



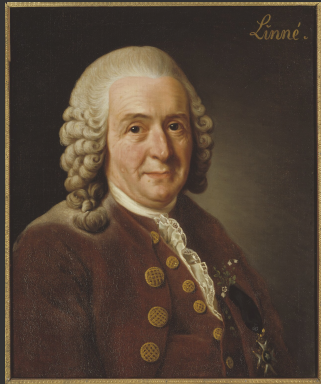
Persistent Homology in Genomics

- Plan:
- ① Review of Evolutionary Biology
 - ② Appearance of non-trivial Topology
& how Persistent Homology can help
 - ③ Example: Influenza

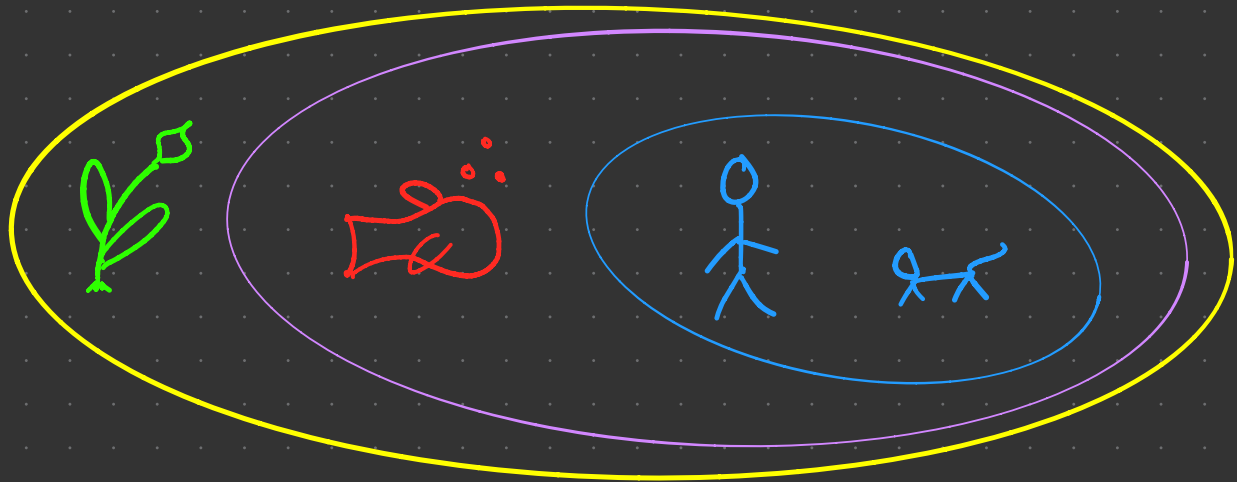
References: [1] "Topology of viral evolution" (Chen, Carlsson, Rabadan)
[2] "TDA for Genomics and Evolution" (Rabadan, Blumberg)

① Review of Evolutionary Biology

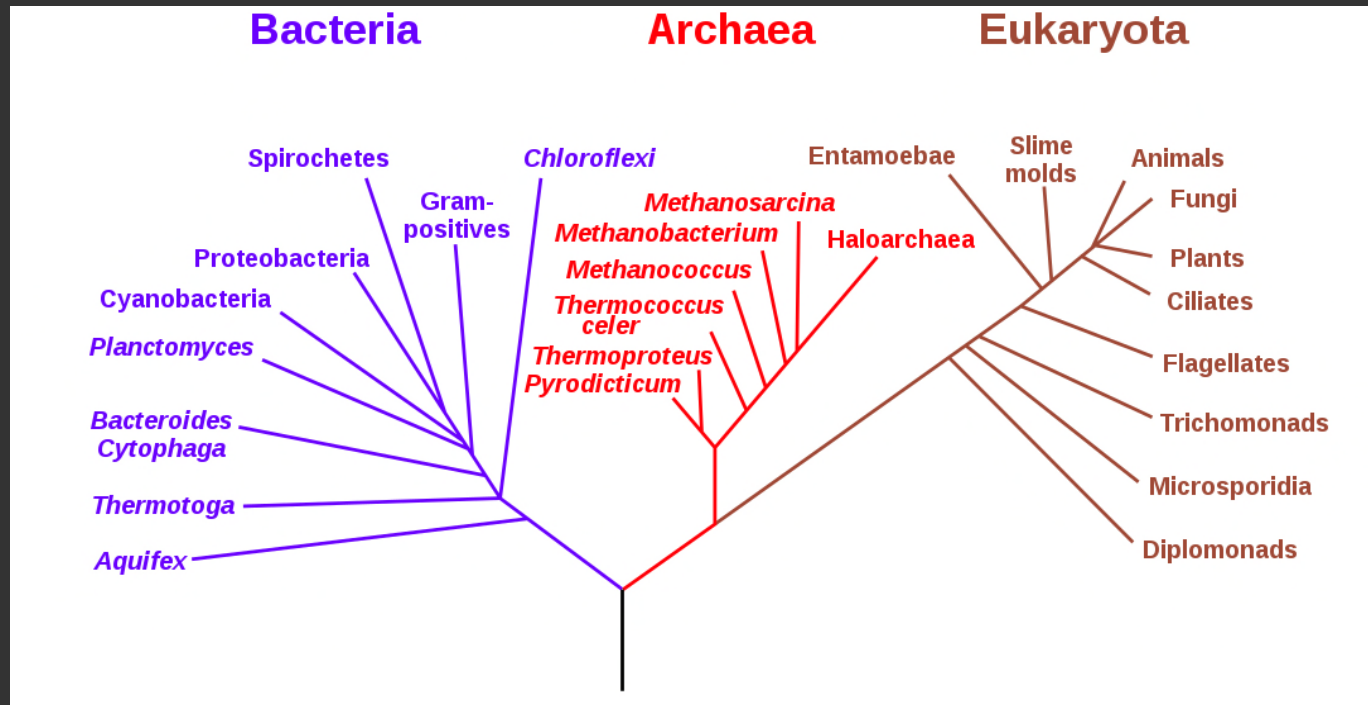
Carl von Linné 1735: Attempt to classify all living organisms on earth



Source: Wiki



Since the 1970s : Availability of molecular data
for determining evolutionary history



Source: Wiki

How does this work?

All information about an organism is stored in a DNA or RNA molecule

DNA . . . ATGCTGCCA . . .
 | | | | | | | |
 . . . TGCATGTC A . . .

RNA . . . GUCAUAAG . . .

