Level 2
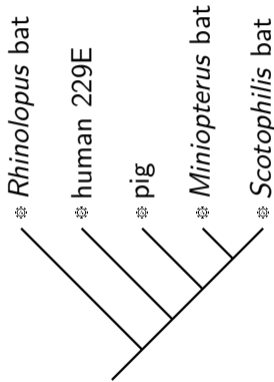
Interpreting phylogenetic trees:

Host switching and zoonosis in Coronaviruses
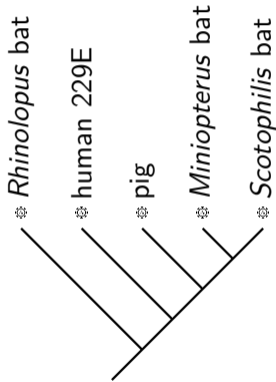
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Level 2

Rhinolopus bat

human 229E

pig

Miniopterus bat

Scotophilis bat

This is a phylogenetic tree showing the relationships of a few **Alpha-coronaviruses**, including one that causes a common cold in humans.

1. Which is the closest relative of the *Miniopterus* bat virus?

2. Is the Pig-A virus more closely related to the Human 229E or to the bat viruses *Miniopterus* bat and *Scotophilis* bat? [with whom do they share a more recent common ancestor?]

3. Is the Human 229E virus more closely related to the *Rhinolopus* bat or the Pig virus?

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4. Name each node on this tree, starting from the root and going up the tree. How many nodes are there?

5. Name each branch. How many branches are there? [do not forget the internal branches!]

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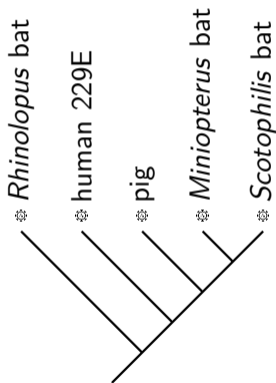
Here is the list of viruses and some of the hosts they infect. Complete the table:

Virus	Host
Rhinolopus bat	bat
human 229E	
pig	pig
Miniopterus bat	
Scotophilis bat	

Can you tell whether the common ancestor of *Miniopterus* bat and *Scotophilis* bat infected a bat, humans or a pig? Identify the host of each virus ancestor on the tree.

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*Rhinolopus* bat

human 229E

pig

Miniopterus bat

Scotophilis bat
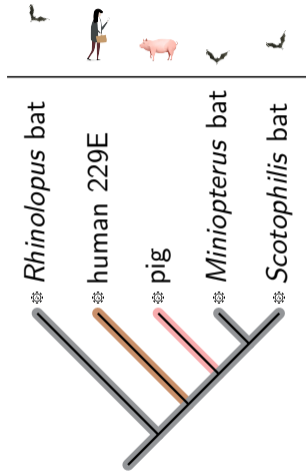
This tree shows the evolutionary history of the movement of the virus from host to host. Branches are coloured by host: gray for bat, brown for human and pink for pig.

For example, if an ancestral branch is gray and one of its descendents is pink, there was a switch from host _____ to host _____.

Particularly, when humans are involved in such host switches, the disease is said to be zoonotic.

Did your answers match this tree?

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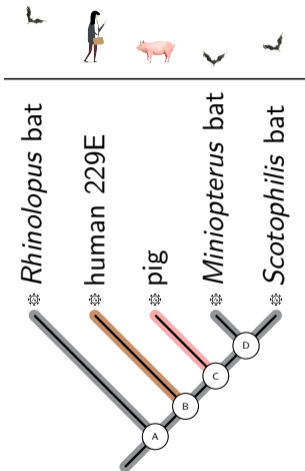
1. What was the host of the oldest ancestral virus [at the root]?

2. Did it switch from this host to any other at any point in its history? Remember each ancestor (node) had two descendents.

Node name	Host switch?	(If host switch) from <u>host</u> to <u>host</u>
Ancestor **A**	no	
Ancestor **B**		
Ancestor **C**		bat **to** pig
Ancestor **D**		

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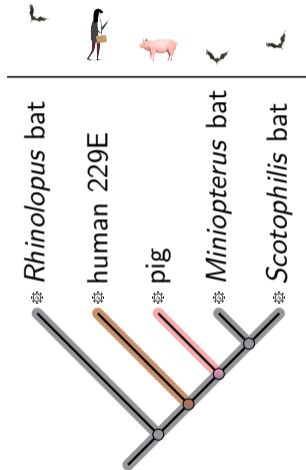

3. The total number of host switches in the history of these viruses is _____

4. The total number of zoonotic events in this history is _____

This is the **Alpha-coronaviruses** group.

