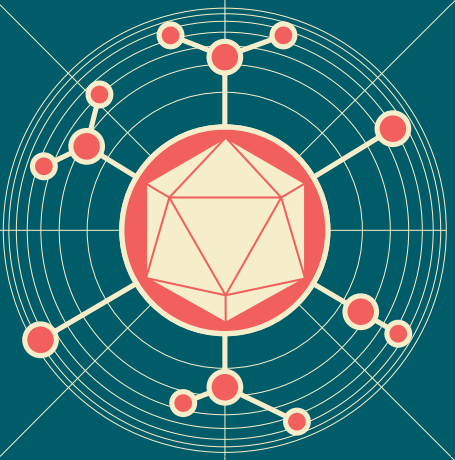


What genomic data could tell us

...through phylodynamics

Philippe Lemey

Rega Institute,

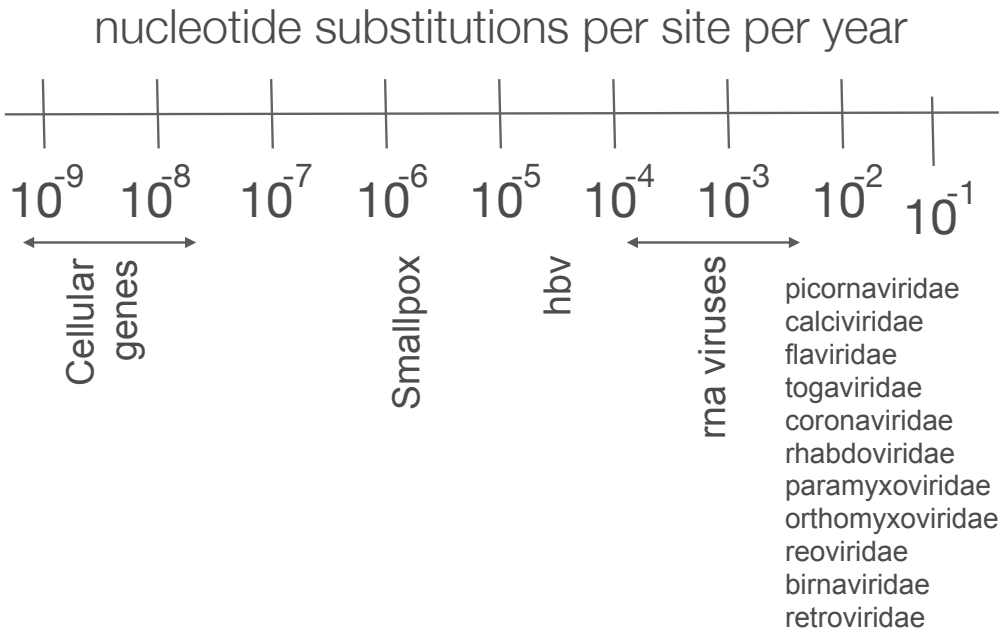
Department of Microbiology,
Immunology and Transplantation

K.U. Leuven, Belgium.

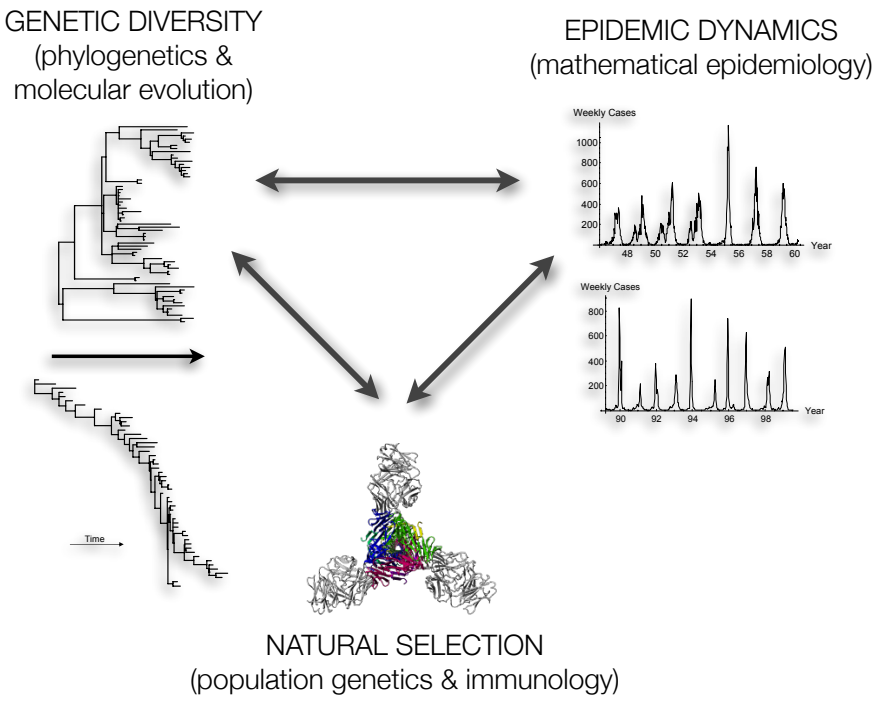
Unifying the epidemiological and evolutionary dynamics of pathogens

> “Rapidly evolving pathogens are unique in that their ecological and evolutionary dynamics occur on the same timescale and can therefore potentially interact.”

Pybus & Rambaut (2009) Nat. Rev. Genetics 10:540-50



Grenfell (2004) Science 303: 327-30



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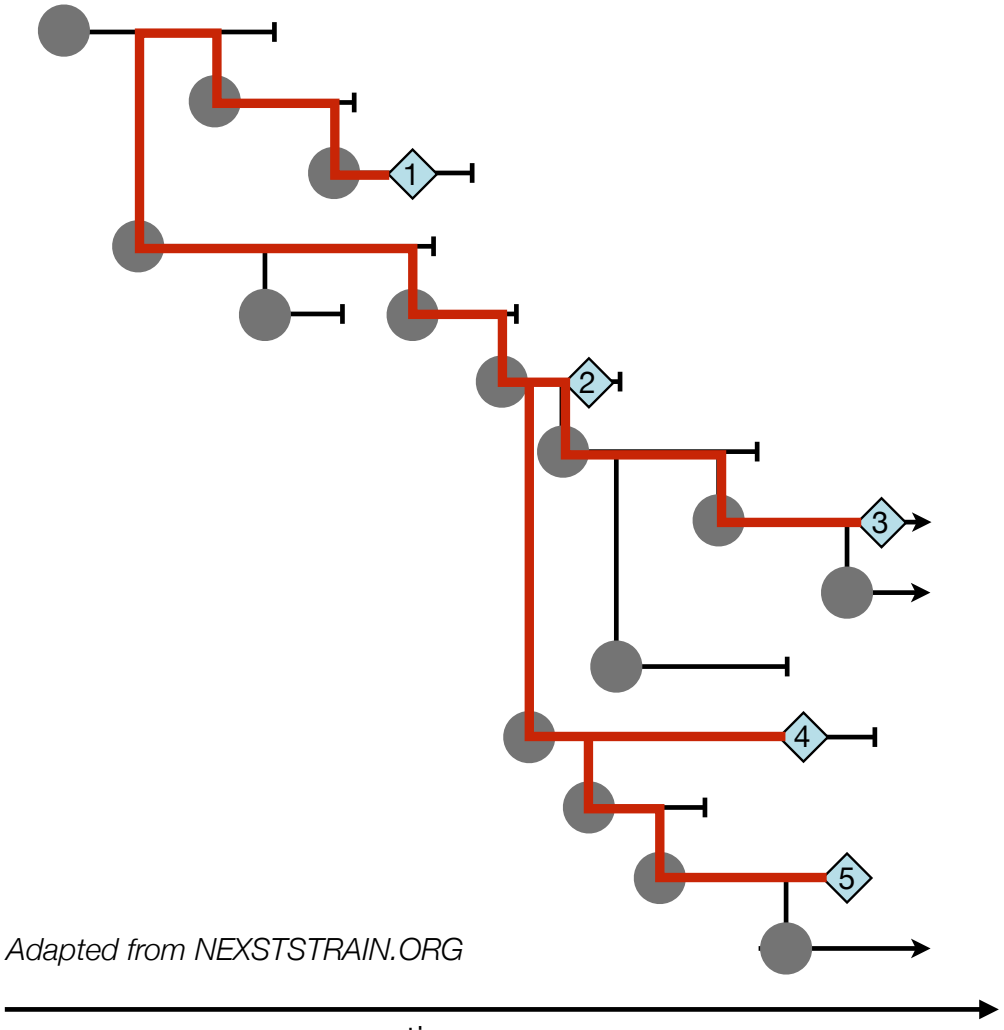
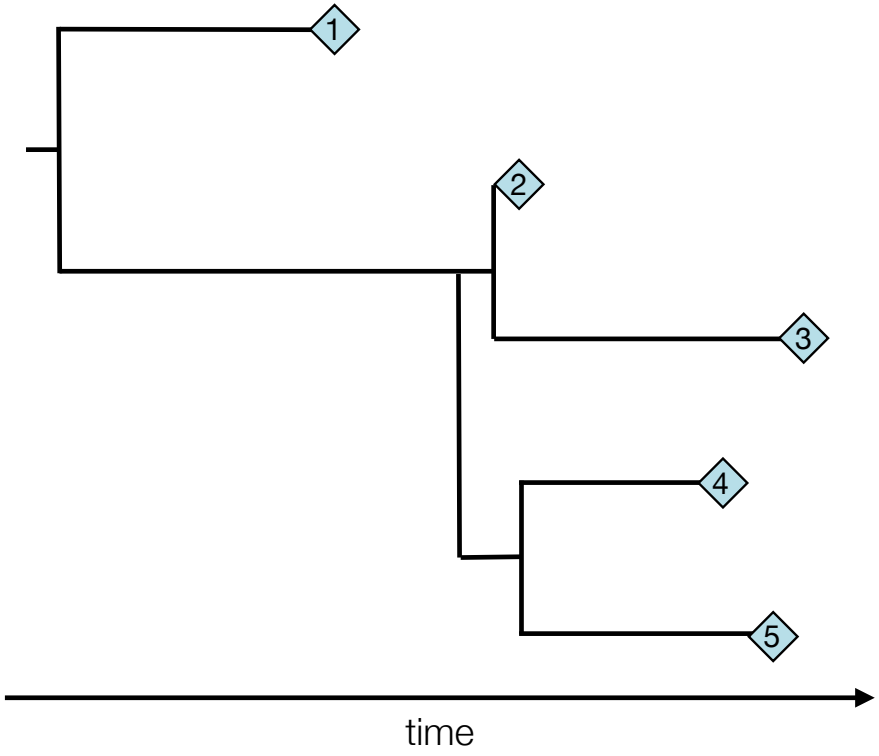


