTION_20170831T120000Z.zip
LOINC Files	LOINC_2.63_Text.zip

From the "Tasks" drop down, select "Import and transform."

5. Clicking on "Activities" will show the progress of the import.
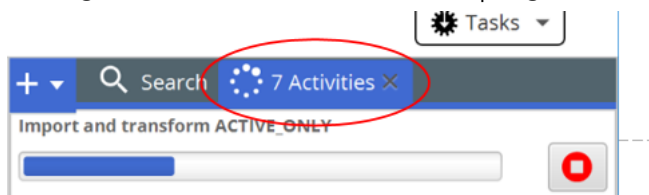
⚠️ **Taxonomy Root known issues**: If you encounter the following error after importing data please quit and restart the SOLOR Viewer. This is a known issue that occurs intermittently on some user's machines. We are actively working to resolve this.

3 Viewing Content

3.1 Taxonomy View

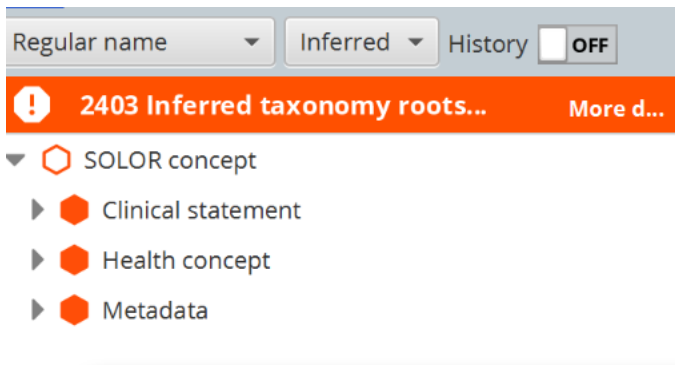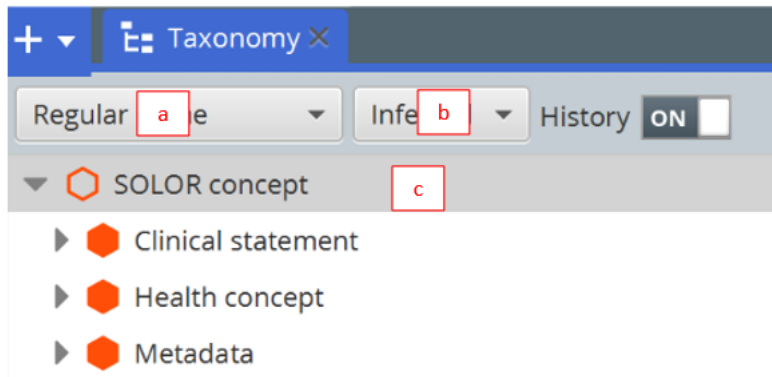Taxonomy view allows the user to browse the content in SOLOR in a tree-like structure. This allows the user to navigate the content from a "top-down" approach – from generic to a more granular concept. By default, the taxonomy view is displayed in the left pane.

Taxonomy view consists of the following:

a. Display name type: Set the display of the concept name in the tree display to show Fully qualified name (Fully Specified Name) or Regular name (Preferred Name)
b. View
   - Stated view: Shows the parent-child lineage that have been stated by a content author
   - Inferred view: Shows the parent-child lineage that have been inferred after classification has taken place
c. Tree display: Displays the tree/branches of SOLOR.
   - There are three top nodes in SOLOR:
       i. Clinical statement: This branch will be available in a future release, to capture clinical models
      ii. Health concept: Main branch that contains Standard (SNOMED, LOINC)
     iii. Metadata: Contains the metadata that are used to store, represent, and display the various data points originating from content authors

To navigate the taxonomy:

