

# Application of Genetics to Anthropological Research Workshop (AGAR - 2018)



**AUGUST 1 - AUGUST 3, *Buffalo, NY***

**THE ORGANIZATION TEAM WELCOMES YOU TO BUFFALO!** Please find below some relevant information with regards to your arrival, lodging, the workshop program, and other activities.

Local organization contact: Omer Gokcumen ([gokcumen@gmail.com](mailto:gokcumen@gmail.com))

Program and content contact: Joanna Malukiewicz ([jmalukie@gmail.com](mailto:jmalukie@gmail.com))

AAAG- or payment related issues: Ellen Quillen ([equillen@wakehealth.edu](mailto:equillen@wakehealth.edu))

In addition here are some phones:

Omer (he/him/his) - 215-704-4829

Joanna (she/her/hers) 732-701-7518

Skyler (he/him/his) - 518-335-0721

Izzy (they/them/theirs) - 505-206-7738

## **Emergency Contact Information**

New York State University Police

(716) 645-2222

Alternatively, use a Blue Light Phone on campus

If off campus, call 911

## WEB ACCOUNTS TO SET-UP PRIOR TO WORKSHOP:

1. Github
  - a. Please set up a basic user account for “Task Automation - Version Control with Git” Session
  - b. <https://github.com>
2. PythonAnywhere
  - a. Registration and workshop instructions are available on this graphic:  
<https://drive.google.com/file/d/1z0c-q-srnKphD5Pv2FFwYVip3e4SC5n5/view?usp=sharing>
  - b. Step 1. Navigate to [https://www.pythonanywhere.com/?affiliate\\_id=003df78d](https://www.pythonanywhere.com/?affiliate_id=003df78d)
  - c. Step 2. Click “Start running Python online in less than a minute!”
  - d. Step 3. Create a Beginner account
  - e. Step 4. Click “Account”
  - f. Step 5. Click “Teacher” tab
  - g. Step 6. Enter “rah” as your teacher’s username.

## SUGGESTED REVIEW MATERIAL PRIOR TO WORKSHOP:

1. Command Line Tutorial
  - a. <https://ryanstutorials.net/linuxtutorial/> (Modules 1-5)
2. Basic Bioinformatics Tutorial
  - a. <https://genomics.sschmeier.com/index.html>
3. Basic Python Tutorial:
  - a. <https://pythonforbiologists.com/introduction/>
4. Git Tutorial
  - a. <https://git-scm.com/book/en/v2> (Chapters 1-3)
5. R Tutorial
  - a. <https://www.youtube.com/playlist?list=PLqzoL9-eJTNBDdKgJgJzaQcY6OXmsXAHU> (First three videos)

## PRIOR TO ARRIVAL:

- Please let us know if you like to join us for Dinner on Wednesday and Thursday so that we can coordinate the commute.
- Please let us know about your arrival times (see below in red).

**LOCATION:** The lodging and the workshop are both located in the North Campus of University at Buffalo. All classes will be held on the second floor of Cooke Hall and the lodging will be provided in the Ellicott Complex. Please see map below and check out the more comprehensive interactive map - <http://www.buffalo.edu/home/visiting-ub/CampusMaps/maps.html>

**ARRIVAL BY AIR:** After you pick up your luggage at Buffalo Niagara International Airport, look outside the airport terminal for Airport Taxi Service. The campus is about 15-20 minutes with Taxi or Uber - and costs approximately \$30 dollars. Note that the UBER service may be a little slow if you are arriving after 10pm. You should tell the drivers that you want to go UB North

Campus - Ellicott Complex/Greiner Hall. If you have any questions please do not hesitate to contact us.

**CHECKING IN TO YOUR ROOMS:** Based on your selection at registration, we have reserved rooms for you in the Ellicott complex (for those who selected the Governor's Hall option) and the adjacent Greiner Hall. It is a beautiful spot near a lake, but it is a maze. To facilitate the check-in process, we will handle all the paperwork and assist you in locating your rooms once you arrive. **As such, it is important for us to know your approximate arrival (meeting place: in front of entrance to Greiner Hall indicated by red arrow) so that we can meet you there with your room keys. Please reply to this email with your expected arrival time at the dorms on Tuesday.**

**PARKING:** If you are driving and need to park your car, please contact [gokcumen@gmail.com](mailto:gokcumen@gmail.com) so that we can arrange a parking permit for you.

