Analyzing Mitochondrial DNA in New World Monkeys

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Focus Points

- Bioinformatics
- New World Monkeys
- Python Script
- Human Genome

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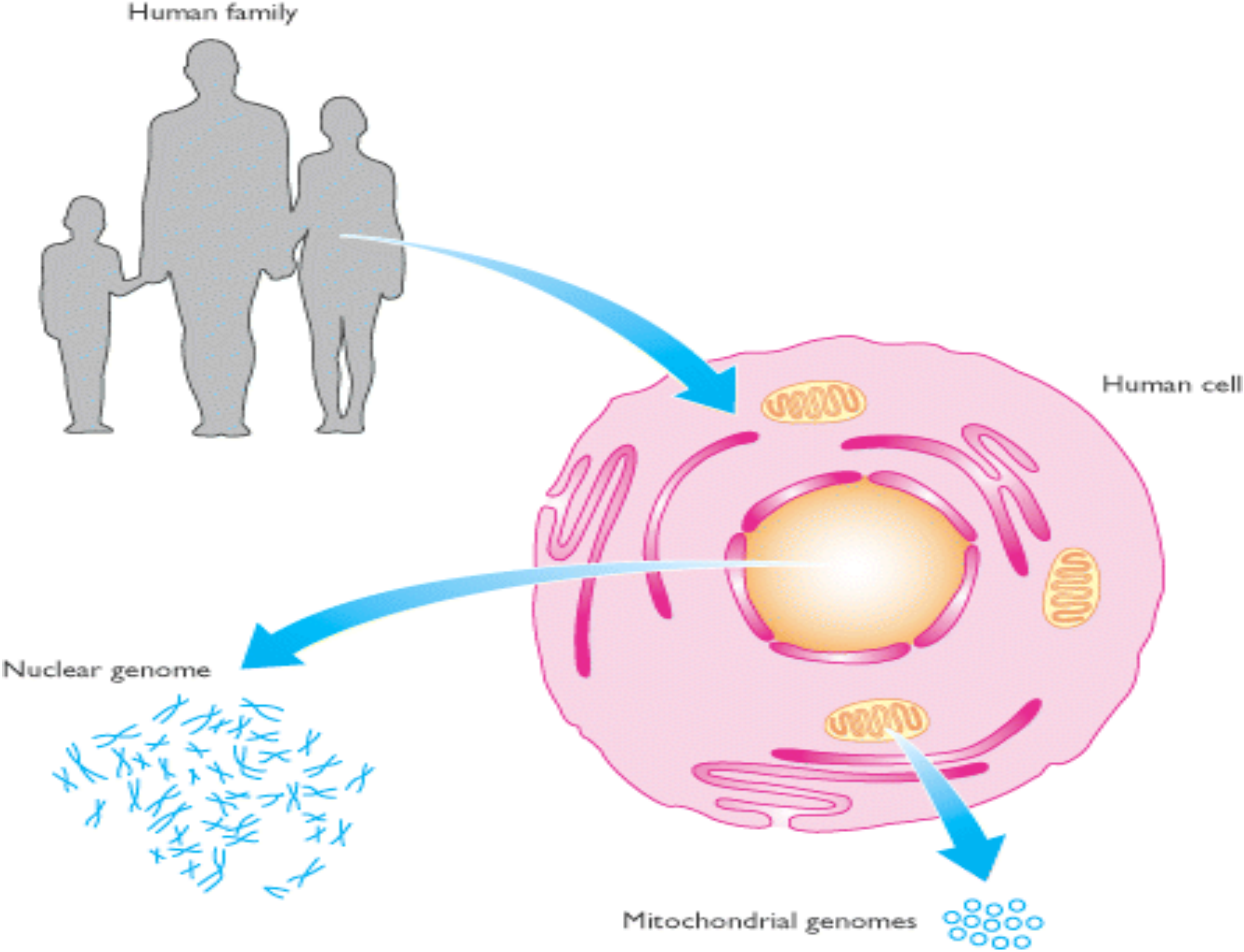
Goals/Purpose

- To find region of Mitochondrial DNA with most variation.
- Learn how to use python script to create programs that compare base pairs and add up the differences.
- At the end of the summer, us five interns will integrate our work.