1. Clicking on the concept itself will populate the "Concept Details" and "Concept Details Table" views if they are linked to the taxonomy.
2. Clicking on the grey arrow pointing to the right will display the immediate children of the concept, and will turn the grey arrow to point downward. Clicking on the grey downward arrow will collapse the expanded view of the concept, hide its descendants, and turn the arrow to point to the right.
3. Each concept will have an icon next to it.
   They symbolize:

   ⬡   Taxonomy root

   ⬡   Primitive single parent

   ⬢   Primitive multi-parent closed

   ⬢   Primitive multi-parent open

   ○   Defined single parent

   ⊕   Defined multi-parent closed

3.2 Simple Search

1. Under the "Search" tab on the right panel, there is a text box, a filter subpanel, and a result subpanel:
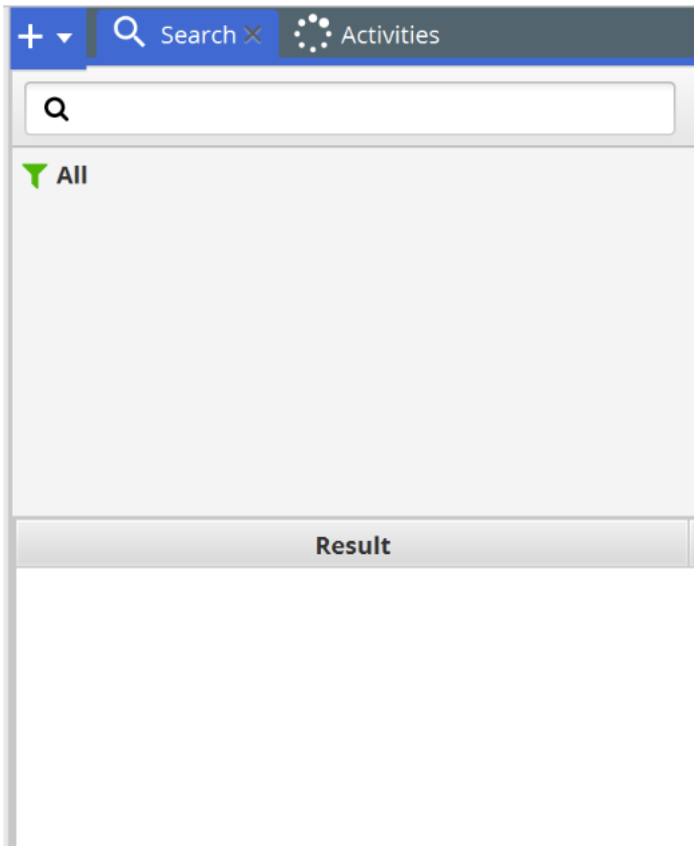
2. Begin searching by typing in search terms in the text box. By default, the search operation will perform against all taxonomies in SOLOR. For example, a search for "staphylococcus" will return results from different taxonomies such as organism, substance, disorder, etc.:

+ ▼ | 🔍 Search ✕ | ⋯ Activities

🔍 staphylococcus

▼ All

Result	
Methicillin resistant staphylococcus aureus positive	
Impetigo due to Staphylococcus aureus	
Staphylococcus immunisation	
Staphylococcus hemolyticus	
Staphylococcus carrier (finding)	
Staphylococcus lugdunensis (organism)	
Staphylococcus pasteuri (organism)	
Staphylococcus aureus meningitis (disorder)	
Staphylococcus epidermidis meningitis (disorder)	
Staphylococcus simulans biovar staphylolyticus (organism)	
Staphylococcus aureus hemolysin antibody (substance)	
Staphylococcus aureus ss aureus (organism)	
Staphylococcus capitis ss capitis (organism)	
Staphylococcus cohnii ss cohnii (organism)	
Staphylococcus delphini (organism)	
Staphylococcus felis (organism)	
Staphylococcus lutrae (organism)	
Staphylococcus muscae (organism)	
Staphylococcus piscifermentans (organism)	
Staphylococcus saprophyticus ss bovis (organism)	