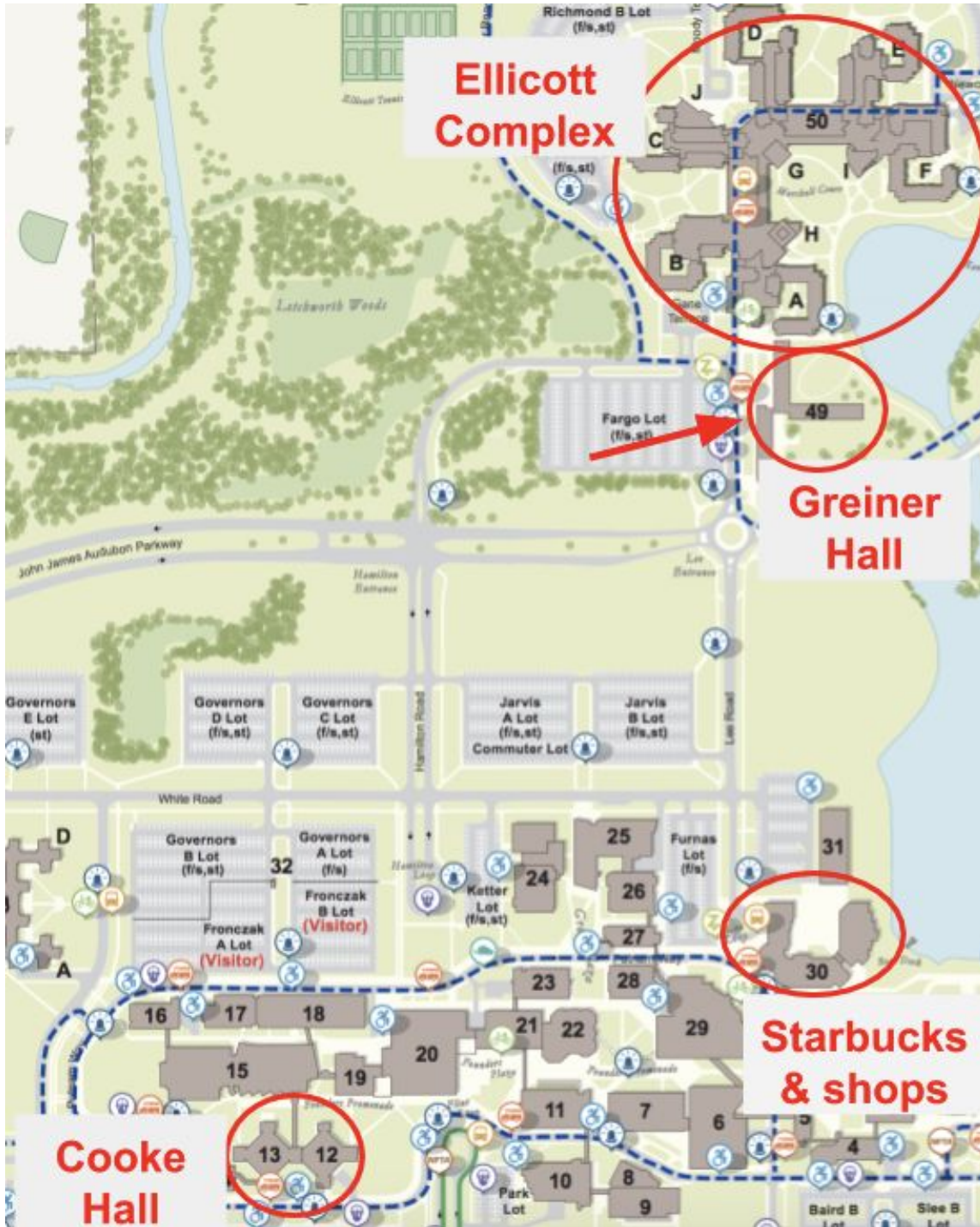
**INTERNET:** There is wireless throughout the campus. It can be accessible through “eduroam” or “UB Guest”

