

BME506
Fall 2023 – Lab 2
Language Basics – Arrays and Command-Line Arguments

Duration: one week.

Note:

1. Every lab assignment must be done individually.
2. When you name a folder or a file, you **should** avoid spaces in those names. For example, if you need to name a folder as **GreenApple**, you should name it as **GreenApple** instead of **Green Apple**. Naming a folder or a file without spaces in the names is to avoid compilation error that may occur while using MinGW build tools (For details, you may see here: http://www.mingw.org/wiki/Getting_Started).
3. **ALL code should be compiled and run on the laboratory computers before submission.**

Goals:

In the following lab, you will continue to work with refining your command of core C/C++ programming constructs, paying particular attention to the use of **1D** and **2D** arrays, **use of command-line arguments** and **use some aspects of cout formatting**.

- Please indent your code properly, include appropriate comments, and use proper names for functions and variables.
- The prototypes of the functions should be in a header file named **Lab2.h**.
- The implementation of the functions should be in a file named **Lab2.cpp**.
- The function **main** should also be in **Lab2.cpp**.
- The code of **Lab2.h** and the partial implementation of **main** (that should go in **Lab2.cpp**) has already been provided in the **Appendix** at the end of this file. You **must** use them in your implementation.

General steps to build the C++ project in Netbeans for Lab2:

1. Create a Netbeans project named **Lab2Proj** while taking care of the NOTE below.

NOTE: While creating the project, please **make sure**

- you set the field “**Project Location:**” appropriately. **Be sure to remember this project location** path. (To keep track of your **Project Location** you may do as follows: Once you have created the project, open a File Explorer, and go into your **Project Location** folder).
- once you have chosen your **Project Location**, enter the word **Lab2Proj** in the field “**Project Name:**”. Notice that your project name gets appended to your **Project Location** path.
- you **UN-CHECK** the checkbox on the left of “**Create Main File**” (We do so since we do not need any file named main.cpp file in this project).
- you Click [**Finish**] to create the project.

- a new folder named **Lab2Proj** has got created automatically under your **Project Location** folder. This **Lab2Proj** folder is your Netbeans *project folder*.
2. Under netbeans project **Lab2Proj**, right-click on the “Header Files” > “New” > “C++ Header File ...”. Set the field “**File Name:**” as **Lab2**. Set the “**Extension:**” as “**h**”. Click [**Finish**].
 3. The file **Lab2.h** is created. Copy the content for the header file from Appendix into this newly create file.
 4. Under netbeans project **Lab2Proj**, right-click on the “Source Files” > “New” > “C++ Source File ...”. Set the field “**File Name:**” as **Lab2**. Set the “**Extension:**” as “**cpp**”. Click [**Finish**].
 5. The file **Lab2.cpp** is created. Copy the content for the source file from Appendix into this newly create file.
 6. In **Lab2.cpp**, add the relevant functions that are intended to solve problems of **Part I**, **Part II**, and **Part III** given below.
 7. Note: At this point, make sure that your two newly created files **Lab2.h** and **Lab2.cpp** exists in the **Lab2Proj** folder.
 8. Right-Click on project **Lab2Proj** >
Select "Properties" >
Click "Run" >
On right, choose "Console Type" to be "Standard Output"
Click [Apply]
Click [OK]
 9. Build the **Lab2Proj** project.
 10. Open a Command Prompt window. Go to the folder **Lab2Proj\dist\Debug\MinGW-Windows** (where **Lab2Proj** is the Netbeans *project folder*). You should see that the executable **lab2proj.exe** has got created in this folder.
 11. Run the executable **lab2proj.exe** from the command prompt.

Important Notes:

1. When your code is error-free, it should build successfully (as seen at the compilation process at Netbean’s “Output” window). **However**, at times, in the Netbean’s *source editor* window, you may notice red line below a built-in method, such as `size()` method of built-in type `string`. You may notice this even if your program has built successfully—For example, in the invocation `str1.size()`, you may see a red line below the word `size`. This is misleading. Such a red line should disappear if you perform the following steps:

Right-Click on project **Lab2Proj** >
Select "Code Assistance" >
Select "Clean C/C++ cache and restart IDE"
2. **If you ever want to remove a project from Netbeans**, right-click on project > click “**Close**”. **AVOID** using “**Delete**” to remove a project from the Netbeans. If you ever remove a project using “**Delete**”, you will have to create a new project all over again to replace the “deleted” project.

