

GenBank/RefSeq Taxonomic Sequence Partitioning

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GenBank

- International Nucleotide Sequence Database Collaboration
- GenBank accession numbers never include an underscore
- NIH genetic sequence database

- Use FASTA files
- Sequence databases

RefSeq

- IRefSeq records consistently use official nomenclature for the gene feature, when available.
- RefSeq collection aims to provide, a complete set of non-redundant, extensively cross-linked, and richly annotated nucleic acid and protein records.

GenBank/RefSeq Taxonomic Sequence Partitioning

- Use of graph analysis
 - Common ancestry
 - Determining phylum
 - Common characteristics

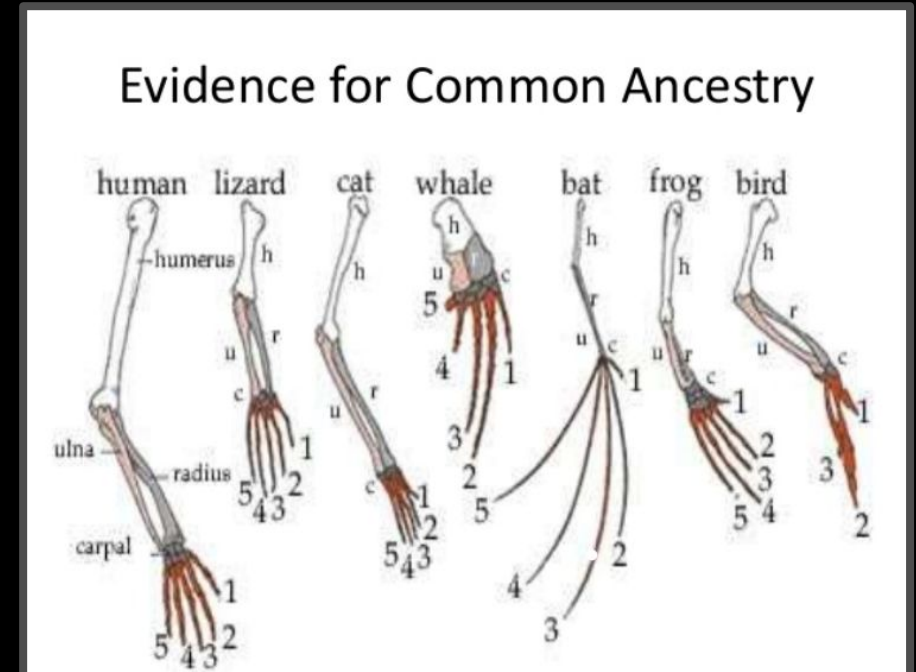
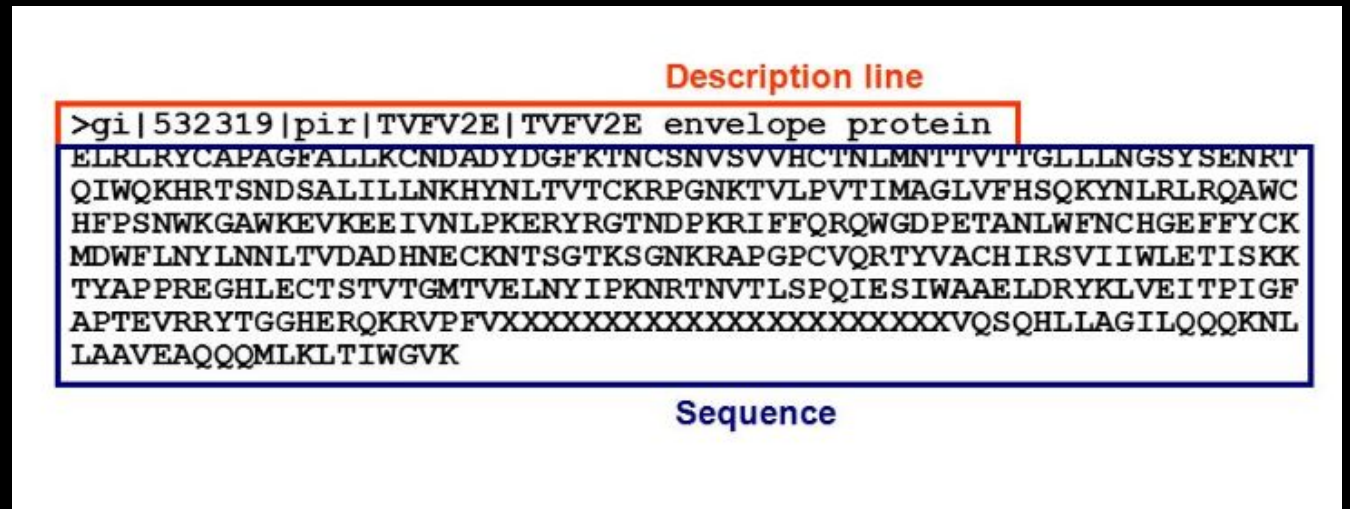