Adenin

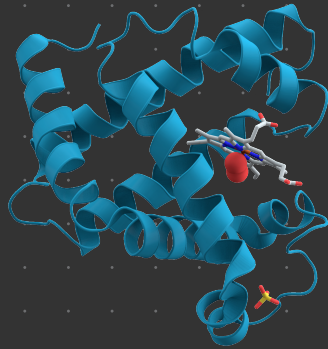
Cytosin

Guanin

Thymin

Uracil

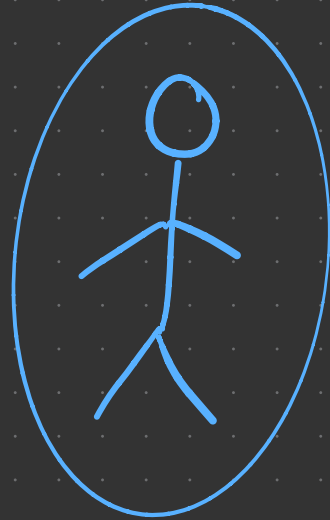
Protein -
Biosynthesis



Proteins



Source: Wiki



Ribosome

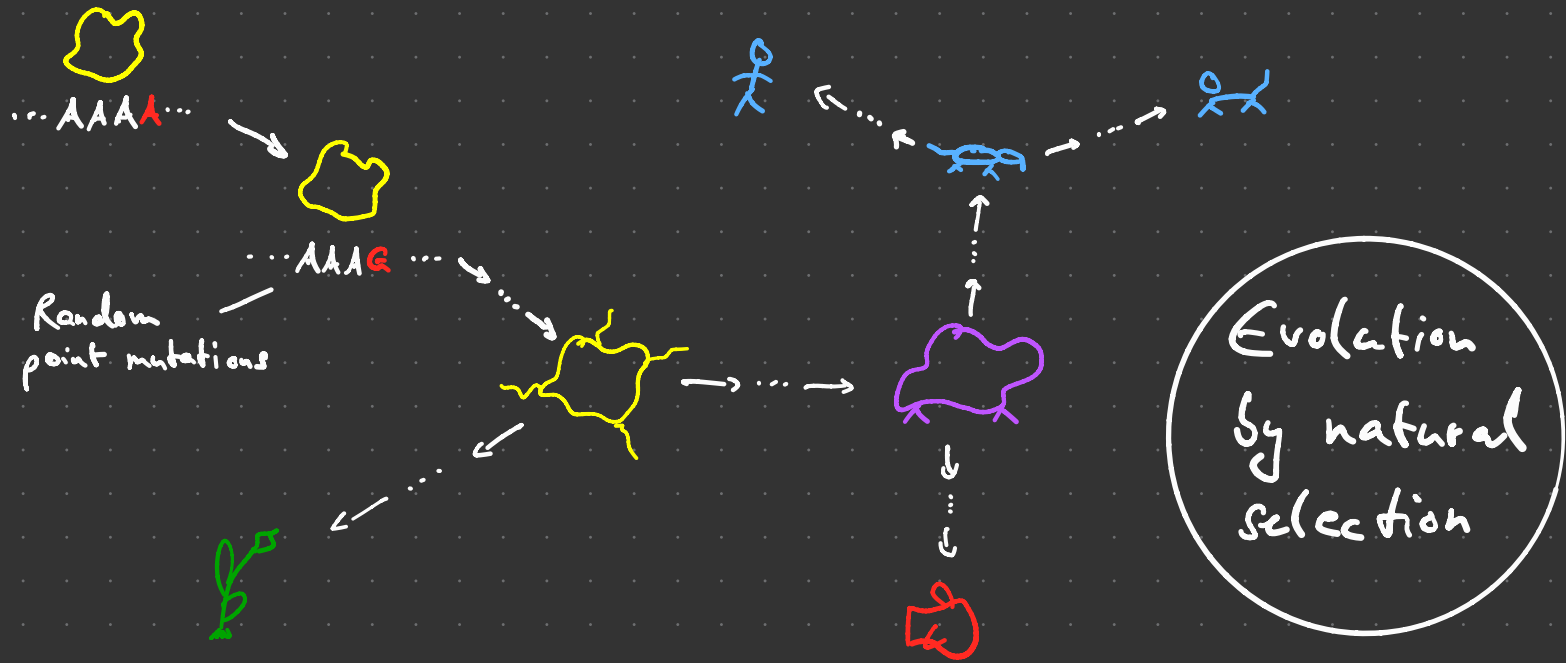


...NESLVP...

Amino Acids

AGCUAGCUA GUCAGUC AGUCAG CAGUC

Simplest mode of reproduction: Clones (Not a realistic depiction!)



Conversely, given

* A number of species    

* together with their genomes AAA, AAG, AGG,
GGG

* and a way to compare them

 AAA _____

 AAG _____

 AGG _____

 GGG _____

... What is the tree?

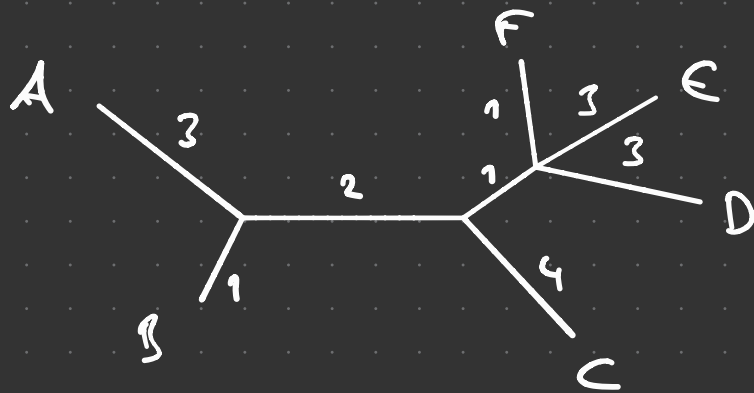
Comparison

Given an alphabet A (here $\#A=4$)
we can define the Hamming-distance
on A^n , $n \in \mathbb{N}$, as

$$d: A^n \times A^n \longrightarrow \mathbb{R} \quad \left(\begin{array}{l} x = AAA \\ y = AAG \end{array} \rightarrow d(x,y) = 1 \right)$$
$$(x, y) \longmapsto d(x,y)$$
$$= \#\{i \in \{1, \dots, n\} \mid x_i \neq y_i\}$$

\Rightarrow For a number of genomes of given length,
we get a finite metric space (X, d_x) .

Def. A tree is a finite, weighted and connected graph without loops and s.t. all vertices have either degree 1 or ≥ 3 .



\implies We get a finite set $\{A, \dots, F\}$ with a "tree metric"

Question: Is there an isometry (at least approximately)

$$(X, d_{\text{Ham}}) \xrightarrow{\sim} (X, d_{\text{Tree}}) ?$$

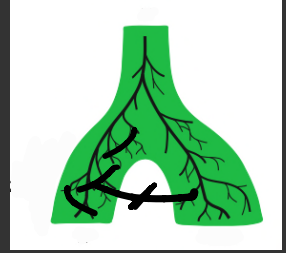
Facts: * Not every metric arises from a tree metric

* There are (heuristic?) algorithms to construct the tree, if possible

→ "Neighbor-Joining"

$$(d_{\text{Ham}}(x, y) - d_{\text{Tree}}(x, y)) \leq \frac{1}{2} \min d_{\text{Tree}}(x, y)$$

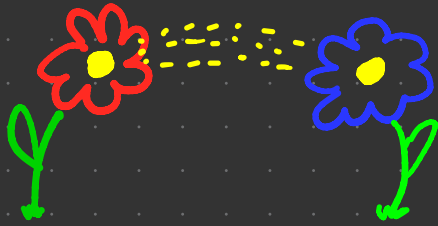
② Appearance of Topology



Source: [2]