In this lab, we will implement a series of functions that:

- simulate an exponential growth equation to model and log bacterial growth.
- allow to model the growth of multiple bacteria (different populations), store results in a 2D array and display the growth of populations in a formatted table

You will need to implement 4 functions:

- **initialize** – it initializes the bacterial sample (prompt the user for k and N_0).
- **calculate** – it calculates and store the bacterial population (over time $t=0$ to 10 hours) in an array.
- **display** – it outputs the growth summary of the single bacterial population from the 1D array, on console
- **twoDdisplay** - it outputs the growth summary of multiple bacterial populations from the 2D array, on console

PART I: Simulate exponential bacterial cell growth

1. This part allows the user to enter parameters k and N_0 that initialize a simple population of bacterial cells $N(t)$, which grows according to the exponential growth equation:

$$N(t) = N_0 e^{kt} \quad ; \text{ where } t=\text{time (hours)}, N_0 = \text{initial population (cells)}; k = \text{growth factor}$$

Examples of possible output from this part:

```
Initializing Bacteria:
Growth factor (k) [0.0-1.0] : 0.13
Initial population (N0) [1-1000] : 25

Growth Summary:

Hour   Population
=====
0      25.000
1      28.471
2      32.423
3      36.925
4      42.051
5      47.889
6      54.537
7      62.108
8      70.730
9      80.550
10     91.732
```

```
Initializing Bacteria:
Growth factor (k) [0.0-1.0] : 0.34
Initial population (N0) [1-1000] : 112

Growth Summary:

Hour   Population
=====
0      112.000
1      157.354
2      221.074
3      310.598
4      436.374
5      613.082
6      861.348
7      1210.149
8      1700.196
9      2388.686
10     3355.979
```

2. Compile the project **Lab2Proj**. Open a Command Prompt window. Go to the folder where the executable **lab2proj.exe** is located. Run the executable from the command prompt (>) as follows:

> lab2proj.exe

PART II: Pass the values of k and N_0 to the program as command-line arguments

1. In this case, we will use $k = 0.24$ and $N_0 = 38$ as example values. When k and N_0 are specified at command-line, the user should **not** be prompted to specify k and N_0 . The output should reflect as shown below.

```
Bacteria Initialized:
  Growth factor (k) = 0.24
  Initial poulation (N0) = 38

  Growth Summary:

  Hour      Population
  ====      =====
  0          38.000
  1          48.307
  2          61.411
  3          78.068
  4          99.244
  5          126.164
  6          160.386
  7          203.891
  8          259.196
  9          329.503
  10         418.881
```

3. Compile the project **Lab2Proj**. Open a Command Prompt window. Go to the folder where the executable **lab2proj.exe** is located. Run the executable at the command prompt (>) where k and N_0 are specified. For example, when k is specified as 0.24 and N_0 is specified as 38, the command-line should look like:
> lab2proj.exe 0.24 38

PART III: Pass the number of bacterial populations as a command-line argument

1. The following example command-line implies that 3 separate bacterial populations are to be tracked and logged when the program is run at the command prompt (>):

> **lab2proj.exe 3**

An example output is shown below:

```
Initializing Bacteria:
  Growth factor (k) [0.0-1.0] : 0.2
  Initial population (N0) [1-1000] : 20

Initializing Bacteria:
  Growth factor (k) [0.0-1.0] : 0.11
  Initial population (N0) [1-1000] : 80

Initializing Bacteria:
  Growth factor (k) [0.0-1.0] : 0.35
  Initial population (N0) [1-1000] : 12

Agar Summary:

  Hour      Population (0)    Population (1)    Population (2)
  =====
    0         20.000         80.000         12.000
    1         24.428         89.302         17.029
    2         29.836         99.686         24.165
    3         36.442        111.277         34.292
    4         44.511        124.217         48.662
    5         54.366        138.660         69.055
    6         66.402        154.783         97.994
    7         81.104        172.781        139.060
    8         99.061        192.872        197.336
    9        120.993        215.299        280.033
   10        147.781        240.333        397.385
```

2. Compile the project **Lab2Proj**. Open a Command Prompt window. Go to the folder where the executable **lab2proj.exe** is located. Run the executable at the command prompt (>) where the number of separate bacterial populations is specified. An example command-line where 3 separate bacterial populations is specified would be as follows:

> **lab2proj.exe 3**

Lab Submission

Deadline: See announcement in D2L for deadline.

