Compgenomics Wiki and Github

Aroon Chande

Lecture 2

Thursday, January 11, 2018

Agenda for today

Quick intro to Comp Genomics

Introduce the class wiki page and Github

Choose your teams

Create your wiki profiles

This is a real world problem, in need of computational solutions



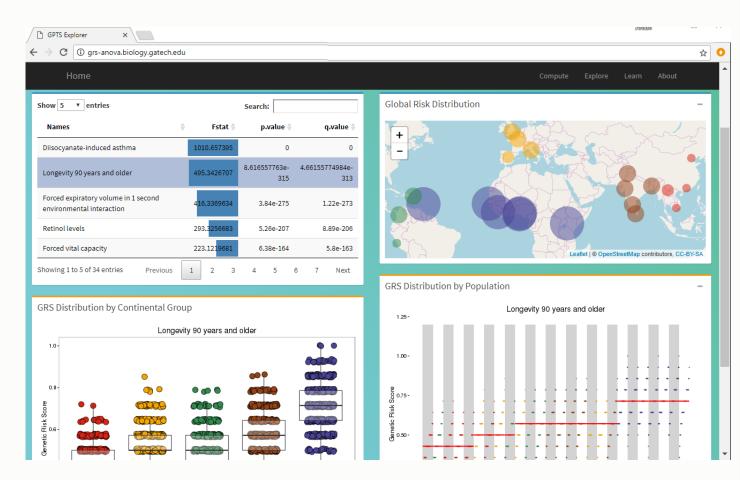
Translating genomics into practice for real-time surveillance and response to carbapenemase-producing Enterobacteriaceae: evidence from a complex multi-institutional KPC outbreak

Jason C. Kwong^{1,2,3,4}, Courtney R. Lane^{4,5}, Finn Romanes⁵, Anders Gonçalves da Silva^{1,4}, Marion Easton⁵, Katie Cronin⁶, Mary Jo Waters⁶, Takehiro Tomita⁴, Kerrie Stevens⁴, Mark B. Schultz^{1,2,4}, Sarah L. Baines^{1,2}, Norelle L. Sherry^{1,2,3}, Glen P. Carter^{1,2}, Andre Mu^{1,2}, Michelle Sait⁴, Susan A. Ballard^{1,4}, Torsten Seemann^{1,7}, Timothy P. Stinear^{1,2} and Benjamin P. Howden^{1,2,3,4}

DOI 10.7717/peerj.4210

Very quick overview of the class

- This is the *tenth* year that this course is being offered.
 - In the end you will produce something like this →



- **Start Early** Most of these processes will take time *i.e.*, don't start immediately after your background presentation, you need to present some preliminary results right after it.
 - **Server people** you have to start even earlier. Setting up the server could be easy or extremely difficult depending on how much you've read and understood about the tool (and your skill level).

• **Document continuously** – It is tempting to leave documentation of your work and results to the end; don't! Document your code, analysis, and results as you go. This results in better documentation and won't leave you awake at 3am the day before your group final presentation

Wiki writing is just as import as analysis documentation.

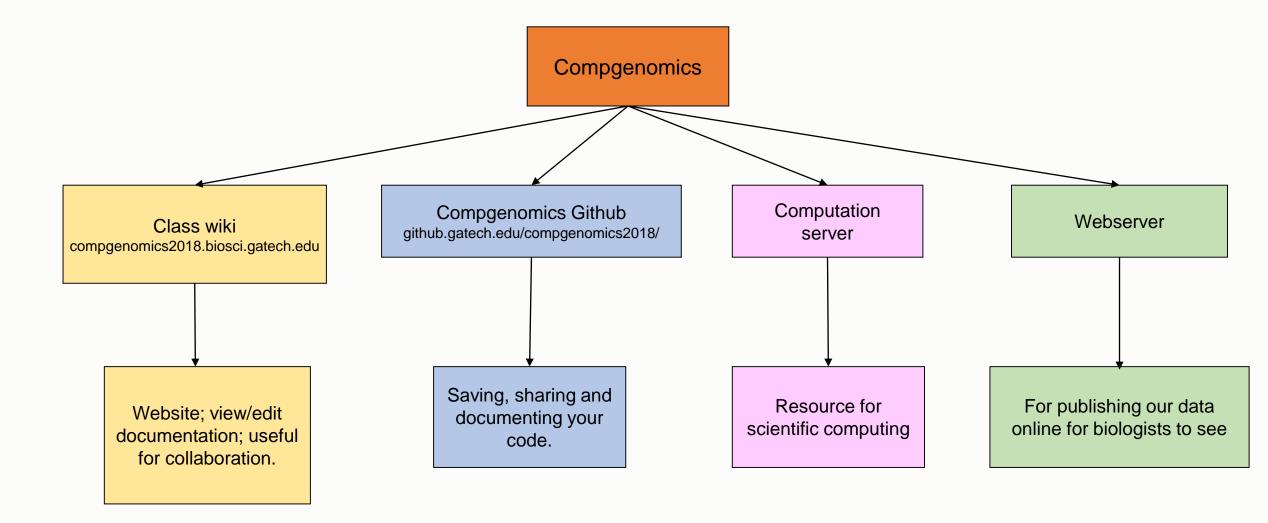
• Stick to an accession convention across the groups when processing genes/proteins – this will avoid confusion, unnecessary mapping and will make sure you do not wind up with duplicates

