

# SETTING UP THE PROGRAMMING ENVIRONMENT



# Outline

- **Recommended local computer settings:**
  - For your laptop/desktop that will complete your homework
- **Server settings:**
  - Linux server : ITS Statistics and Computation service.
- **Very Basics of UNIX**
- **Submitting your first homework assignment.**

# Setting up your local computer

Operating systems: Microsoft Windows or Mac OS X

- 1. Setup terminal**
- 2. Setup development tools**
- 3. Install R**
- 4. Install Rstudio**
- 5. Install Anaconda (python + jupyter)**

# Windows : terminal & development tools

- **Install MobaXterm at <http://mobaxterm.mobatek.net/download.html>**
  - Using “Installer edition” will place the MobaXterm executable at C:\Program Files (x86)\Mobatek\MobaXterm Personal Edition
- **Download plugins at <http://mobaxterm.mobatek.net/plugins.html> and copy them to the directory where MobaXterm executable is.**
  - CygUtils.plugin: <http://mobaxterm.mobatek.net/CygUtils.plugin>
  - C++ development tools:  
<http://mobaxterm.mobatek.net/plugins/Development.mxt3>
  - Git: <http://mobaxterm.mobatek.net/plugins/Git.mxt3>
  - Type **'grep', 'g++', 'git'**, to verify that these plugins are installed.

# Mac : terminal & development tools

- Terminal : nothing to do, terminal is available at **/Applications/Utilities/Terminal.app**
- Install command line tools for Xcode
  - Go to App Store and install Xcode
  - or run  
**\$ xcode-select --install**
- Install homebrew and git
  - Follow installation instruction at <https://brew.sh/>
  - Then, run  
**\$ brew install git**

# Windows & Mac : R and Rstudio

- Download and install latest R at  
<https://cran.cnr.berkeley.edu/bin/windows/base/>  
<https://cran.cnr.berkeley.edu/bin/macosx/>
- Download RStudio at  
<https://www.rstudio.com/products/rstudio/download/#download>
- Install **tidyverse**, **devtools**, **Rcpp**, and **RcppArmadillo**  
> `install.packages(c("tidyverse", "devtools", "Rcpp", "RcppArmadillo"))`

# Windows & Mac : Anaconda

- Download the full anaconda package (python 3.6) at <https://www.anaconda.com/download/>
  - Or download miniconda at <https://conda.io/miniconda.html> (and install individual packages as needed)
- Install "R Essentials" conda package  
`$ conda install -c r r-essentials`  
(Windows users:  
run "Anaconda Prompt" at Start Menu to get the prompt)

# Windows Only : Additional Steps

- Need to install Rtools to use development tools  
<https://cran.r-project.org/bin/windows/Rtools/>
- Run MobaXterm to include Anaconda directories into your \$PATH environment.

```
echo 'export  
PATH=/mnt/c/Users/[YourWindowsUserName]/Anaconda3:/mnt/c/Users/[YourWindowsUserName]/Anaconda3/Scripts:/mnt/c/Users/[YourWindowsUserName]/Anaconda3/Library/bin:$PATH' >> ~/.bashrc
```



# Testing your local settings

- Run Terminal (or MobaXterm)
- Connect to ITS Statistics and Computation Server
  - Verify that you have AFS account  
[http://www.itcs.umich.edu/scs/access\\_problems.php#MFILETEST](http://www.itcs.umich.edu/scs/access_problems.php#MFILETEST)
  - Set up your AFS access if you don't have one  
[http://www.itcs.umich.edu/scs/access\\_problems.php#AFSPROVISION](http://www.itcs.umich.edu/scs/access_problems.php#AFSPROVISION)
  - Type **"ssh scs.dsc.umich.edu [Enter]"** in the terminal
  - Type your Kerberos password
- Did you successfully log in?