**DINING AND OTHER SHOPS:** There is a Starbucks and multiple Tim Horton’s coffee shops in the campus. There are also multiple dining options and a CVS for convenience items. Starbucks - a convenient mid-point in the campus is highlighted in the map. You can find other locations here - <https://myubcard.com/dining/locations> - and here <https://myubcard.com/shops/vendors>

If you feel adventurous, other off-campus options are:

Duff's Famous Wings: 3651 Sheridan Dr, Amherst, NY 14226 - 1.5 Miles (716) 834-6234  
Break'n Eggs Express: 1280 Sweet Home Rd, Buffalo, NY 14228 - 0.2 Miles (716) 688-6068  
Burrito Bay - 2341 Millersport Highway Getzville, NY 14068 - 1.1 Miles (716)-688-6070

Coffee and light pastries will be available in the mornings and lunch will be provided on August 1-3 (during the workshops). The dinner will not be provided but dinner events will be organized for those who want to join.



## **PROGRAM**

### **AUGUST 1**

#### **9AM - 9.30AM INTRO**

#### **9.30AM - 12pm - Task Automation - Version Control with Git**

*Instructor: Dr. Joanna Malukiewicz (German Primate Center, Instituto Adolfo Lutz, Universidade Federal do Vale São Francisco)*

Info: Introduction to command line, version control, and automation.

#### **12PM - 1.30PM LUNCH**

#### **1.30PM - 4PM - The Basics of Read Mapping and Variant Calling**

*Instructor: Dr. Tim Webster (Arizona State University and University of Utah)*

Info: Introduction to sequencing reads (fastq files), read mapping (SAM/BAM files), and variant calling (VCF files).

Topics also include read trimming and quality control, duplicate removal, and BAM file analysis and exploration. Run alignment pipeline starting with a raw fastq file and producing a raw VCF file.

#### **4PM-4.30PM - COFFEE BREAK**

#### **4.30PM - 7PM - The basics of VCF files**

*Instructor: Dr. Maria Nieves-Colón (Arizona State University and LANGEBIO-CINVESTAV)*

Info: VCF format and introduction to variant filtering.

Output data details: Filtered VCF files, SNP density, Fst, Tajima's D.

Run variant filtering and analysis pipeline starting with a raw VCF file and producing population genetic metrics from a filtered VCF.

### **AUGUST 2**

#### **8.30AM - 10.30AM - Data Management in R**

*Instructor: Dr. Ellen Quillen (Wake Forest University School of Medicine)*

Info: Basics of manipulating data in Tidy R, Tidyverse, Bioconductor, etc.

#### **10.30AM - 11.00AM - COFFEE BREAK**

#### **11.00AM -1.00PM - Statistical Considerations**

*Instructor: Christopher Clukay (University of Florida)*

Info: Basics of multiple testing correction methods and selection

Optimize computing time by taking advantage of multiple processors

**1.00PM - 2.00PM LUNCH**

**2.00PM - 3.15PM - Molecular genetic and genomic analysis of gene variants**

Instructor: Dr. R. Antonio Herrera (Stony Brook University)

Info: Identifying sources of variation and the role of mutation in the evolution of DNA sequence and gene function. Using python, we will explore aspects of molecular genetic and genomic function of identified variants and generate hypotheses about their effect on gene function.

**3.15PM - 3.45PM - COFFEE BREAK**

**3.45PM - 5.00PM - Structural Variants and Haplotype Interval Matching**

Instructors: Dr. Omer Gokcumen and Yen-Lung Onta Lin (University of Buffalo)

Info: Investigate genomic outliers and associated haplotypes for their impact on gene expression function, loss of function variants, etc.

**AUGUST 3**

**9.00AM -12PM - Admixture and Genetic Introgression Analysis**

Instructor: Dr. Krishna Veeramah (Stony Brook University)

Info: Applying  $f$  and  $D$  statistics using the ADMIXTOOLS package to infer population admixture

**12PM - 1.30PM LUNCH**

**1.30PM - 4.30PM - Data Visualization in R**

Instructor: Dr. Genevieve Housman (University of Chicago)

Info: Basics of Visualizing Data in R using ggplot2 and Gviz

**5PM- BARBEQUE**