## Teaching Notes

### By *Shawna Reed*

*Shawna.reed@quinnipiac.edu*

**Course Information**

Department: Biomedical Sciences

Level**Upper Undergraduate**

Course type: **Both**

Students: **Life Science and Pre-Health Majors**

Number of Students: 20-45 per class, 16-18 per lab

**Module Information**

Original Module Name: 1. Introduciton to BLAST, 3, Databases, 6 Phlyogenetics (combined)

Link to Original: <https://qubeshub.org/community/groups/gsfmn/final>

Modified Module Name: BLAST and Horizontal Gene Transfer

Files associated:

* Assignment QUBES\_BLAST\_ASSIGN
* F19\_P3\_GenomeSolver (Slide Deck)

Modification Learning Goals:

* Become familiar with BLAST and be able to use it for homology searches
* Be able to interpret BLAST results
* Picking a best match for a query sequence
* Identify an unknown sequence
* Use BLAST to compare evolution of other sequences to 16S identity in the same genus of bacteria
* Analyse BLAST results and compare to previous results
* Use BLAST to find Chlamydia with integrated phage sequences
* Analyse BLAST results to compare phage-derived genes and their distribution

**Teaching Notes**

*(Think about what you would like to read about this activity if you came back to it in 2 years)*

Suggestions for this section (not all required, and extras always welcome):

* What did you change and why?
	+ I changed many of the modules and combined them to use only NCBI BLAST to analyze genomic sequences for horizontal gene transfer. My lecture and lab time was constrained and I could not add multiple lectures to teach about new bioinformatic tools
* How did the activity go?
	+ What went well and why?
		- When I had time to lecture the students through, they seemed to understand that the phage genes were horizontally transferred
	+ What went wrong and why?
		- The students, as expected had a lot of trouble with BLAST and viewing and interpreting trees. If I had time I might move to using MEGA to compare sequences, and also do the activity in-class so we can talk through issues together. I would add a part where they draw out the 16S sequences, make a table of the Chlamydia species and compare the distribution of the genes.
* What was the prep like?
	+ How much time went into prep?
		- Probably about 3-4 hours
	+ Did you have to do any prep (i.e. grow cultures, grow seeds, order supplies) ahead of implementation?
		- No
* Would you do this activity again?
	+ - Yes
	+ What would you change in the future?
		- Change the activity as above, and do a more careful scaffolding to explain horizontal gene transfer
* What do you wish you’d known before you ran the activity?
	+ The students don’t really understand phylogenetic trees
* Is there anything else you would like to make note of?
* How does this activity fit in your overall course curriculum?
	+ Helps the students understand big data and horizontal gene transfer
* In what ways, if any, did you modify your teaching practice with this activity?
	+ I would not have done any activities about this topic, and would have spent less time discussing genomics and horizontal gene transfer.