Figure 0: common ancestry

FASTA

- The universal format standard in the field of bioinformatics
- FASTA stores a variable number of sequence records



The diagram illustrates a FASTA format entry. It consists of two main parts: a description line and a sequence. The description line is highlighted with a red border and contains the text: `>gi|532319|pir|TVFV2E|TVFV2E envelope protein`. The sequence is highlighted with a blue border and contains a single line of amino acid codes: `ELRLRYCAPAGFALLKCNDADYDGFKTNC SNVSVVHCTNLMNTTVTTG LLLNGSYSENRT
QIWQKHRTSND SALILLNKHYNLTVTCKRPGNKT VLPVTIMAGLVFHSQKYNLRLRQAWC
HFPSNWKGAWKEVK EIVNLPKERYRG TNDPKRIFFQRQWGD PETANLWFNCHGEFFYCK
MDWFLNYLNNLTVDADHNECKNTSGTKSGNKRAPGPCVQRTYVACHIRSVIIWLETISKK
TYAPPREGHLECTSTVTGMTVELNYIPKNRTNVTLS PQIESIWAAELDRYKLVEITPIGF
APTEVRRYTGGHERQKRVPFVXXXXXXXXXXXXXXXXXXXXXXXXXVQSQHLLAGILQQQKNL
LAAVEAQQQMLKLT IWGVK`. The labels "Description line" and "Sequence" are placed above and below their respective sections.

```
>gi|532319|pir|TVFV2E|TVFV2E envelope protein
ELRLRYCAPAGFALLKCNDADYDGFKTNC SNVSVVHCTNLMNTTVTTG LLLNGSYSENRT
QIWQKHRTSND SALILLNKHYNLTVTCKRPGNKT VLPVTIMAGLVFHSQKYNLRLRQAWC
HFPSNWKGAWKEVK EIVNLPKERYRG TNDPKRIFFQRQWGD PETANLWFNCHGEFFYCK
MDWFLNYLNNLTVDADHNECKNTSGTKSGNKRAPGPCVQRTYVACHIRSVIIWLETISKK
TYAPPREGHLECTSTVTGMTVELNYIPKNRTNVTLS PQIESIWAAELDRYKLVEITPIGF
APTEVRRYTGGHERQKRVPFVXXXXXXXXXXXXXXXXXXXXXXXXXVQSQHLLAGILQQQKNL
LAAVEAQQQMLKLT IWGVK
```

Figure 1: FASTA Format

Type	Format(s)	Example(s)
local (i.e. no database reference)	lcl integer	lcl 123
	lcl string	lcl hmm271
GenInfo backbone seqid	bbs integer	bbs 123
GenInfo backbone moltype	bbm integer	bbm 123
GenInfo import ID	gim integer	gim 123
GenBank	gb accession locus	gb M73307 AGMA13GT
EMBL	emb accession locus	emb CAM43271.1
PIR	pir accession name	pir G36364
SWISS-PROT	sp accession name	sp P01013 OVAX_CHICK
patent	pat country patent sequence-number	pat US RE33188 1
pre-grant patent	pgp country application-number sequence-number	pgp EP 0238993 7
RefSeq	ref accession name	ref NM_010450.1
general database reference (a reference to a database that's not in this list)	gnl database integer	gnl taxon 9606
	gnl database string	gnl PID e1632
GenInfo integrated database	gi integer	gi 21434723
DDBJ	dbj accession locus	dbj BAC85684.1
PRF	prf accession name	prf 0806162C
PDB	pdb entry chain	pdb 1I4L D
third-party GenBank	tpg accession name	tpg BK003456
third-party EMBL	tpe accession name	tpe BN000123
third-party DDBJ	tpd accession name	tpd FAA00017