Adapted from NEXSTSTRAIN.ORG

Phylogeny



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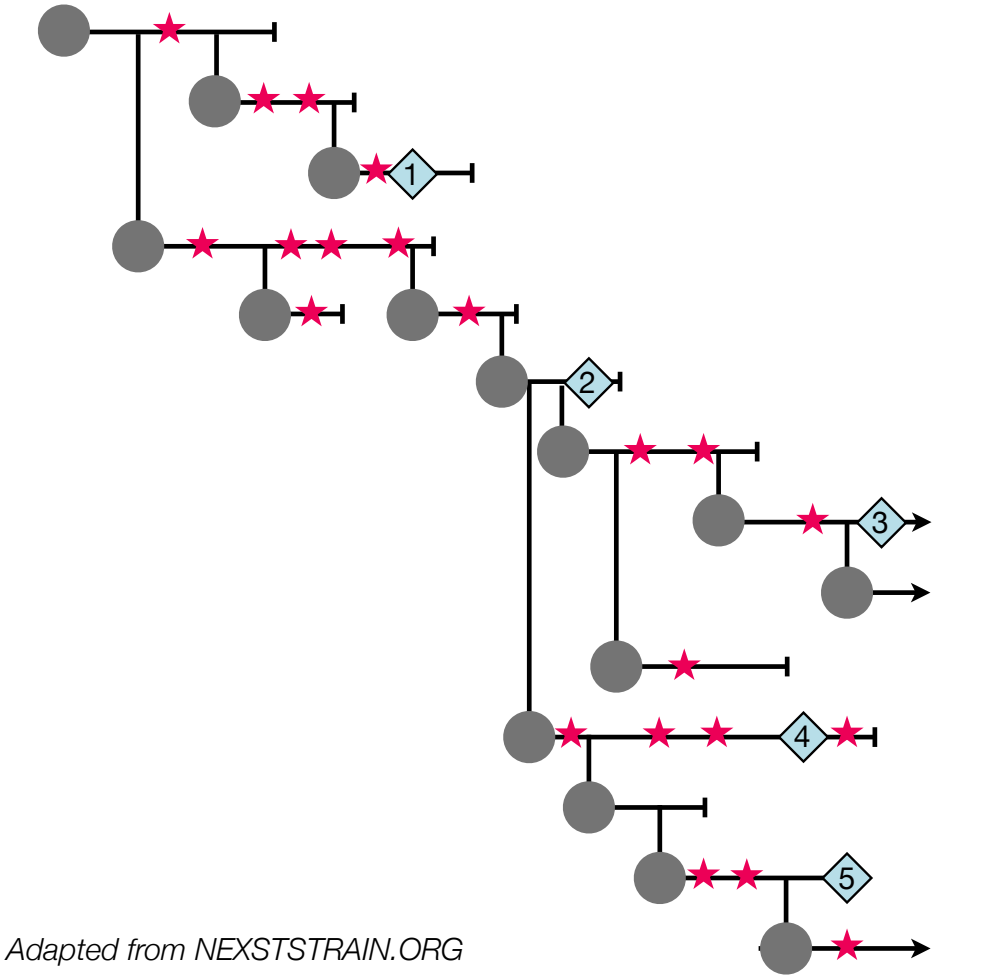
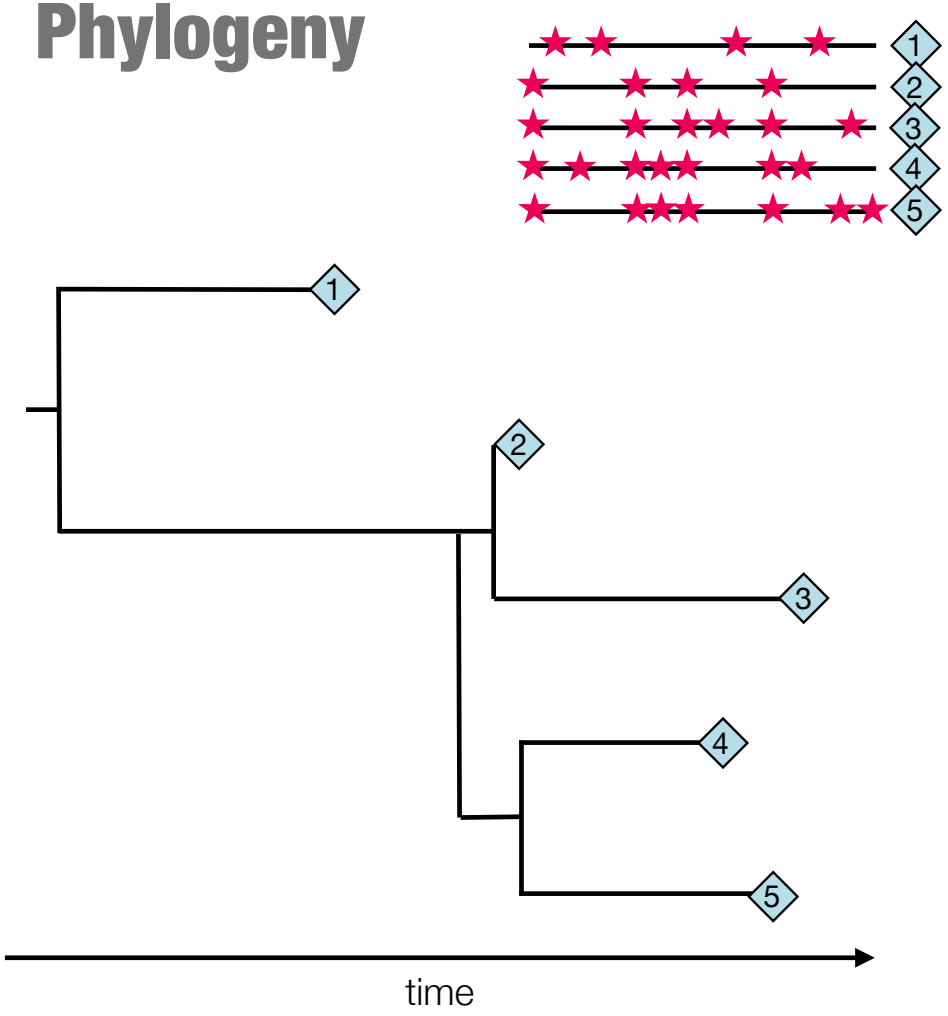