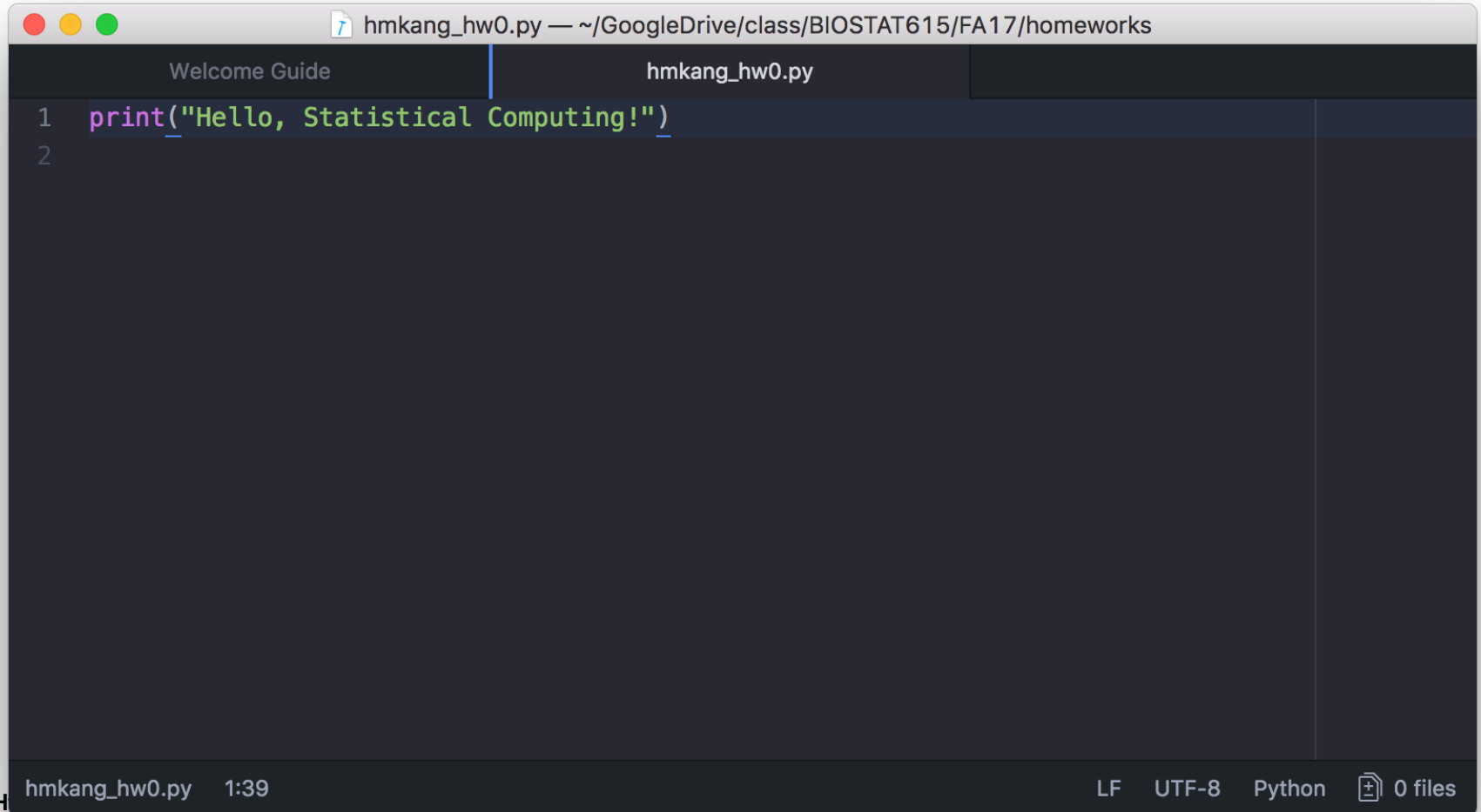
# Homework Assignment 0

- **You need to write three programs**
  - One python, One R, and One C++ program
- **Each problem should perform the same task**
  - Printing out “Hello, Statistical Computing!” to the screen
- **Verify your code runs correctly at SCS server**
  - It should run in **scs.dsc.umich.edu** not only in your laptop
- **Name your codes exactly this way**
  - If your UMICH username is hmkang(@umich.edu), for example,
    - **hmkang\_hw0.py , hmkang\_hw0.r, hmkang\_hw0.cpp** (All lowercase)
- **Attach three individual files separately to**  
**BIOSTAT.vron3jfg9g14axan@u.box.com**  
**(You will receive a confirmation email if submitted)**

# Starting with your favorite editor

- **For python and C++, pick your favorite editor**
  - Atom (Windows & Mac)
  - Code Writer (Windows)
  - Vim / GVim (Windows & Mac)
  - Emacs (Windows & Mac)
  - Sublime Text (Windows & Mac – Proprietary)
- **For R, you can use RStudio as an editor**
  - Or use one of the editors above
    - For Atom, install '**language-r**' package to support syntax highlighting for r language.