NCBI Identifiers

NCBI FASTA defined format
for sequence identifiers

Figure 3: database identifiers table

Nucleic Acid Code ↕	Meaning ↕	Mnemonic ↕
A	A	A denine
C	C	C ytosine
G	G	G uanine
T	T	T hymine
U	U	U racil
R	A or G	pu R ine
Y	C, T or U	p Y rimidines
K	G, T or U	bases which are K etones
M	A or C	bases with aM ino groups
S	C or G	S trong interaction
W	A, T or U	W eak interaction
B	not A (i.e. C, G, T or U)	B comes after A
D	not C (i.e. A, G, T or U)	D comes after C
H	not G (i.e., A, C, T or U)	H comes after G
V	neither T nor U (i.e. A, C or G)	V comes after U
N	A C G T U	N ucleic acid
-	gap of indeterminate length	

Sequence Representation

Sequences may be protein sequences or nucleic acid sequences, and they can contain gaps or alignment characters

Figure 4: Sequences table

Taxonomy

How Are Organisms Classified?

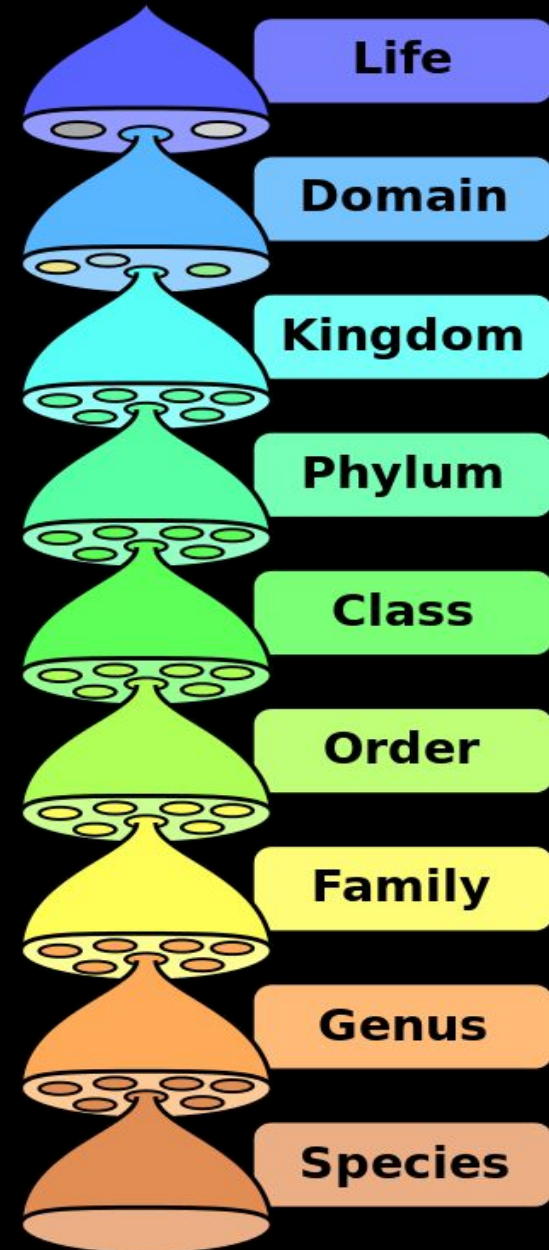


Figure 5: Modern Taxonomic Hierarchy

What are taxa?