Adapted from NEXSTSTRAIN.ORG

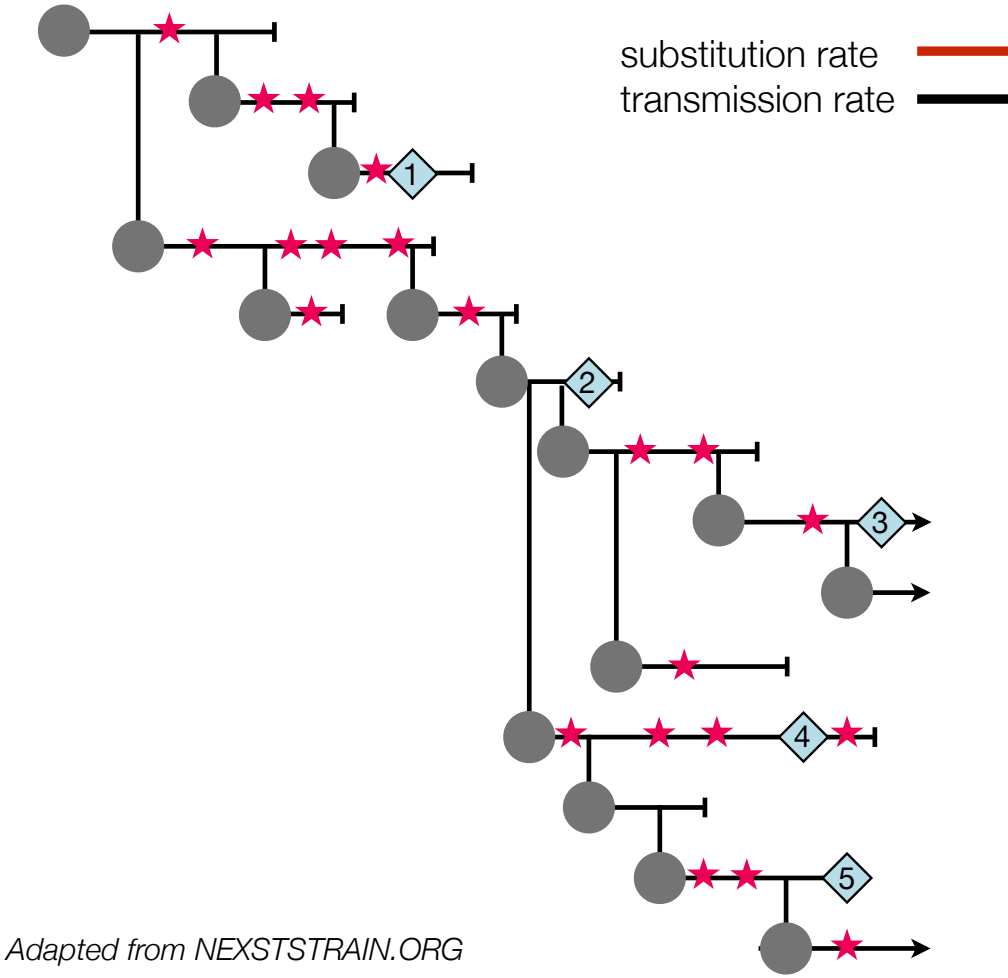
time

Phylogeny



time

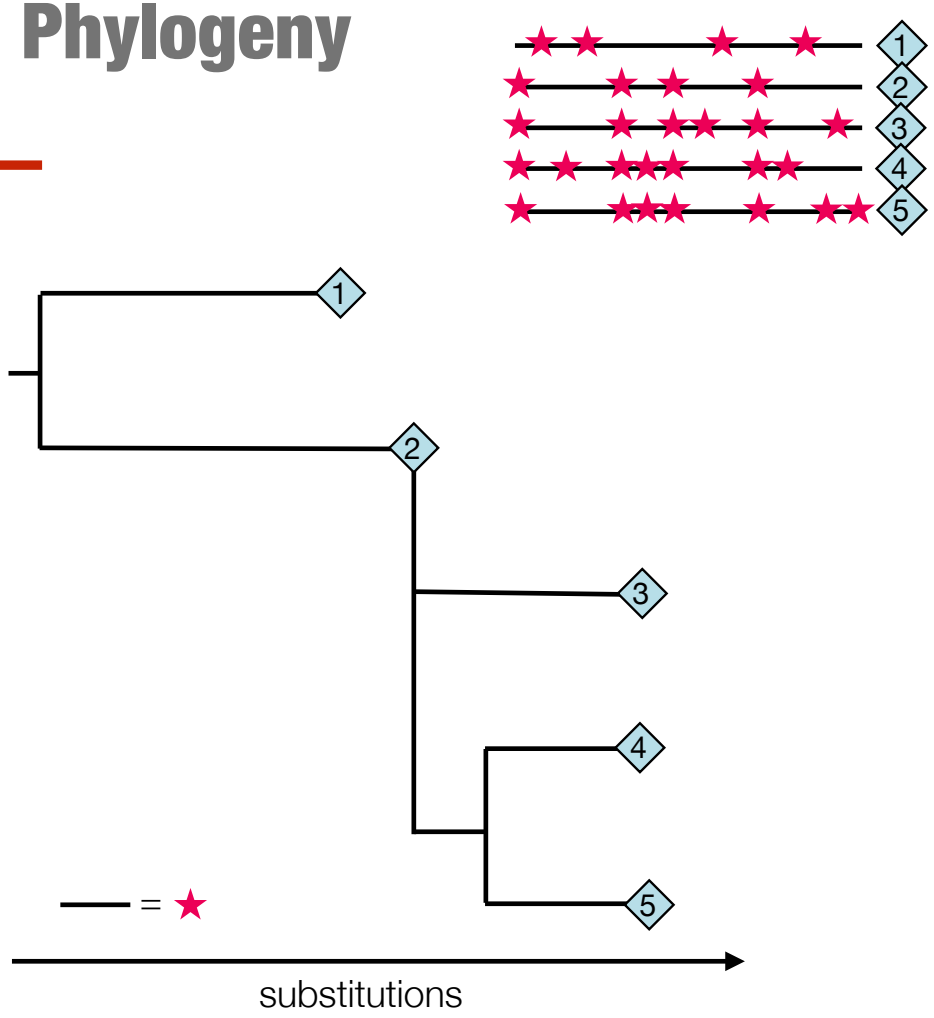
Transmission history



Adapted from NEXSTSTRAIN.ORG

time

Phylogeny



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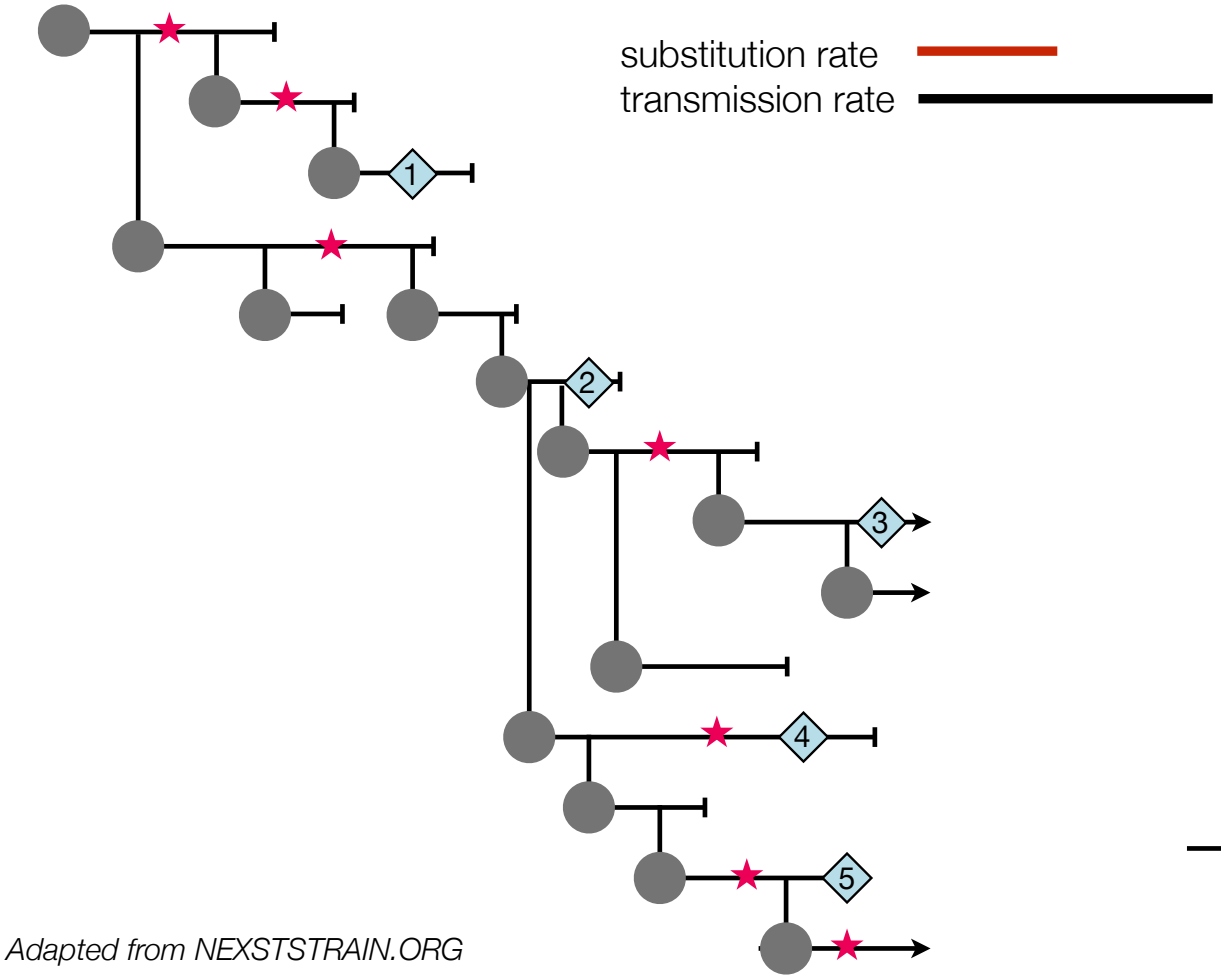
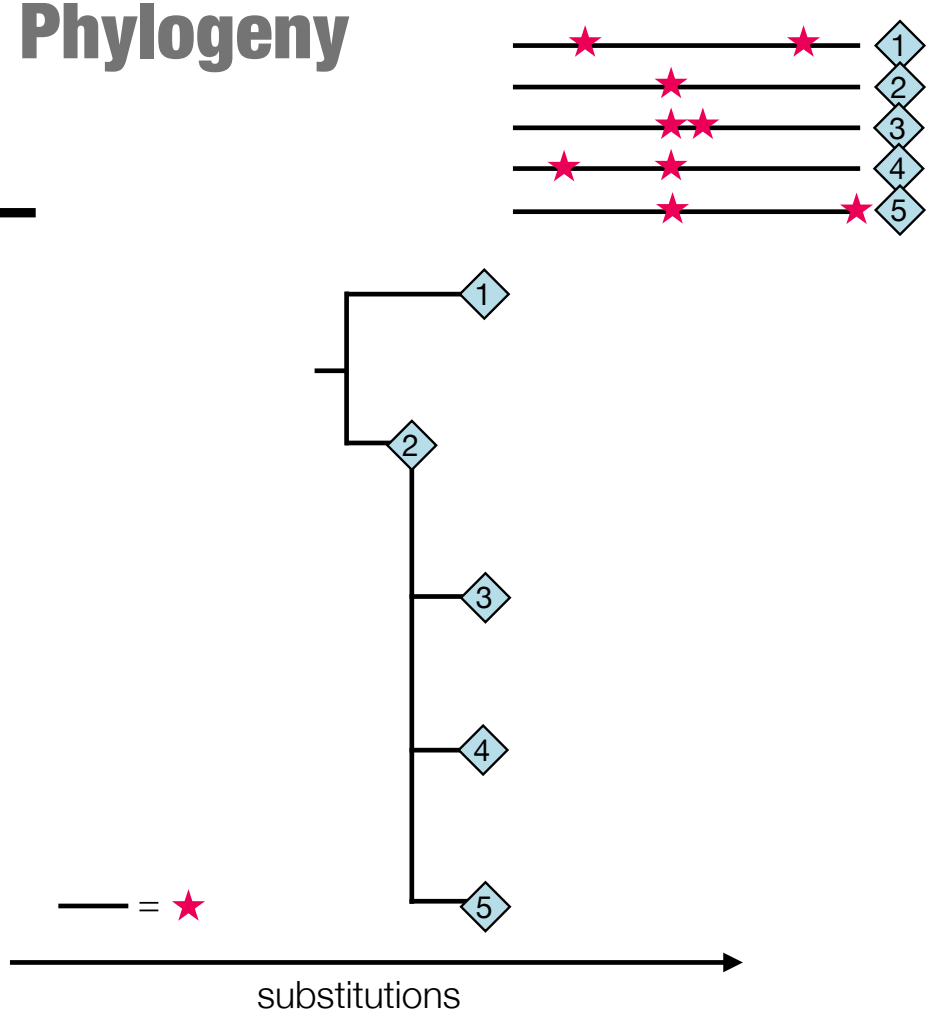