Background Information

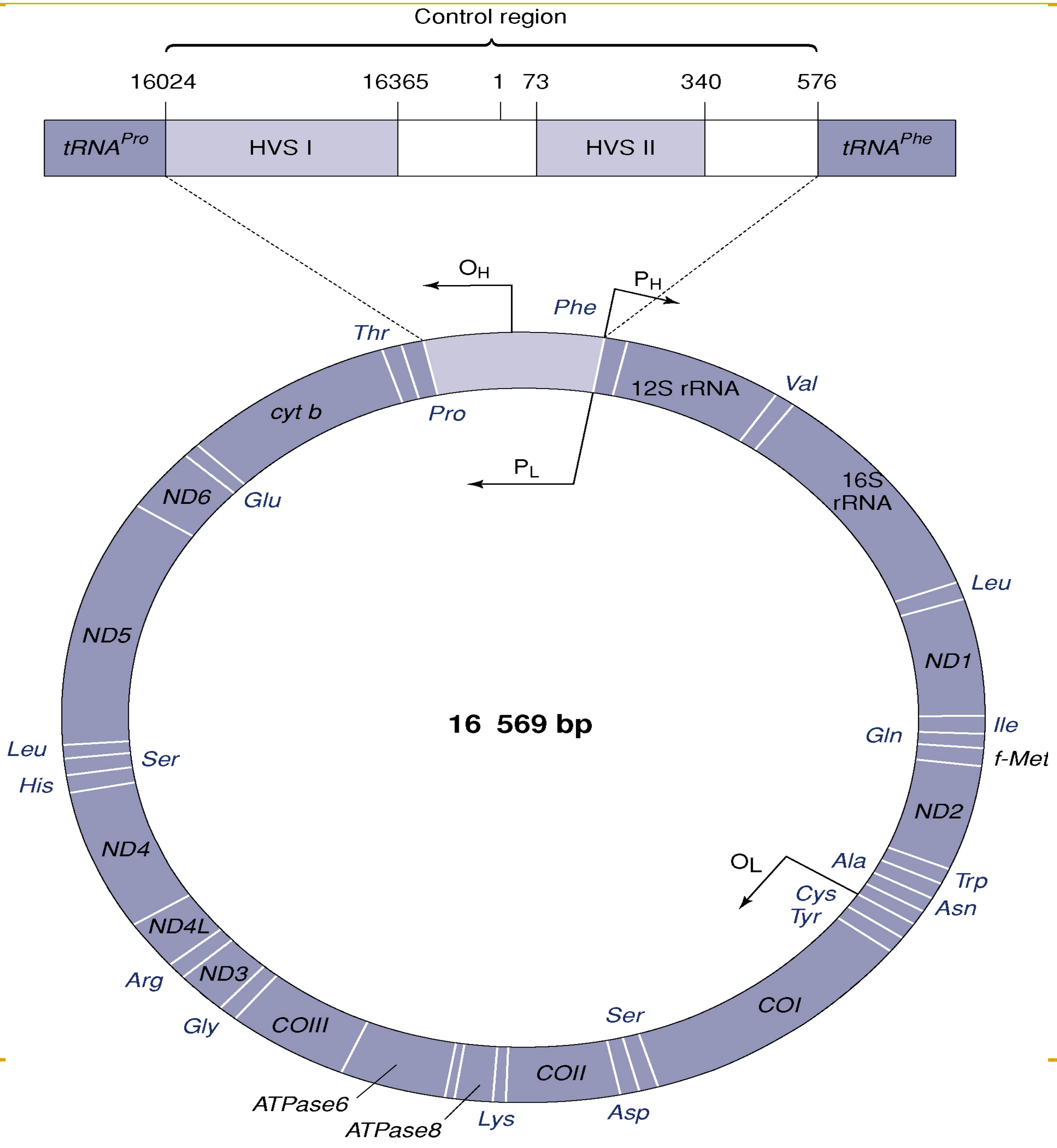
- Bioinformatics is the use of computer science, mathematics, and information theory to model and analyze biological systems, especially systems involving genetic material.