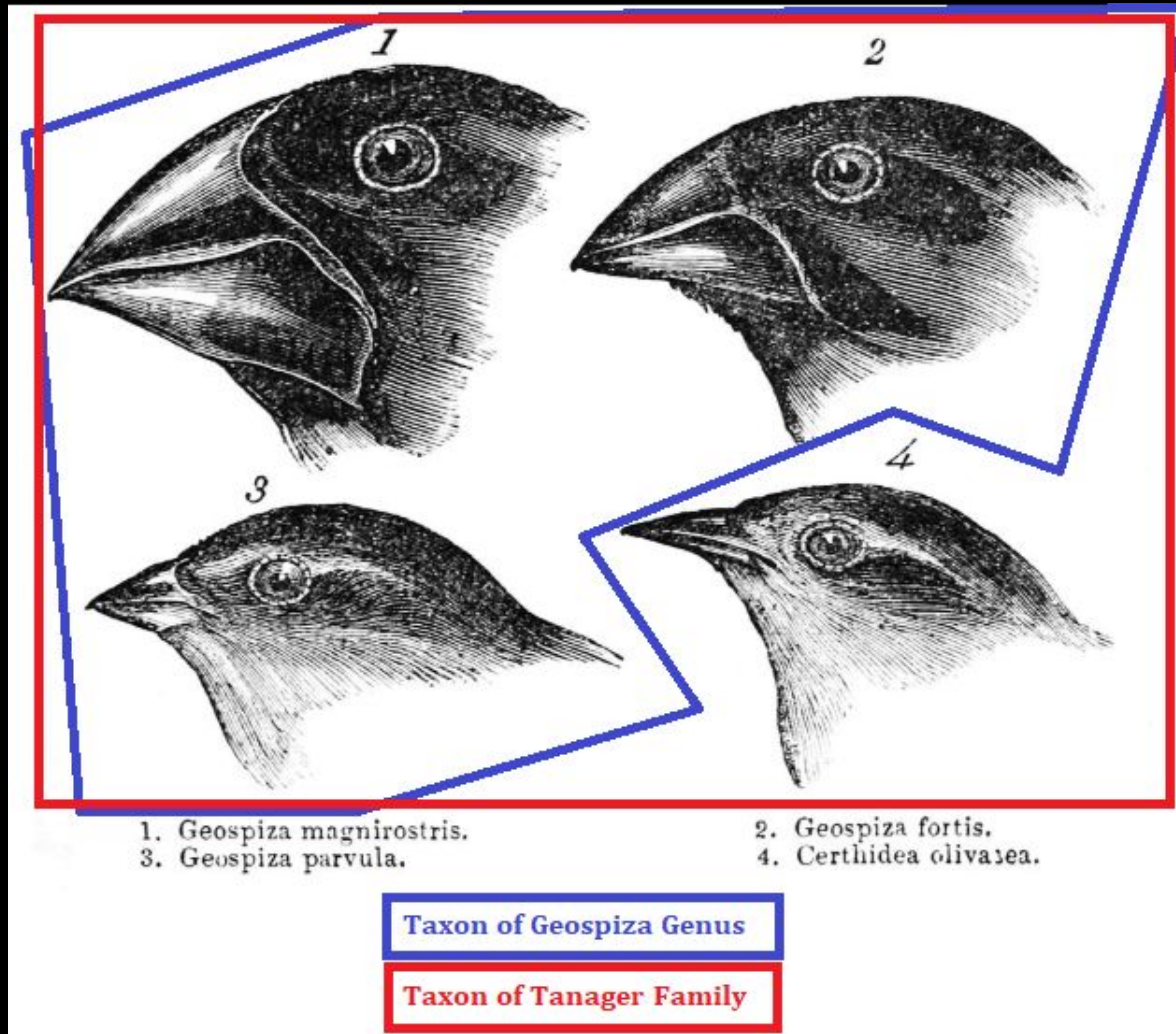
Taxon (Rank)	Chimpanzee 	Humans 	Asian Elephant 	Drosophila 
<i>Kingdom</i>	Animalia	Animalia	Animalia	Animalia
<i>Phylum</i>	Chordata	Chordata	Chordata	Arthropoda
<i>Subphylum</i>	Vertebrata		Vertebrata	
<i>Class</i>	Mammalia	Mammalia	Mammalia	Insecta
<i>Order</i>	Primates	Primates	Proboscidea	Diptera
<i>Superfamily</i>			Elephantoidea	
<i>Family</i>	Hominides	Hominidae	Elephantidae	Drosophilidae
<i>Subfamily</i>		Homininae		Drosophilinae
<i>Genus</i>	Pan	Homo	Elephas	Drosophila
<i>Species</i>	Simia troglodytes	Sapiens	Elephas maximus	Drosophila melanogaster