Adapted from NEXSTSTRAIN.ORG

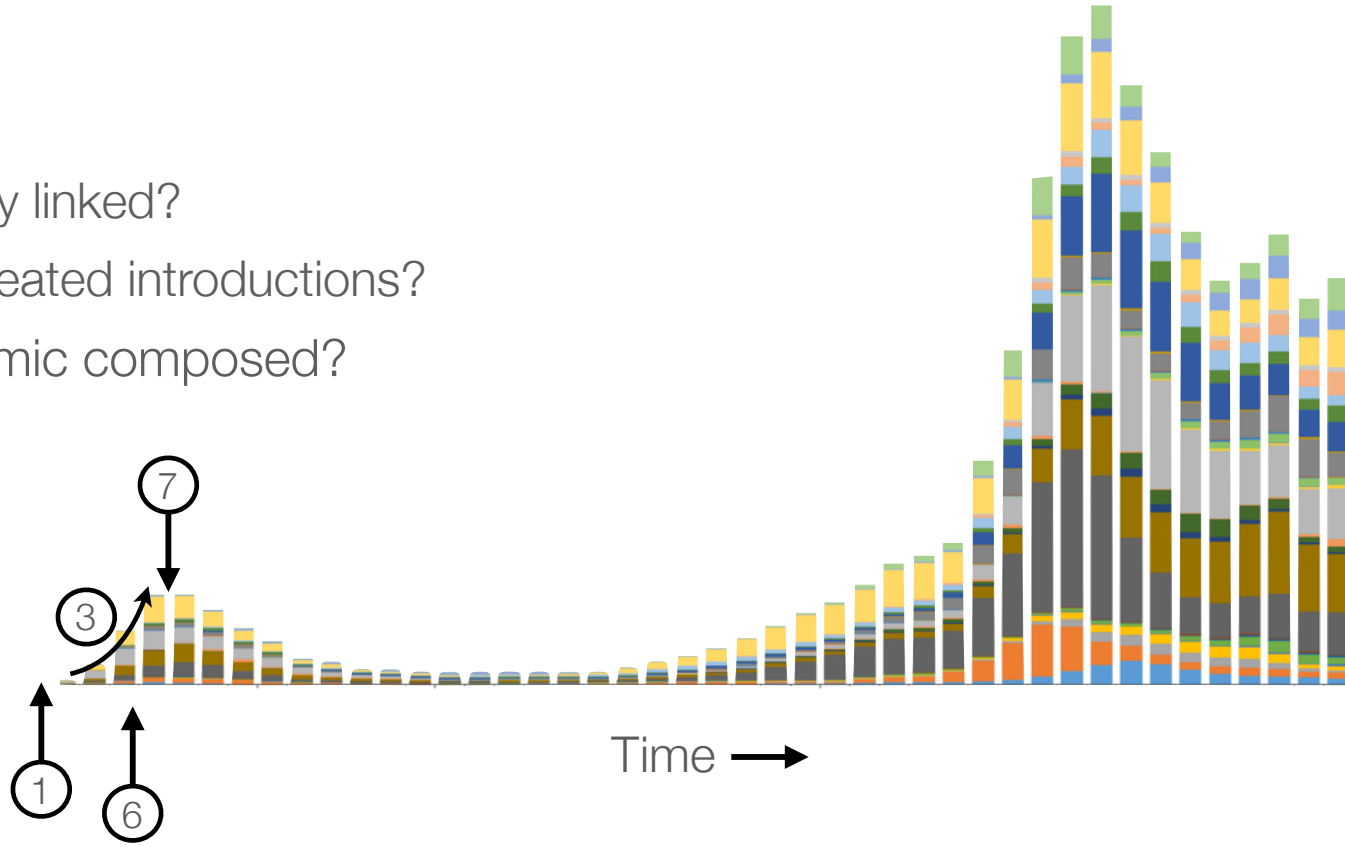
time

Phylogeny



Epidemiological questions

1. When did an epidemic start?
2. Where did it come from, how many introductions?
3. How fast is it transmitting?
4. In what direction is it spreading?
5. Are hosts X, Y & Z epidemiologically linked?
6. Local transmission or repeated repeated introductions?
7. Of how many strains is the epidemic composed?
8. What adaptations has it accrued?
9. ...