* Implication of the "tree-paradigm" is that species have to be reproductively isolated

* But there are counter-examples: (Already known to Darwin)

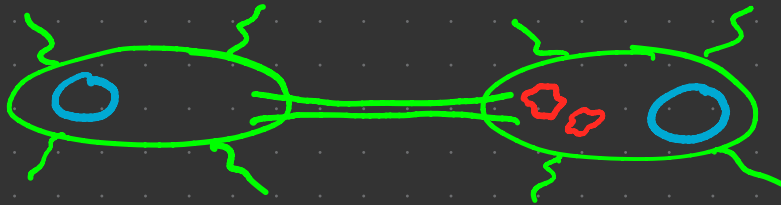


Fertile (!)
hybrids of
plants

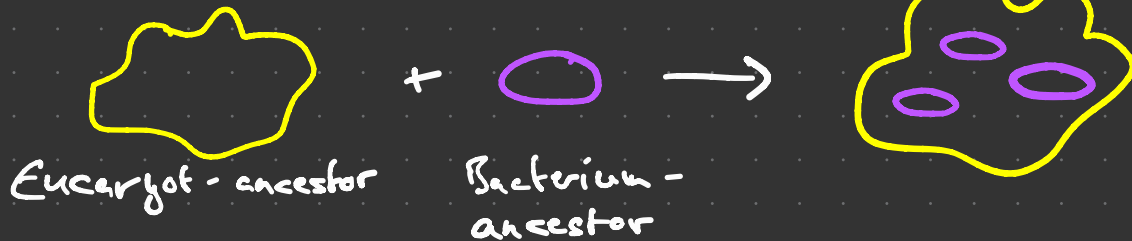
(E.g. some orchids)

Many more examples of "horizontal" evolution or "reticulate events"

* "Conjugation" of bacteria & archaea

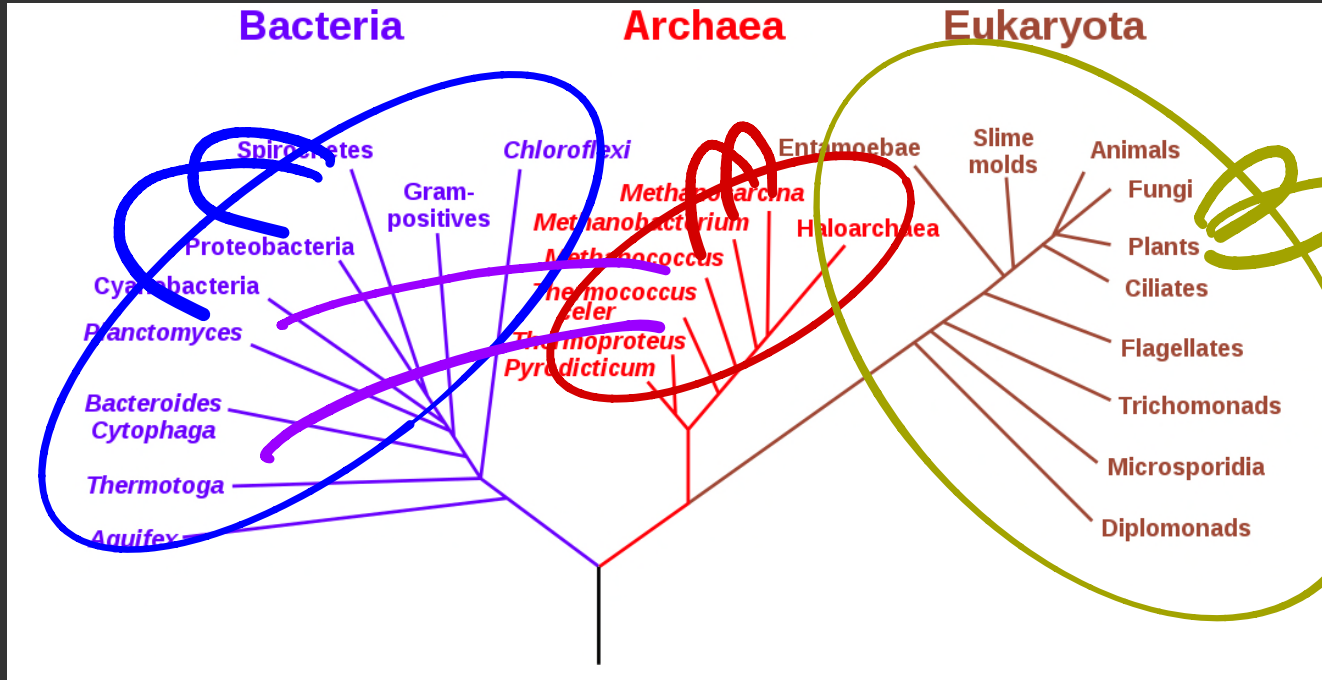


* Symbiotes

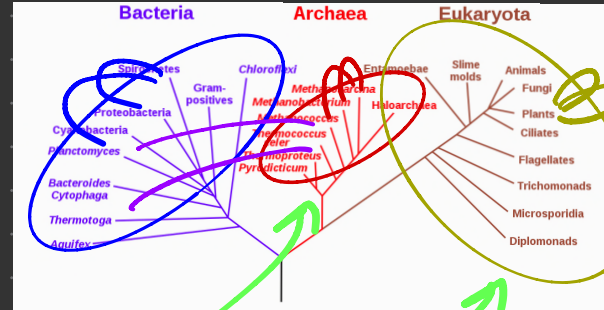


Eucaryotic
cell with
mitochondria

Tree of Life ?



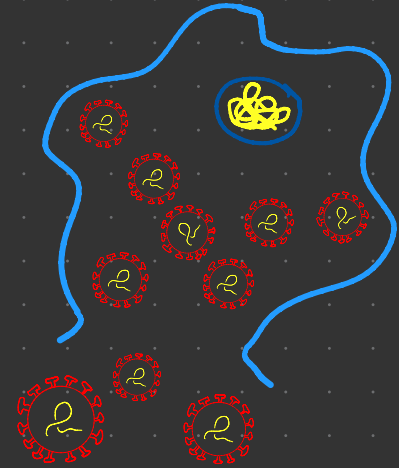
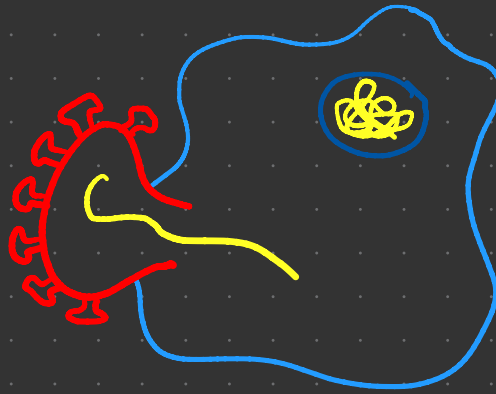
One more thing...



