**Phyloinformatics**

Assignment-6

Answer the following questions

1.Describe the structure of ‘Tree of life’ project.

Answer: The Tree of Life (ToL) is basically just a collection of materials documenting the diversity of the world's organisms. The conceptual and navigational structure of the Tree of Life web site is based upon the phylogenetic relationships among the creatures it catalogues and describes.

Tree of Life project's structure consists of:

* Hierarchical Relationships Between Groups of Organisms

So basically all organisms that are alive today or that have lived on this planet in the past are part of one large, genetically connected group: Life on Earth. The three major groups of living things:

* Eubacteria
* Archaea
* Eukaryotes ; is the containing group for a variety of groups including plants, animals, and fungi; animals is the containing group for several groups including sponges, cnidarians, and Bilateria; Bilateria is the containing groups for many groups like arthropods, molluscs, and nematodes, etc.

Life on Earth. Each of these major subgroups of Life is itself divided into a multitude of hierarchically nested subgroups.

* Categories of Tree of Life Pages

branches, leaves, other articles, notes, and treehouses; The structural backbone of the Tree of Life project consists of leaf and branch pages, which present the scientific core content of the Tree of Life collection. Each of these pages provides a synopsis of the most important characteristics of a particular group of organisms. Tree of Life leaf and branch pages are categorized according to four different [page status levels](http://tolweb.org/tree/home.pages/pagestatus.html) based on their completeness and review status.

Leaf Pages

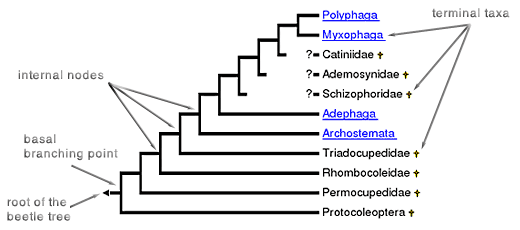
ToL leaf iconLeaf pages are Tree of Life pages about the terminal groups, i.e., the tips, of the tree of life. What this means is that the group of organisms that a leaf page is about is not further subdivided into independent genetic lineages or subgroups. Tree of Life leaf pages are most often pages about individual species; however, leaf pages are not defined by the rank of a given group; rather, if a species is divided into subspecies, varieties, or strains, and if Tree of Life authors decide to devote separate Tree of Life pages to these subgroups, then the pages for the subspecies, varieties, or strains, would be the leaf pages. Here are some examples of Tree of Life leaf pages: [The Vampire Squid](http://tolweb.org/Vampyroteuthis_infernalis), [The Tailed Frog](http://tolweb.org/Ascaphus_truei), [The Salamanderfish of Western Australia](http://tolweb.org/Lepidogalaxias_salamandroides), [Bembidion levettei](http://tolweb.org/Bembidion_levettei) (a carabid beetle), [Pelegrina aeneola](http://tolweb.org/Pelegrina_aeneola) (a jumping spider).

Branch Pages

* Branch pages are Tree of Life pages about groups of organism that can be divided into subgroups representing distinct genetic lineages. For example, a branch page may be about a group of related species, or it may be about a genus, a family, or a group of related families. Tree of Life branch pages always feature a phylogenetic tree or a list of taxa providing an overview of the subgroups included in the group that the branch page is about. Here are some examples of Tree of Life branch pages:
* [eukaryotes](http://tolweb.org/Eukaryotes)
* [sea cucumbers](http://tolweb.org/Holothuroidea)
* Terrestrial Vertebrates
* [Agaricomycotina](http://tolweb.org/Agaricomycotina) (a group of fungi),
* [dobsonflies](http://tolweb.org/Megaloptera).
* Links Between Tree of Life Pages

the Tree of Life tree diagram

In order to put the information about individual groups in a phylogenetic context, Tree of Life branch pages feature a tree diagram (or a list of subgroups if relationships among subgroups are unknown). Tree diagrams provide an overview of the phylogenetic relationships among subgroups. For example, the tree diagram of the [beetle](http://tolweb.org/coleoptera) page (Coleoptera) looks like this:



The tree diagram on the beetle (Coleoptera) page showing the relationships between the major beetle subgroups.

The basal branching point in the Coleoptera tree represents the ancestor of all beetles. This ancestor diversified over time into several descendent subgroups, which are represented as internal nodes (branching points) and terminal taxa at the tips of the beetle tree.

