

AstroBio web application is available at :

<http://ec2-3-135-218-7.us-east-2.compute.amazonaws.com:3000/>

MultiStress Explorer application is available at:

<http://ec2-3-16-161-145.us-east-2.compute.amazonaws.com:3838/ShinyApplication/>

To host [AstroBio](#) web App and database Locally, follow these steps:

### STEP 1: Download

- Node Js <https://nodejs.org/en/download/>
  - Node version 8.9.4+ is preferred
  - NPM version 6.13.0+ is preferred
- Mongodb <https://www.mongodb.com/try>
  - mongodb version 4.2.1+ is preferred
- Ensure you have npm and node installed. You can check by writing the following commands in terminal
  - node --version
  - npm -- version

### STEP 2: Clone/Download program locally:

1. Go to repository:  
[https://github.com/igemsoftware2020/Concordia\\_Montreal/tree/1.0.0](https://github.com/igemsoftware2020/Concordia_Montreal/tree/1.0.0)
2. Click on the Code button in green, and copy the HTTPS link
3. Go to the directory where you wish to store the program code, and write the following:
  - a. git clone  
[https://github.com/igemsoftware2020/Concordia\\_Montreal/tree/1.0.0](https://github.com/igemsoftware2020/Concordia_Montreal/tree/1.0.0)
  - b. Program files are now available locally under the name:  
**Concordia\_Montreal/**
  - c. **Concordia\_Montreal/** will be bald to recognize it as the main root folder for the repository.

### STEP 3: Setting up database:

1. Windows:
  - a. Create an empty folder, name it "db" in the following directory C:\data\db in your windows machine
  - b. Once the folder is created, go to terminal and navigate to the following directory C:\Program Files\MongoDB\Server(version)\bin

- c. Once in bin directory, write the command "mongod", mongod is now hosted in default port 27017
  - d. In case you wish to run your mongod in another port, please make sure to edit code and adjust port number accordingly
  - e. Mongod can now be accessed via the mongo command.
  - f. Once mongod is set locally, the program will be able to execute.
  - g. All necessary libraries are already included in the package that comes with this repository.
2. MacOS:
- a. Install Homebrew and XCode
  - b. You also have the option to install mongod from terminal
    - i. brew update
    - ii. brew install mongod
    - iii. mkdir -p /data/db
      - 1. If permission was needed,
        - a. sudo chown -R id -un /data/db
        - b. Then write password
    - iv. mongod
    - v. Mongod can now be accessed via the mongo command
  - c. Alternatively, one can also install it as follow:
    - i. brew tap mongodb/brew
    - ii. brew install mongodb-community@4.4
    - iii. brew services start mongodb-community@4.4
    - iv. mongod --config /usr/local/etc/mongod.conf --fork
    - v. Mongod can now be accessed via the mongo command
    - vi. Once mongod is set locally, the program will be able to execute.
    - vii. All necessary libraries are already included in the package that comes with this repository.
3. Linux:
- a. Create repository file that can be accessed with yum command after choosing which version to install
  - b. Choose version from here:  
<https://repo.mongodb.org/yum/amazon/2013.03/mongodb-org/>
  - c. Assuming we are going for version 4.4, create /etc/yum.d/mongodb-org-4.4.repo and add the following in the file:
    - i.
 

```
[mongodb-org-4.4]
name=MongoDB Repository
baseurl=https://repo.mongodb.org/yum/amazon/2013.03/mongodb-org/4.4/x86_64/
```

```
gpgcheck=1
enabled=1
gpgkey=https://www.mongodb.org/static/pgp/server-4.4.asc
```

- d. Once added, write the following commands
  - i. `sudo yum install -y mongodb-org`
  - ii. `sudo systemctl start mongod`
  - iii. You can verify status, `sudo systemctl status mongod`
  - iv. Start mongodb service, `sudo systemctl enable mongod`
  - v. Mongodb can now be accessed via the mongo command
  - vi. Once mongodb is set locally, the program will be able to execute.
  - vii. All necessary libraries are already included in the package that comes with this repository.
  - viii. You can stop mongodb service, `sudo systemctl stop mongod`

## Running AstroBio Application

- Go to the cloned program directory where `package.json` and `app.js` are and write the following command:
  - `npm start`
  - Program will run on port 3000
  - Application can be accessed locally on <http://localhost:3000/>
  - The program is currently running [here](#) on Amazon Elastic Compute Cloud

## Installation for MultiStress Explorer Application

- This application requires many packages in order to run successfully.
- Therefore, we have created a `setup_shiny.R` which can be found in the repository in the following directory:
  - **Concordia\_Montreal**/`scripts/R/shinyApp/setup_shiny.R`
  - Running the `setup_shiny.R` code will install needed packages
- Now you can run `app.R` in Rstudio and explore the shiny app. The program can be found in **Concordia\_Montreal**/`scripts/R/shinyApp/app.R`
- The program is currently running [here](#)

## Installation for R scripts, transcriptomics analysis

- All R programs for data analytics are included in the following two directories:
  - **Concordia\_Montreal**/scripts/R/DEA/
  - **Concordia\_Montreal**/scripts/python
- To set up all required packages for data analytics, run setup.R program which can be found in **Concordia\_Montreal**/scripts/R/DEA/setup.R
- Before running the program, make sure that all directories are set properly and points to the right files
- Using Rstudio, you can run any of the GSE####.R scripts and generate the differential expression analysis results.

### Code to install all needed packages to run AstroBio Multistress Explorer

```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")

install.packages("dplyr", "shiny", "sjmisc", "ggplot2", "factoextra")

BiocManager::install("Biobase")

BiocManager::install("ComplexHeatmap")
```

### Code to install all needed packages to run gene differential expression analysis

```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")

BiocManager::install()

BiocManager::install("GEOquery")

BiocManager::install("Biobase")

BiocManager::install("limma")

BiocManager::install("edgeR")

BiocManager::install("arrayQualityMetrics")

install.packages("devtools")

devtools::install_github("aryoda/R_enumerations@v0.3.0-beta")
```