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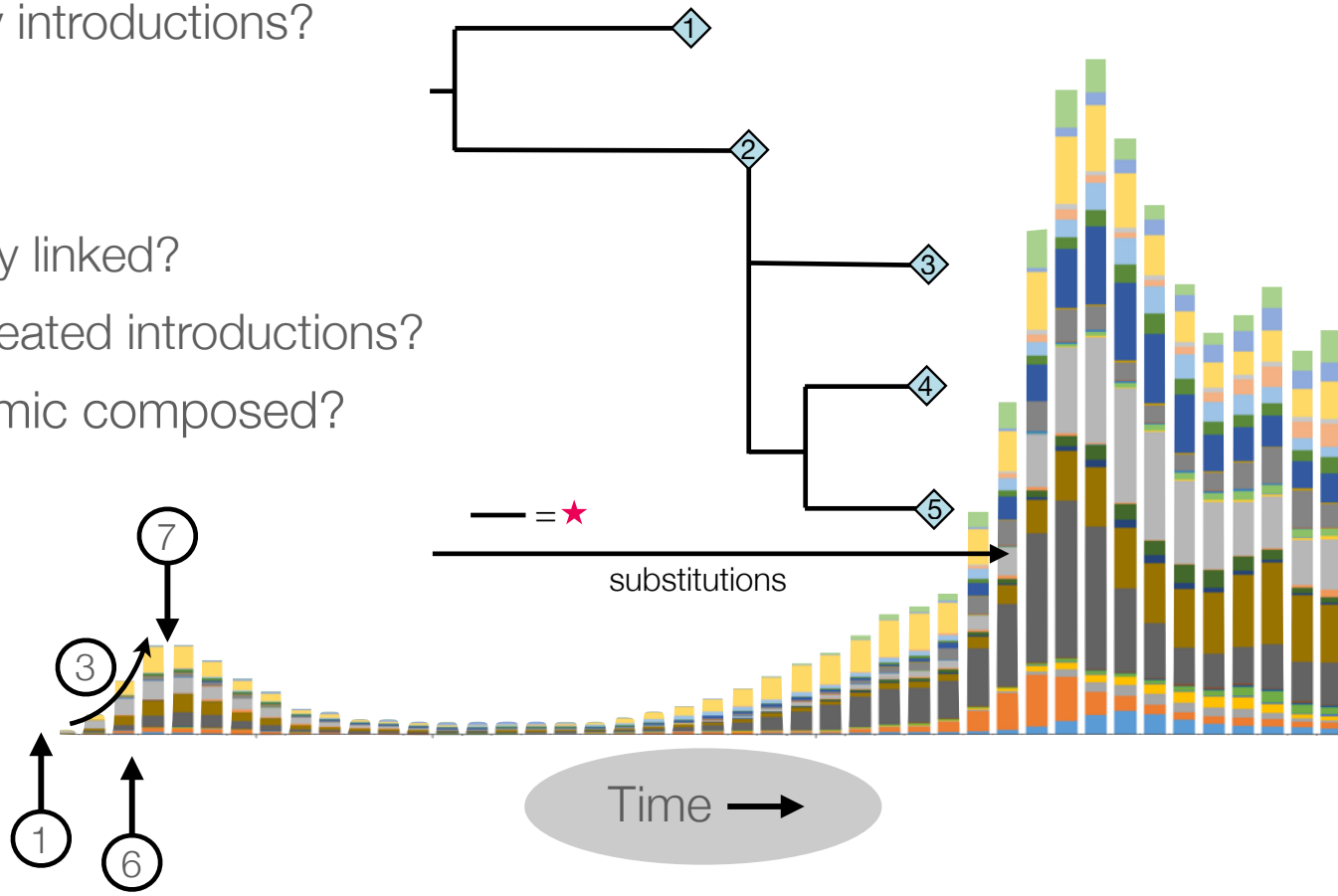
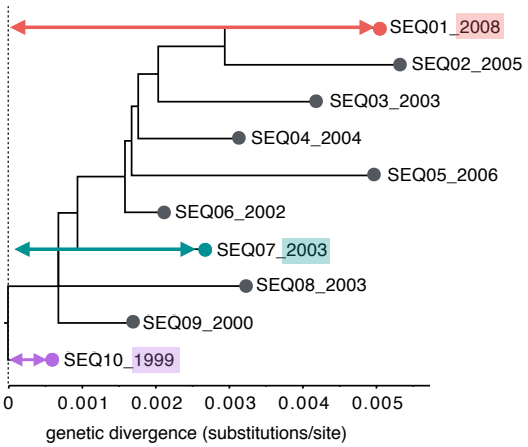
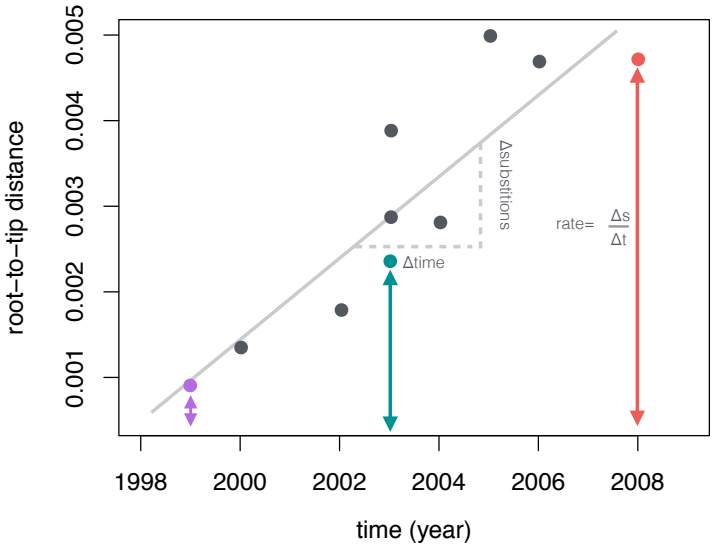


Phylodynamic inference: time

Substitutions

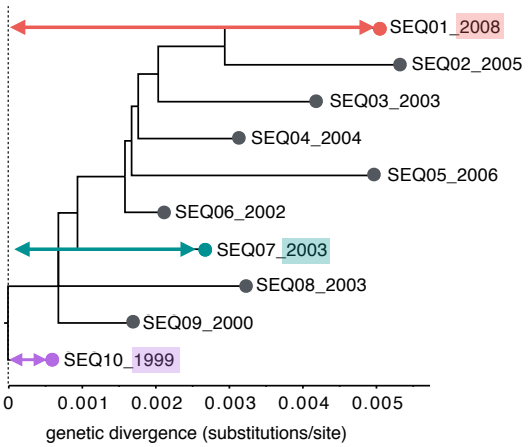


Evolutionary rate

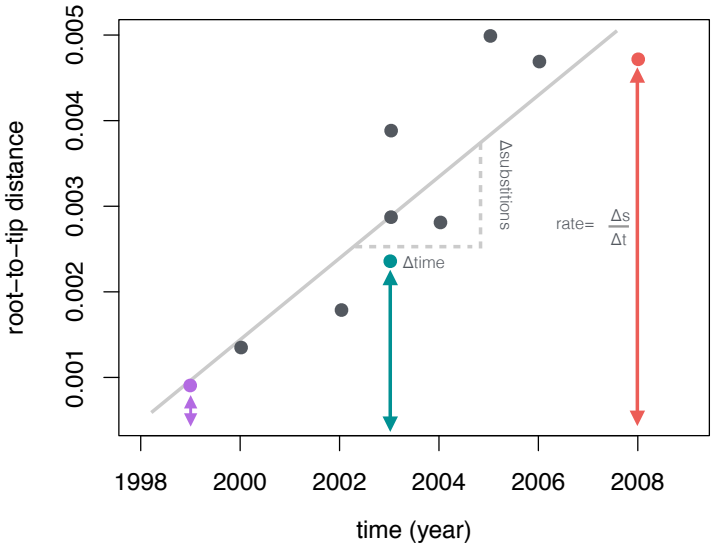


Phylodynamic inference: time

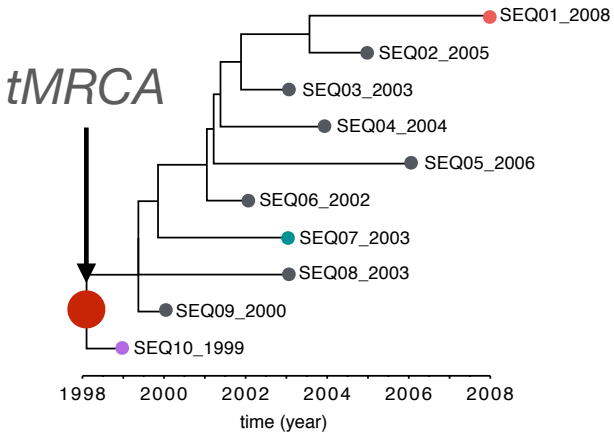
Substitutions



Evolutionary rate



Time



Molecular clock

Epidemiological questions

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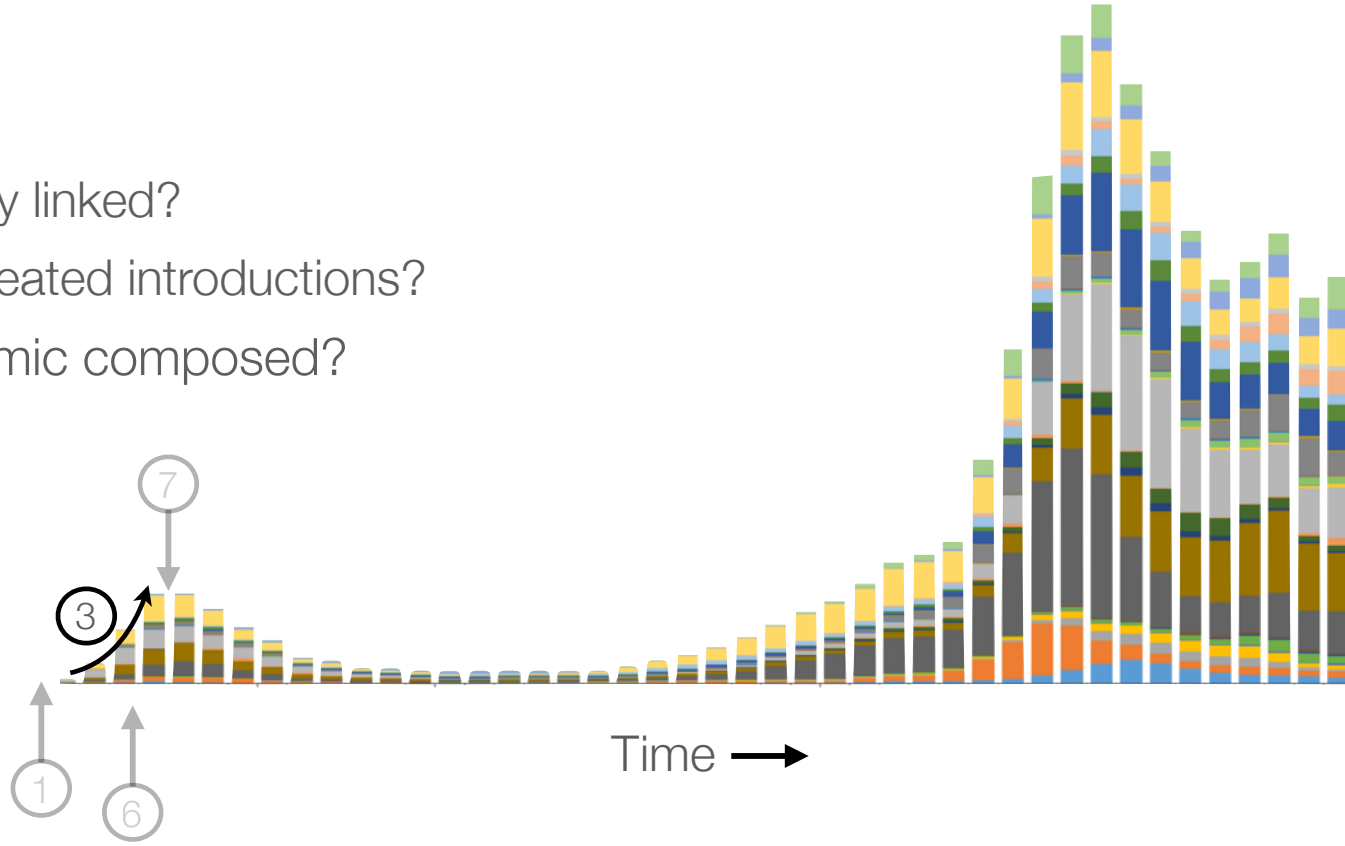
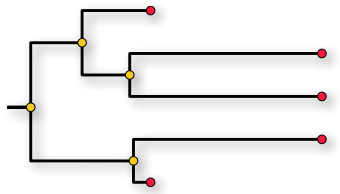
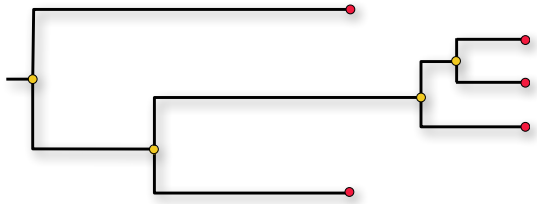
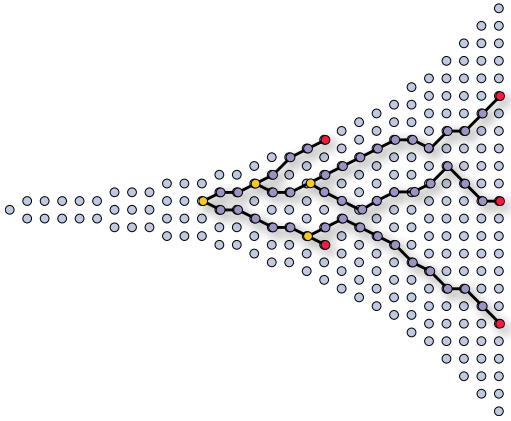


