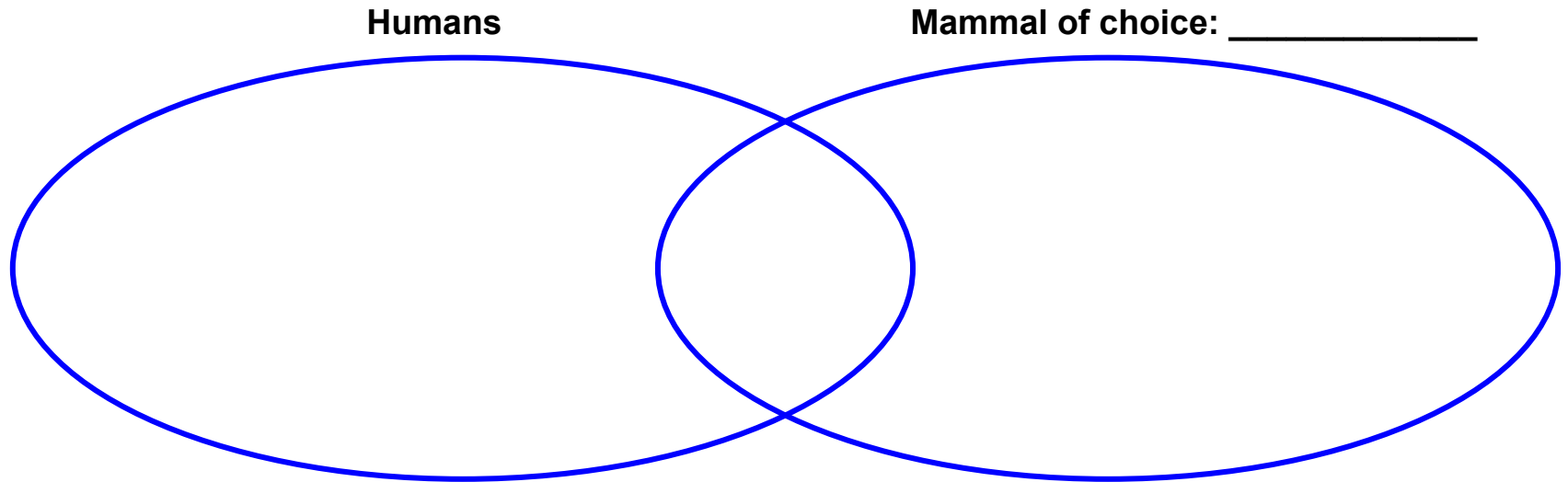


Pseudogenes and Using Python to Compare Gene Mutations in Humans and Other Organisms

By Dana Russell and Johana Uitto

Catalyst

Create a Venn-Diagram in groups of 4 comparing/contrasting the characteristics of Humans and another mammal of your choice.



Follow-Up Questions

1. What makes these organisms have these characteristics?
1. Why were some of these characteristics able to stay the same in two different organisms?
1. What happened to the genes that are no longer seen in humans?

Pseudogenes are...



Fake / imitating



A unit of DNA that codes for a particular trait

A section of a chromosome that is non-functional and an imperfect copy of a functional gene.

Write your assigned pseudogene in the box next to the matching function.

Pseudogene	Function
	associated with the growth of a tail (and general development)
	associated with a type of white blood cell
	associated with the production of Vitamin C
	associated with the immune system
	associated with fur-like body hair
	associated with the immune system
	associated with the processing of uric acid
	associated with repairing DNA damaged by UV radiation

Let's compare!

1. Go to GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>).
 - a. Search assigned gene
 - b. Click on the link for your gene
 - i. Under “Analyze this sequence”, click “Run BLAST”. Alternatively, copy the accession number of the gene and visit the BLAST website (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>)
 - ii. Check the box for your gene (the first option). Check the box for an unrelated organism (scroll down to an organism with a non-human scientific name).
 - iii. Click Download → FASTA (Aligned Sequence).
2. Go to <http://www.ebi.ac.uk/Tools/msa/muscle/>
3. Copy the contents of the file that you generated in BLAST into the box.
 - a. Change the output format to Pearson/FASTA.
 - b. Hit “Submit”.
 - c. Hit “Download Alignment File”
 - d. Right Click → Save As → “gene_name.fasta”. For example, WNT3A would be wnt3a.fasta
 - e. Save the file to the desktop
4. Run pseudogene.py

Conclusion

Take a screenshot of your results in
Python

Conclusion Questions

1. What types of mutations did you see between the human pseudogene and the functioning gene? Do you think that these types of mutations always have a large impact?
2. Do you think that non-functioning genes have more or fewer mutations than a functioning gene? Support your answer.
3. Why do biologists study pseudogenes?
4. Why do biologists use computers to study genomes?