

Characterizing SARS-CoV-2 transmission clusters using phylogenies and metadata in DYNAMITE

COVEME 2021

Brittany Rife Magalis, PhD

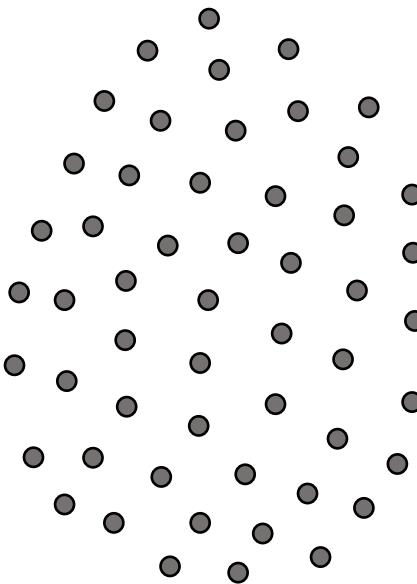
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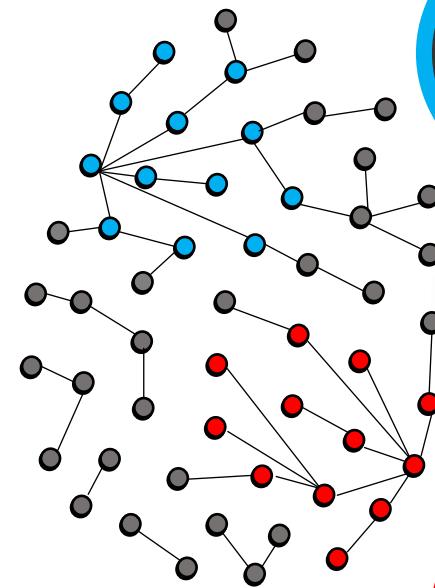
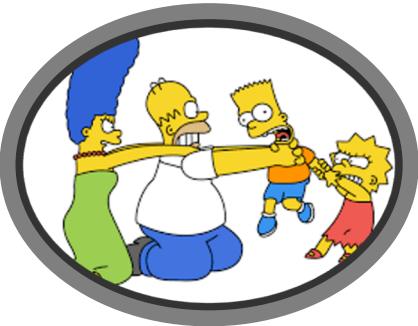
Identifying transmission clusters within a regional epidemic

How do we identify clusters of transmission?

• Infected individual

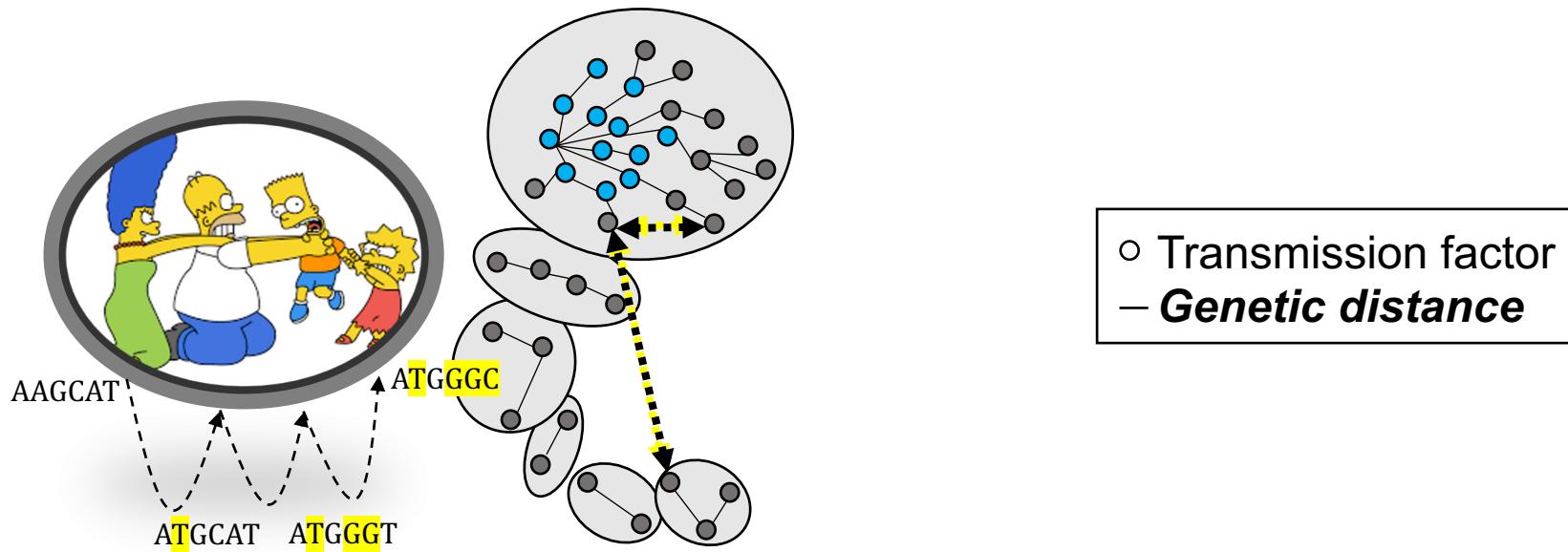


Identifying transmission clusters within a regional epidemic



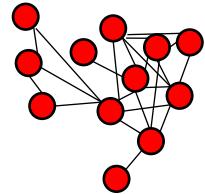
- Transmission factor
- Transmission event

