

Brief introduction to Perseus

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You will find Perseus and instructions to download it and install it here:

<http://www.sas.upenn.edu/~vnanda/perseus/>

Vidit Nanda

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The **Perseus** Software Project for Rapid Computation of Persistent Homology

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[Basic Information and Usage](#)

[Persistent Homology of **Cubical** Toplexes](#)

[Persistent Homology of **Simplicial** Toplexes](#)

[Persistent Homology of **Vietoris-Rips** Complexes](#)

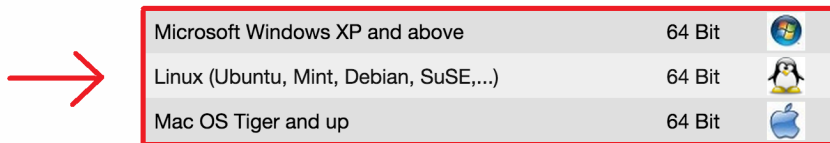
[Visualizing the Output: Persistent Homology via Intervals](#)




[Software License and Citations](#)

Click on the icon for your operating system in order to download the executable file or download the source code as a zipped file:

Download or Compile

Click on the icon for your operating system in order to download the suitable executable file. The current version is **4.0 Beta**.



Microsoft Windows XP and above	64 Bit	
Linux (Ubuntu, Mint, Debian, SuSE,...)	64 Bit	
Mac OS Tiger and up	64 Bit	

Once you have the file corresponding to your operating system, see "Basic Information and Usage" below. If you'd prefer to compile the software from source yourself instead, keep reading.

The source code is also available as a zipped file [here](#). Download this to a directory where you have read/write permissions. You can now Use any C++ compiler to compile the main file **Pers.cpp**. The choice of compiler depends mainly on your operating system. Microsoft Windows users have various compiler options such as the open-source [mingw](#), or the complete integrated development environment provided by the somewhat pricey [Microsoft Visual Studio](#). Mac users will probably require a hefty [Xcode](#) download and installation on their systems.

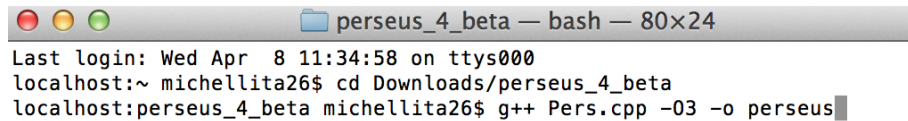
If using the [gcc](#) compiler from the command line, just go to the directory with the extracted source files and type:

```
g++ Pers.cpp -O3 -o perseus
```

Of course, you can replace "perseus" in the command above with any executable name of your choice.

Warning for New Users: The current version is not compatible with the [Clang compiler](#) (default on new Macs) or the recent [gcc 4.9](#). For now, new users can either get a genuine gcc for their machines or use the pre-compiled executable. Thanks to Steve and Ken Ferry for pointing out the clang issue and to Marcio Gameiro for the gcc issue. These will be resolved in the next (Beta 5) version of Perseus.

Once you download Perseus you can open up a terminal and change the directory to access Perseus. Assuming that Perseus is in the Downloads directory, you will need to type **cd Downloads/perseus_4.beta**. In order to compile it, you need to type **g++ Pers.cpp -O3 -o perseus**.

A terminal window titled "perseus_4_beta — bash — 80x24". The terminal shows the following commands and output:

```
Last login: Wed Apr 8 11:34:58 on ttys000
localhost:~ michellita26$ cd Downloads/perseus_4_beta
localhost:perseus_4_beta michellita26$ g++ Pers.cpp -O3 -o perseus
```

Make sure the file containing your data is located in the Perseus directory.

There are several ways to input your data. The website provides a thorough explanation on how to input your data points as a points with uniform birth times, points with different birth times and as a distance matrix.

For example, if you wanted to input your data as points with uniform birth times, you need to add (at the top) the number of coordinates per vertex (the dimension of your data), the scaling factor (almost always you should set this equal to 1), the step size (by how much will you increase the radius on each step) and the number of steps. Underneath you should have your data points and at the end of every row you should add the associated initial radius (you should set this $r = 0$).

You could do this on the terminal by typing **pico name_of_your_data_set** (you should replace “name_of_your_data_set” by the name of your file), and then typing the necessary numbers on top. Use **control + X** to exit and **control + O** to save. Alternatively, you could do this on any text editor without using the terminal.

Figure 1: Example of file format for points with uniform birth times

```
3: the ambient dimension, i.e., the number of coordinates per vertex.
1 0.01 100: the radius scaling factor  $k=1$ , the step size  $s=0.01$ , the number of steps  $N=100$ 
1.2 3.4 -0.9 0.5: the vertex (1.2, 3.4, -0.9) with associated radius  $r = 0.5$ 
2.0 -6.6 4.1 0.3: the vertex (2.0, -6.6, 4.1) with associated radius  $r = 0.3$ 
and so on!
```

Finally, once your file has the correct format, you can type **./perseus rips name_of_your_data_set** and it will compute the persistent homology of this complex and you can find the results in the **output.txt** file that will appear on your Perseus directory.