

## Prep Work

- Clone <https://github.com/EthanDayley/asd-siloing-exploratory>
- Ensure that the following are installed on your machine:
  - MySQL
  - Python 3
  - Jupyter
  - The following Python packages:
    - pandas
    - matplotlib
    - numpy
    - scikit-learn
    - gensim
    - phate
    - Wordcloud
- Download GoogleNews-vectors-negative300.bin from <https://github.com/mmhaltz/word2vec-GoogleNews-vectors> to the word\_embeddings folder in the asd-siloing-exploratory repository.
- Create a MySQL database called asd\_siloing.
- In your repository, run mysqlsh -u <username> -h localhost -f .\scripts\generate\_tables.sql.

## Materials Gathering

NOTE: Unless otherwise stated, all command line operations listed below should be conducted from the top level of the local asd-siloing-exploratory repository.

- In a web-browser, navigate to <https://www.ncbi.nlm.nih.gov/pmc/> and input a search term.
- From the results page, select the menu labeled "Send to:" and select "File", with a "PMCID List" format.
- Move the downloaded list to the "search" folder of the local asd-siloing-exploratory repository and rename it to "pmc\_result.txt".
- Run: `py -n 90000 .\scripts\select-article-subset.py -i .\search\pmc_result.txt -o .\search\article-test-subset.txt`
- Run: `py .\scripts\download_abstracts.py`
- Run: `py .\scripts\fetch_article_info.py`
- Run: `mysqlsh -u <username> -h localhost -f .\scripts\distinct_journals_query.sql --sql 1> journal_list.txt`
- Run: `py .\scripts\generate_journal_query.py`
- Run: `py .\scripts\chunk_journal_query.py`
- In a web browser, navigate to <https://www.ncbi.nlm.nih.gov/nlmcatalog>
- Take the output of the chunk\_journal\_query script and run each query individually in the NLM Catalog. Make sure to download the results in XML format and move each of them to journal\_classification\nlm\_catalog\_results.
- Run: `py .\scripts\extract_source_info.py`

**Validation**

- See the `data_analysis\validation.ipynb` Jupyter notebook

**Final Clustering**

- See the `data_analysis\cluster_analysis.ipynb` Jupyter notebook