Project 2: HetIONet

Course: Big Data Technology

Student: Fabiola Li Wu

Instructor: Arezoo Bybordi

Due Date: Monday, April 28th, 2025

Data: HetIONet (nodes.tsv and edges.tsv)

Q1: For each drug, compute the number of genes and the number of diseases associated with the drug. Output results with the top 5 number of genes in descending order.

- 1. Filter all the edges with source = 'Compund'
- 2. Filter all the genes and diseases from step 1.
- 3. Map every compound < compoundID, 1>
- 4. Group the maps by the compoundID e.g. <compundID, genesAmount> and <compundID, diseaseAmount>
- 5. Sort the map by its values.
- 6. Prints out the first 5 compoundID, amount of genes, and amount of diseases associated with the drug(compound)

```
Query 1: Top 5 compounds with most genes associated, and their associated diseases
Query 2: Query 2: Top 5 diseases with drugs associated Query 3: Names of top 5 compounds with most genes associate. Press 0: EXIT
Enter the query number: 1
Query 1: Top 5 compounds with most genes associated, and their associated diseases
Compound ID
                        Genes
                                    Diseases
Compound::DB08865
Compound::DB01254
                        564
                                    17
7
                        532
Compound::DB00997
Compound::DB00570
                        523
Compound::DB00390
```

- Q2: Compute the number of diseases associated with 1, 2, 3,..., n drugs. Output results with the top 5 number of diseases in descending order.

- 1. Filter all the compounds that have disease in their target.
- 2. Map <disease, drugsAmount> e.g: disease1 has 4 drugs related to it -> <disease1, 4>
- 3. Filter out the diseases with amount greater than n.
- 4. Map <drugAmount, drugAmountAmount>. For example: <disease1, 4>, <disease4, 4>, <disease10, 4> -> <4, 3>
- 5. Print out.

- Q3: Get the name of drugs that have the top 5 number of genes. Output the results.

- 1. Filter all the edges with source = 'Compund'
- 2. Filter all the genes and diseases from step 1.
- 3. Map every compound < compoundID, 1>
- 4. Group the maps by the compoundID e.g. <compundID, genesAmount>
- 5. Sort the map by its values.
- 6. Print out the first 5 compound name by getting it from the nodes.tsv file, and the amount of genes.