Prerequisite Terminologies:

In order to have a thorough understanding of the main topic, you should have the basic concept of the following terms:

- Microarray
- Gene Expression Analysis
- Tissue Microarray

Introduction:

Microarray analysis techniques are used in interpreting the data generated from experiments on DNA (Gene chip analysis), RNA, and protein microarrays, which allow researchers to investigate the expression state of a large number of genes, in many cases, an organism's entire genome in a single experiment. Gene expression microarrays provide a snapshot of all the transcriptional activity in a biological sample. The power of these tools has been applied to a range of applications, including discovering novel disease subtypes and identifying underlying mechanisms of disease or drug response. Most microarray technologies, such as Affymetrix and Agilent, provide commercial

data analysis software alongside their microarray products. There are also open source options that utilize a variety of methods for analyzing microarray data. ArrayExpress is one of the repositories recommended by major scientific journals to archive functional genomics data from microarray and sequencing platforms to support reproducible research.

Steps:

- Open the homepage of the ArrayExpress database, which you can access from [here](#).
- Go to the 'Browse' tab to browse the ArrayExpress database to select a particular dataset on which you want to perform microarray analysis.
- On the 'Browse' page, you'll find accession IDs of particular experiments available on ArrayExpress database.
- The other information such as title, type of the search protocol, organism, assays, processed data and raw data is also provided on the browse page.
- Search results can be filtered using the drop down menus at the top of the results table. They can be filtered by:
  - **Organism:**
    Select the organism of your interest.
  - **Experiment type ((DNA assay, RNA assay, amplicon sequencing, metabolomic profiling, protein assay):**
  - Select the experiment type as 'RNA assays' because we need only transcription profiling by assays for microarray analysis.
  - **Technology (array assay, high-throughput sequencing, mass spectrometry):**

- ○ Select technology as 'Array assay' for the sake of microarray analysis.
- ○ **ArrayExpress data only** - experiments submitted directly to ArrayExpress, not imported from the NCBI Gene Expression Omnibus (GEO). Use the 'ArrayExpress data only' checkbox to activate this filter.
- After selecting a filter, click on the 'Filter' button on the right hand side to filter the experiments.
- Click on any accession ID of the experiment, it'll take you to the page of that particular experiment where you can find the following information:
  - ○ **Status:** provides the information that when that particular experiment was submitted, updated and released.
  - ○ **Organism:** mention the organism name.
  - ○ **Sample:** Provide a detailed sample information and links to further data.
  - ○ **Array:** Provides information of the array type.
  - ○ **Protocol:** Provide detailed protocol information.
  - ○ **Description:** Provide a detailed description of the particular experiment to understand it in a much better way.
  - ○ **Experiment type:** Information of the experiment type.
  - ○ **Files:** Following files are provided related to the particular experiment:
    - ■ Investigation description
    - ■ Sample and data relationship
    - ■ Raw data (Intensity values that are being calculated from the microarray images)
    - ■ Processed data

- ■ Array design

Note: These files are important for the microarray analysis. We'll see how to retrieve these files in the next section of this video.

Summary:

In this video tutorial of Microarray analysis, we learned about the microarray analysis techniques and their applications. We also got to know about the ArrayExpress database and how to select a particular experiment to get started with the microarray analysis.