SARS-CoVs is a species of Beta-coronaviruses that include forms that cause SARS and COVID-19 diseases in humans, bats, civet cats and pangolins. The story of this group is much more complicated and we will try to understand why this is.

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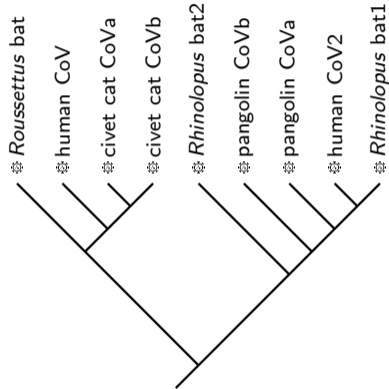
Here is the **Beta-coronaviruses** tree and the list of hosts they infect:

Virus	Host
Human CoV2	human
Rhinolopus bat1	bat
Rhinolopus bat2	bat
Human CoV	human
Roussettus bat	bat
Pangolin CoVa	pangolin
Pangolin CoVb	pangolin
Civet cat CoVa	civet cat
Civet cat CoVb	civet cat

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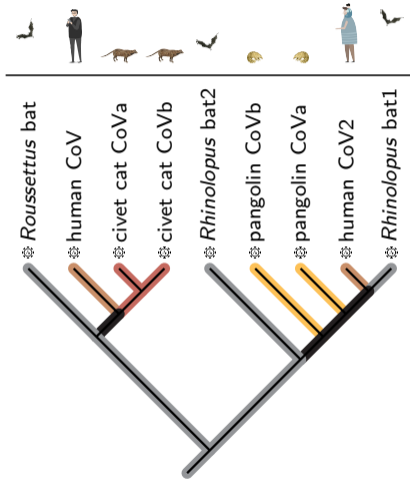
This tree shows you the evolutionary history of host switches, i.e., when and where on the tree the SARS-CoVs viruses went from one host species to another host species. Branches are coloured by host: gray for bat, brown for human, yellow for civet cat and red for pangolin.
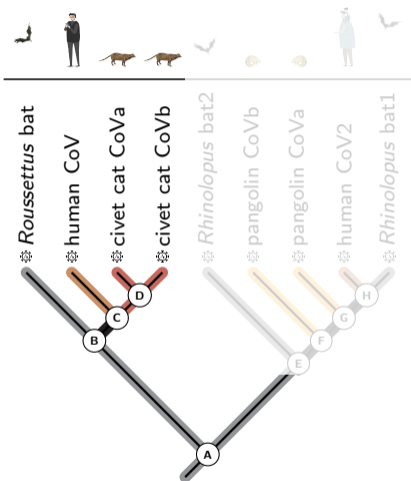
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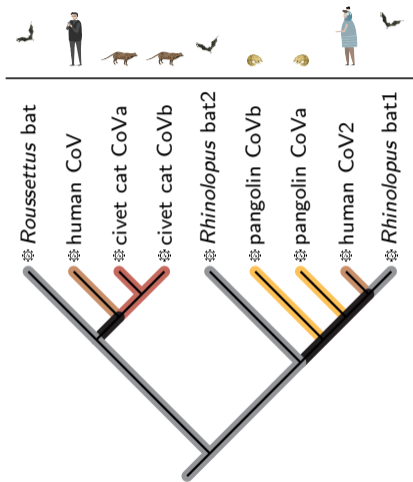
If an ancestral branch is gray and one of its descendents is yellow , there was a switch from host _____ to host _____. Black thick lines mark a virus lineage for whom we cannot tell who the host was. If an ancestral branch is thick black and one of its descendents is gray , there may have been a switch, but we are not sure what it was. As you can see, there are many black thick branches in this tree. Mark them.