3. To limit the search in a taxonomy, simply drag any concept, for example "Organism (SOLOR)," from the taxonomy panel to the filter subpanel in the search panel, click on the search box and hit enter to perform search with the same text string, or enter a new text string:
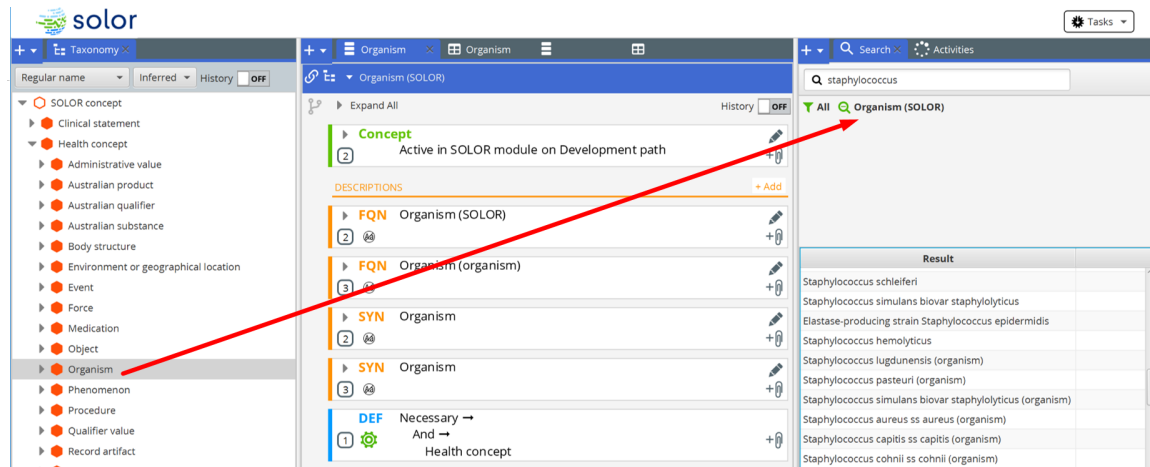
Note: Clicking on the filtered node, e.g. Organism (SOLOR), will remove it from the filter sub-panel.

Note: Multiple filtering nodes can be placed into the filter sub-panel, e.g. performing a search and limiting to "Phenomenon" or "Procedure taxonomy". The filtering functionality is set to "All" AND (X OR Y).

Note: In SOLOR, Findings and Observable Entities are combined into the "Phenomenon (SOLOR)" taxonomy.

4. Clicking on a search result entry will populate "Concept details" and "Concept details table" tabs that are linked to search.

Concept Details

Concept Details Table

			author time	module path
COMPONENT	RF2 legacy relationship implication **Necessary but not sufficient concept definition** Staphylococcus aureus		User 2002-01-31 00...	SNOMED CT® ... Development ...
STR	SCT identifier assemblage **3092008** Staphylococcus aureus		User 2002-01-31 00...	SNOMED CT® ... Development ...
▸ SYN	Staphylococcus aureus		User 2007-07-31 00...	SNOMED CT® ... Development ...
▸ SYN	Micrococcus pyogenes var. aureus		User 2007-07-31 00...	SNOMED CT® ... Development ...
▸ SYN	Staphylococcus pyogenes aureus		User 2007-07-31 00...	SNOMED CT® ... Development ...
▸ SYN	Staphylococcus pyogenes citreus		User 2007-07-31 00...	SNOMED CT® ... Development ...
▸ FQN	Staphylococcus aureus (organism)		User 2007-07-31 00...	SNOMED CT® ... Development ...
REL	RF2 stated relationships Is-a Staphylococcus, coagulase positive (Stated) Staphylococcus aureus		User 2008-07-31 00...	SNOMED CT® ... Development ...
REL	RF2 inferred relationships Is-a Staphylococcus, coagulase positive (Inferred) Staphylococcus aureus		User 2002-01-31 00...	SNOMED CT® ... Development ...
MEMBER	Microorganism reference set Staphylococcus aureus		User 2010-05-31 00...	SNOMED Clini... Development ...
MEMBER	Organism foundation reference set Staphylococcus aureus		User 2009-11-30 00...	SNOMED Clini... Development ...
MEMBER	National Health Service laboratory isolate simple reference set Staphylococcus aureus		User 2006-10-02 00...	SNOMED CT U... Development ...