Figure 5: Taxonomy table

Taxa



Passeriformes --->

Tanager ---->
Emberizidae --->

Geospiza ----->

magnirostris /fortis/ ---->
parvula/**olivacea** ----->

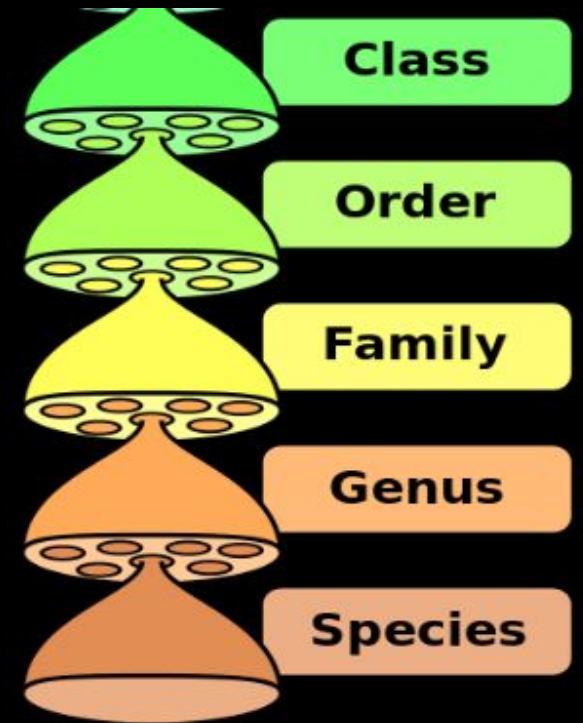


Figure 6: Darwin's finches by John Gould

Taxonomic Sequence

- Graph complex networks of organisms
 - Nodes are organisms
 - Links are similarities between organisms
- Taxonomic sequences are better recognized as a phylogenetic trees.

Trees

- Fundamental Data Structure
 - Root Node
- Directed Graph
 - Single parent
 - Arbitrary amount of children
- Good for Hierarchical Organization

