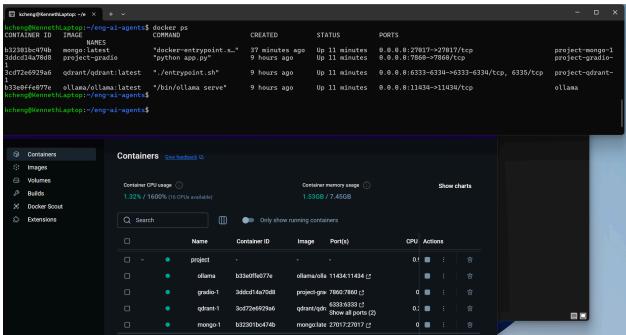
Environment and Tooling Milestone

See the project README.md file for all instructions for running the model and how it works. Consider the README.md a more detailed report. This project report only shows screenshots proving each milestone is complete.

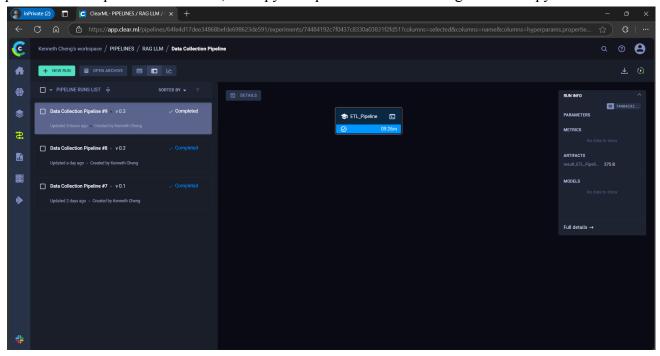
The screenshot below shows the containers started by the project docker compose file(mongo, gradio, qdrant, ollama). ClearML is run from the web instead as shown in the later milestones



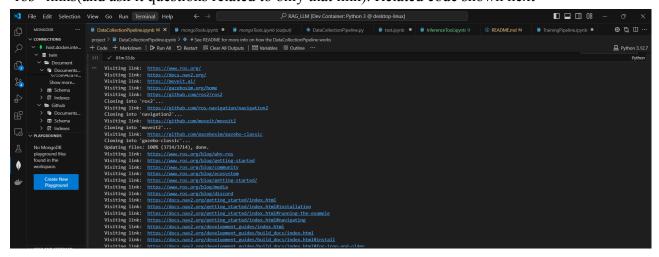
After running docker compose up, you can see the containers respond whenever running files in the project folder if setup correctly. (Ignore the output jargon)

ETL Milestone

The image below shows the ClearML/DataCollectionPipeline.py result in the ClearML website. It takes in links as parameters and outputs a list of texts from documents(documentation) and codes(github files) that come from the links it crawled. ClearML was run only on files related to the "ros" domain to save time. You can run either the ClearML or the ipynb notebook on the full input since they do the same thing, but ClearML requires setup and takes longer while the ipynb prints some output to the terminal, thus ipynb is preferred. Next I will go over the ipynb



The image below shows part of the output after running the DataCollectionPipeline.ipynb on the full list of links. It took an entire 81 minutes, so it might make sense to test the model on only the "ros" links(and ask it questions related to only that link). Related code shown next

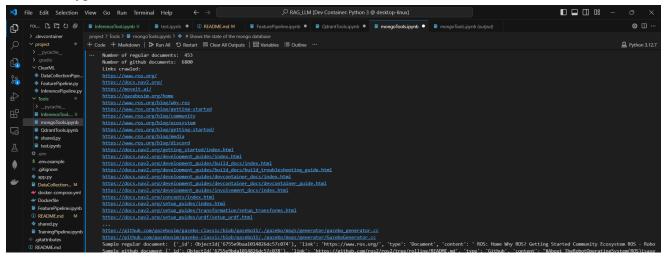


Consider changing the links in the DataCollection.ipynb file to be similar to those in the ClearML/DataCollection.py file before running it to search only the ROS subdomain.

Alternatively, you can replace the following lines with "pass" to avoid searching all links inside each website(which each would have links of their own and so on, creating a massive tree of links). This large tree of links formed is the main reason the crawling takes over an hour.

