Jonah's eye genetics project

Intro:

I am interested in finding and counting the genetic differences between the eyes of nocturnal and diurnal animals, and looking at the genetic differences between eyes of animals that are evolutionarily far apart. I have two questions, what are the genetic differences between the eyes of nocturnal and diurnal animals?, and a secondary question, is there a large amount of evolutionary convergence and parallelism between the eyes of species that have evolved to be nocturnal or diurnal as mammals?

Evolutionary convergence is where two unrelated species evolve the same trait independently. Evolutionary parallelism is where two species that share a common ancestor use a gene from said common ancestor to help them both evolve the same trait. A diagram of this is available in figure one, on the next page.

For this project nocturnality means that the animal is either awake primarily after sunset and before sunrise or gathers most of its food and water underground. An animal is diurnal if it is awake primarily after sunrise and before sunset and, while it may burrow, gathers most of its food and water overground. Some differences between nocturnal and diurnal animals is that nocturnal eyes are often larger, with especially large pupils, have more rods per cones than diurnal animals, making them often colourblind, they often have a Tapetum Lucidium, which is a reflective membrane at the back of the eye, and have thicker, larger and more curved lenses than diurnal animals[2].

I think that I can mostly answer the first question, and I can somewhat answer the part of the second question that involves convergence, but I do not think I can find parallelism using my method.

To try and answer these questions, I am using some python programs I have written. These programs look at the genetic differences in some genes. The genes are being compared with other species inside some phylogenic subtrees, which are selected parts of a wider phylogenic tree and between these subtrees to see how eyes from further apart species differ. These subtrees are shown in figure 2 (on the next page). I am comparing the genes by getting some alignments of genes used in eye development. An alignment is a group of sequences, all for the same gene, but for the version of that gene in many different species. The link to the list of species found in the alignments can be found below in the resources section[1]. A list of "letters" in the same position across all of the species is called a column and the individual sequences are called rows.

I have 7 of these alignments, which are from the UCSC table browser(on their bioinformatics website at genome.ucsc.edu), and I am counting the genetic differences between the species in the alignment, which are changes in the "letters" that make up a gene from species to species, for example if in one spot in the alignment, humans might have an A, while tarsiers might have a T. These "letters" are actually molecules, adenine, guanine, cytosine and thymine. However, there isn't always a letter, sometimes there is just a gap, represented here as a "-". These entire column is removed here, because dashes often signal an intron. An intron is a portion of DNA that does not code for anything. The opposite of this is an exon, which is what codes for proteins. I then store these counts and also how many times there isn't a difference. The number of differences are then divided by the number of times there isn't a difference plus the number of times there isn't a difference and the results are stored. Then, the results are

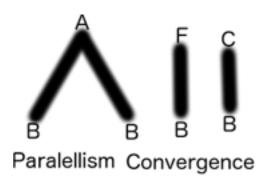
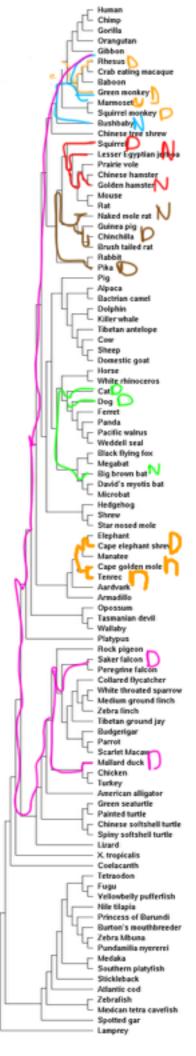


Figure 1



filtered to only show species in the aforementioned phylogenic subtrees, or only to show particularly low or high differences. Then the subtrees can then be averaged to compare different groups of species with one another.

Question:

My main question is: What are the genetic differences between the eyes of nocturnal and diurnal animals? Another question I'd like to answer is: How much evolutionary convergence and parallelism is there between the eyes of species that have evolved to be nocturnal or diurnal?