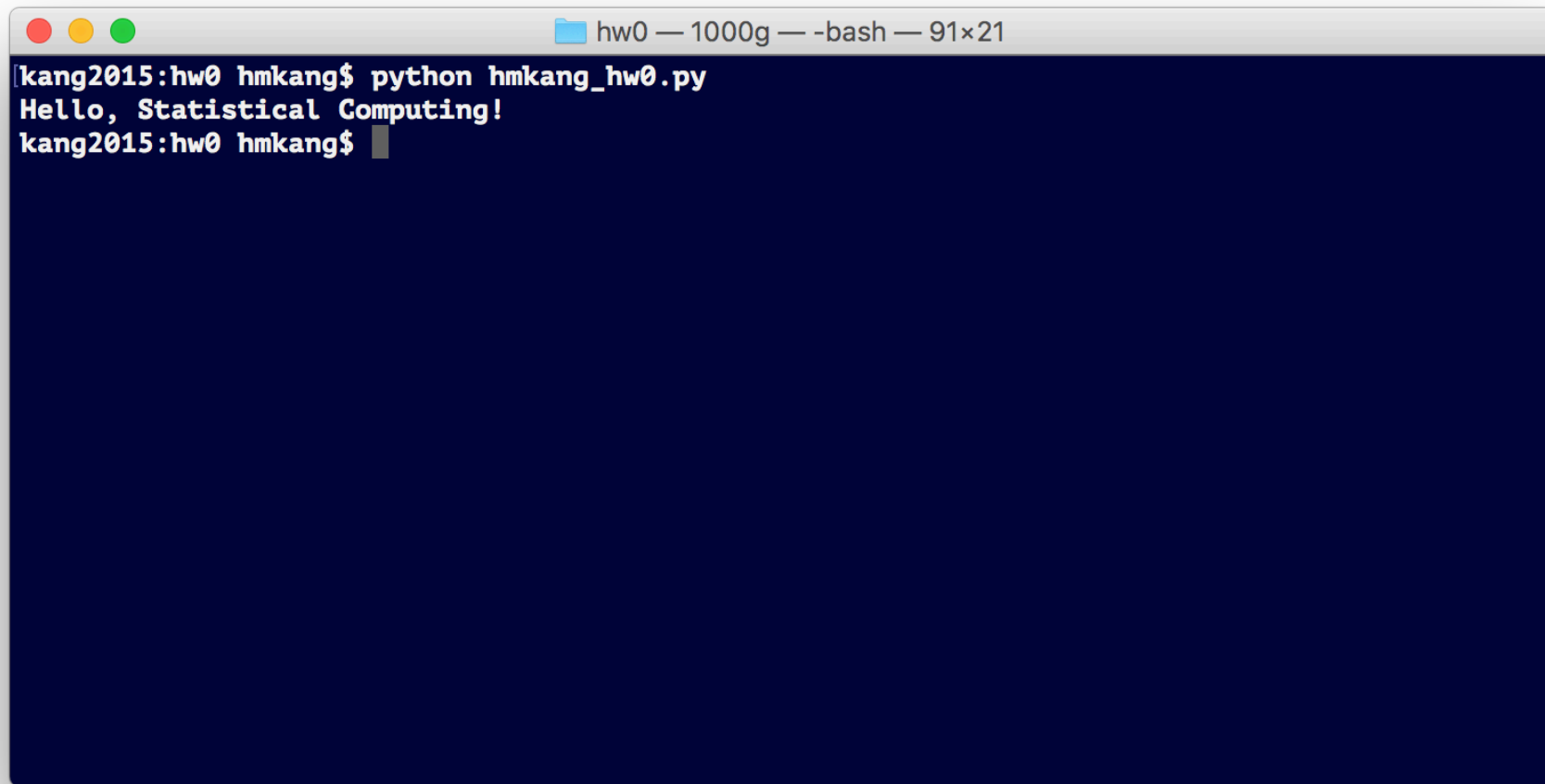
# Create a python code



The image shows a code editor window with a dark theme. The title bar at the top indicates the file is `hmkang_hw0.py` located at `~/GoogleDrive/class/BIOSTAT615/FA17/homeworks`. The editor has two tabs: `Welcome Guide` and `hmkang_hw0.py`. The `hmkang_hw0.py` tab is active, showing a single line of Python code: `print("Hello, Statistical Computing!")`. The code is color-coded: `print` is purple, the opening quote is green, the string content is green, and the closing quote is green. The line number 1 is visible on the left. The bottom status bar shows the file name `hmkang_hw0.py`, the time `1:39`, and the encoding `LF UTF-8 Python`. There is also a file explorer icon and `0 files` on the right.

```
1 print("Hello, Statistical Computing!")
```

