9. To run a different alignment method, change the method argument from “ClustalW” to “Muscle” or ”ClustalOmega”

10. There are gaps. When only looking at overlapped sequences as the amoA gene length was inconsistent there were 13 gaps.

11. 644

12. 41.6%

14. The two most closely related amoA gene were the two different strains of Nitrosococcous oceanii. The most distantly related were the uncultured beta-proteobacteria and the uncultured marine archea