Hypotheses:

I think that when there is a switch in an animals waking hours there will be a moderate difference between their diurnal relatives, particularly in the lens and retina, because nocturnal eyes are usually fairly different from eyes of diurnal animals. The birds will probably have a large difference from the mammals, because they are evolutionarily far away from each other. There will be a moderate difference from between the different groups (primates, rodents and the other mammals), because many types of animals have quite different eyes, such as rodents and primates, and a large difference between an animal that switched to being nocturnal or diurnal and an animal who is far apart and has the opposite waking hours, because combining the differences between eyes of animals that are far apart evolutionarily and the moderate difference between animals that are awake at different times should add up to make a large difference.

Procedure:

- Find some phylogenic subtrees that have one change from being nocturnal to diurnal or vice versa. The bird tree is an exception to this, but it is just there look for differences between mammalian and avian eyes, not for the difference between nocturnal and diurnal eyes
- 2. Get some eye development genes found in the group of species that you are looking at, in this case, mammals. I chose CRYGB, OTX1, PAX6, PDE6B, SIX6, TULP 1, and VSX2. For more information on what these genes do, see the gene ontology[4]
- 3. Find the gene alignments for all of the genes that were chosen in step one.
- 4. Write a program that counts the differences in the alignments on every combination of species.
- 5. Run this program on each gene to see the differences between the nocturnal and diurnal animals in a tree, to tell the differences between the nocturnal and diurnal animals in the tree and to detect convergence and parallelism. If there are very few differences between the genes of the two species then that indicates convergence.

Program:

The code is split into three main programs, stuffGetter, stuffDoer and stuffReader. StuffGetter counts the genetic differences between the genes and stores the number of differences and the number of pairs in the sequence, then stores that in a file as a dictionary. StuffDoer reads that file and divides the number of differences by the number sames. StuffReader reads the results from stuffDoer and turns them into a spreadsheet, making the results easier to analyze.

Results:

The results for my experiment, along with my programs can be found at https://github.com/mrtopsyt/IrisGenomeProject. In some genes, particularly those associated with the lens, my first hypothesis is supported, however in a majority of the genes there is little to no difference. My second hypothesis, that when comparing the rhesus macaque to birds there will be a large difference was supported in every gene, although the differences varied wildly, being especially high in PAX6. Close analysis of the general spreadsheets (the sheets that contain every species) could reveal examples of convergence, however I do not have time to do this, leaving the rest of my hypotheses neither supported or contradicted.

Conclusion:

My questions were "What are the genetic differences between the eyes of nocturnal and diurnal animals" and "how much convergence and parallelism is there in the evolution of the eye when animals evolved eyes that allowed them to be awake at different times." I gathered some data which showed that there is a wide difference in the similarity of eyes in small groups. I did not gather sufficient data to show convergence or parallelism, though closer examination of my existing data, especially if compared with how closely related species are could help to support or contradict my hypotheses. The data I have supports my first hypothesis in genes associated with the lens, but is contradicted in other genes. My second hypothesis is supported in every gene and I did not get enough data to support or contradict my other hypotheses.

My experiment could be improved by factoring in how related species are and how through closer analysis of the data. An issue I noticed is that many of the genes I chose have purposes outside of the eye and the differences I have noticed could be due to an adaptation in another, possibly unrelated function.

Resources:

The eye development genes come from the genome ontology project. They are on the internet at geneontology.org.

The gene alignments and phylogenic tree come from the UCSC genome browser at genome.ucsc.edu

[1]: https://genome.ucsc.edu/cgi-bin/hgTrackUi?

hgsid=481435187_Ld6djzJgnb2LbqLj3uibAuB26qv1&c=chr4&g=cons100way. This is also where the phylogenic tree used in figure 2 comes from.

[2]: http://archives.evergreen.edu/webpages/curricular/2011-2012/m2o1112/web/nocturnal_mammals.html

[3]: http://biopython.org/wiki/Multiple_Alignment_Format. The biopython project, which made the man parser.

[4]: geneontology.org

This code and the