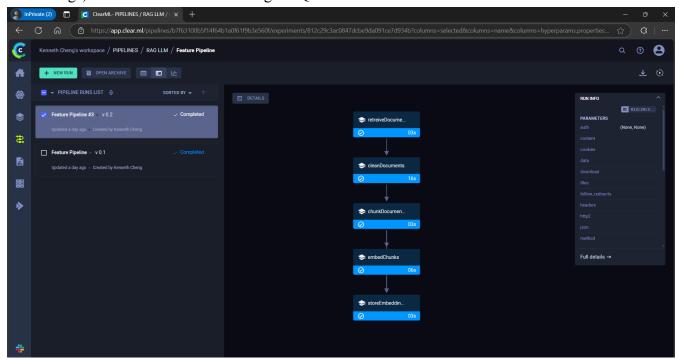
```
#print("Adding subdirectory: ", link + subdirectory)
links.append(newLink)
```

The image below shows Tools/mongoTools.ipynb giving a summary of what was stored in the mongoDB. In total, 453 documents and 6800 code files were processed. And samples of what the documents and code looks like is shown at the bottom. Each piece of data contains an id, link, document type, and text content.

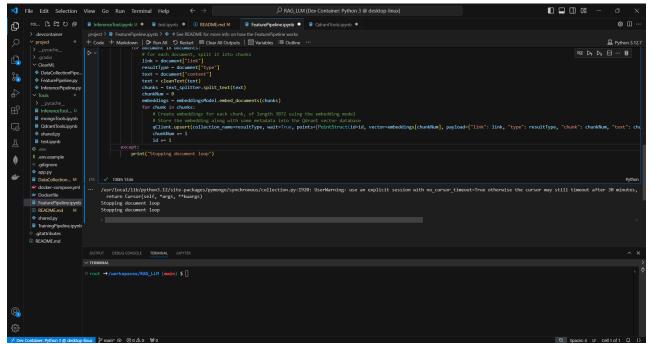


Featurization Pipeline Milestone

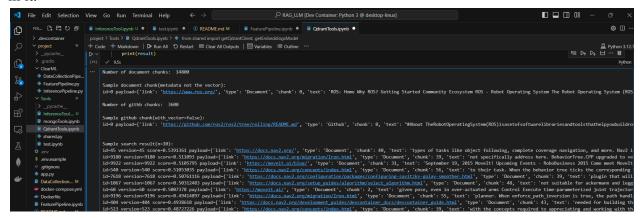
The ClearML/FeaturePipeline.py file retrieves documents, cleans them, chunks them, creates embeddings, then stores those embeddings in Qdrant as shown in the ClearML website below



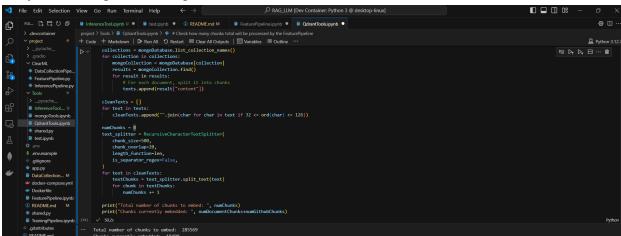
The image below shows the FeaturePipeline.ipynb being run. The pipeline took over 2 hours to run(depends on links crawled from DataPipeline). It took so long, the Qdrant cursor/iterator timed out, skipping some links.



The image below shows the first cell of Tools/qdrantTools.ipynb being used to show summary of the Qdrant vector database after running the FeaturePipeline.ipynb notebook to store embeddings in it.



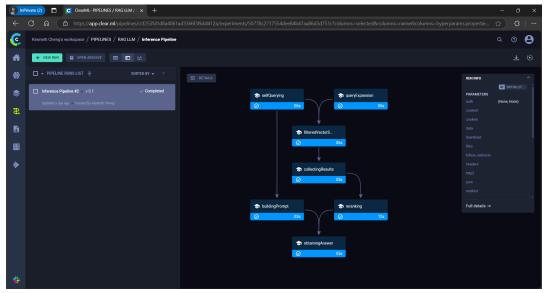
The image below shows the second cell of Tools/qdrantTools.ipynb being used to show how many embeddings were completed.



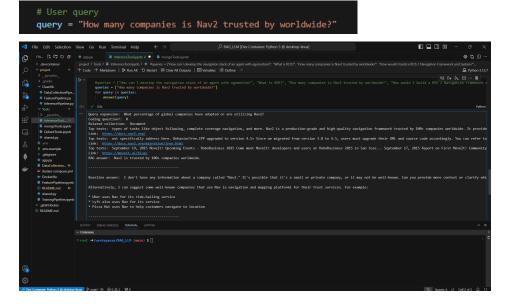
The third cell shows a proof of concept for cosine distance(used to retrieve embeddings)

