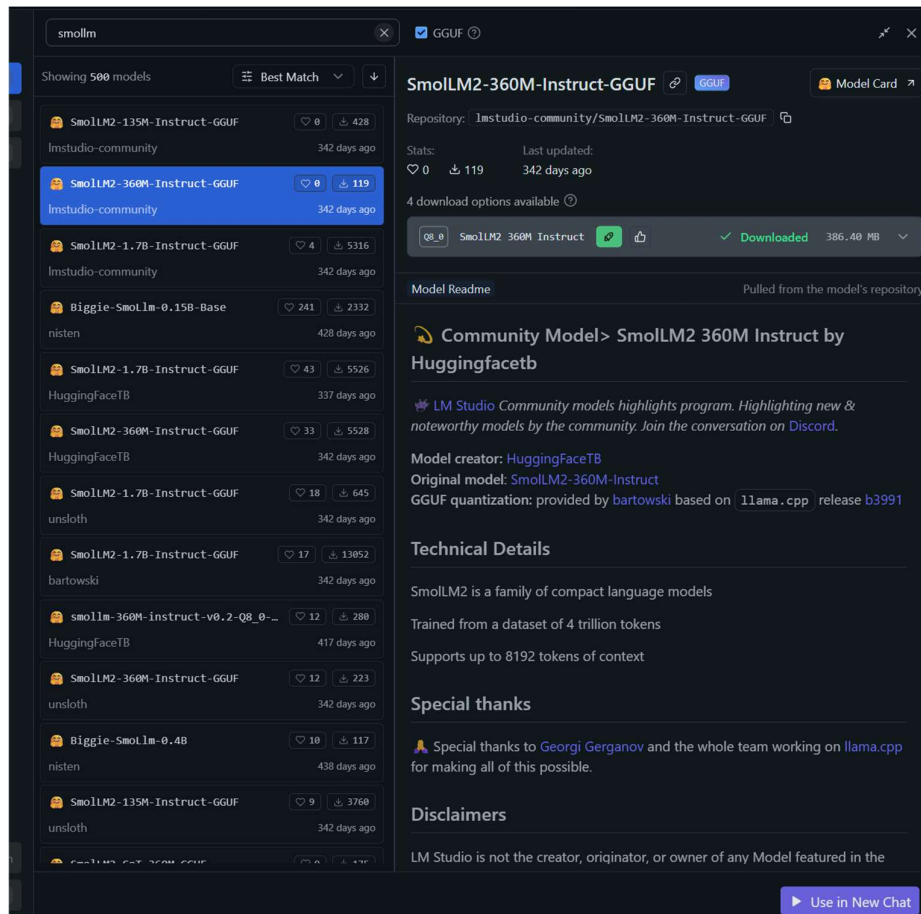**Setup:**

Download the zip file containing the files from Brightspace, extract its contents in an empty folder in your local hard drive **NOT Onedrive**.

You should have 10 files in the same folder, with these names:

A0_validator.py

A1_aggregator.py

A2_preparator.py

maininterface.py

environment.yml

run.bat

taxonomy1.csv
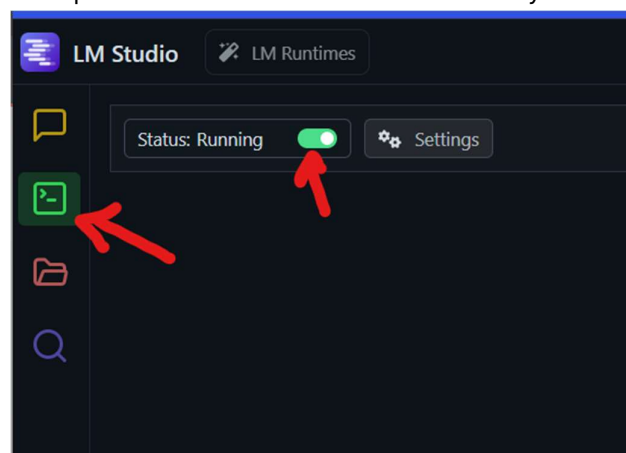
taxonomy1_2.csv

taxonomy2.csv

taxonomy2_2.csv

**Steps to run the tool:**

1. Install Anaconda https://www.anaconda.com/download/success
   1.1 Click on "Distribution Installers" and download the version that suits your operating system (Windows, Mac, Linux).
   1.2 Double click on the executable and follow the default install instructions. "Create shortcuts", "Register Anaconda3 as the system python 3.xx".
   1.3 You can untick "Launch Anaconda Navigator" and "Getting Started with Anaconda Distribution".
   1.4 If the installation is successful, you should be able to find "Anaconda Prompt" and "Anaconda Navigator" in your programs.
2. Install LM Studio for your operating system https://lmstudio.ai/download
   2.1 Follow the default instructions on the installer and launch the program once it has been installed.
   2.2 When the program starts, they will ask you to download a model. You can ignore that. Click on the "Discover" tab (purple magnifying glass) found on the left side panel.
   2.3 On the new panel that has opened search for the model **"smollm2-360m-instruct" (Q8_0 of 386,40 MB)**. Find it in the list and download it. This is a very small LLM, it may be prone to hallucinations.

2.4 Once the model is downloaded, you should be able to go to the "Chat" panel in LM studio and chat with your own local large language model (LLM). Possibly not as good as paid versions such as ChatGPT, but this one is free, local, secure and private.

2.5 Go to developer mode and enable the server by clicking "Status Running"



3. Go back to the folder where the files you downloaded from Brightspace are located. Start the tool setup by double clicking on the "run.bat" file.

    3.1 A command window will open, select "[1] Setup and Run HCAI System".

    3.2 Proceed by typing "y".

3.3 The program will now install the correct Python version, along with all the necessary packages to make the tool run. This can take a few minutes (10-15min). Once all is installed, the tool will open in your browser.

If the application does not open and you get the following error:
ERROR conda.cli.main_run:execute(xx): `conda run streamlit run maininterface.py` failed.

1. Make sure you have installed anaconda or miniconda: search for "anaconda prompt" in your computer.
2. Execute anaconda prompt and a command prompt will appear.
3. Navigate to the folder where maininterface.py is located using the command: *cd "your folder location"*
4. Run the command: *conda activate hcai_env*
5. Run the command: *streamlit run maininterface.py*

**If you encounter any of the following issues, restart the whole application:**

**Known bugs:**
- **Going from Agent 1 The Aggregator back to Agent 2 The Preparator results in an error**
- **In Agent 1 The Aggregator, during the taxonomy construction, clicking the elements in the visualization may result in infinite reloading or the interface disappearing completely**
- **In Agent 1 The Aggregator, categories and characteristics yet to be placed may disappear. If that happens just add them manually.**