# Check whether it runs locally



A terminal window with a dark blue background and white text. The window title bar shows three colored buttons (red, yellow, green) on the left, and a folder icon followed by the text "hw0 — 1000g — -bash — 91x21" on the right. The terminal content shows the command "python hmkang\_hw0.py" being executed, followed by the output "Hello, Statistical Computing!". The prompt "kang2015:hw0 hmkang\$" is visible at the end of the line.

```
kang2015:hw0 hmkang$ python hmkang_hw0.py
Hello, Statistical Computing!
kang2015:hw0 hmkang$
```

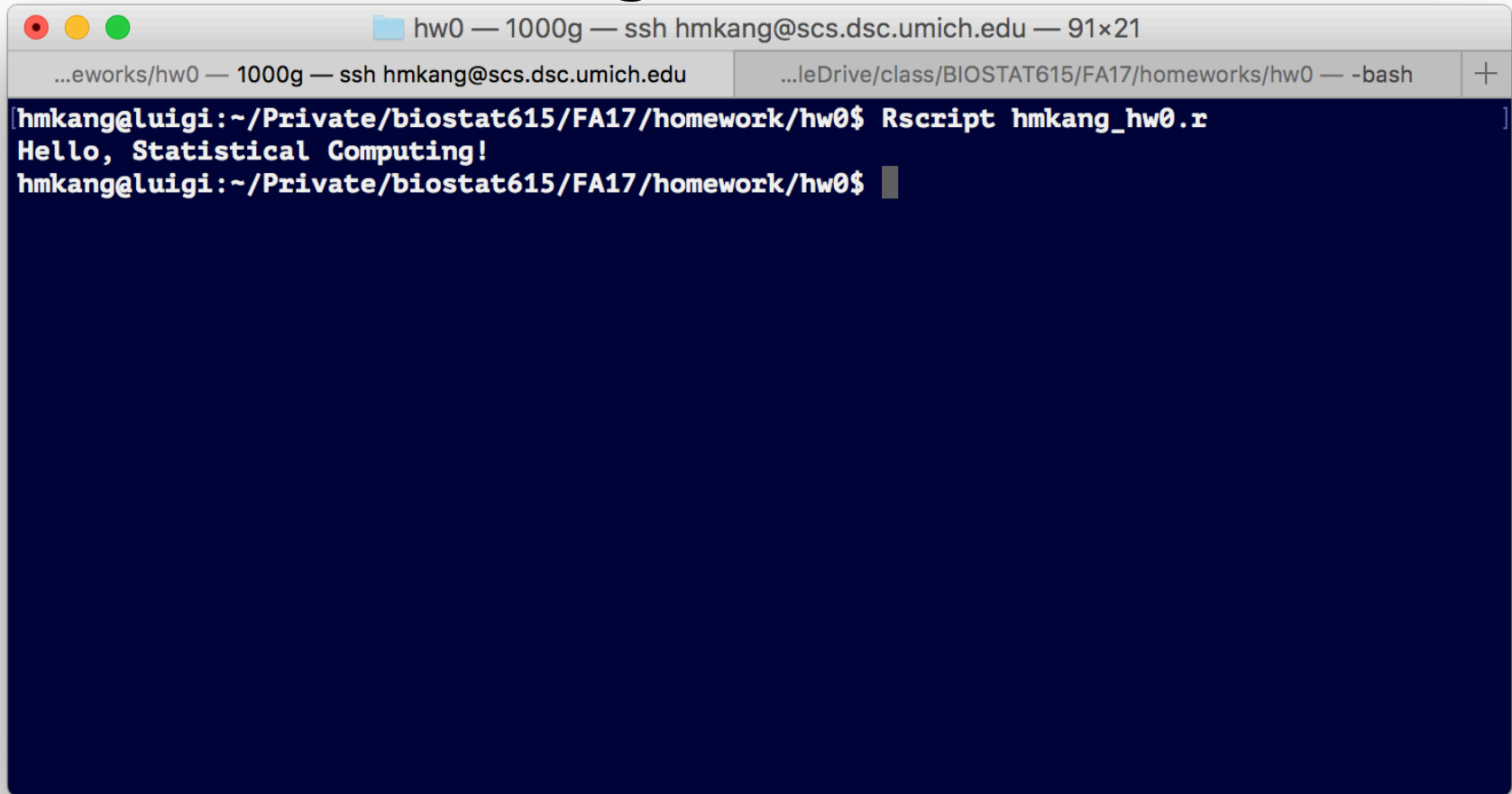
# Working on the SCS servers

- **You must to use SCS server to verify that your programs (compile and) run correctly in one of the SCS servers, as the instructors will evaluate your program in the same environment.**
- **It will be challenging to get used to UNIX environment, if you do not have previous experiences.**
  - If you are a UNIX newbie, use the online course at <https://www.codecademy.com/learn/learn-the-command-line> (free parts only) to learn the basics of UNIX.