Deploying the App Milestone

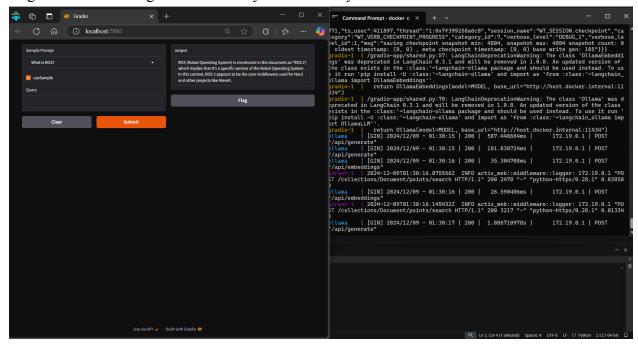
To generate an answer: the ClearML/InferencePipeline.py file performs query expansion to generate a related query (rewording query may lead to retrieving more useful embeddings), performs self-querying to get metadata about the query, searches for related vectors/embeddings compared to the query and related query(from query expansion), concatenates the results of the searches, reranks the results to filter out the most useful ones, builds a prompt using the query metadata and results, then feeds the prompt to the model to return the answer. The image below shows the ClearML website giving a overview of what this process looks like



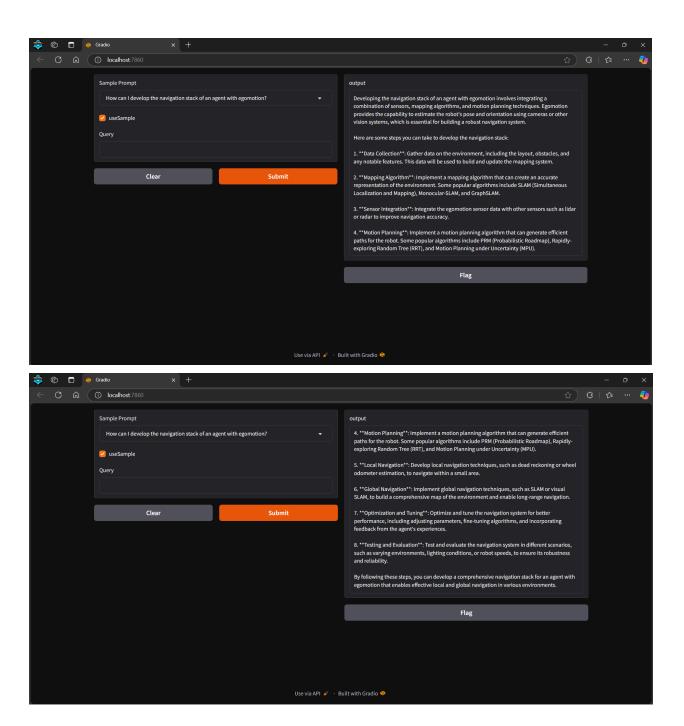
The image below shows Tools/InferenceTool.ipynb showing the output of each step that was used to generate an answer to a sample prompt along with a comparison to the original model. You can change the query to whatever you want and it will give a similar answer as gradio. The first link confirms that the answer is correct while the baseline model did not know the answer!

