Introduction to the training course

Course materials

- Course materials are available here:
  https://github.com/eachambers/UNAMtraining

- Please feel free to ask questions

- I want this to be useful for you!

What you should have already

- A laptop (doesn't matter which OS)
- A UT EID with access to TACC
- Have already set up multi-factor authentication for TACC
- Be connected to the university's wifi network (utexas)

DATA

- What is RADseq / what do the data look like?
- Using cluster computing (TACC)
- How to work with bash / CLI

Processing

- How does ipyrad work & what do we need to look out for?
- Finalizing data assembly on TACC

Analysis

- Building trees with RAxml (on TACC)

Visualization

- Learning about tidy data
- Visualizing trees in ggplot & ggtree
- Running analyses in R

Structure of the course and materials

Conceptual lecture

Practical tutorial

take home work (not always!)

Log in to TACC Frontera using a **secure shell** on your computer. You will need your TACC user ID, your password, and to have set up multi-factor authentication (*if you want, you can paste the line below to log into TACC*).

Course schedule

	Topic	Practical tutorial	Relevant links/other material
DATA	1.1 Welcome 1.2 RADseq basics 1.3 Bash/CLI	1t. Bash/CLI basics	Becca Tarvin RADseq
Processing	2.1 RADseq bioinformatics 2.2 Intro to TACC	2t. Getting set up and running jobs in TACC	
	3.1 iPyrad basics 3.2 Running iPyrad	3t. iPyrad on TACC	iPyrad CLI
Analysis	4.1 Phylogenetics 4.2 Trees on TACC	4t. RAxML on TACC	
	5.1 Tidy data in R	5t. tidyverse in R	Tidyverse course materials (Claus Wilke)
Visualization	6.1 Data visualization in R	6t. ggplot and ggtree in R	RStats grad student course (2016, 2017)