

Name:

Bioinformatics Take Home Test #4

Due Date Monday 10/26/2015 before class

(This is an open book exam based on the honors system -- you can use notes, lecture notes, online manuals, and text books.)

Teamwork is not allowed on the exams, write down your own answers, do not cut and paste from webpages. If your answer uses a citation, give the source of the quoted text.)

All questions worth 1pt

1. According to Hennig a natural taxonomy should be based on which of the following?
 - A. shared primitive characters.
 - B. shared derived characters.
 - C. homoplasies.
 - D. non-shared derived characters.
 - E. None of the above.
2. Which of the following is true regarding genome rearrangements?
 - A. They occur frequently in evolution.
 - B. They are often responsible for erecting species barriers.
 - C. They can trigger speciation events.
 - D. Closely related organisms show fewer genome arrangements than more distantly related organisms
 - E. All of the above.
3. True/False In BLAST searches using only a single genome as target, proteins can have more than one match because of paralogy.
4. What is GC strand bias (based on location with respect to the origin and terminus of replication)?
 - A. There are more GC dinucleotide simple repeats near the origin.
 - B. The G versus C content of the leading strand versus lagging strand changes.
 - C. The CG versus AT content of a genome changes.
 - D. The GC versus AT content of the leading strand versus lagging strand changes.
 - E. None of the above.
5. Which of the following is NOT an advantage of performing BLAST on the command line?
 - A. It is easy to BLAST an entire genome against another entire genome
 - B. The same script to perform command line BLAST searches can be reused anytime one wants to add a BLAST step to a pipeline.
 - C. It is simple enough for anyone, even people with no computer skills, to point and click their way to results.
 - D. It is possible to write a script to run 100,000 BLAST searches in one go
 - E. Scripted BLAST searches can be put into a pipeline with other computer scripts, to perform a complex task for you, leaving one free to do other things
6. In the unix operating system, which command would one use to check if a file is in the current directory?
 - A. ls
 - B. cat
 - C. pwd
 - D. cd
 - E. qlogin
7. In the unix operating system, which command would one use to enter a subdirectory?
 - A. ls
 - B. chmod
 - C. pwd
 - D. cd
 - W. qlogin
8. In the principle component analysis, JALVIEW uses which of the following to define protein space?
 - A. The presence or absence of a conserved sequence motif to define protein space.
 - B. A tree based on percent identity to define groups that are close to each other in sequence space.
 - C. Each alignment column as a dimension to define protein space.
 - D. GC bias on the leading versus lagging strand.
 - E. None of the above.

9. What is a Principle Component Analysis?

- A. A way to visualize n-dimensional protein space by projecting it onto a 2-dimensional screen.
- B. BLAST is used to identify common motifs that together using domain shuffling make up the components of a large number of proteins.
- C. A measure of how many rearrangements a genome has undergone.
- D. A method for detecting duplicated genes.
- E. None of the above.

14. Which of the following is NOT one of the possible fates of a recently duplicated copy of a gene?

- A. Decay, loss of function, and piece-wise deletion.
- B. Gain a homing endonuclease domain and turn into an intein.
- C. Subfunctionalization (Both copies retain only part of the original function).
- D. Neofunctionalization (Acquires a new function).
- E. Sit around semi-permanently as junk DNA.

15. Which of the following is NOT an example how a new gene can be created?

- a) Through mutations
- b) Left over DNA of viruses or other genetic parasite being repurposed
- c) Golgi Apparatus packaging of proteins
- d) Gene duplication followed by neofunctionalization
- e) None of the above

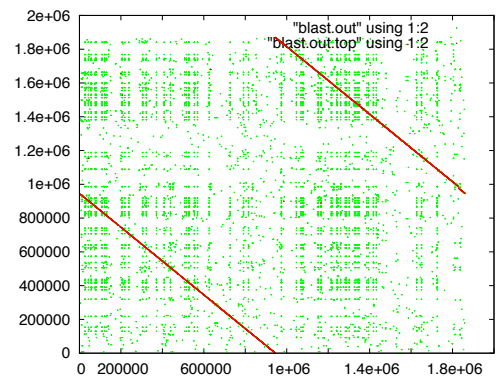
16. True/False Most duplicated genes go on to perform a new functions in an organism.