Identifying transmission clusters within a regional epidemic

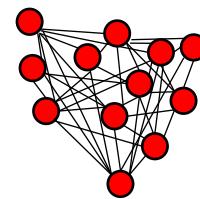


But why a phylogeny?

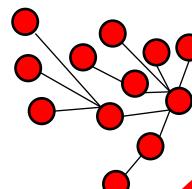
(*Filtered* pairwise
genetic distances)



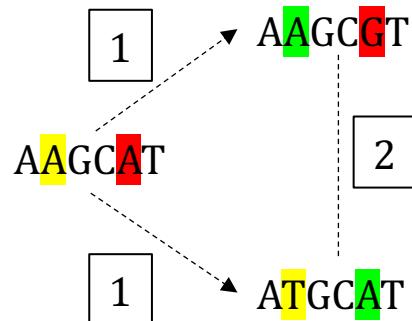
(Pairwise genetic
distances)

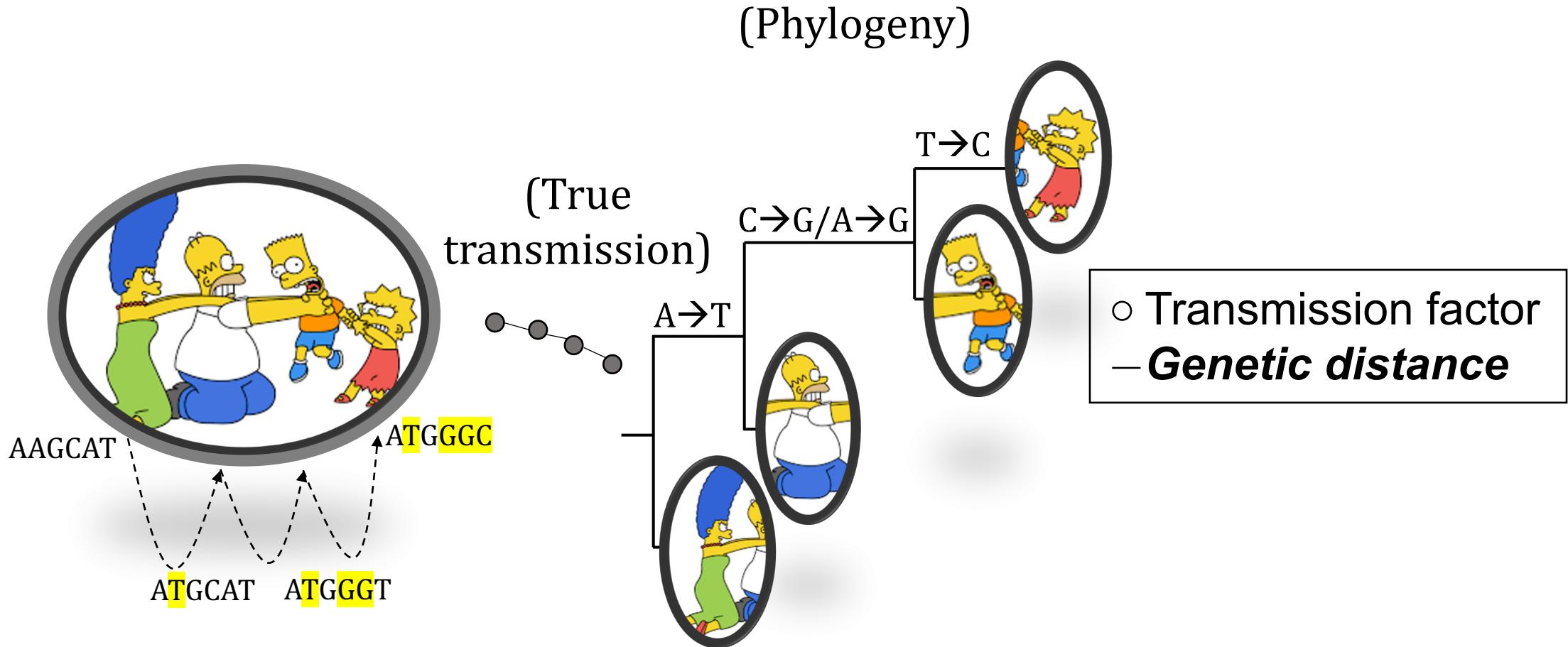


(True
transmission)