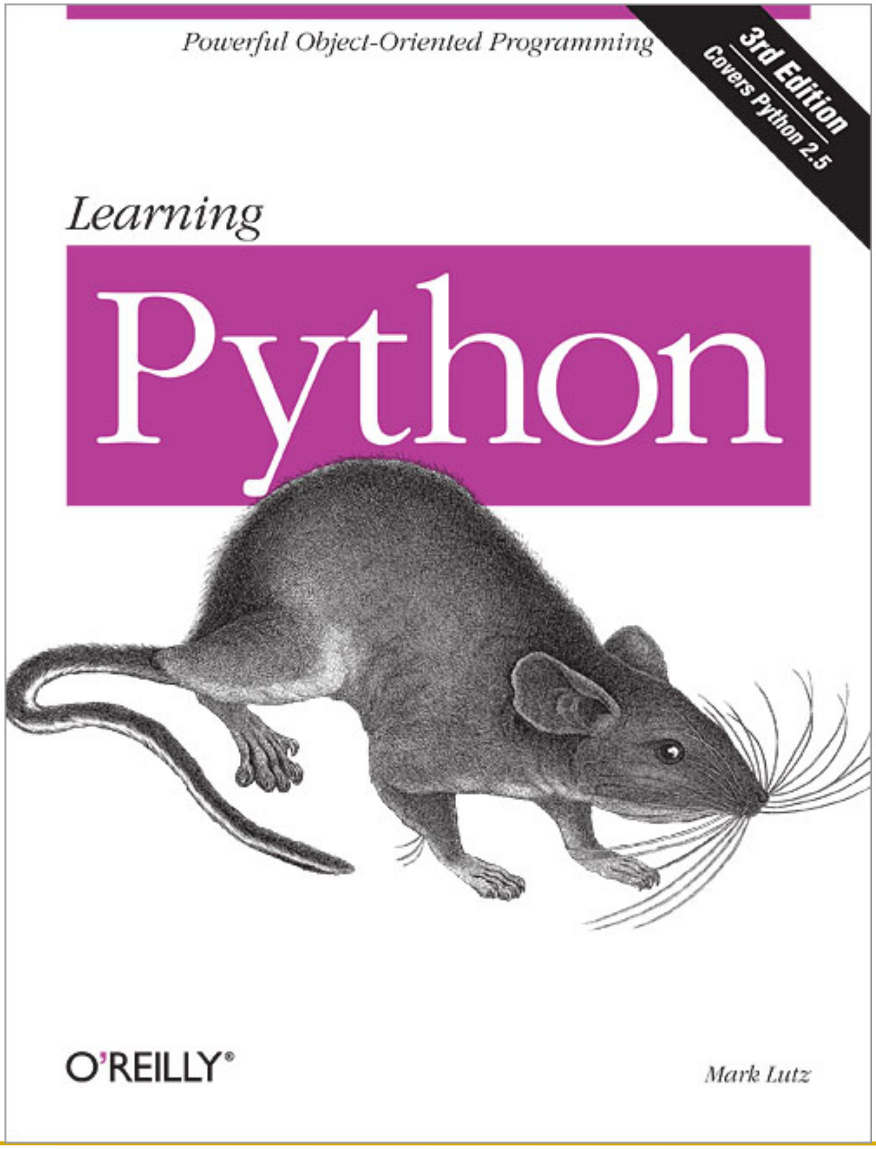
New World monkeys are limited to tropical forest environments of southern Mexico, Central, and South America.


Human family
Human cell
Nuclear genome
Mitochondrial genomes

What is mitochondrial DNA?

Mitochondria are structures within cells that convert the energy from food into a form that cells can use. Although most DNA is packaged in chromosomes within the nucleus, mitochondria also have a small amount of their own DNA. This genetic


Control region
16024
16365
1
73
340
576
tRNA^Pro
HVS I
HVS II
tRNA^Phe
O_H
P_H
Phe
Thr
Pro
12S rRNA
Val
cyt b
P_L
Glu
ND6
16S rRNA
Leu
ND5
ND1
16 569 bp
Ile
Gln
f-Met
Leu
Ser
His
ND2
ND4
O_L
Ala
Trp
Cys
Tyr
Asn
ND4L
Arg
ND3
COI
Gly
COIII
Ser
COII
ATPase6
ATPase8
Lys
Asp