* The root on the left, the diagram shows that the ancestral beetle lineage gave rise, on the one hand, to members of the extinct Paleozoic group Protocoleoptera, and on the other to the ancestor of the remaining beetles. This ancestor in turn split into a species that gave rise to the extinct family Permocupedidae, and another that gave rise to the remainder of the beetles.
* The terminal taxa in the diagram, where we see Polyphaga and Myxophaga on adjacent branches. The ancestral species of these two groups split in two parts

1.To give rise to one species that was the ancestor of the Polyphaga.

2.Another species that was the ancestor of the Myxophaga.

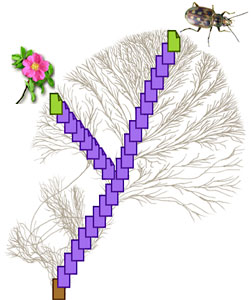
Even though it isn't shown on this diagram, the splits implied in this tree probably happened in the Permian period, before the time of the dinosaurs.

* Exploring the Tree of Life

travelling from the root to the leaves

The taxon list on each Tree of Life branch page is linked to the trees/lists of the pages for related groups. All Tree of Life pages taken together therefore present current ideas about the structure of the entire evolutionary tree of living things (at least to the extent that the project has been developed so far). Following the links up and down the tree, you can wander along the branches, exploring the diversity of many different kinds of organisms, while at the same time being reminded of the genetic connectedness of all of Life.

You may begin you journey at the root of all Life on Earth, travelling up the tree through levels of ever less inclusive groups, all the way up to the leaf pages of individual species or subspecies. Or you may start your exploration on a leaf page, following the link to its containing group and then moving through ever more inclusive containing groups, all the way down to the root.



-Links between taxon list on each Tree of Life pages let visitors explore the evolutionary tree of life from the bottom up or from the top down.

2. Explain the significant findings of Human, Chimp and Gorilla phylogeny considering

mtDNA, rRNA and proteins. Draw a phylogenetic tree based on the reported facts.

Answer:

Relatively small differences in genotype can lead to dramatic differences in phenotype: for example, chimpanzees and humans differ in only about 5% of their genomes. Africa was formerly inhabited by extinct apes closely allied to the gorilla and chimpanzee; and as these two species are now man’s nearest allies, it is somewhat more probable that our early progenitors lived on the African continent than elsewhere. The most commonly used recent definition is: Hominid – the group consisting of all modern and extinct Great Apes (that is, modern humans, chimpanzees, gorillas and orang-utans plus all their immediate ancestors).

It is analyzed that the sequence divergence amongst the three species that is, gorilla, chimpanzee and human varying from Hominidae and Pongidae. Apart from the genomic phylogeny, it is compared that the protein and rRNA phylogenies to increase the importance of phylogenetic analysis. The proteins selected are from the mitochondrial origin as mtDNA which codes for mitochondrial proteins, mutate at a higher rate compared to nuclear DNA, so as to give a more useful, magnified view of the diversity present in a population, and its history.

We are only about 96 percent the same as our closest relatives, chimpanzees. It has been analyzed that the phylogeny between three members of the Hominidae family that is, human, gorilla and chimpanzee using parsimony, BIONJ and PHYML methods and calculated the sequence divergence between them using in silico restriction digestion. For analysis, they have taken the genome, 12s and 16s rRNA and a set of 13 proteins coded by the mitochondrial DNA. Phylogeny based upon mitochondrial genome, 12s and 16srRNA supported the chimpanzee-human clade. Mitochondrial genome phylogeny was not found to predict the correct phylogeny by any of the three methods. However, some mitochondrial proteins were also found to be supporting the chimpanzee-gorilla clade. Moreover, not a single protein was found for which the phylogeny predicted by parsimony, BIONJ and PhyML methods were same. PhyML and BIONJ methods were found to predict correct phylogeny often. However, neither mitochondrial genome, rRNA nor any of the mitochondrial proteins was found for which the three methods predicted similar results. In an attempt to analyze the phylogenies more clearly, it is calculated that the sequence divergence between the genome of these three organisms. The results suggest the human mitochondrial genome to have diverged more from gorilla in comparison to chimpanzee. Even considering the evolutionary process to be influenced more by point mutation, it was analyzed that the digested sites of these three organisms and achieved the similar results. At ±2 error, human mitochondrial genome was found to have diverged 95.7% from gorilla genome compared to the 95.8% divergence of chimpanzee genome. No similar cut sites were found between human and chimpanzee at 0, ±1 and ±2 errors. This indicate gorilla to be having similarity with both human and chimpanzee at increased levels of error and hence to be the common ancestor.