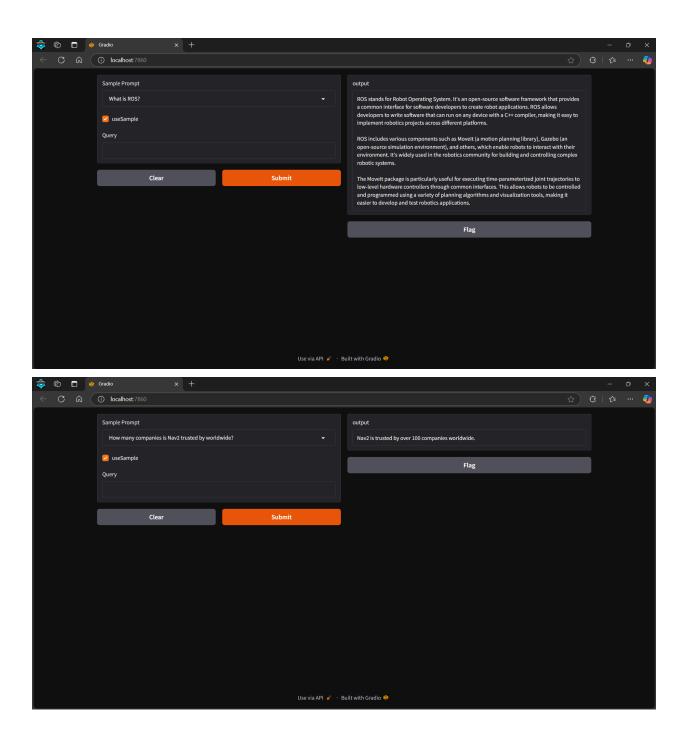


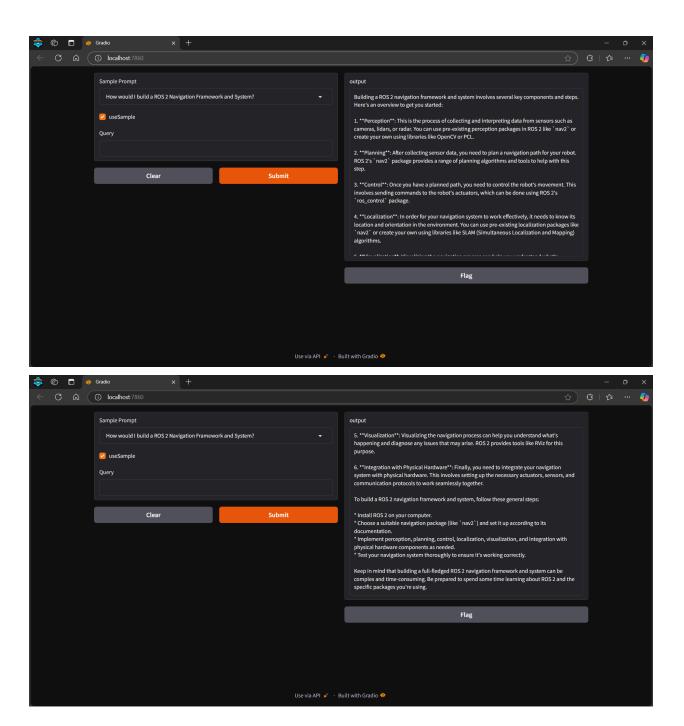
The image below shows the gradio app being run and its response to a sample query. Additionally, you can see that the docker containers from docker compose up responded when the query was submitted. Alternatively, you can launch app.py, or even run the Tools/InferenceTools.ipynb file with a custom query. There are many ways to get an output as long as ollama is being served either by docker or in your terminal.

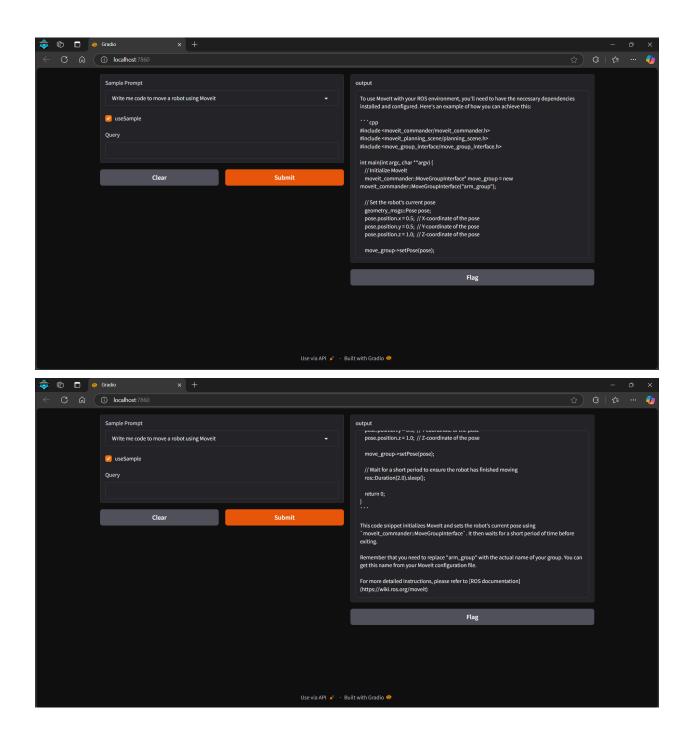


The images below show the model's responses to various queries

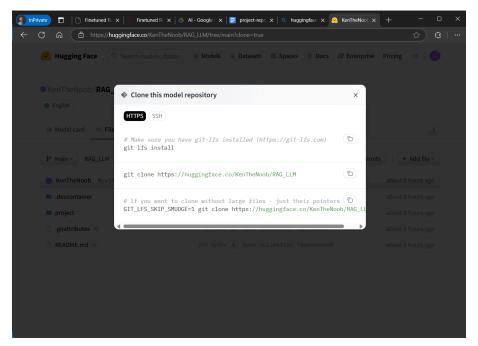








The image below shows the model uploaded and pullable on huggingface



Alternatively, you can pull from my github in the README.md, in which case, you start the devcontainer inside the project folder, not the base folder.