DEF	EL++ stated form assemblage
	Staphylococcus aureus
	Necessary →
	  And →
	    Staphylococcus, coagulase positive
			User
			2018-01-13 04...
				SOLOR overla...
				Development ...

DEF	EL++ inferred form assemblage Staphylococcus aureus		User 2018-01-13 04...	SOLOR overla... Development ...

5. Clicking on another search result entry will refresh the content of these two tabs.

6. If data is not being displayed, please refer to "Links" under section 2.2.1.

3.2.1 Simple Search Example – Gentamycin
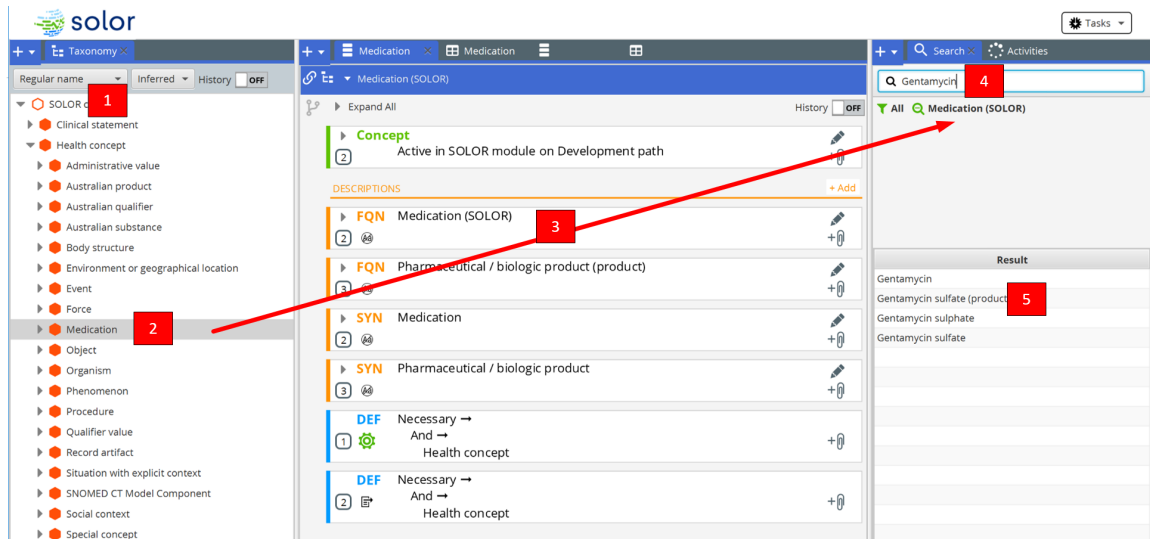
1. Expand "SOLOR concept" in the Taxonomy panel
2. Select "Medication" under "Health concept"
3. Drag "Medicine" to the Search Panel
4. Type in "Gentamycin" and hit Enter
5. Result is show in the Result sub-panel