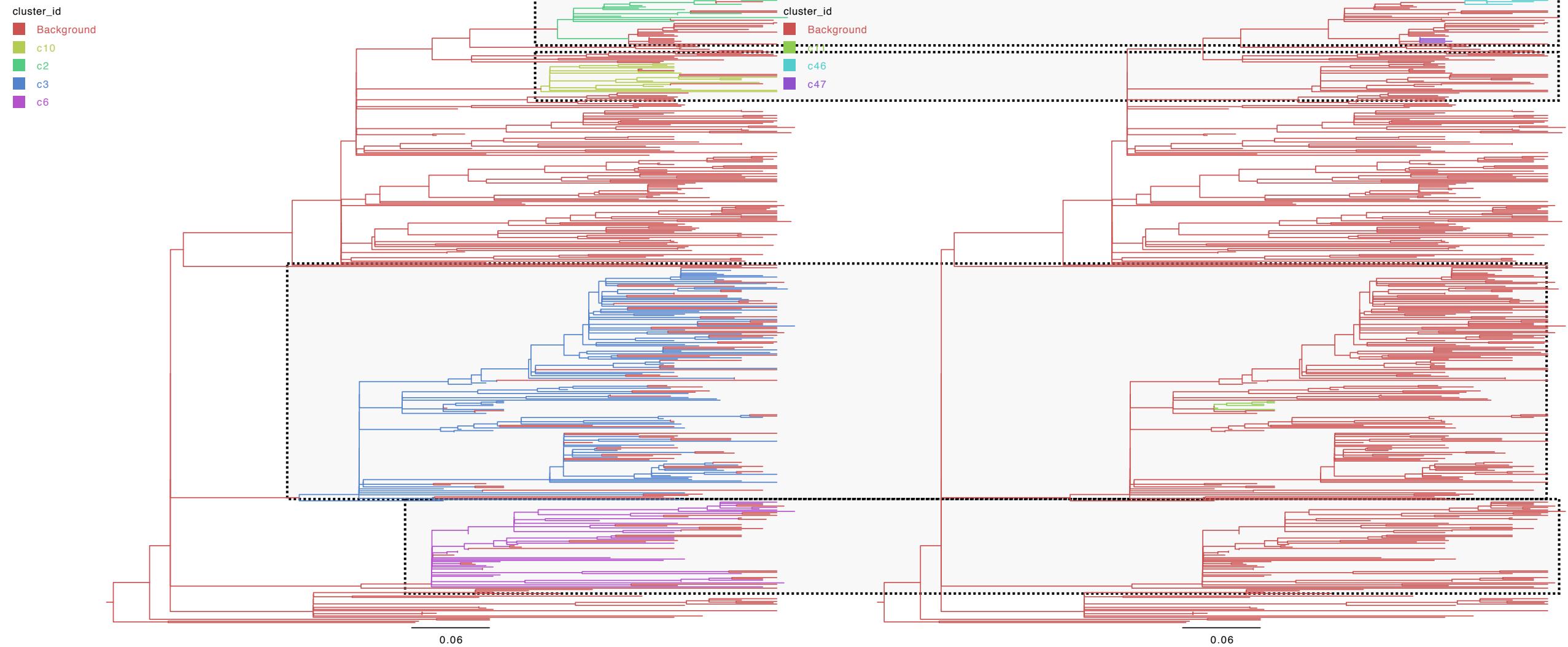


- Transmission factor
- ***Genetic distance***



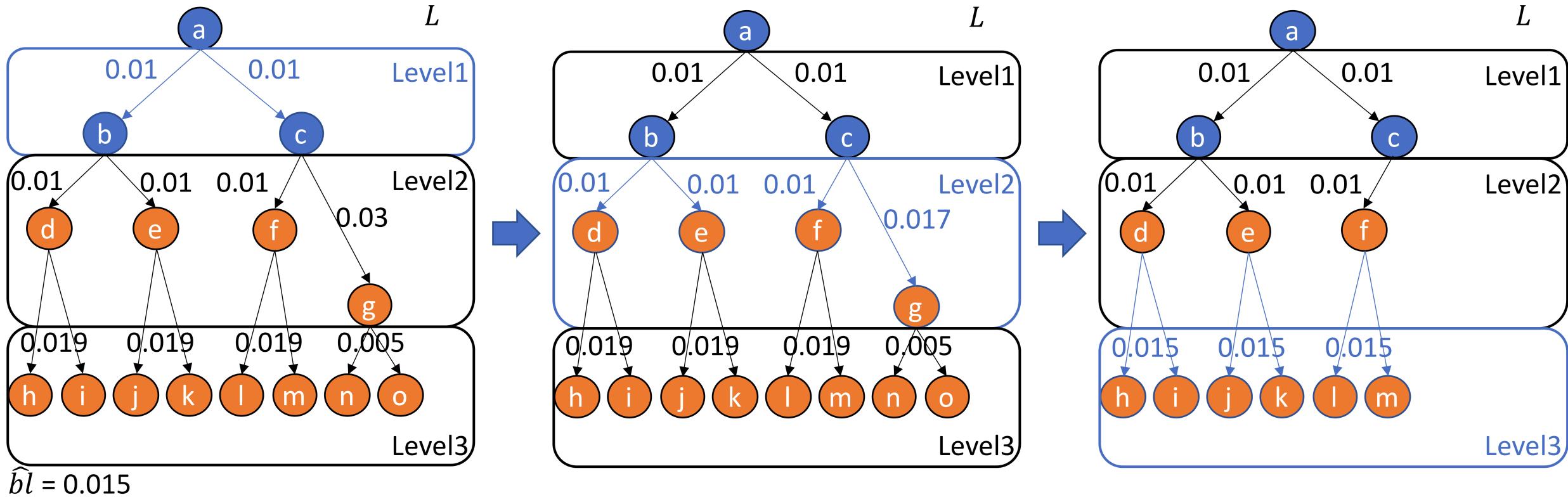


Why DYNAMITE?



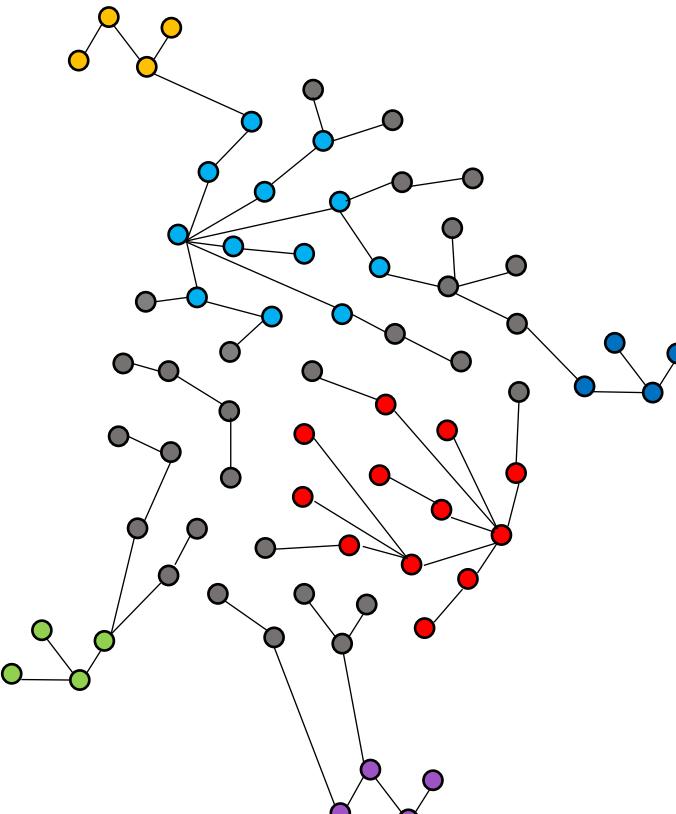
