Default Clinical Pipeline

The Default Clinical Pipeline is a great place for the new user of a binary installation to start. New developers should look at the `ctakes-examples` project to start.

The Default Clinical Pipeline produces the most commonly desired output from cTAKES. This includes annotations for Anatomical sites, Signs/Symptoms, Procedures, Diseases/Disorders and Medications. For each annotation there are normalized UMLS CUIs, plus values for negation, uncertainty and subject.
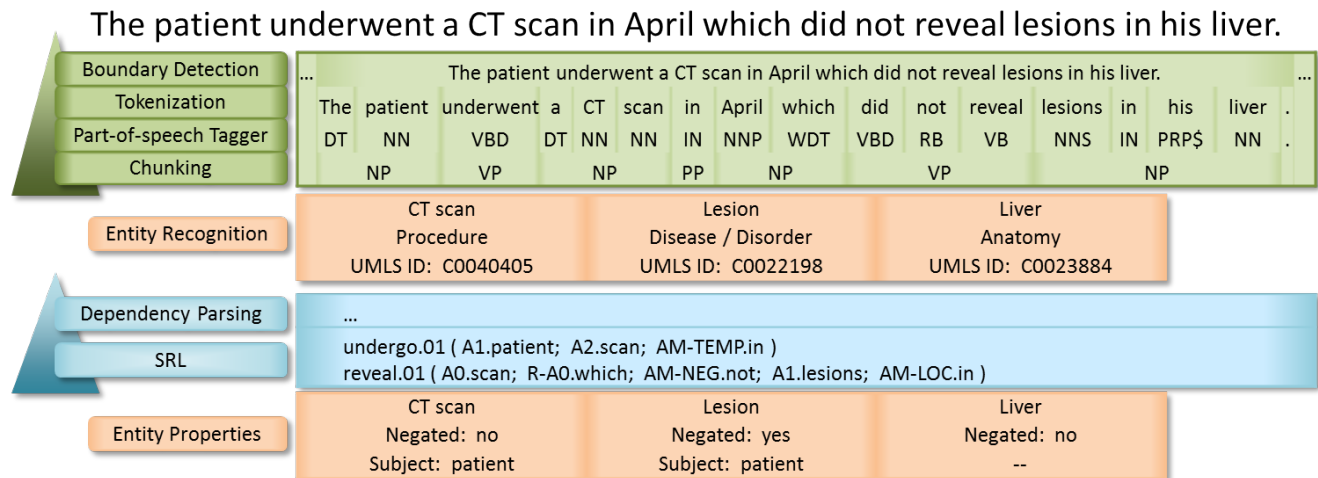

Figure 1. A sample sentence processed by the Default Clinical Pipeline.

Step-by-step guide

Run via command line.

1. Execute bin/**runClinicalPipeline** `-i` *inputDirectory* `--xmiOut` *outputDirectory* `--user` *umlsUsername* `--pass` *um lsPassword*

The pipeline will write log information to the screen and will write an XMI file for each file in `inputDirectory` and its subdirectories. The directory tree below `inputDirectory` will be mirrored in `outputDirectory`.

You can view information in the XMI files using the UIMA Cas Visual Debugger (CVD).

1. Execute bin/**runctakesCVD**
2. Select **File > Read Type System File**
3. Select `TypeSystem.xml` in `resources/org/apache/ctakes/typesystem/types/`
4. Select **File > Read XMI CAS File**
5. Select any `.xmi` file in your `outputDirectory`

Selections in the tree on the left can provide highlighting in the document text on the right. Browsing annotations is not necessarily straightforward. Reference the CVD main area documentation for how to use the CVD. See the cTAKES 4.0 Component Use Guide for cTAKES annotations and attributes.

For cTAKES 4.0, if **runClinicalPipeline** fails with "ERROR PipelineBuilder - No Collection Reader specified.", verify that you used -i *inputDirectory*

> ⓘ The command line bin/**runClinicalPipeline** runs the Piper File `DefaultFastPipeline.piper` in `resources/org/apache/ctakes /clinical/pipeline/`

Related articles

- Piper Files
- Default Clinical Pipeline
- Piper File Submitter GUI
- Simple Pipeline Fabricator GUI