Viruses

Reproduction of viruses

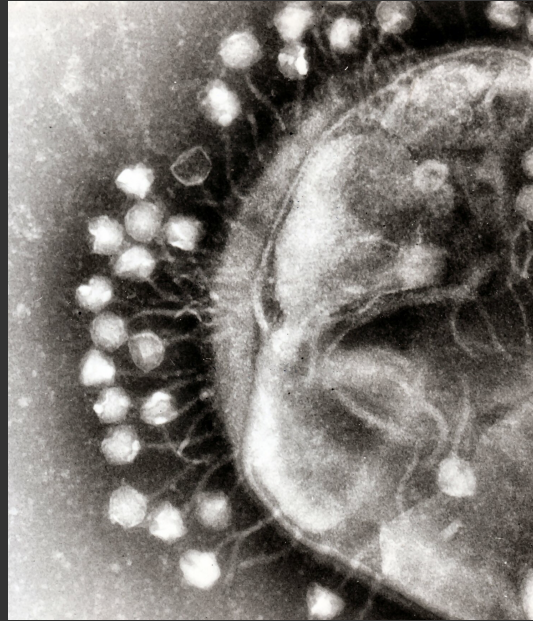
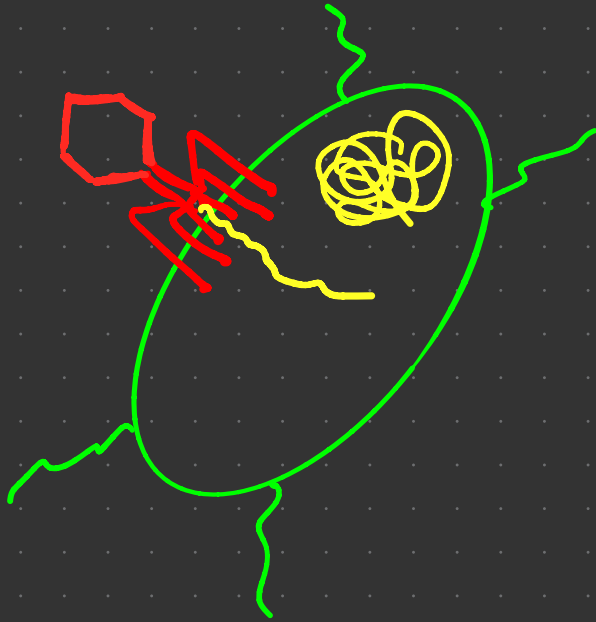
Viruses need a host to replicate



* If genome is built into gametes, it is inherited

⇒ 5-8% of human genome

Also for bacteria / archaea - "Bacteriophages"



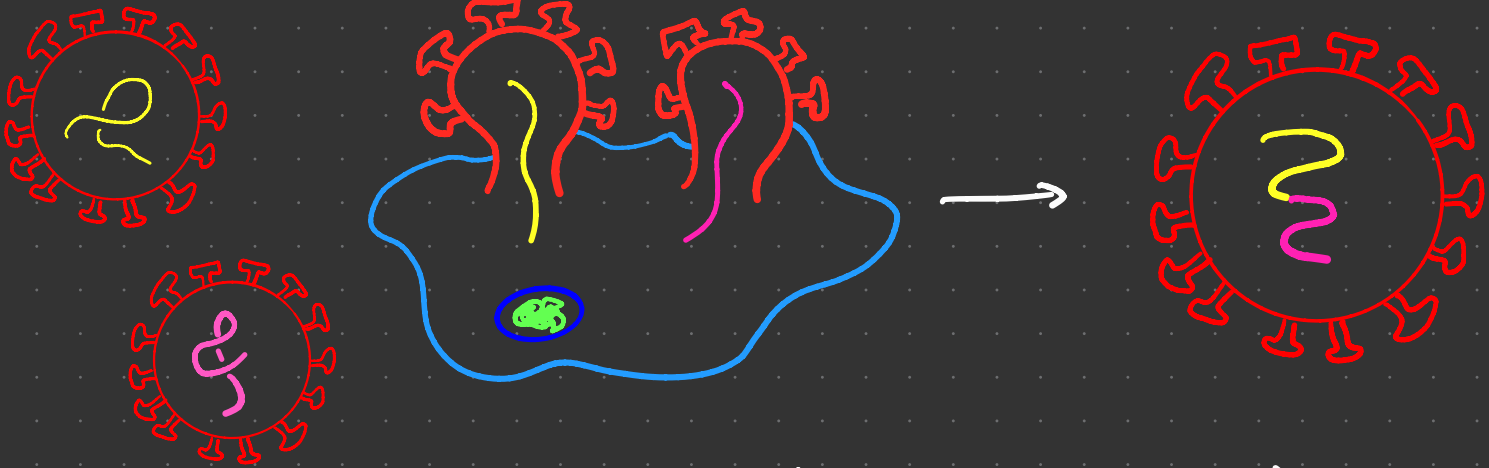
Source: Wiki

(Possibly responsible for the 2011 "EHEC" outbreak)

There is also mixing of genetic material between viruses

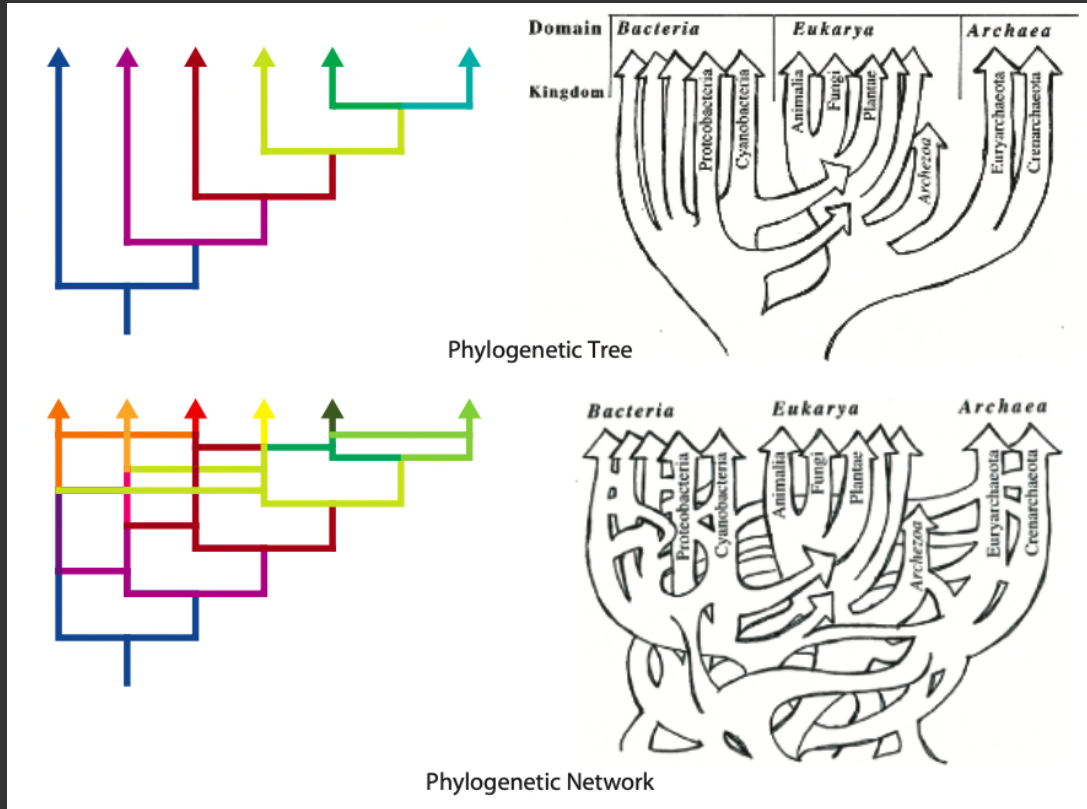
"Coinfection"