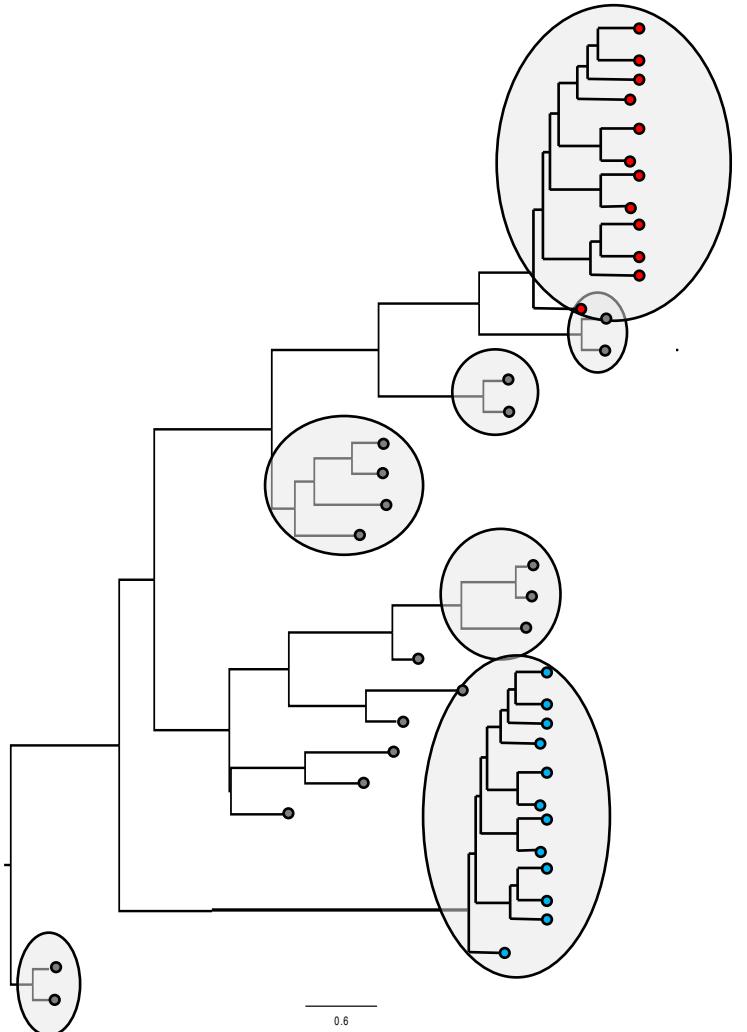
Not limited to monophyletic clades and can incorporate sampling time information to put restraints based on known serial interval