# Verify that it runs on SCS server

1. Login in to the server - `$ ssh scs.dsc.umich.edu`
2. Create a directory (a suggestion)  
`$ mkdir --p ~/Private/biostat615/FA17/homework/hw0`
3. From another terminal, copy your python file to there  
`$ scp username_hw0.py username@scs.dsc.umich.edu:Private/biostat615/FA17/homework/hw0/`  
*(Or use MobaXterm or other GUI tools that supports SCP/SFTP file transfer)*
4. From the other terminal, change the working directory  
`$ cd ~/Private/biostat615/FA17/homework/hw0/`
5. Run the code and verify that it works  
`$ python username_hw0.py`

# Do the same thing in R

A terminal window with a light gray title bar and a dark blue background. The title bar contains three colored window control buttons (red, yellow, green) on the left, a folder icon and the text 'hw0 — 1000g — ssh hmkang@scs.dsc.umich.edu — 91x21' in the center, and a plus sign on the right. Below the title bar is a tab bar with two tabs: the first tab is labeled '...eworks/hw0 — 1000g — ssh hmkang@scs.dsc.umich.edu' and the second tab is labeled '...leDrive/class/BIOSTAT615/FA17/homeworks/hw0 — -bash'. The terminal content shows a command prompt 'hmkang@luigi:~/Private/biostat615/FA17/homework/hw0\$' followed by the command 'Rscript hmkang\_hw0.r'. The output of the command is 'Hello, Statistical Computing!'. The prompt is followed by a cursor. The terminal window is set against a white background.

```
hmkang@luigi:~/Private/biostat615/FA17/homework/hw0$ Rscript hmkang_hw0.r
Hello, Statistical Computing!
hmkang@luigi:~/Private/biostat615/FA17/homework/hw0$
```