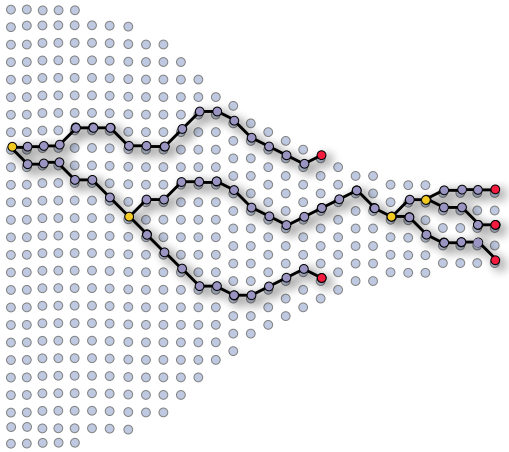
Phylodynamic inference: the coalescent



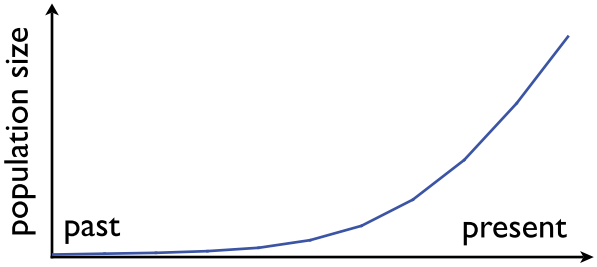


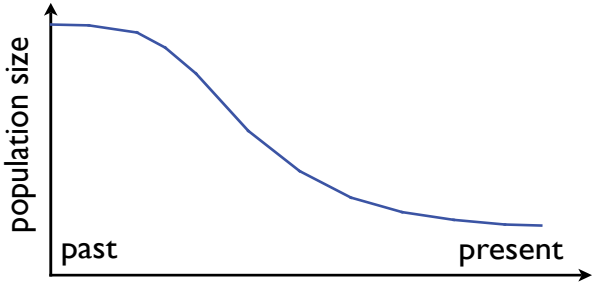
Phylogeny or
Genealogy





The coalescent relates the rate at which sampled 'individuals' find their common ancestors to population size





Population size

Epidemiological questions

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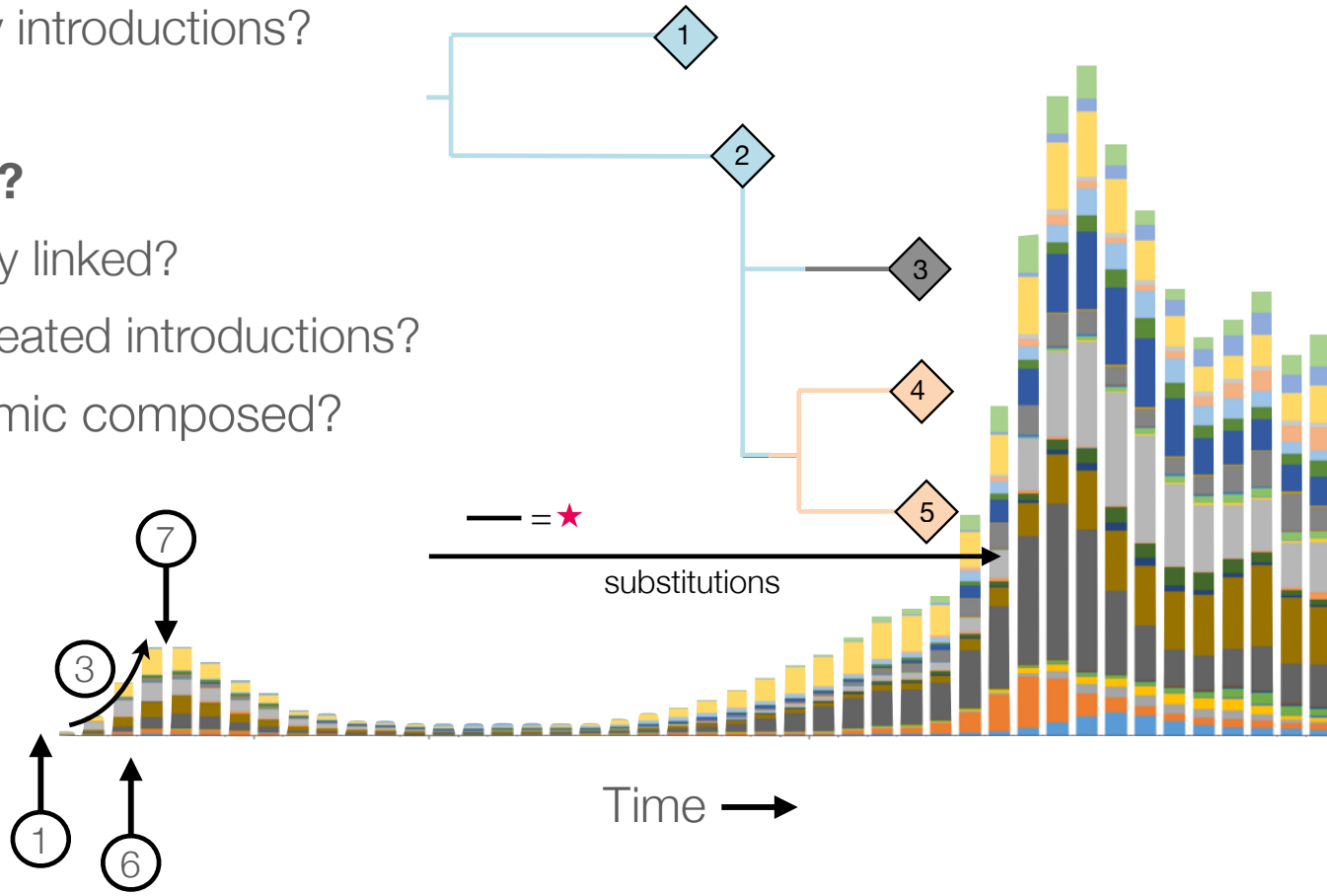
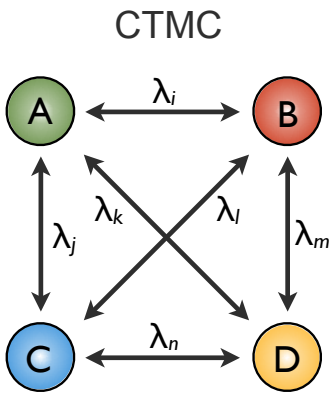
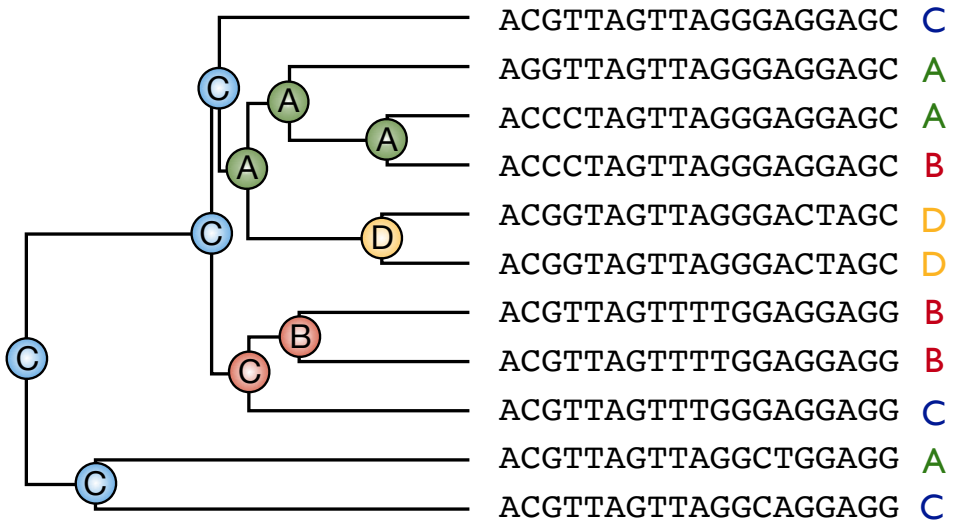
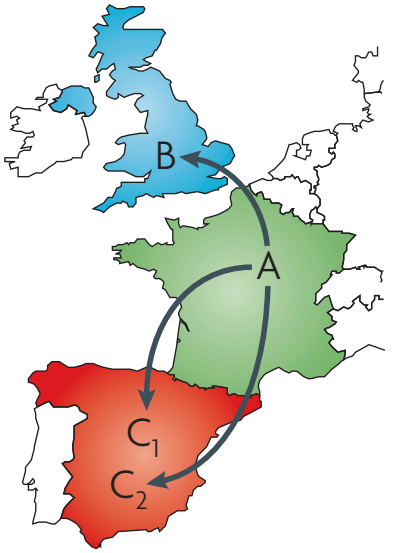