 Have proper channels for exchange of data – again, this avoids confusions

• Everyone likes the new stuff – Try to search for what is recent in the literature and attempt to use it along with the classical tools

 Understand what you are doing – don't blindly follow what other classes have done, have a proper understanding and basis of what you are doing

CompGenomics Resources



Course Wiki page

http://compgenomics2018.biosci.gatech.edu/

• The course wiki page is a public display of your work

• Lectures, readings, and all other course material can be found here

 We will not be using T-square, other than to send email announcements to the class

Previous wiki pages

 We are using different hosting infrastructure this year, past CompGenomics wiki pages can be found at:

compgenomics[2009-2016].biology.gatech.edu

 Use previous classes as a reference for what kind of documentation is expected

Don't reinvent the wheel

Or at least, don't reinvent it every time

Scientific research is building and expanding on existing knowledge

- For some of the tasks you'll be given, there may only be one "great" way to do them
 - We won't penalize doing the same thing as previous years if you provide your own, data-driven reasoning

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Wiki accounts

 All students are required to create a wiki account and contribute to the wiki

 In order to register you must use your "user@gatech.edu" email address

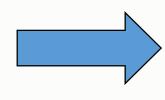
You have until Monday, January 15th to register an account

Wiki Accounts

 The wiki is public and where your collaborators, other scientists, and maybe future employers will see your work

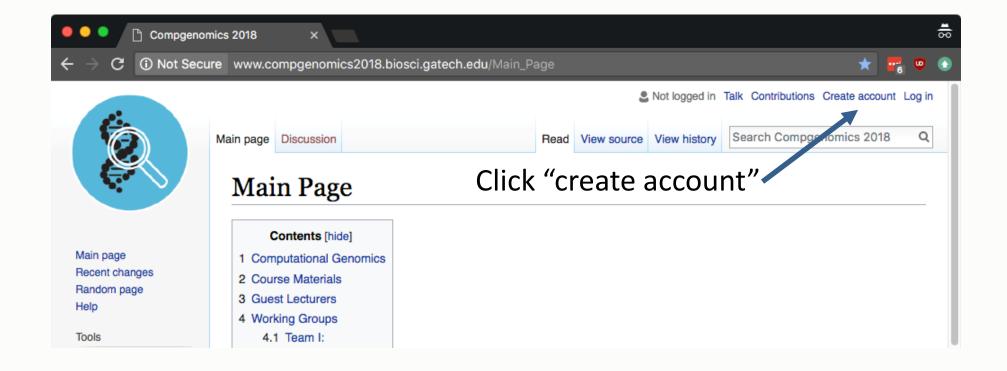
• Once we have assigned groups, add yourself on the Profiles page. Be sure to include a picture.



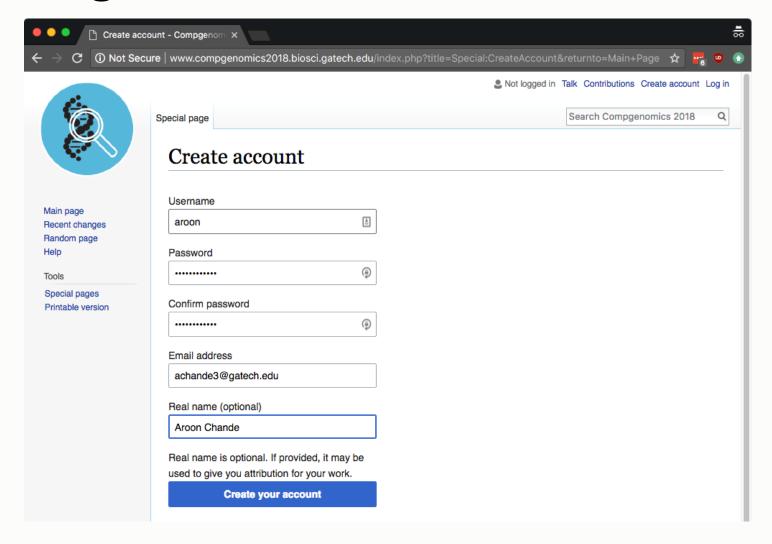




Account registration



Account registration



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Class Github

https://github.gatech.edu/compgenomics2018/

- I'll talk more about what git and source code management are next week on Tuesday
- This site will contain all your code, raw analysis and other work product
- During the semester, these data will be private, afterwards they will be open-sourced (on Github.com)

Why use git?

 Git and other source code management (SCM) tools are very useful for storing and tracking the files and scripts you create when working

• It provides an audit trail of who made what changes, when

 Use and proficiency with SCM is quickly becoming a required skill in both industry and the public sector (i.e. CDC)

Why use git?

• Git keeps everyone accountable

Keep collaborative files in one place

Provides a platform to organize, document, and share your work

Github student pack

https://education.github.com/pack

 Get free and discounted access to AWS (Cloud servers), DigitalOcean (Virtual servers), and other useful software tools

 Great for learning and refining some of the skills you'll learn this semester

Group selection