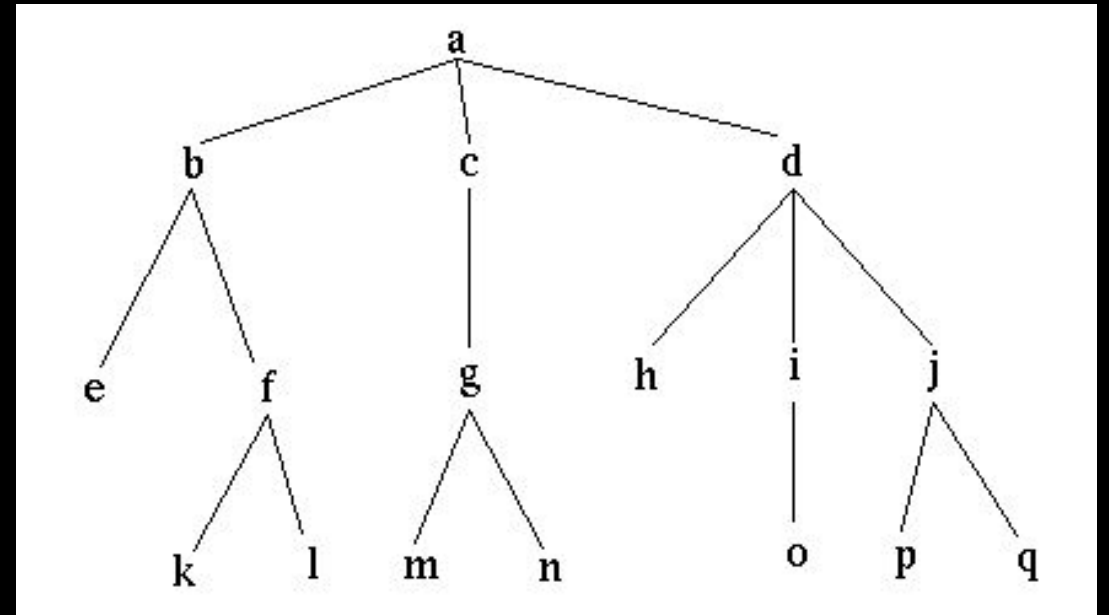


Figure 2: Example Tree

Phylogenetic trees

Phylogenetic trees are usually based on morphological or genetic homology

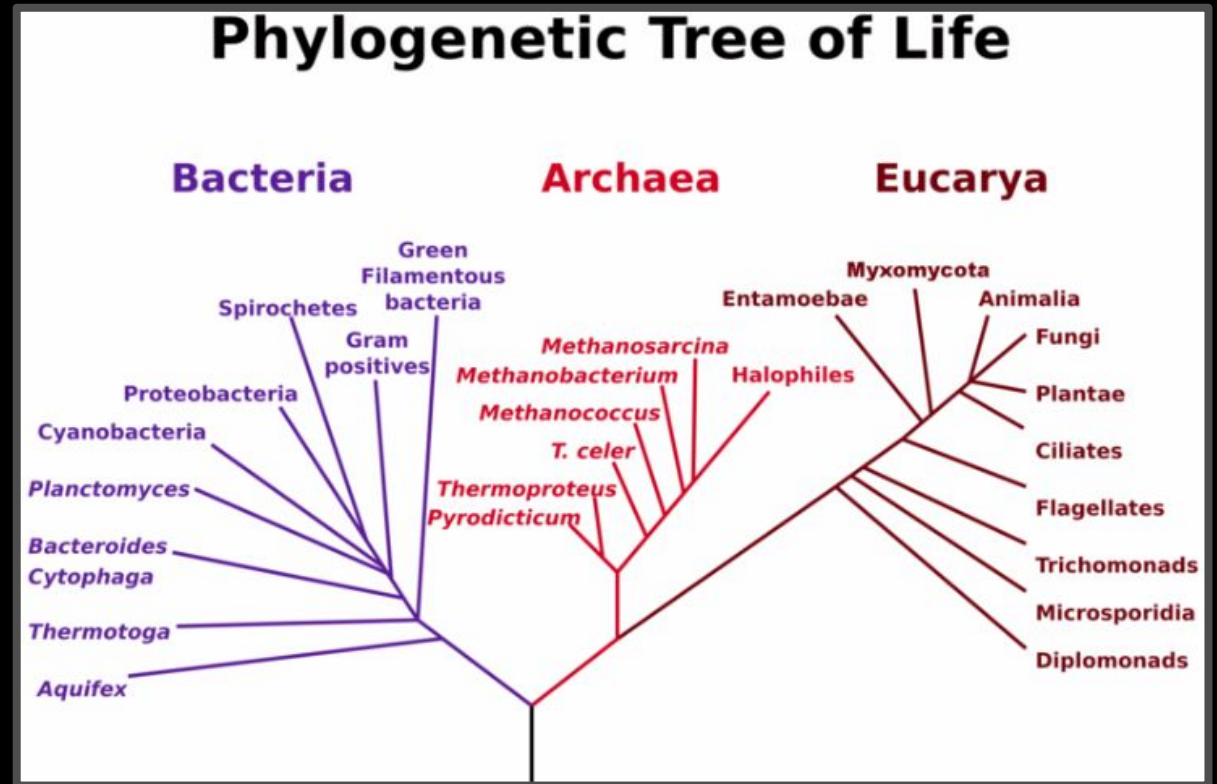


Figure 7: Phylogenetic tree of life

Development

Plan and Current Status

'GenBank/RefSeq Taxonomic Sequence Partitioning' - ???

- Retrieve NCBI Taxonomy Data
- Parse Taxa into Tree
- Make observations (...profit!)

