Objective
- Provide an ideal software pipeline which can supply valid, reproducible and reliable correlation networks.

Motivation and background
- Correlation networks are ideal to describe the relationship between the expression profiles of genes.
- When genes corresponding to a particular part of the body becomes not expressed, it leads to impairment or mutation.
- We want to identify genes that are expressed in concert to healthy development of a cell can be identified and even changes leading to disease can be detected.
- However, this concept is not fully applied due to lack of benchmarking studies confirming universal applicability.
- Our aim is to explore the robustness of gene expressions by comparing structural similarities of commonly developed networks using big data infrastructures.

Methodology
1. Dataset extraction from NCBI
2. Data cleaning and processing
3. Data conversion
4. Finding the overlapping edges
5. Correlation networks creation
6. Statistical data analysis

Hypothesis
- We want to compare genes expressed under different conditions but originating from the same platform and the same organism (Mus musculus, or mouse), to see if the correlation is consistent between experiments (because it is always there) or not (because it is unique). Our null hypothesis is that the correlation does not vary widely always (that is, there is a certain range) or not (because it is unique). Our null hypothesis is that the correlation is consistent between experiments (because it is always there) or not (because it is unique).

Dataset Selection
- Studied all the model organisms and selected mouse for our study.
- Used selenium web automation tool to extract top hundred datasets with highest number of samples.
- Finalized GSE 6514 dataset as it is satisfying our criteria of ‘same organism (mouse), same platform (GPL1261), same tissue (Brain’). It has the highest number of samples (90) out of all eligible datasets.
- Used java program to find out all the possible overlapping edges by pair-wise comparison of all 18 networks, or a total of 153 combinations.

Data Cleaning and Conversion
- Cleaned the raw dataset using excel and converted the data by suing Perl software from Dr. Cooper to create correlation.
- Subdivided the dataset into 18 small datasets (5 samples each for a dataset)
- Used java program to find out all the possible overlapping edges by pair-wise comparison of all 18 networks, or a total of 153 combinations.

Results - Networks
- Converted huge network images into tables by using Neo4j
- Analysing all the 153 network images and related tables.
- Working on a java program which takes a file with all the unique edges from all of those network files.
- As of now, we couldn’t find any common edge in all of those network files.
- Use of Neo4j
- Used a tool named Neo4j to create correlation networks which takes edge files as input.
- It is a graph DBMS and a tool to visualize networks.
- Uses Cypher Query Language.