**Summary of class discussions**

The summaries follow sequentially as given in class and urls as found notes on comparative studies. Please go over pages, then summaries, then review pages again.

You should be able to determine which habitat to save or evaluate the biodiversity in the examples given on the web pages. For the medical examples, you should be able to interpret trees given.

The class as a whole did an excellent job on summarizing the webpages and the following summaries should help you in learning the material on the webpages quickly.

***Conservation issues***

Conservation 08 Summary

All areas have species dying off, this is inevitable (biodiversity will half in the next 100 years). We need to decide how to choose where to put preservation efforts to save the most species. Recent conservation efforts are looking at overall species diversity in different areas. Modern preservation techniques focus on preserving an entire ecosystem over a specific species. So, by selecting areas with the most diverse phylogenetic trees there are the most benefits and the most species saved for your effort.

Conservation 10

The higher the biodiversity, the more valuable the ecosystem. Biodiversity should be calculated based on numbers and objective criteria. There are three steps to calculate the value of the ecosystem.

To calculate currency value of an ecosystem you must create a phylogenetic tree of the species in the ecosystem. Then, to figure out the amount of change you calculate the “length” of each branch. Longer branches will represent more change for that species. Lastly, you measure this value or richness by adding the branch lengths of the species that are present in the ecosystem of interest.

These steps allow you to obtain a currency value for the ecosystem and evaluate the biodiversity in the area.

* Branch length corresponds to the amount of evolutionary or genetic change. Longer branches= more change. Branch lengths can be calculated based on differences in SNPS between different groups.
* The currency value of an ecosystem is determined by adding the branch lengths of the species present in the ecosystem of interest.
* A community of organisms is likely to fare better against environmental stressors if it has a higher currency value relative to a community with a lower value. This is because currency value is calculated based on evolutionary and genetic change over time. Groups of species exhibiting greater genetic diversity than other groups are more likely to be able to deal with environmental changes.
* If an environment has low biodiversity currency, it may still be desired because it has an endangered, endemic, or sparse species.
* If a choice needs to be made, it would be better to concentrate conservation efforts on communities with the highest currency rating, as these have the greatest biodiversity to conserve.

Biomass considerations

Ecosystems with a higher biodiversity of plants produce a higher biomass. This translates into more food in the form of plant mass for animals, producing more oxygen and absorbing more greenhouse gases. The larger the genetic distance between plant species the more productive the ecosystem because they would have evolved to occupy distinct niches. It is not possible to preserve all species in a habitat. Evolutionary distance can be measured using a phylogenetic tree where the length of the branches is proportional to the evolutionary change that occurs on that branch. Specifically, they looked at 29 experiments that varied the species in the ecosystem and the branch length was a more reliable predictor of biomass than the number of species. To preserve functioning ecosystems, we should focus on increasing the evolutionary distance between species.

*Medical summaries.*

HIV

HIV is a modern disease in comparison to other ancient illness such as Parkinson’s and diabetes. It was first discovered in 1987 but was theorized to lurk in human populations for a long time before. A research team, lead by Michael Worobey, determined that HIV consisted of evolving populations instead of only existing as static infectious particles. It is especially fast at evolving within these populations because of its high mutation rate. As the virus infects more individuals, different versions of it appear, creating a tree-like network which can be conveniently mapped using a phylogenetic tree.

They discovered that the subtype M, the most common form of HIV, existed well before previously thought and it originated in Africa due to the consumption of chimpanzees in the form of SIV.

In 2010, scientists found a new strain of HIV that orginated from gorillas. The RNA sequence was different and resembled a virus in gorillas. It evolved specialized traits to infect humans and has jumped from chimps at least 3 times and at least once from gorillas.

In 2015, HIV spread quickly in Kinshasa and migration moved the virus quickly. It then jumped to humans at least 13 separate times due to global travel.

SARS

Biologists collected sample of the SARS virus’s genetic material from different sources. They created an evolutionary tree that showed that the infected civet and human SARS viruses were similar to each other. The most important piece of information from this tree was that the civet and human virus was branched within a clade of bat viruses, this means the ancestor of the civet and human strains seem to have been a bat virus at one point. It is concluded that the path of transmission occurred when civets came in contact with infected bats. The virus infected civets and then evolved and then was transmitted to humans most likely at the live animal market.

HLA genes

HLA genes are very diverse (and vary from person to person) and   
have evolved several mutations over time due to rapid adaptation of   
pathogens placing a stronger selection of genetic variation.   
  
HLA genes are important to evolutionary history and the human genome.   
Origins of populations shaped these mutations and variations of the HLA   
genes and understanding these variation lineages can help identify compatible  
donors whose genes contain similar mutations.    
  
i.e. transplants (the closer the match in HLA genes between donor and recipient  the more likely the procedure will be successful), blood donors, etc

Taxol

Phylogenies are important because they allow us to study species that are not very well known and from those predictions we can do useful things such as extract a cancer treatment compound called taxol from close relatives of the Pacific Yew. Taxol was originally discovered in the Pacific Yew, but it was inefficient and expensive to extract, however, the European Yew was discovered to have a similarly effective compound that produced taxol much more effectively. Later it was discovered that a fungus growing on the European Yew produced taxol even more efficiently.