2	2	131567	superkingdom			0	0	11	0	0	0	0	0	0	0	0	
3	6	335928	genus		0	1	11	1	0	1	0	0	0	0	0		
4	7	6	species	AC	0	1	11	1	0	1	1	0	0	0			
5	9	32199	species	BA	0	1	11	1	0	1	1	0	0	0			
6	10	1706371	genus		0	1	11	1	0	1	0	0	0	0			
7	11	1707	species	CG	0	1	11	1	0	1	1	0	0	0			
8	13	203488	genus		0	1	11	1	0	1	0	0	0	0			
9	14	13	species	DT	0	1	11	1	0	1	1	0	0	0			
10	16	32011	genus		0	1	11	1	0	1	0	0	0	0			
11	17	16	species	MM	0	1	11	1	0	1	1	0	0	0			
12	18	213421	genus		0	1	11	1	0	1	0	0	0	0			
13	19	18	species	PC	0	1	11	1	0	1	1	0	0	0			
14	20	76892	genus		0	1	11	1	0	1	0	0	0	0			
15	21	20	species	PI	0	1	11	1	0	1	1	0	0	0			
16	22	267890	genus		0	1	11	1	0	1	0	0	0	0			
17	23	22	species	SC	0	1	11	1	0	1	1	0	0	0			
18	24	22	species	SP	0	1	11	1	0	1	1	0	0	0			
19	25	22	species	SH	0	1	11	1	0	1	1	0	0	0			
20	27	49928	species	HE	0	1	11	1	0	1	1	0	0	0			
21	28	49928	species	HE	0	1	11	1	0	1	1	0	0	0			
22	29	28221	order		0	1	11	1	0	1	0	0	0	0			
23	31	80811	family		0	1	11	1	0	1	0	0	0	0			
24	32	31	genus		0	1	11	1	0	1	0	0	0	0			
25	33	32	species	MF	0	1	11	1	0	1	1	0	0	0			
26	34	32	species	MX	0	1	11	1	0	1	1	0	0	0			
27	35	32	species	MM	0	1	11	1	0	1	1	0	0	0			
28	38	47	species	AD	0	1	11	1	0	1	1	0	0	0			
29	39	80811	family		0	1	11	1	0	1	0	0	0	0			
30	40	39	genus		0	1	11	1	0	1	0	0	0	0			
31	41	40	species	SA	0	1	11	1	0	1	1	0	0	0			
32	42	39	genus		0	1	11	1	0	1	0	0	0	0			
33	43	42	species	CF	0	1	11	1	0	1	1	0	0	0			
34	44	39	genus		0	1	11	1	0	1	0	0	0	0			
35	45	44	species	ML	0	1	11	1	0	1	1	0	0	0			
36	47	39	genus		0	1	11	1	0	1	0	0	0	0			
37	48	47	species	AG	0	1	11	1	0	1	1	0	0	0			