"Recombination"



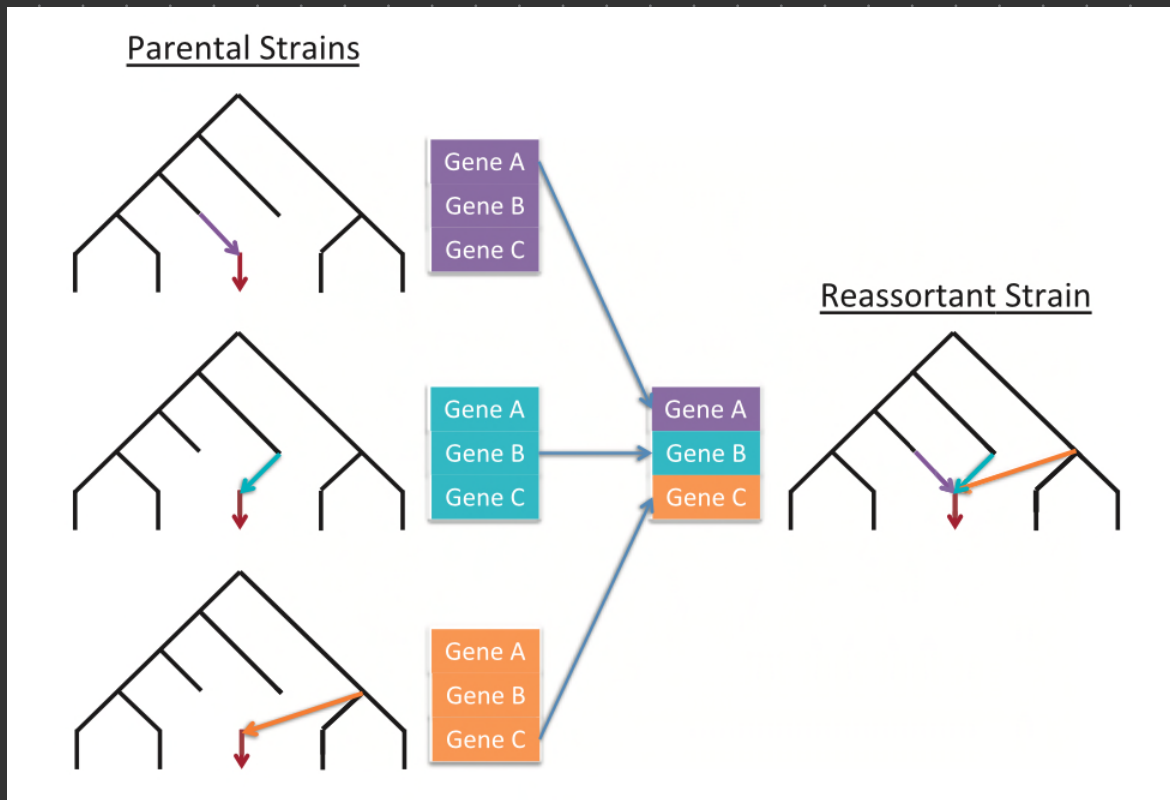
(see Example)

Instead of a tree, we need a network



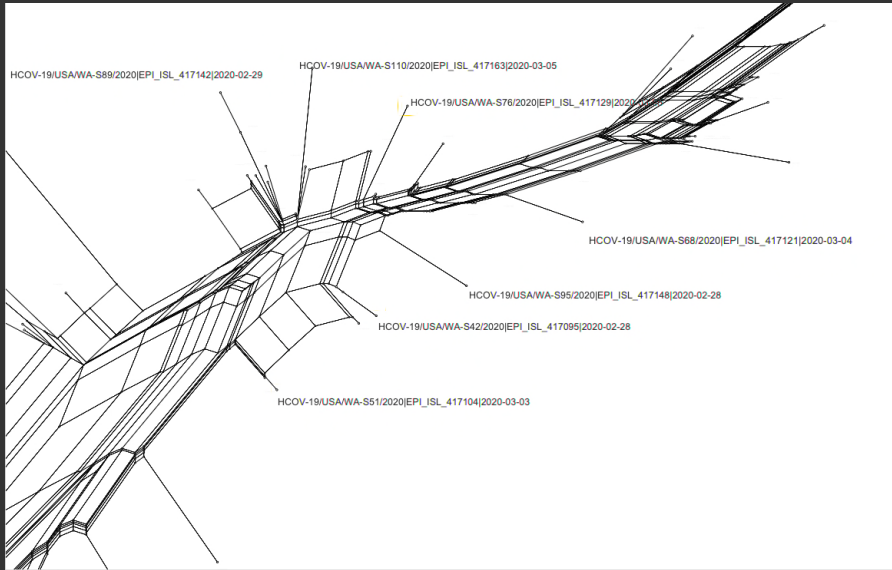
Source: [2]

In principle, it is possible to construct the network



Source: [2]

However, this seems to be extremely difficult
in real life, due to \times computational complexity
 \times biological interpretation
issues



← "split - Network"

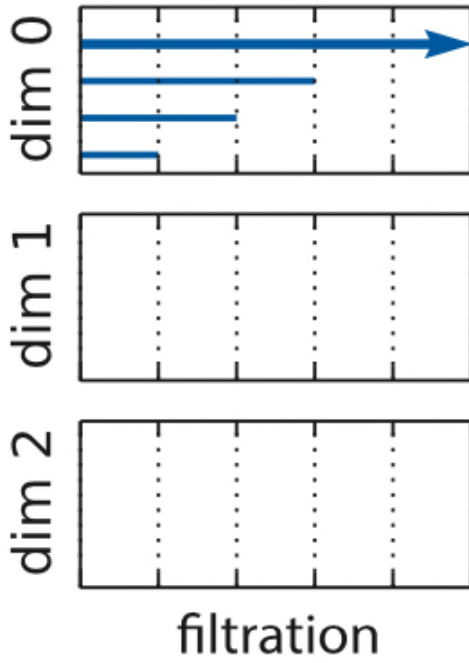
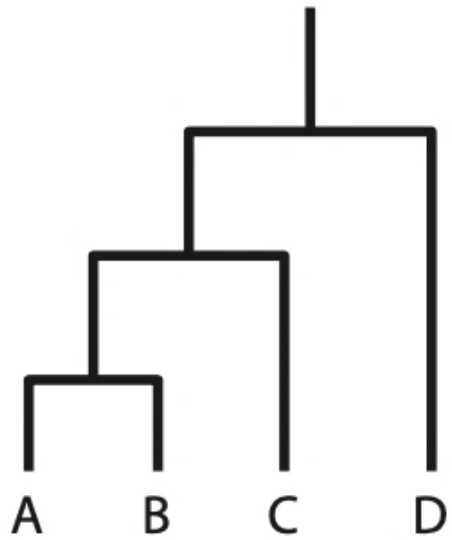
Hard to get
relevant information

How Persistent Homology is able to help

Philosophy: * Evolution happens in a complicated, high-dimensional space (?) and we want to know its structure.