How does DYNAMITE work?



- Now includes similar acceptance approach based on sampling time and serial interval (time between symptom onset in donor and recipient)
 - e.g., 6 days for SARS-CoV-2 [Rai et al., 2021]

Identifying transmission clusters within a regional epidemic



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(Transmission)

What are the risk factors for transmission of SARS-CoV-2?

Relevant geographical and temporal sampling

FLACO-BLAST



FLoridA COvid Basic Local Alignment Search Tool



Searches and aligns “local” sequence segments (rather than entire sequence) and scores according to similarity

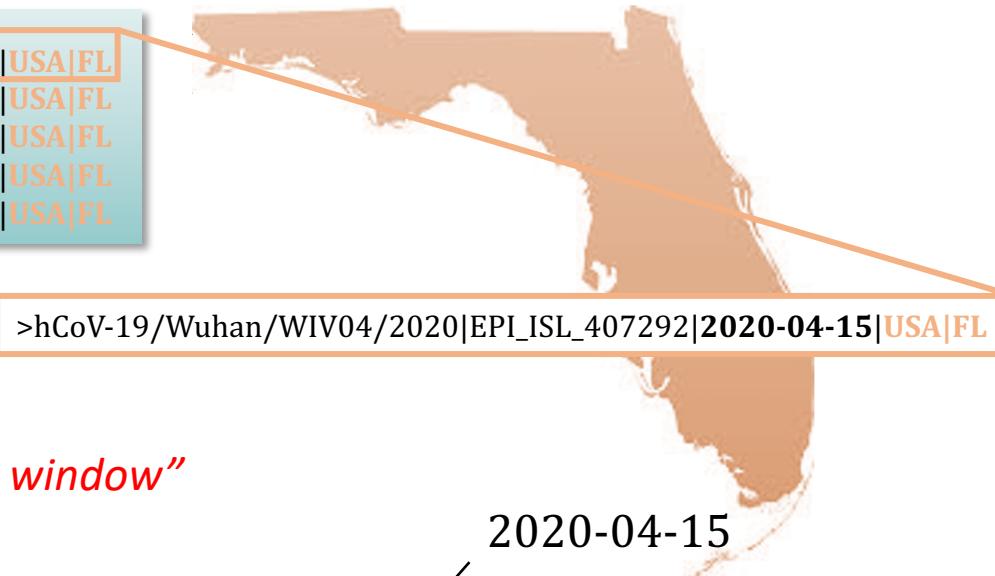


For information on GISAID sequence retrieval and FLACO-BLAST, see Alberto Riva’s breakout session!

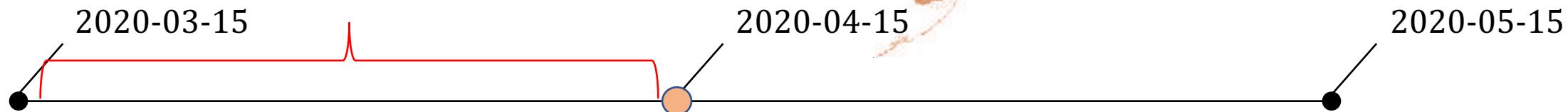
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FLACO-BLAST

>hCoV-19/Wuhan/WIV04/2020|EPI_ISL_407292|2020-04-15|USA|FL
>hCoV-19/Wuhan/WIV04/2020|EPI_ISL_407296|2020-05-15|USA|FL
>hCoV-19/Wuhan/WIV04/2020|EPI_ISL_407297|2020-06-15|USA|FL
>hCoV-19/Wuhan/WIV04/2020|EPI_ISL_407312|2020-07-15|USA|FL
>hCoV-19/Wuhan/WIV04/2020|EPI_ISL_407313|2020-08-15|USA|FL



“Transmission window”



ID	%
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402137 2020-04-10 Spain	100
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402128 2020-04-01 Taiwan	99
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402129 2020-03-21 UK	98.9
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402164 2020-03-30 Spain	98
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402114 2020-03-15 China	98

ID	%
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402137 2020-04-16 Spain	100
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402128 2020-04-20 Germany	100
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402129 2020-04-21 UK	99
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402164 2020-05-01 Germany	98
>hCoV-19/Wuhan/WIV04/2020 EPI_ISL_402114 2020-05-11 Spain	98

>hCoV-19/Wuhan/WIV04/2020|EPI_ISL_402137|2020-04-10|Spain
>hCoV-19/Wuhan/WIV04/2020|EPI_ISL_402137|2020-04-16|Spain
>hCoV-19/Wuhan/WIV04/2020|EPI_ISL_402128|2020-04-20|Germany

For information on GISAID sequence retrieval and FLACO-BLAST, see Alberto Riva’s breakout session!