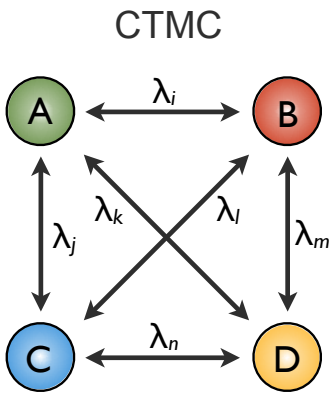
Phylodynamic inference: spatial diffusion

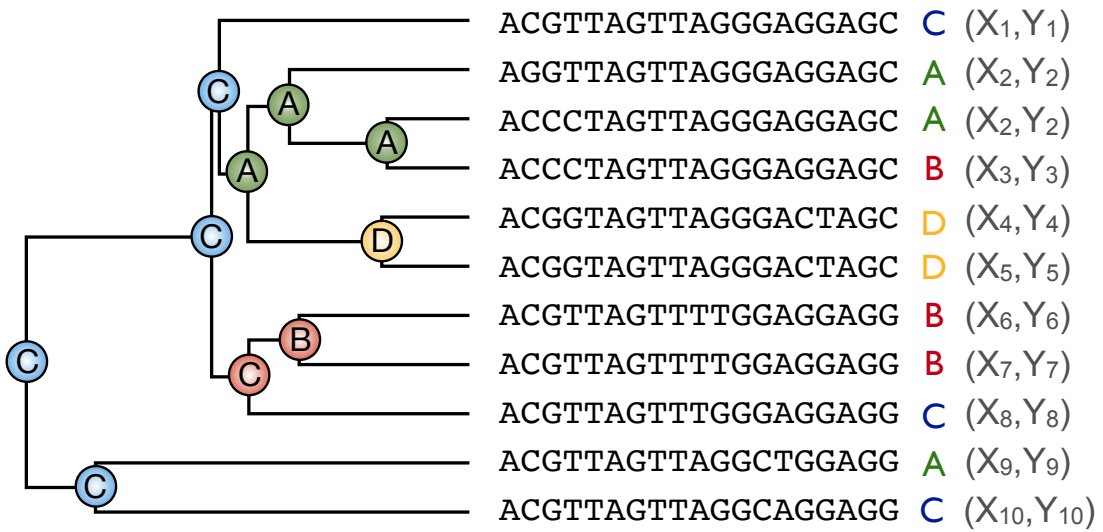


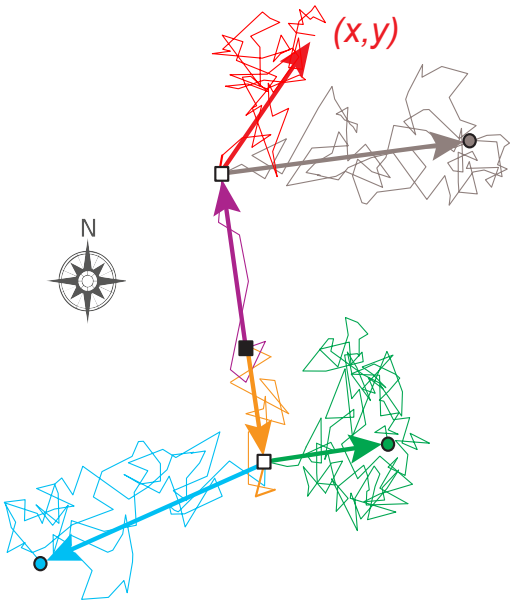


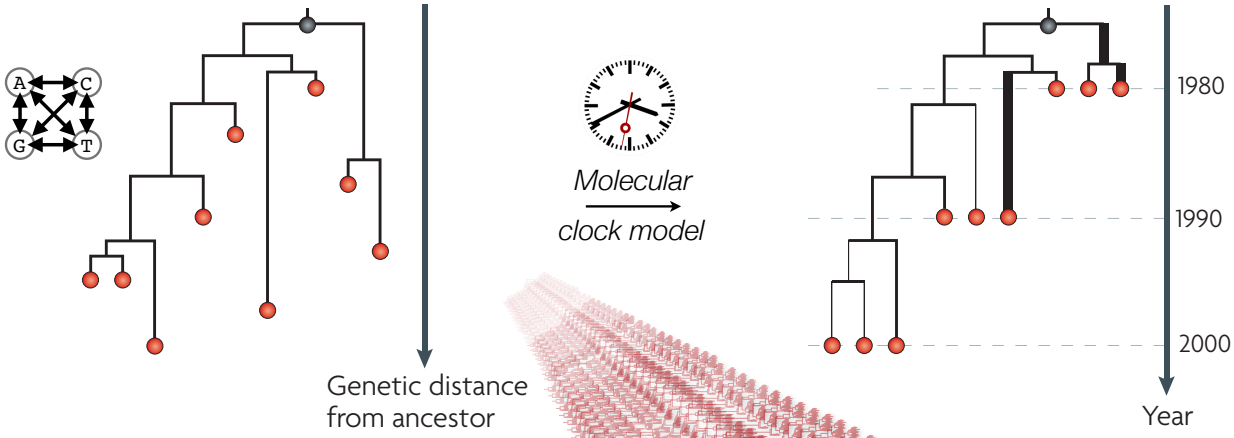


Phylodynamic inference: spatial diffusion

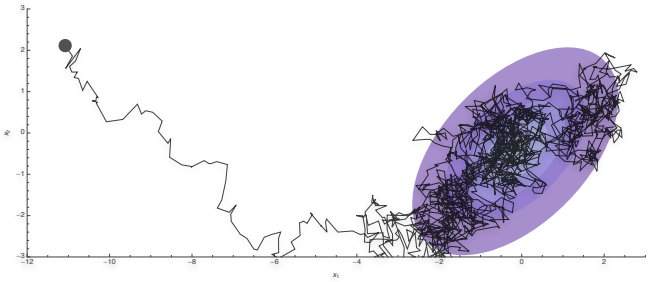


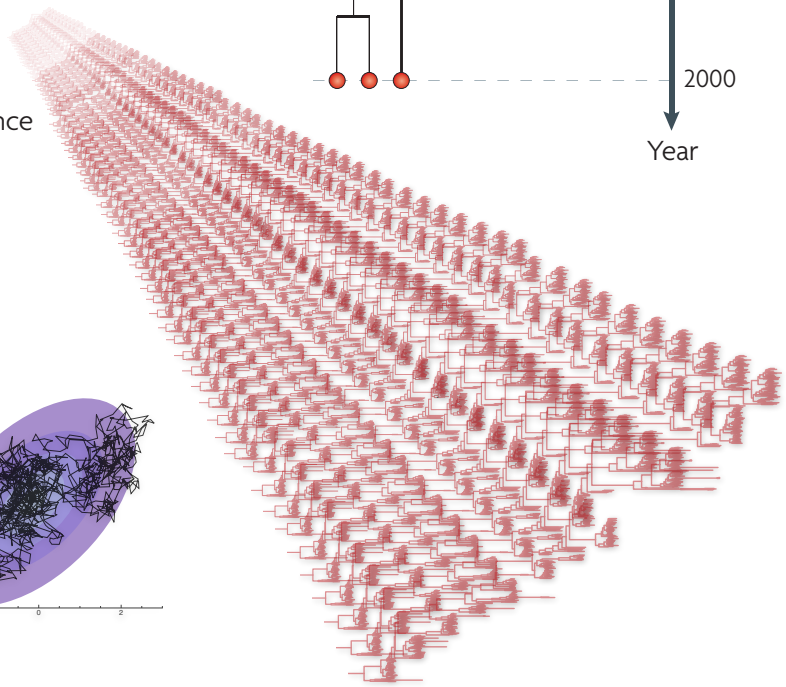


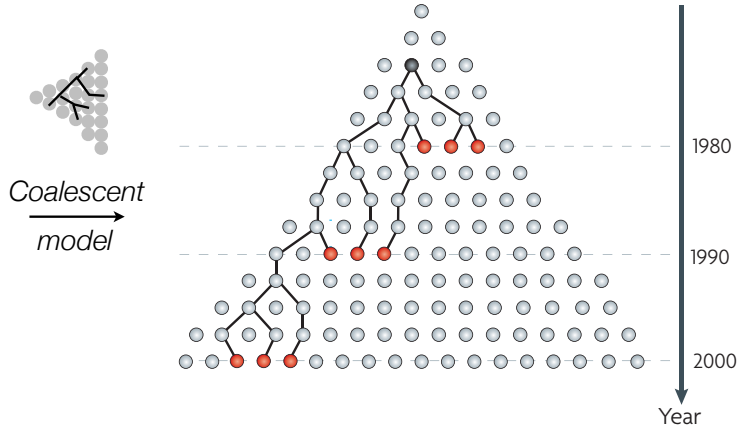


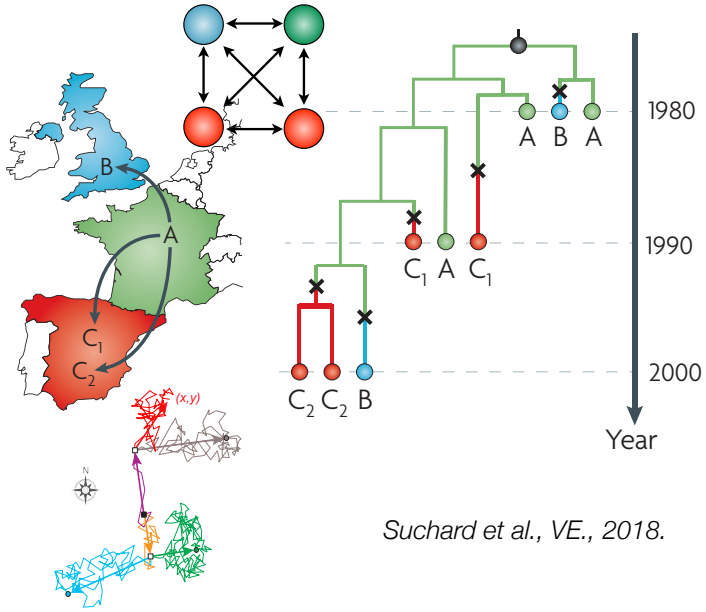


Pybus and Rambaut, NRG, 2009.









BEAST: Bayesian phylodynamics

Suchard et al., VE., 2018.

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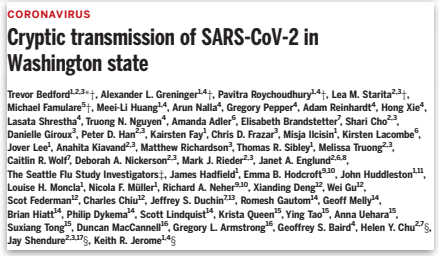
CORONAVIRUS

Timing the SARS-CoV-2 index case in Hubei province

Jonathan Pekar[1,2], Michael Worobey[3]*, Niema Moshiri[4], Konrad Scheffler[5], Joel O. Wertheim[6]*

The Huanan Seafood Wholesale Market in Wuhan was the early epicenter of the COVID-19 pandemic

Michael Worobey[1]*, Joshua I. Levy[2], Lorena Malpica Serrano[1], Alexander Crits-Christoph[3], Jonathan E. Pekar[4,5], Stephen A. Goldstein[6], Angela L. Rasmussen[7,8], Moritz U. G. Kraemer[9], Chris Newman[10], Marion P. G Koopmans[11,12], Marc A. Suchard[13,14,15], Joel O. Wertheim[16], Philippe Lemey[17,18], David L. Robertson[19], Robert F. Garry[18,20,21], Edward C. Holmes[22], Andrew Rambaut[23], Kristian G. Andersen[2,24]*



CORONAVIRUS

Cryptic transmission of SARS-CoV-2 in Washington state

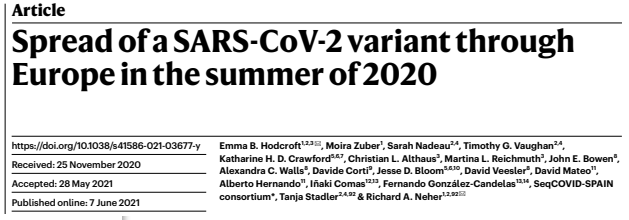
Trevor Bedford[1,2,3]*†, Alexander L. Greninger[1,4]†, Pavitra Roychoudhury[1,4]†, Lea M. Starita[2,3]†, Michael Famulare[5]†, Mee-Li Huang[1,4], Arun Nalla[4], Gregory Pepper[4], Adam Reinhardt[4], Hong Xie[4], Lasata Shrestha[4], Truong N. Nguyen[4], Amanda Adler[6], Elisabeth Brandstetter[7], Shari Cho[2,3], Danielle Giroux[3], Peter D. Han[2,3], Kairsten Fay[1], Chris D. Frazar[3], Misja Ilcisin[3], Kirsten Lacombe[6], Jover Lee[1], Anahita Kiavand[2,3], Matthew Richardson[3], Thomas R. Sibley[1], Melissa Truong[2,3], Caitlin R. Wolf[7], Deborah A. Nickerson[2,3], Mark J. Rieder[2,3], Janet A. Englund[2,6,8], The Seattle Flu Study Investigators‡, James Hadfield[1], Emma B. Hodcroft[9,10], John Huddleston[1,11], Louise H. Moncla[1], Nicola F. Müller[1], Richard A. Neher[9,10], Xianding