ALL code should be compiled and run on the laboratory computers before submission.

Create a folder. Name it as YourLastname_YourFirstname_bme506_Labnumber.

Example: If student name is John Smith, the name of folder should be

Smith_John_bme506_Lab2.

Copy your Netbeans *project folder*, **Lab2Proj**, in the above folder. Make sure the folder **Lab2Proj** contains your two files **Lab2.h** and **Lab2.cpp**.

The above folder must also contain a duly filled and signed standard cover page. The cover page can be found on the departmental web site:
[Standard Assignment/Lab Cover Page](#)

Compress the above folder as a single zip file that is named according to the following rule:
YourLastname_YourFirstname_bme506_Labnumber.zip.
Example: Smith_John_bme506_Lab2.zip.

Upload the above zip file on D2L through the "Assessment" > "Assignments" link.

Note: If the code does not compile, the submission will receive a ZERO mark.

Appendix

#include <iomanip>

is a library with functions that can manipulate the formatting of variables passed to the output stream (cout). For instance, using the function 'setw(X)' in an output stream will use up to X characters to display the next variable in the stream (right-justifying the output).

```
cout << setw(8) << 2.6796 << endl;
cout << setw(8) << 2.67 << endl;
-----
      2.6796
      2.67
```

Similarly, functions like setprecision(X) can be used within the stream to control the number of significant digits, or decimal places to display when outputting variables.

[see <http://www.cplusplus.com/reference/iomanip/> for more details and examples of usage: particularly the links relating to setw, setprecision, setfill and setbase (which is used to convert output to hexadecimal, binary and formats relating to bases other than decimal)]

Command line arguments

We can pass arguments directly into our program at runtime (without having to request input from cin). For instance, if we call the executable of our program with an extended string that includes a whitespace separated list of string values, then these may be accessible by the main() routine. To enable such usage, main() must be declared in order to accept these arguments:

```
int main(int argc, char *argv[]) { ... }
```

Here, argc contains the number of whitespace separated strings on the command-line, and argv is an array of pointers to char objects (i.e. null terminated strings). For example, if our executable was called "myexe", and we called the program from the terminal using:

```
myexe hello 4 3.812 bme506
```

The command line string contains 5 whitespace separated substrings (*argc* = 5); and each would be stored as a string in the *argv* array:

```
argv[0] = "myexe"
argv[1] = "hello"
argv[2] = "4"
argv[3] = "3.812"
argv[4] = "bme506"
```

We can therefore extract and use these arguments to control our program (e.g. as input to control flow statements like if/then/else or switch).

#include <cstdlib> provides access to standard C library functions (e.g. *atoi()* or *atof()*) which can be used to convert strings of numeric values into numeric values (when assigning to int's or double's)

e.g. `int myInt = atoi(argv[4]);`

In your Lab2.h file, the code should be as follows:

```
#ifndef LAB2_H_
#define LAB2_H_
#include <iostream>

using namespace std;

void initialize(double& k, int& n0);
void calculate( const double k, const int n0, double array[]);
void display(const double array[]);
void twoDdisplay(int num, const double arr[][11]);

#endif /* LAB2_H_ */
```

In your Lab2.cpp file, the #include statement and the function main should be as follows. Fill the body of function main as required.

```
#include <iostream>
#include <iomanip>
#include <cmath>
#include <cstdlib>
#include "Lab2.h"

//implement the function initialize
//implement the function calculate
//implement the function display
```

```

//implement the function twoDdisplay

int main(int argc, char* argv[]) {
    double k;
    int n0;
    if (1 == argc) { //Part I
        //WRITE THE CODE FOR Part I HERE.
        ...
    }
    else if (2 == argc) { //Part III
        //WRITE THE CODE FOR Part III HERE.
        ...

    }
    else if (3 == argc) { //Part II
        //WRITE THE CODE FOR Part II HERE.
        ...

    }
    else {
        cout << "Number of command-line arguments "
              << "(including the name of the program) "
              << "should be three or less." << endl;
    }
} //end of main

```