17. True/False Plastids are descended from free living Cyanobacteria (also sometimes called blue green algae).

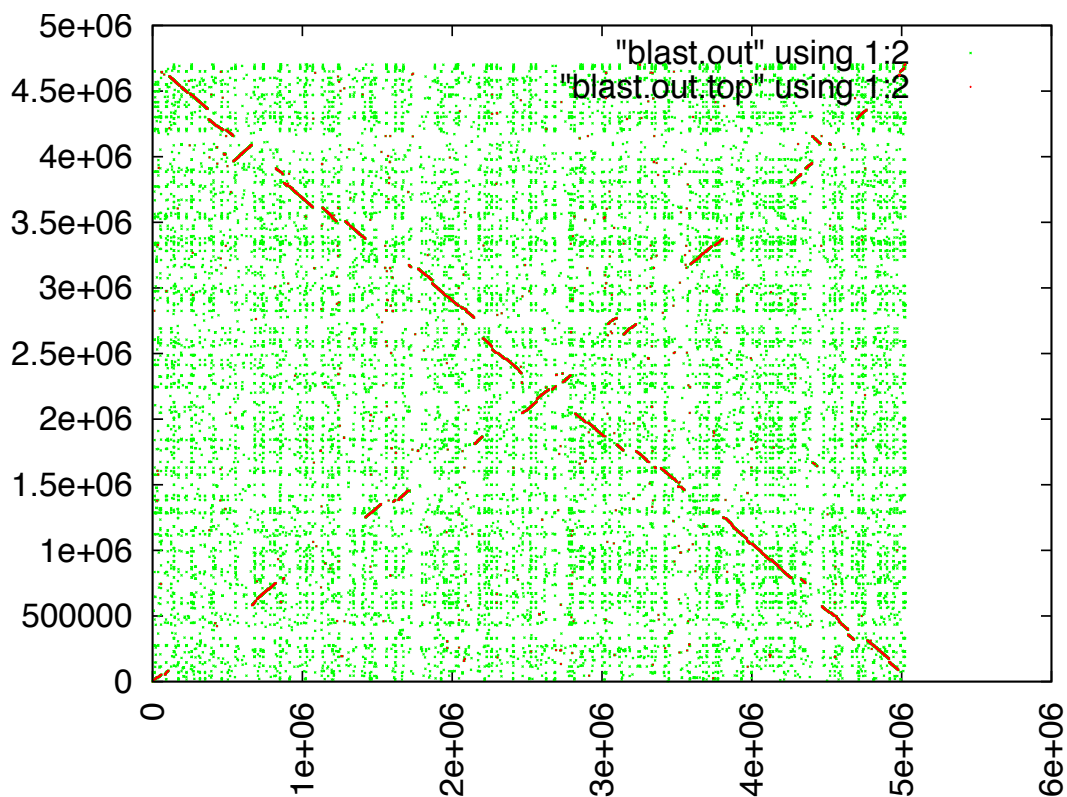
18. True/False There are many unrelated Eukaryotes that acquired the ability to photosynthesize by capturing as an endosymbiont an Eukaryote with a plastid endosymbiont. This is called secondary endosymbiosis.

19. What happened in the plot on the right?

- A. Two nearly identical genomes were used, but the origin of replication was miscalled in one.
- B. One large genome inversion, involving about half of the genome
- C. One round of whole genome duplication, so that every gene is present in one of the two genomes twice and only once in the other
- D. These genomes are so divergent that synteny can no longer be observed.
- E. There is a strong strand bias.



20. About how many genome rearrangement events are needed to produce the following graph?



21. A monophyletic group of organisms that is defined by which of the following?

- A) synapomorphy
- B) autapomorphy
- C) paraphyly
- D) polyphyly
- E) symplesiomorphy
- F) homoplasy

22. A paraphyletic group of organisms that is defined by which of the following?

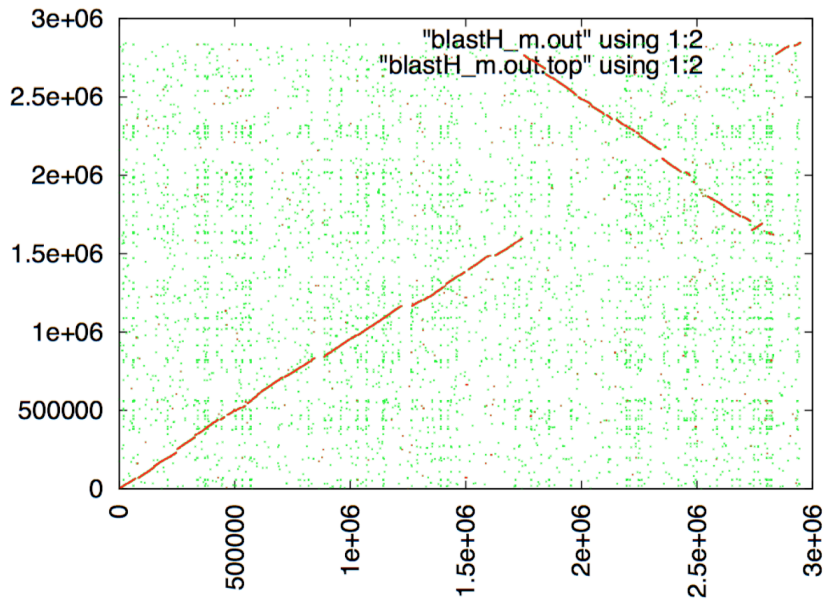
- A) synapomorphy
- B) autapomorphy
- C) paraphyly
- D) polyphyly
- E) symplesiomorphy
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22. A polyphyletic group of organisms that is defined by which of the following?

- A) synapomorphy
- B) autapomorphy
- C) paraphyly
- D) polyphyly
- E) symplesiomorphy
- F) homoplasy

23. What happened in the plot below?

- A. Two nearly identical genomes were used, but the origin of replication was miscalled in one.
- B. One large genome inversion, involving about half of the genome
- C. One round of whole genome duplication, so that every gene is present in one of the two genomes twice and only once in the other
- D. These genomes are so divergent that synteny can no longer be observed.
- E. There is a strong strand bias.



Extra credit (2pts):

Assuming that the figure in question 20 represents the comparison between two circular genomes, draw the recombination events that could have turned the gene order in one genome into the gene order in the other genome.