Deng[12], Wei Gu[12], Scot Federman[12], Charles Chiu[12], Jeffrey S. Duchin[7,13], Romesh Gautom[14], Geoff Melly[14], Brian Hiatt[14], Philip Dykema[14], Scott Lindquist[14], Krista Queen[15], Ying Tao[15], Anna Uehara[15], Suxiang Tong[15], Duncan MacCannell[16], Gregory L. Armstrong[16], Geoffrey S. Baird[4], Helen Y. Chu[2,7]§, Jay Shendure[2,3,17]§, Keith R. Jerome[1,4]§

Article

Untangling introductions and persistence in COVID-19 resurgence in Europe

https://doi.org/10.1038/s41586-021-03754-2
Received: 4 February 2021
Accepted: 22 June 2021

Philippe Lemey[1,2]✉, Nick Ruktanonchai[3,4], Samuel L. Hong[1], Vittoria Colizza[5], Chiara Poletto[5], Frederik Van den Broeck[5,6], Mandev S. Gill[1], Xiang Ji[7], Anthony Levasseur[8], Bas B. Oude Munnink[9], Marion Koopmans[9], Adam Sadilek[10], Shengjie Lai[3], Andrew J. Tatem[3], Guy Baele[1], Marc A. Suchard[11,12] & Simon Dellicour[1,6]✉



Article

Spread of a SARS-CoV-2 variant through Europe in the summer of 2020

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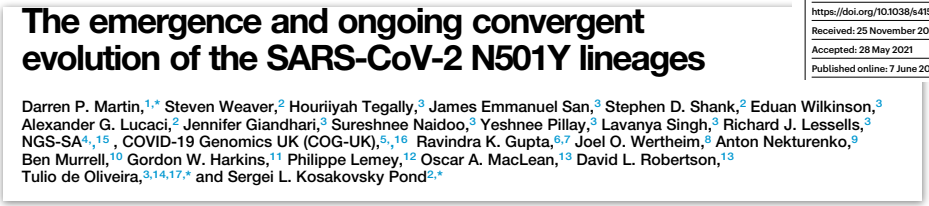
Received: 25 November 2020
Accepted: 28 May 2021
Published online: 7 June 2021

Emma B. Hodcroft[1,2,3]✉, Moira Zuber[1], Sarah Nadeau[2,4], Timothy G. Vaughan[2,4], Katharine H. D. Crawford[5,6,7], Christian L. Althaus[8], Martina L. Reichmuth[9], John E. Bowen[5], Alexandra C. Walls[5], Davide Corti[9], Jesse D. Bloom[5,6,10], David Veesler[5], David Mateo[11], Alberto Hernando[11], Iñaki Comas[12,13], Fernando González-Candelas[13,14], SeqCOVID-SPAIN consortium*, Tanja Stadler[2,4,92] & Richard A. Neher[1,2,92]✉



The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages

Darren P. Martin,[1,*] Steven Weaver,[2] Houriiyah Tegally,[3] James Emmanuel San,[3] Stephen D. Shank,[2] Eduan Wilkinson,[3] Alexander G. Lucaci,[2] Jennifer Giandhari,[3] Sureshnee Naidoo,[3] Yeshnee Pillay,[3] Lavanya Singh,[3] Richard J. Lessells,[3] NGS-SA[4,,15] , COVID-19 Genomics UK (COG-UK),[5,,16] Ravindra K. Gupta,[6,7] Joel O. Wertheim,[8] Anton Nekturenko,[9] Ben Murrell,[10] Gordon W. Harkins,[11] Philippe Lemey,[12] Oscar A. MacLean,[13] David L. Robertson,[13] Tulio de Oliveira,[3,14,17,*] and Sergei L. Kosakovsky Pond[2,*]