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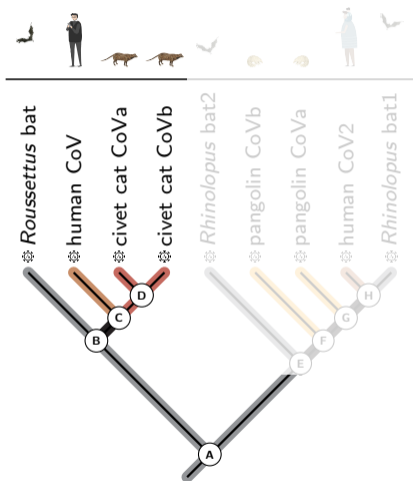
1. What was the host of the oldest ancestral virus [node **A** at the root]?

2. In the SARS clade (left):

    (i) Node **B**: What was the host of the common ancestor of bat, human and civet cat CoVs?
    (ii) Node **C**: What was the host of the common ancestor of human and civet cat CoVs?
    <u>human / civet cat</u>
    (iii) Node **D**: What was the host of the common ancestor to both civet cat CoVs?

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Level 2

3. From which animal did the virus 'jump' to humans?

4. From which animal did the virus 'jump' to civet cats?

5. Did the virus jump to bats from any other animal? Can we be sure?
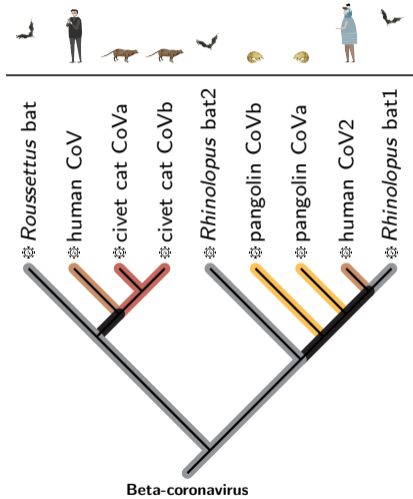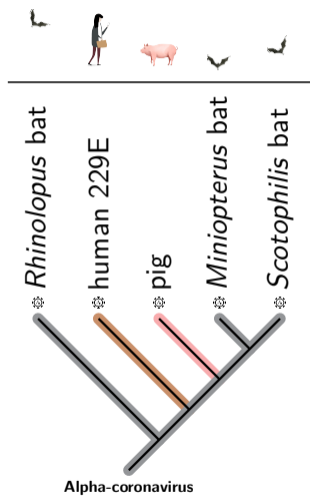
6. Which of these was a zoonotic event?

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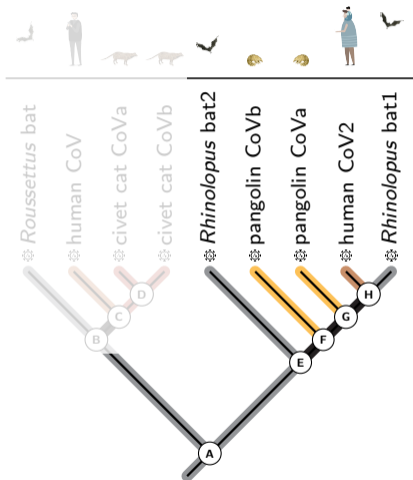
7. In the CoViD-19 clade (right):

   (i) Node **E**: What was the host of the common ancestor of bat, human and pangolin CoVs?
   (ii) Node **F**: What was the host of the common ancestor of bat, human and pangolin CoVs?
   (iii) Node **G**: What was the host of the common ancestor of bat, human and pangolin CoVs?
   (iv) Node **H**: What was the host of the common ancestor of bat and human CoVs?
   (v) We do not know what the host at node **G** was – human, or pangolin. From which animal did the virus come to humans? Can we be sure?

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Level 2

Alpha-coronavirus

Rhinolopus bat · human 229E · pig · Miniopterus bat · Scotophilis bat

Beta-coronavirus

Roussettus bat · human CoV · civet cat CoVa · civet cat CoVb · Rhinolopus bat2 · pangolin CoVb · pangolin CoVa · human CoV2 · Rhinolopus bat1

Finally, compare the evolutionary histories of the **Alpha-coronaviruses** and **Beta-coronaviruses** presented here. They represent two different lineages in this tree, and so must have different histories in terms of both, the viruses themselves and the hosts they infect.

Do they have any shared history?

How do their histories differ?

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