* How is this structure related to relevant information about evolution, e.g. type, scale & statistics of reticulate events.

Hint: Reticulate events prevent contractibility of the network.

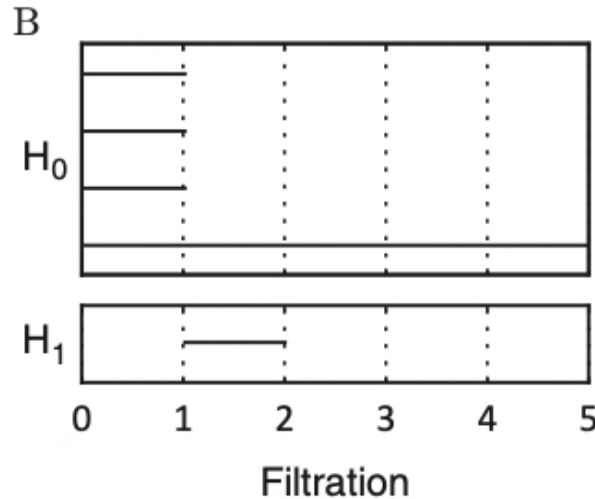
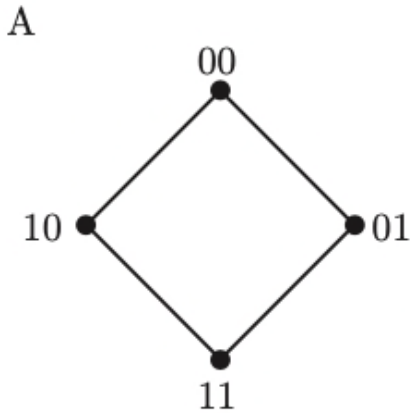


Source: [2]

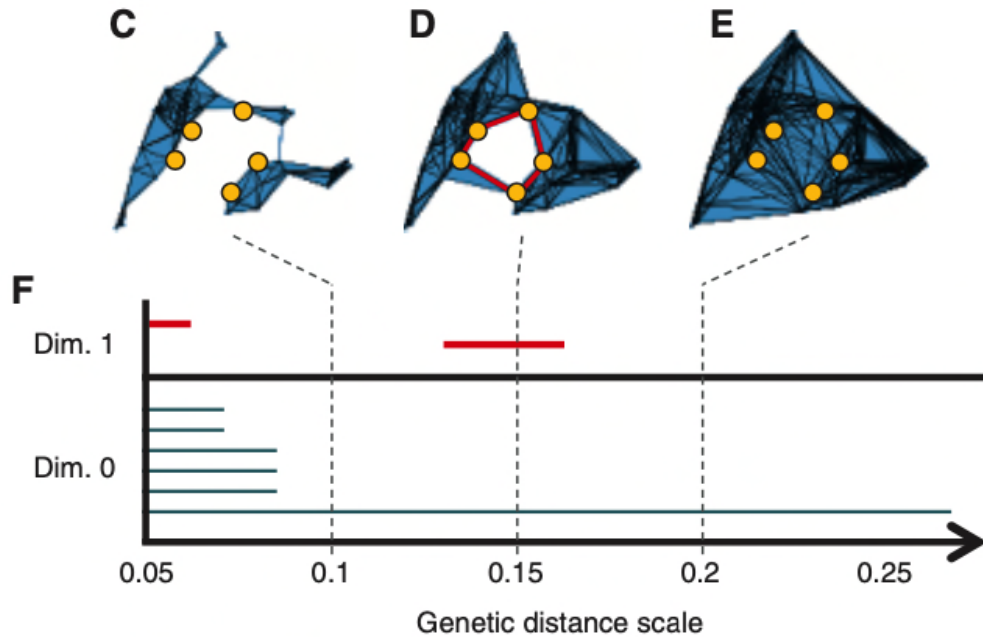
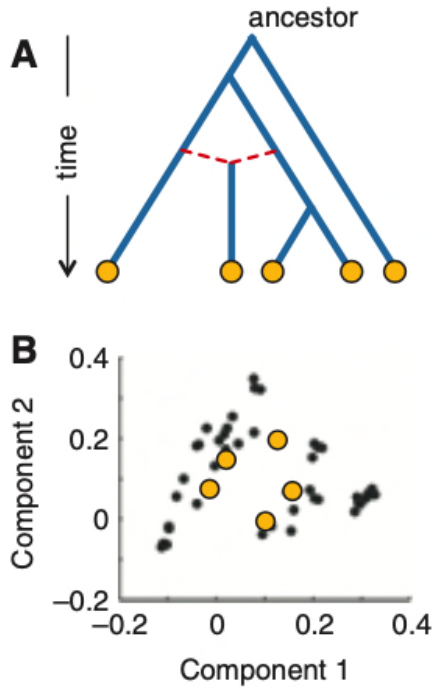
Simplest example

Suppose $\mathcal{A} = \{0, 1\}$

* Every site only mutates once ("infinite-sites assumption")



For a realistic example :



Source : [27]

Theorem (Chan, Carlsson, Rabadan)

(X, d_x) a tree-like finite metric space, $\varepsilon \geq 0$.

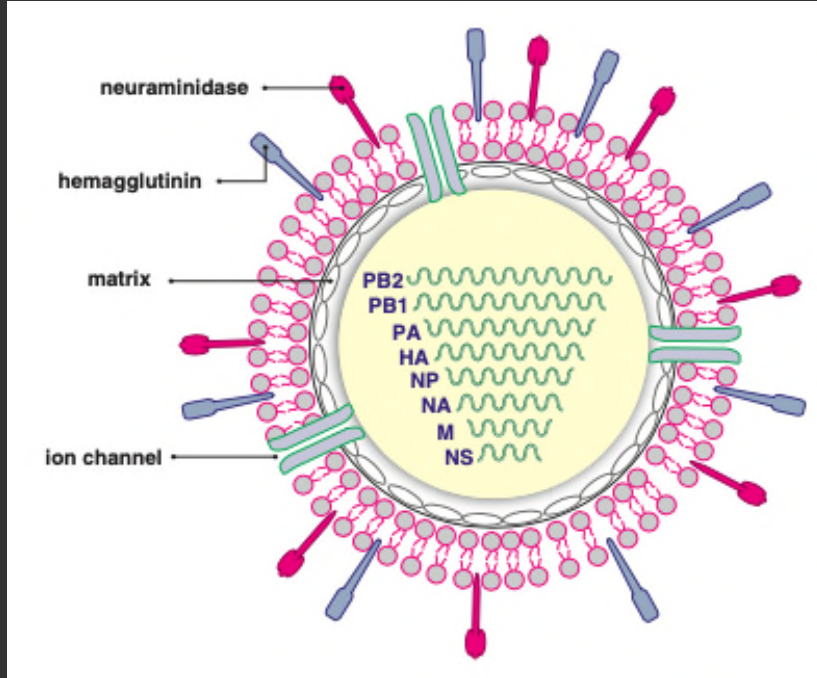
Then $H_i(\text{VR}_\varepsilon(X, d_x)) = \{0\}$ for $i \geq 0$.