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Alberto Riva, PhD

Evidence of “VAXers” as high-risk groups and potential transmitters?

Do “VAXers” cluster together in the tree or demonstrate evidence of transmission?

Step 1: FLACO-BLAST Delta sequences in FL against GISAID

Step 2: Align sequences using ViralMSA

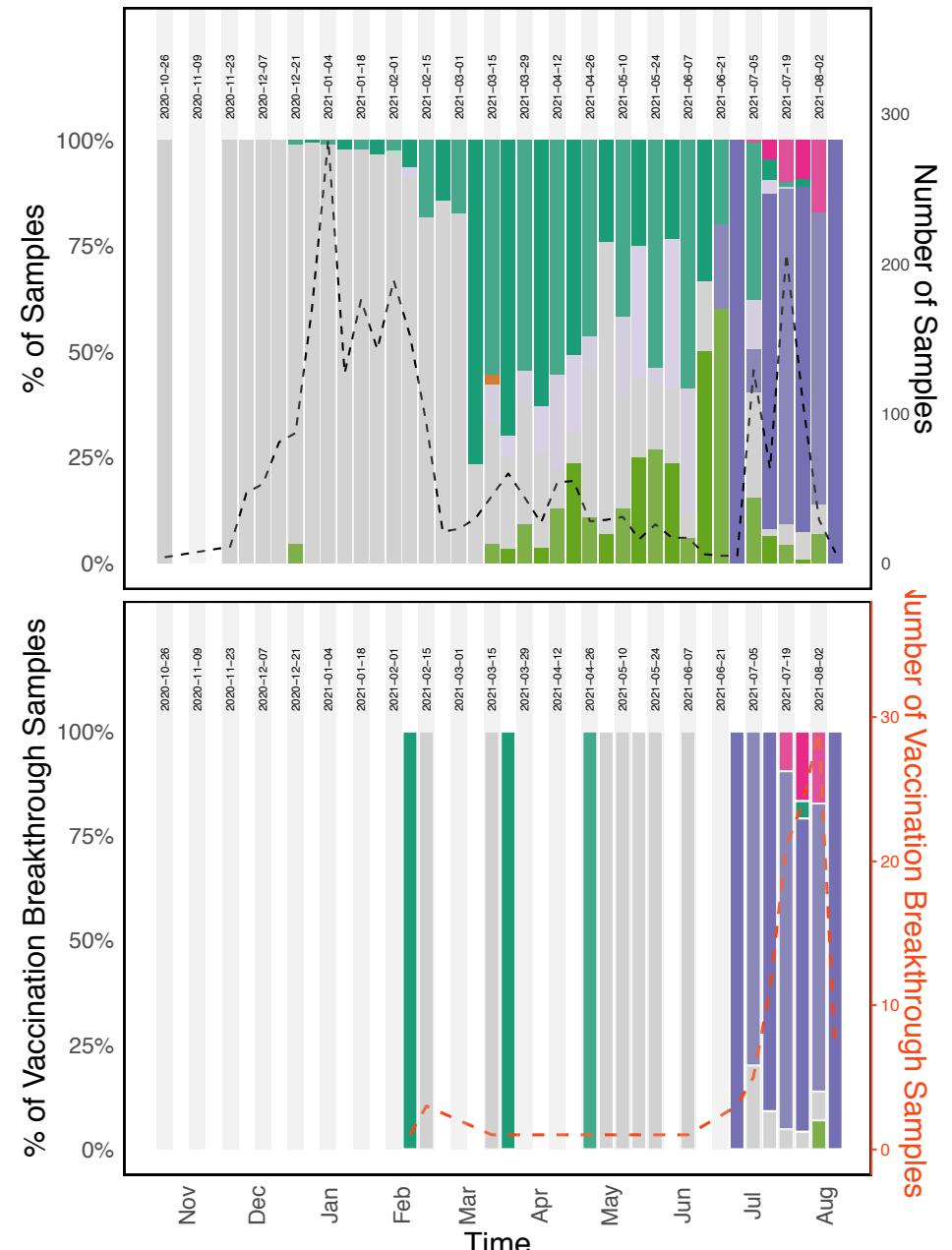
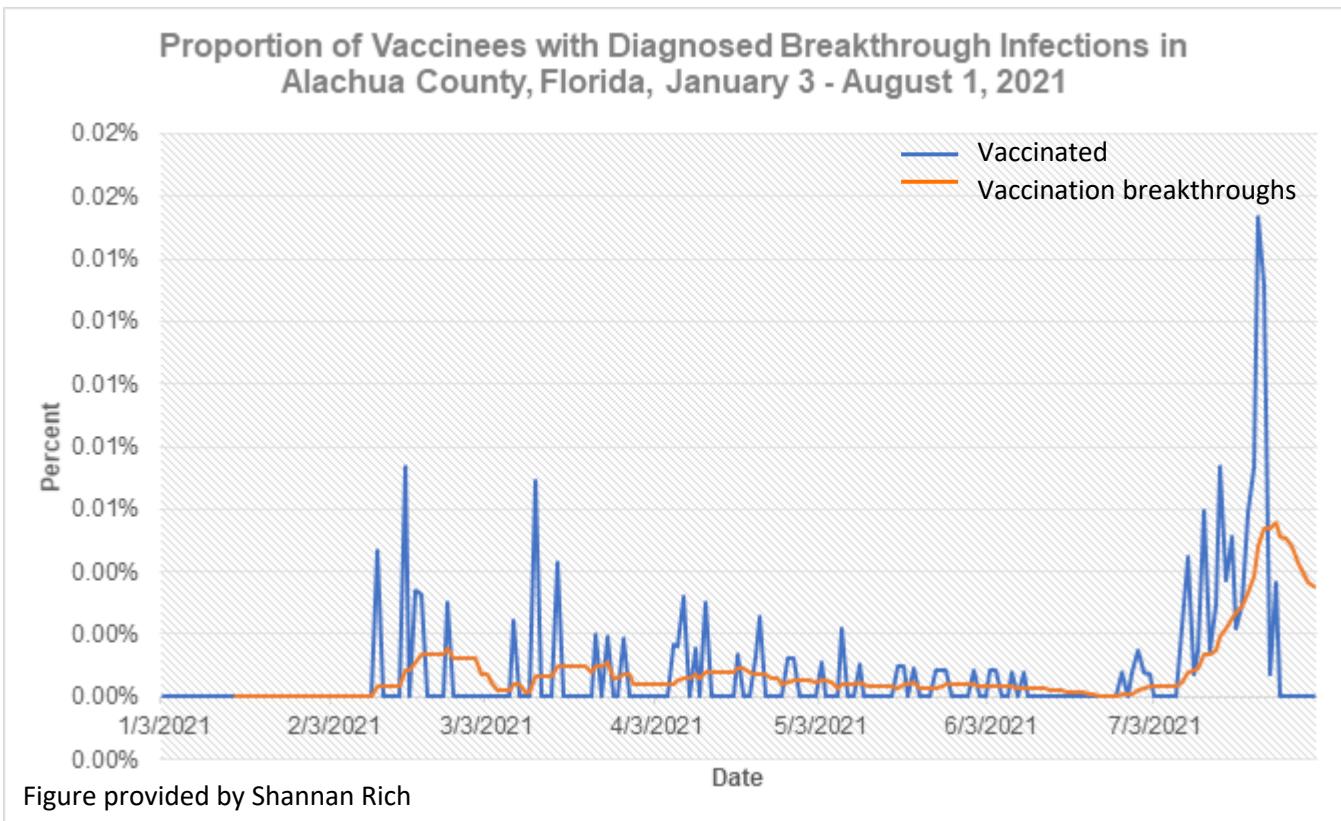
Step 3: Mask problematic sites