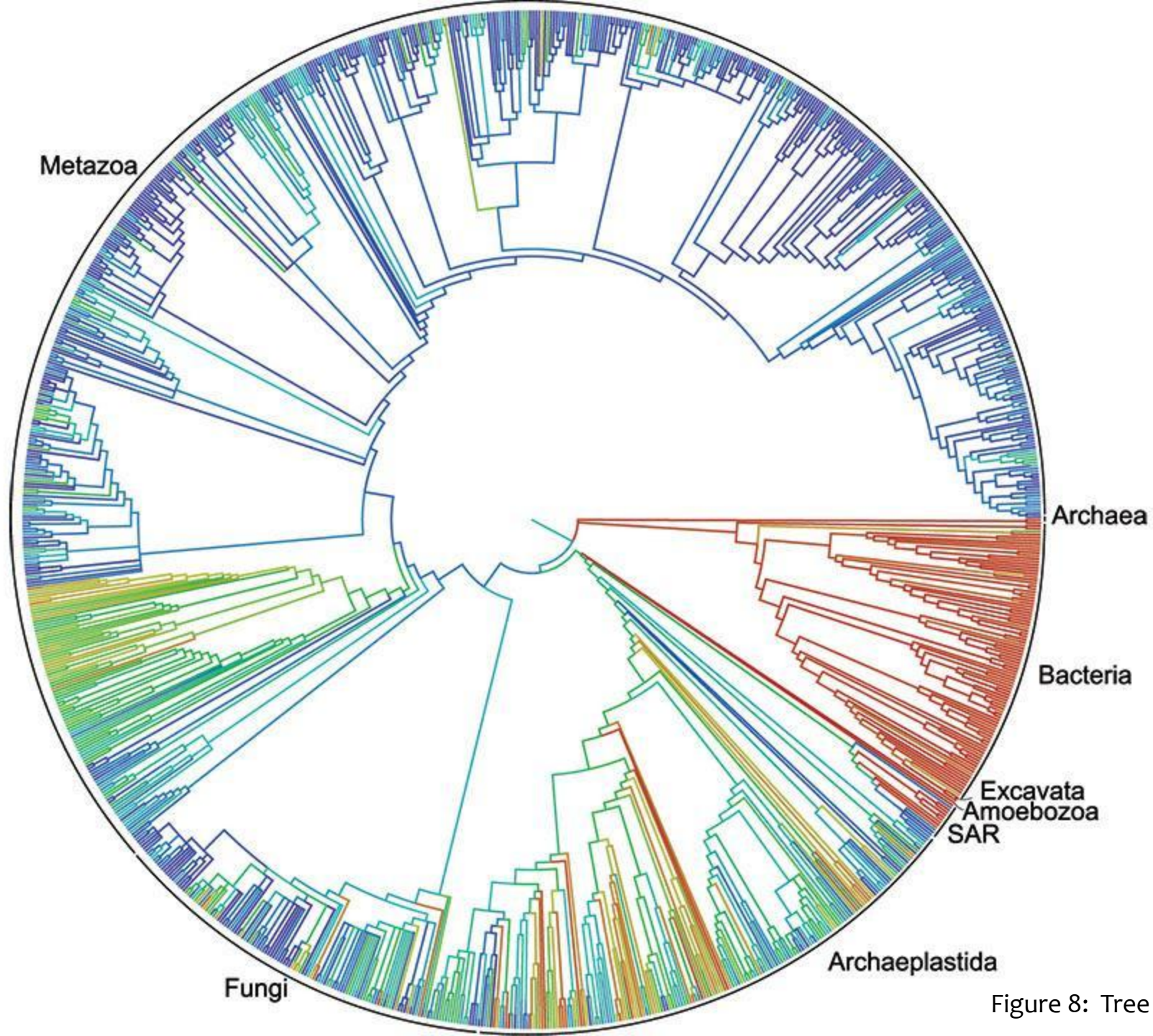


Figure 8: Tree of Life

Retrieve NCBI Data

- URLLIB + TQDM
- Caching
 - MD5

```
(env) [chance@yotsugi Taxa]$ python main.py
Checking for cached taxa data... Not found
Downloading and Preparing data...
taxdmp.zip: 64%|██████████| 31.0M/48.1M [00:20<00:18, 906kBytes/s]
```

Figure 9: retrieving data

Parsing into Tree

- CSV Parsing
- NetworkX
- pyplot
 - slow

2	2	131567	superkingdom			0	0	11	0	0	0	0	0	0	0	
3	6	335928	genus			0	1	11	0	0	1	0	0	0	0	
4	7	6	species	AC	0	1	11	1	0	1	1	0	0	0	0	
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20	27	49928	species	HE	0	1	11	1	0	1	1	0	0	0	0	
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22	29	28221	order		0	1	11	1	0	1	0	0	0	0	0	
23	31	80811	family		0	1	11	1	0	1	0	0	0	0	0	
24	32	31	genus		0	1	11	1	0	1	0	0	0	0	0	
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36	47	39	genus		0	1	11	1	0	1	0	0	0	0	0	
37	48	47	species	AG	0	1	11	1	0	1	1	0	0	0	0	

Figure 10: Taxonomy nodelist

Challenges and Plans

- Slow Plot Generation
 - More Power!
 - Gephi
 - Subtrees
- Taxa IDs
 - Name Associations
- Analysis
 - PageRank
 - Node Distributions
- QOL Improvements
 - Name lookup
 - Global tree caching

Figure 11: names.dmp

```
[chance@yotsugi .taxa_data]$ head names.dmp
1      |      |      |      |      |      |      |      |      |      |
1      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
2      |      |      |      |      |      |      |      |      |      |
[chance@yotsugi .taxa_data]$
```

	all	root	Bacteria	Monera	Procaryotae	Prokaryota	Prokaryotae	bacteria	eubacteria	prokaryote	synonym	scientific name	scientific name	in-part	in-part	in-part	in-part	blast name	genbank	common name	in-part
				Monera <Bacteria>	Procaryotae <Bacteria>	Prokaryota <Bacteria>	Prokaryotae <Bacteria>	bacteria <blast2>		prokaryote <Bacteria>											

Figure 12: Monsoon Logo



GitHub

<https://github.com/bioinformatics-spr19/Taxa>



In conclusion

- Taxonomy is a work in progress.

Thank You