\Rightarrow Topological obstruction: L^∞ -norm on bars.

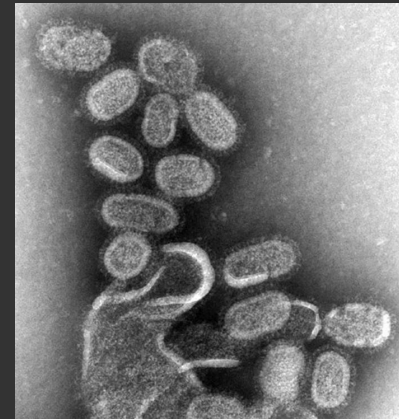
(Identification of "noise" by usual stability results - GH-metric sounds bottleneck-metric)

Example: Influenza

- * RNA virus
- * 8 "segments"
- * mutates very fast



Source: [2]

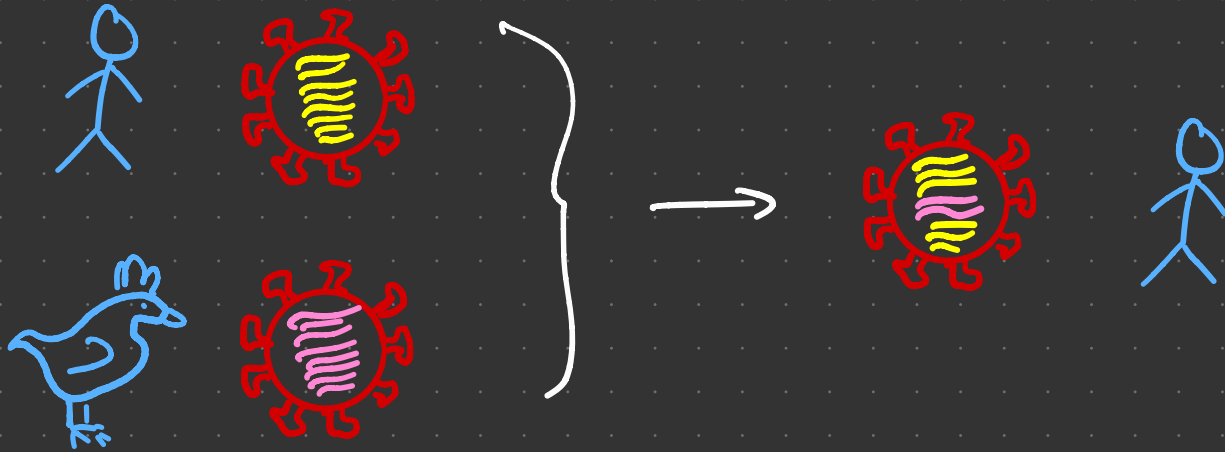


Source: Wiki

In principle two modes of evolution:

- * vertically $\sim 10^{-3}$ substitutions / nucleotide-year
- * horizontally, through infections

Important feature: "Reassortment"

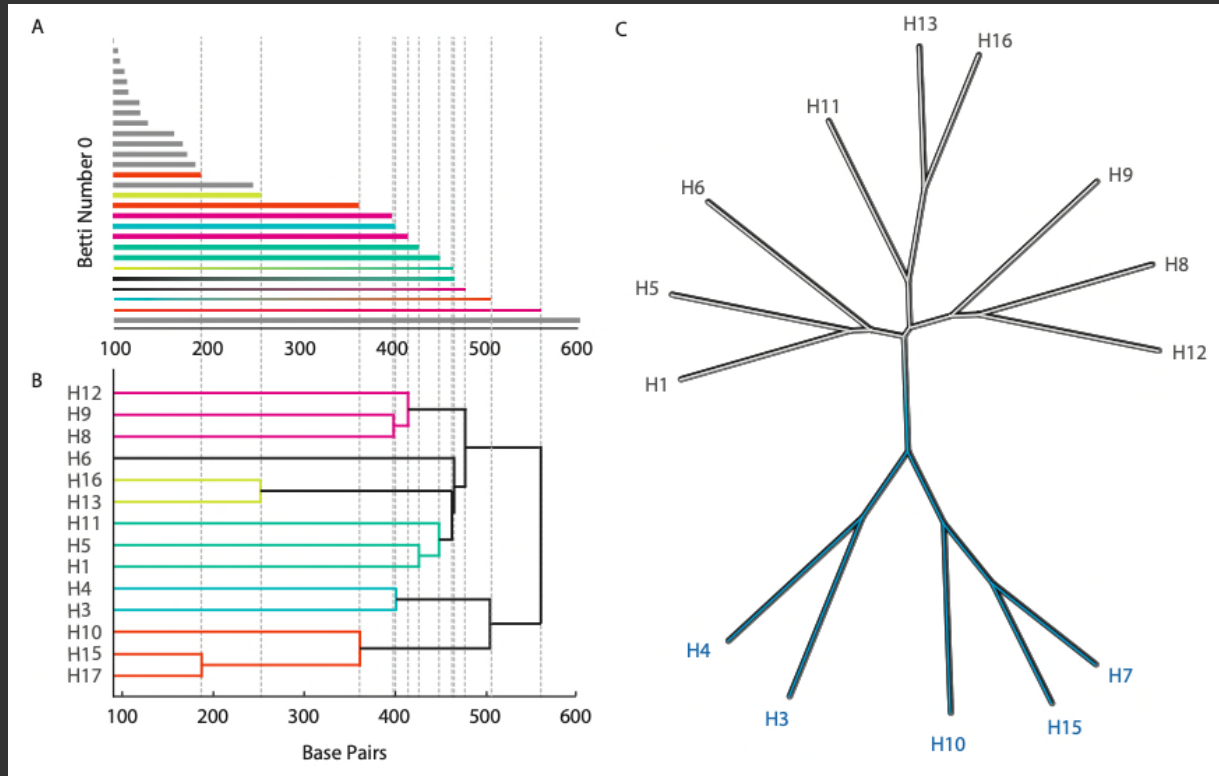


Questions concerning vaccines etc.

- * Reassortment hotspots?
- * Location?
- * Rate?
- * History?