3.2.2 Simple Search Example – LOINC Code
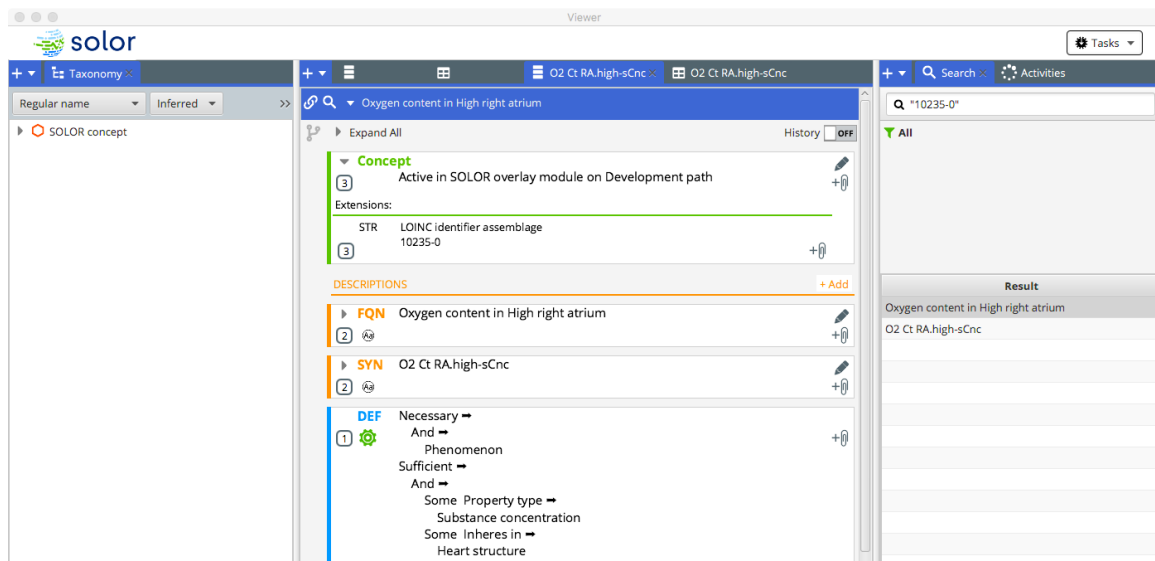
1. Type in a LOINC code that you want to search for be sure to include "" around the LOINC code "10235-0" and hit Enter
2. Result is show in the Result sub-panel

3.2.3 Search Syntax

Simple search implements the Lucene query package. Below are examples of frequently used Lucene searches. For a complete list of the Lucene query syntax, please visit: [https://lucene.apache.org/core/7_0_0/queryparser/org/apache/lucene/queryparser/classic/package-summary.html - Overview](https://lucene.apache.org/core/7_0_0/queryparser/org/apache/lucene/queryparser/classic/package-summary.html).

3.2.3.1 Terms

1. Terms could be Single Terms or Phrases
   a. Single Term: composed of a single word
      i.   Example: nose
   b. Phrase: Composed of a group of words surrounded by double quotes
      i.   Example: "nose bleed"

⚠ **Note on Default Conjunction Operator:** OR is the default conjunction operator. Therefore, *nose bleed* (without the double quotes), will automatically become: nose OR bleed, and will return results such as *dry nose, bull nose,* and *Gastrointestinal bleed.*

3.2.3.2 Wildcards

1. "?" will perform a single character wildcard search.
   a. Example: a?duct will return "Procedure to abduct extremity" as well as "Vocal cord does not adduct on phonation"
2. "*" will perform multiple character (0 or more) wildcard search.
   a. Example: h*at will return terms with the word heat, hemostat, or houseboat.

3.2.3.3 Boolean Operators

1. OR is the default conjunction operator.
   a. Therefore, nose bleed (without the double quotes), will automatically become: nose OR bleed, and will return results such as dry nose, bull nose, and Gastrointestinal bleed.
2. AND: Having the word AND (all capitalized) will require both terms to match.
   a. Example: tibia AND fibula.

   ⚠ **Note on Phases:** Phrases can be used. Example: *"tibia and fibula" AND fracture* will require that the result contains both "tibia and fibula" as well as "fracture", such as "Open fracture of upper end of tibia and fibula."
3. "+" will require the term must exist.
   a. Example: *+tibia fibula* will return "Proximal shaft of tibia" as well as "Insertion of bone growth stimulator into tibia and fibula"

4. "NOT" will exclude the term after "NOT."
    a. Example: *tibia NOT fibula* will return terms with only *"tibia"* in the text.
5. Grouping is achieved via parentheses.
    a. Example: (tibia NOT fibula) AND fracture will only return terms that contains "tibia" and "fracture," while excluding any terms that also contains "fibula."