Step 4: Screen for recombination

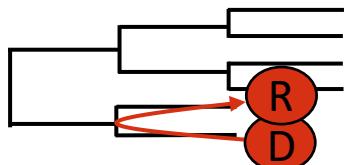
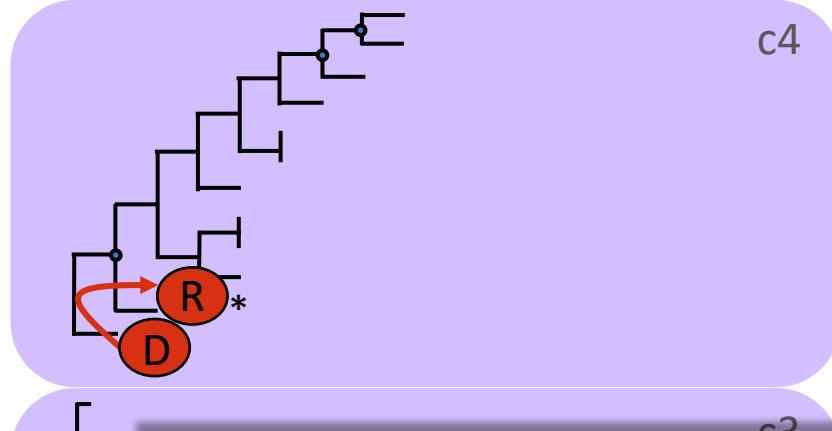
Step 5: Added sequences to existing phylogeny using UShER