⇒ Use TDA

For one segment:

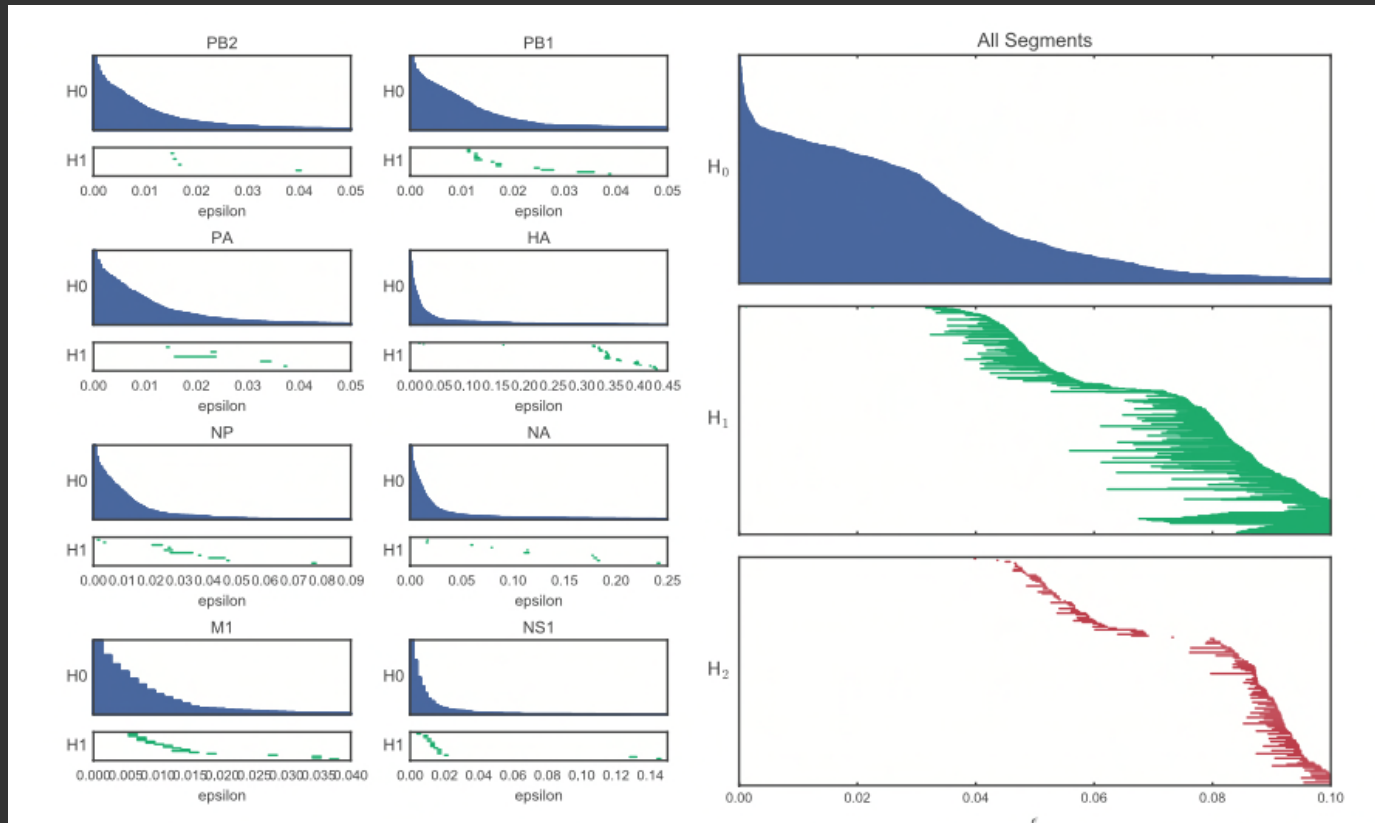


Only relevant
homology
in dim. 0

→ no
recombination

Source: [2]

For the whole genome:



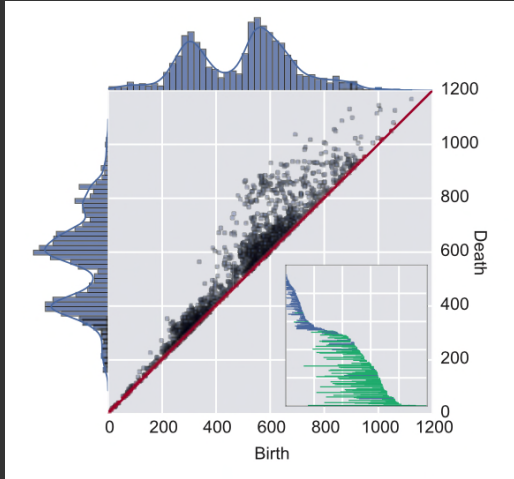
Source: [27]

Barcodes provide useful information:

- * cycles correspond to reticulate events of various types
- * Statistics of cycles reveal reassortment hotspot preserving vital functions
- * Reassortment location and rates

In particular, there is interesting information

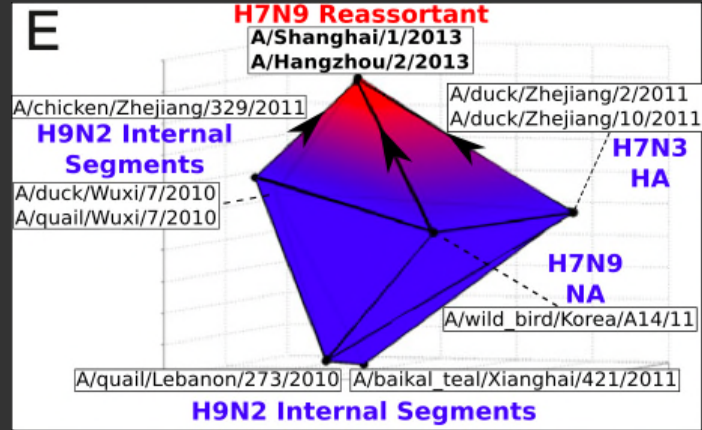
... in the persistence diagram



Source: [2]

Intra- & Inter-subtype reassortments

... in higher dim. cycles



Source: [2]

Triple reassortment lead to 2013 H7N9 avian flu outbreak in China.

Persistent Homology	Viral Evolution
Filtration value ϵ	Genetic distance (evolutionary) scale
0-dimensional Betti number at filtration value ϵ	Number of clusters at scale ϵ
Generators of 0-dimensional homology	A representative element of the cluster
Hierarchical relationship among generators of 0-0-dimensional homology	Hierarchical clustering
1-dimensional Betti number	Number of irreducible recombination/reassortment events
Generators of 1-dimensional homology	Recombinant/reassortant events
Generators of 2-dimensional homology	Complex horizontal genomic exchange
Number of higher dimensional generators in time frame	Lower bound on recombination/reassortment rate
Non-zero high dimensional homology (topological obstruction to phylogeny)	No phylogenetic representation

Source: [2]

Summary

- * Persistent homology provides a new way to think about evolution beyond trees & networks
- * Barcodes and their statistics yield insights into evolutionary history on earth and pathogens
- * Possible applications for vaccines, antibiotics and pandemics