4 Exiting the SOLOR Viewer

The SOLOR Viewer has writing processes when the application is quitting. "Activities" panel will show the progress during the exiting process:
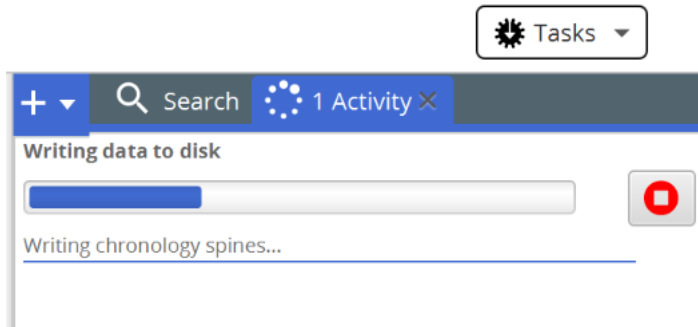
> ⚠️ **DO NOT force quit or hit 'X'** (quit application icon on the upper right-hand side) multiple times.

Doing so may require a re-installation of the SOLOR Viewer. Be patient and the application will quit when the writing processes is completed. Clicking on the "Activities" tab will show the writing progress.

5 Uninstalling the SOLOR Viewer

To uninstall the SOLOR Viewer, go to the installation folder where the SOLOR Viewer was installed. Double click on the uninstall icon (Windows: uninstall.exe; Mac: SOLOR Viewer Uninstaller.app), and the uninstallation process will begin.

⚠️ Note: If the user requires a re-installation, please make be sure to move or have copies of the downloaded terminology files that have been moved into the *data\to-import folder*. Failure to do so may require downloading the terminology files again. If the folder is not empty, please delete the entire folder before re-installing the SOLOR Viewer.

6 Reporting a Problem or Request an Enhancement

If the user finds an error in this documentation, a bug within the SOLOR Viewer application, or would like to propose an enhancement, please use SOLOR JIRA (https://healthservices.atlassian.net/projects/SOL/summary) to submit an issue[3].

6.1 JIRA Create Issue

1. Click on "Create" button located at the top of the banner.
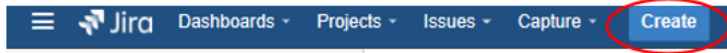
This will bring up a "Create issue" page:

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[3] If the user would like to register as a SOLOR JIRA participant, please visit http://hspconsortium.org/contact/ to submit a registration request

a. <u>Project</u>: Be sure to select **"SOLOR & ISAAC & KOMET (SIK)."**
b. <u>Issue Type</u>: Select the most appropriate type. Typically, it will be "Bug" or "Task."
c. <u>Summary</u>: Enter a brief (one [1] sentence) summary of the issue.
d. <u>Description</u>: Enter as much information as possible regarding the issue.
   - Note: If the user entering issues is an unregistered JIRA user, please enter contact information in this field so that appropriate personnel could reach the user if needed.
e. <u>Priority</u>: Select the most appropriate priority level.
   - Blocker: Blocks development and/or testing work, production could not run
   - Critical: Crashes, loss of data, or severe memory leak

f. Project: Be sure to select **"SOLOR & ISAAC & KOMET (SIK)."**

g. Issue Type: Select the most appropriate type. Typically, it will be "Bug" or "Task."

h. Summary: Enter a brief (one [1] sentence) summary of the issue.

i. Description: Enter as much information as possible regarding the issue.

   - Note: If the user entering issues is an unregistered JIRA user, please enter contact information in this field so that appropriate personnel could reach the user if needed.

j. Priority: Select the most appropriate priority level.