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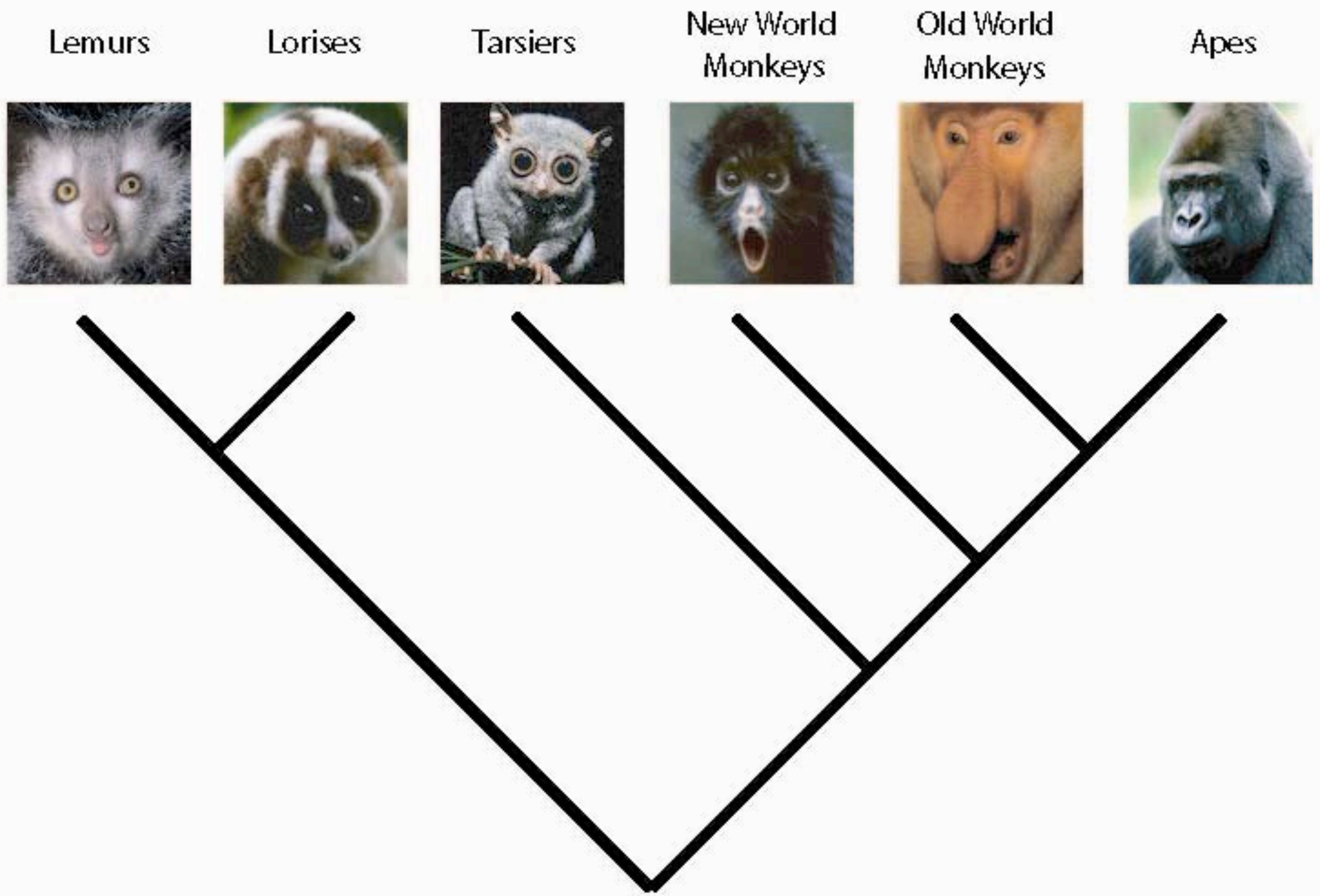
Python Script

Python is a dynamic object-oriented programming language that can be used for many kinds of software development. Linux/Unix

```
#! /usr/bin/python

spotHolder = 0

count = 0

while spotHolder < len(bigfoot) :

        bp1 = bigfoot[spotHolder]
        bp2= chimp[spotHolder]

        if bp1 != bp2:
               count =count + 1
               print bp1 + "" + bp2 + "Mismatch at bp" + str(spotHolder + 1) + "!"
        else:
               print bp1 + "." + bp2
        spotHolder = spotHolder+ 1
print "Number of mismatches: " + str(count)
length = len(bigfoot)
numMatches = length - count
percentMatch = float(numMatches) / float(length)
```

Examples Of Comparing Mitochondrial DNA

Cebus_albifrons
GTGGCAACACCAGCTCAACTAGGCCTACAAAACGCTACATCCCCCATT
Aotus_lemurinus
ATGGCAACACCAGCTCAACTAGGCCTACAAAACGCTACGTCTCCTATT


Lemurs
Lorises
Tarsiers
New World Monkeys
Old World Monkeys
Apes

References

http://www.python.org/

http://anthro.palomar.edu/primate/prim_5.htm

http://ghr.nlm.nih.gov/chromosome=MT

Acknowledgements

- Mentor : Dr. Todd Disotell
- Co-Mentor: Christina Bergey
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- The Audience

Questions