Step 6: Use DYNAMITE clustering algorithm to identify clusters of transmission

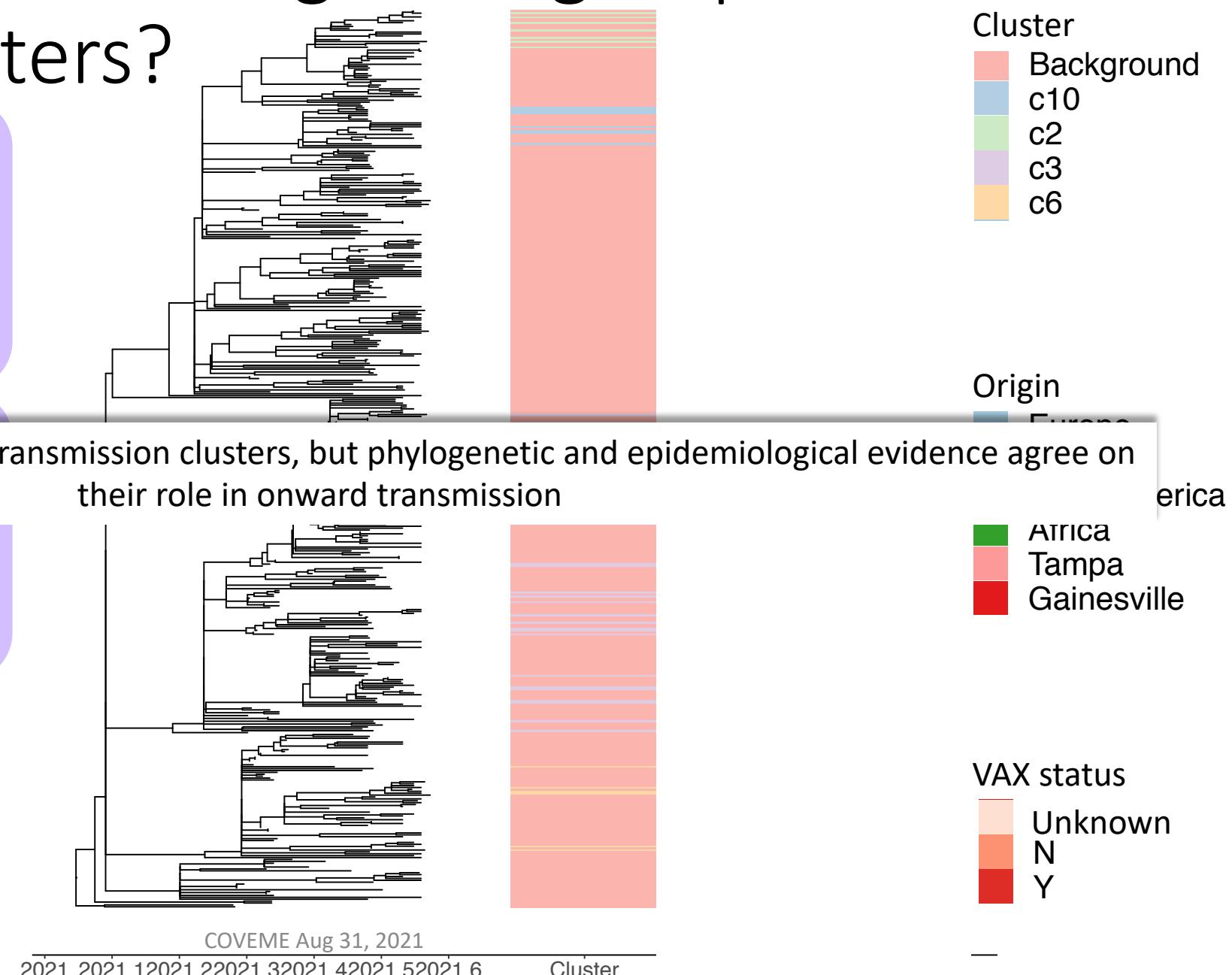
Evidence of “VAXers” as high-risk groups and potential transmitters?



Evidence of “VAXers” as high-risk groups and potential transmitters?



5E-05
subs/site



DEMO

DYNAMITE tutorial and material found in <http://tinyurl.com/coveme2021>

Additional material:

DYNAMITE: a phylogenetic tool for identification of dynamic transmission epicenters

 Brittany Rife Magalis, Simone Marini, Marco Salemi, Mattia Prosperi

doi: <https://doi.org/10.1101/2021.01.21.427647>

<https://github.com/ProsperiLab/DYNAMITE>