   - Blocker: Blocks development and/or testing work, production could not run
   - Critical: Crashes, loss of data, or severe memory leak
   - Major: Major loss of function
   - Minor: Minor loss of function, or other problem where easy workaround is present
   - Trivial: Cosmetic problem like misspelled words or misaligned text

k. Attachment: Please include a screenshot or relevant document if applicable.[4]

l. Create another: If there are more than one issue to be reported, clicking on this checkbox will allow the user to create additional issues after clicking on "Create button" (h).

m. Create button: Click on this button when ready to submit the issue.

Note: If the user knows the appropriate values to enter for remaining fields, please input the information. Otherwise, it is acceptable to leave those fields empty.

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[4] This function will not be available for non-registered users.

7 Troubleshooting

7.1 Minimum OS and Hardware Configuration

The installer checks for a minimum memory configuration for Mac and Windows of 8 GB for the installer to continue the installation process; otherwise, the installation process will not complete.

Apple:

       Operating System: macOS Sierra 10.12.6 or higher

       Processor: 2.6 GHz

       Memory: 8 GB

Windows:
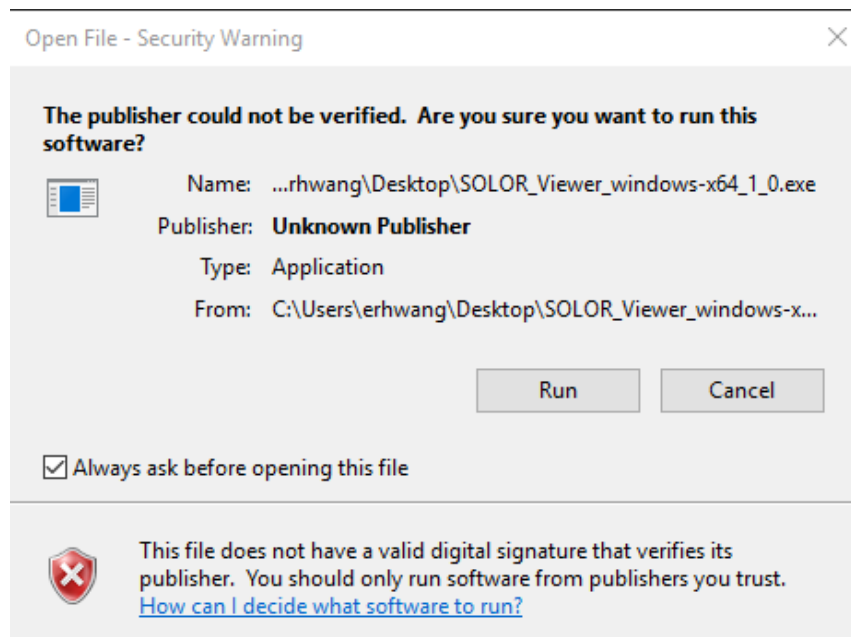
       Operating System: Windows 10

       Processor: 2.6 GHz

       Memory: 8 GB

7.2 Unidentified Developer

⚠️ Mac users: If the user receives a messaging stating that the "'SOLOR Viewer Installer App' cannot be opened because it is from an unidentified developer," go to System Preferences' Security & Privacy tab, and click the "Open Anyway" button next to the message "SOLOR Viewer Installer.app."

7.3 Data File Sizes

If the user experiences issues importing the SNOMED CT and LOINC please check that the downloaded zip files in **bytes are**:

Terminology	Bytes on Mac	Bytes on Windows
SNOMED CT International	416,419,383	406,660
SNOMED LOINC Collaboration	3,660,960	3,576
LOINC Files	6,732,541	6,575

8 Known Issues

8.1 Taxonomy Root

⚠️ **Taxonomy Root known issues**: If you encounter the following error after importing data please quit and restart the SOLOR Viewer. This is a known issue that occurs intermittently on some user's machines. We are actively working to resolve this.