# For C++, use this code.

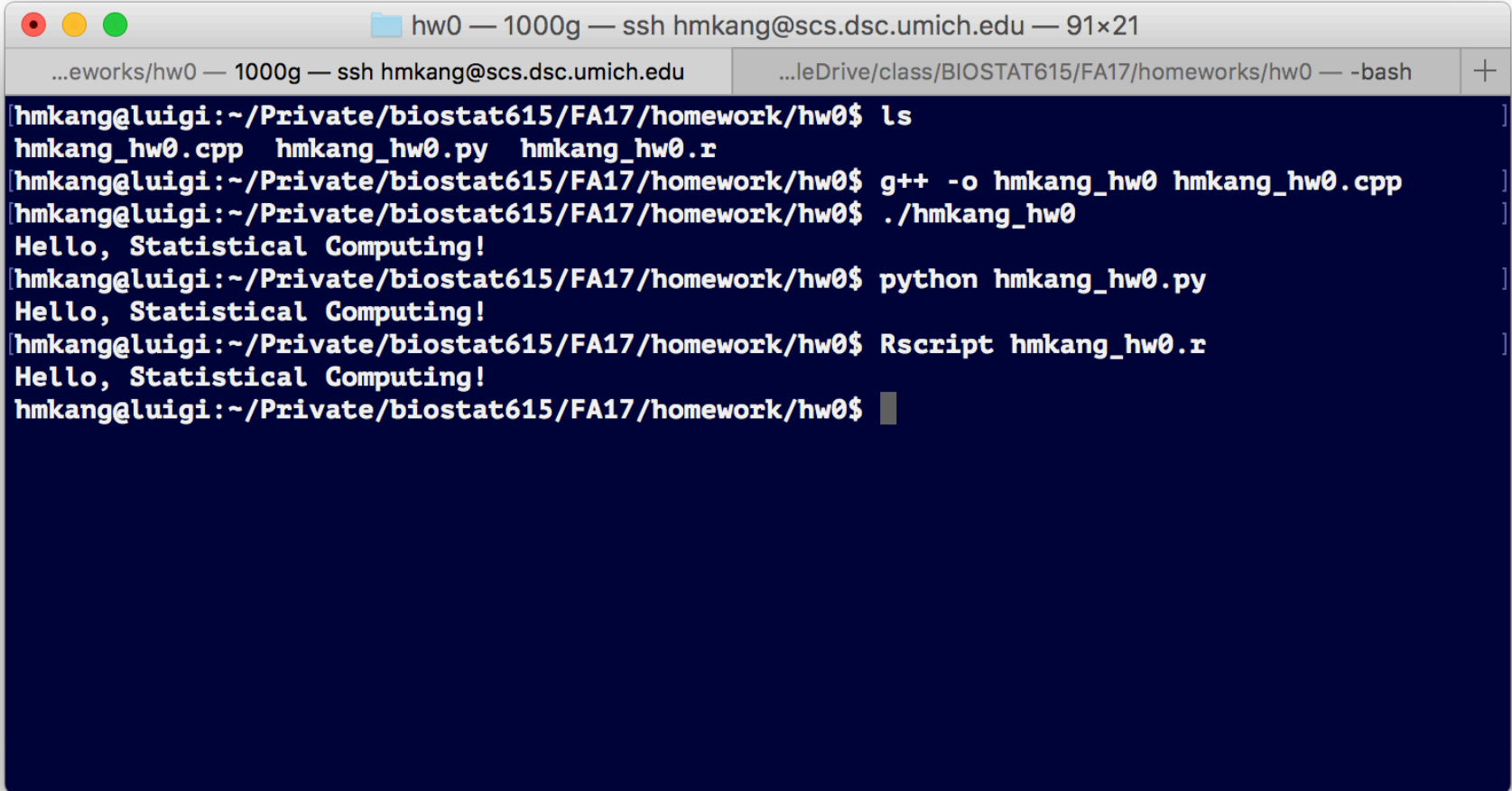


The image shows a screenshot of a C++ code editor window. The title bar at the top reads "hmkang\_hw0.cpp — ~/GoogleDrive/class/BIOSTAT615/FA17/homeworks". Below the title bar, there are three tabs: "Welcome Guide", "hmkang\_hw0.py", and "hmkang\_hw0.cpp". The "hmkang\_hw0.cpp" tab is active, showing the following C++ code:

```
1  #include <iostream>
2
3  int main(int argc, char** argv) {
4      std::cout << "Hello, Statistical Computing!" << std::endl;
5      return 0;
6  }
7
```

The code is highlighted with a light blue background. The editor window has a dark theme. At the bottom of the window, there is a status bar that shows "hw0/hmkang\_hw0.cpp 5:12", "LF", "UTF-8", "C++", and "0 files".

# Verify that it works at SCS server



```
hw0 — 1000g — ssh hmkang@scs.dsc.umich.edu — 91×21
...eworks/hw0 — 1000g — ssh hmkang@scs.dsc.umich.edu  ...leDrive/class/BIOSTAT615/FA17/homeworks/hw0 — -bash +
hmkang@luigi:~/Private/biostat615/FA17/homework/hw0$ ls
hmkang_hw0.cpp hmkang_hw0.py hmkang_hw0.r
hmkang@luigi:~/Private/biostat615/FA17/homework/hw0$ g++ -o hmkang_hw0 hmkang_hw0.cpp
hmkang@luigi:~/Private/biostat615/FA17/homework/hw0$ ./hmkang_hw0
Hello, Statistical Computing!
hmkang@luigi:~/Private/biostat615/FA17/homework/hw0$ python hmkang_hw0.py
Hello, Statistical Computing!
hmkang@luigi:~/Private/biostat615/FA17/homework/hw0$ Rscript hmkang_hw0.r
Hello, Statistical Computing!
hmkang@luigi:~/Private/biostat615/FA17/homework/hw0$
```

# Send exactly three files by email

- Send an email to **BIOSTAT.vron3jfg9g14axan@u.box.com**  
(This is for HW0 only. Address for HW1 will be different)
- Any title, and and text body
- Attach three files as separate attachments (in one email)
- File names must be
  - **username\_hw0.py**
  - **username\_hw0.r**
  - **username\_hw0.cpp** (All lowercase)
- Check your mailbox to confirm the receipt of homework

# Summary

- **Basic setup for homework assignments and implementation of lecture materials.**
- **Assignment 0 due is Tuesday September 12 by 8:30am**
- **No hard copy submission is required.**