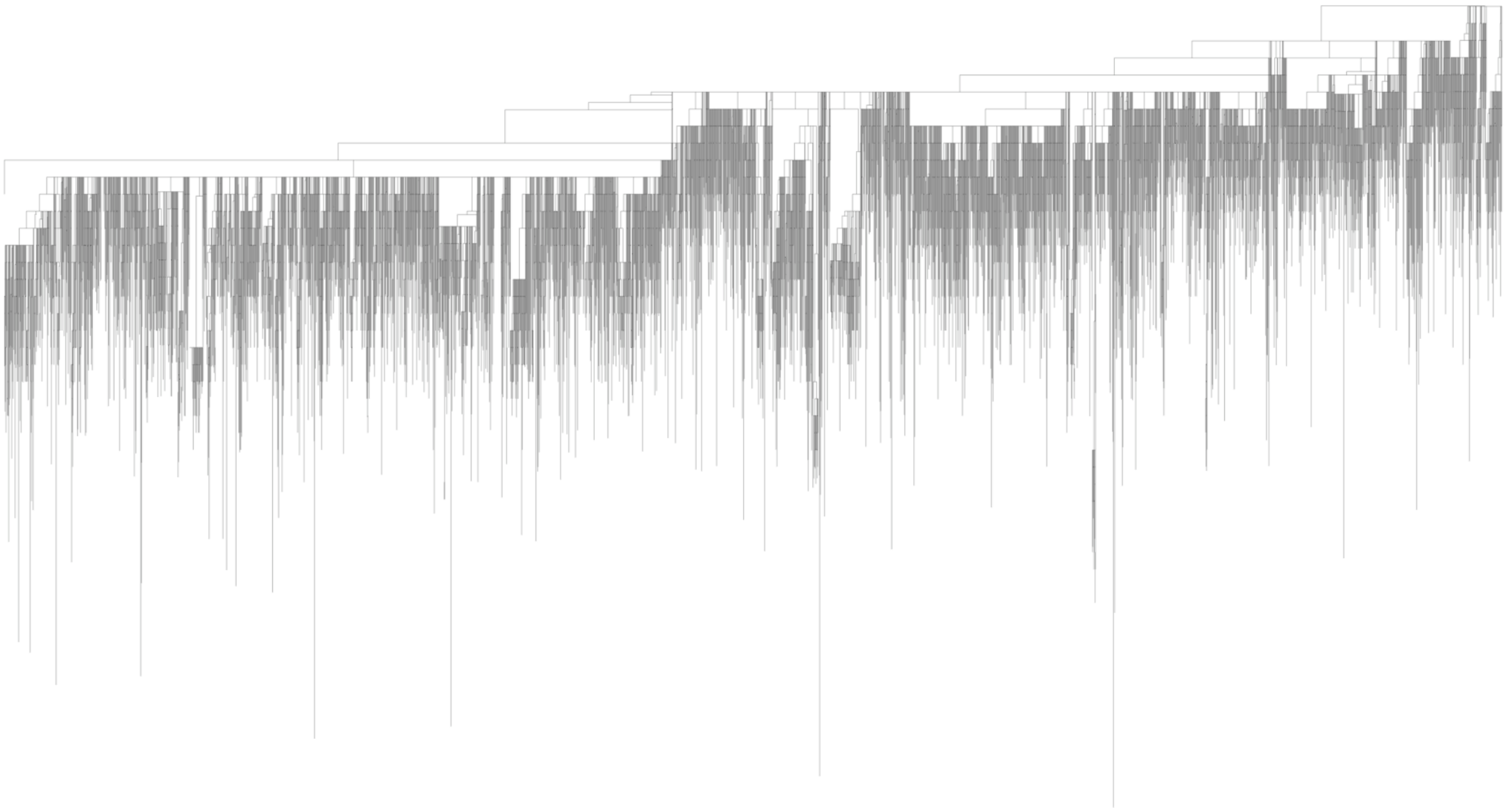
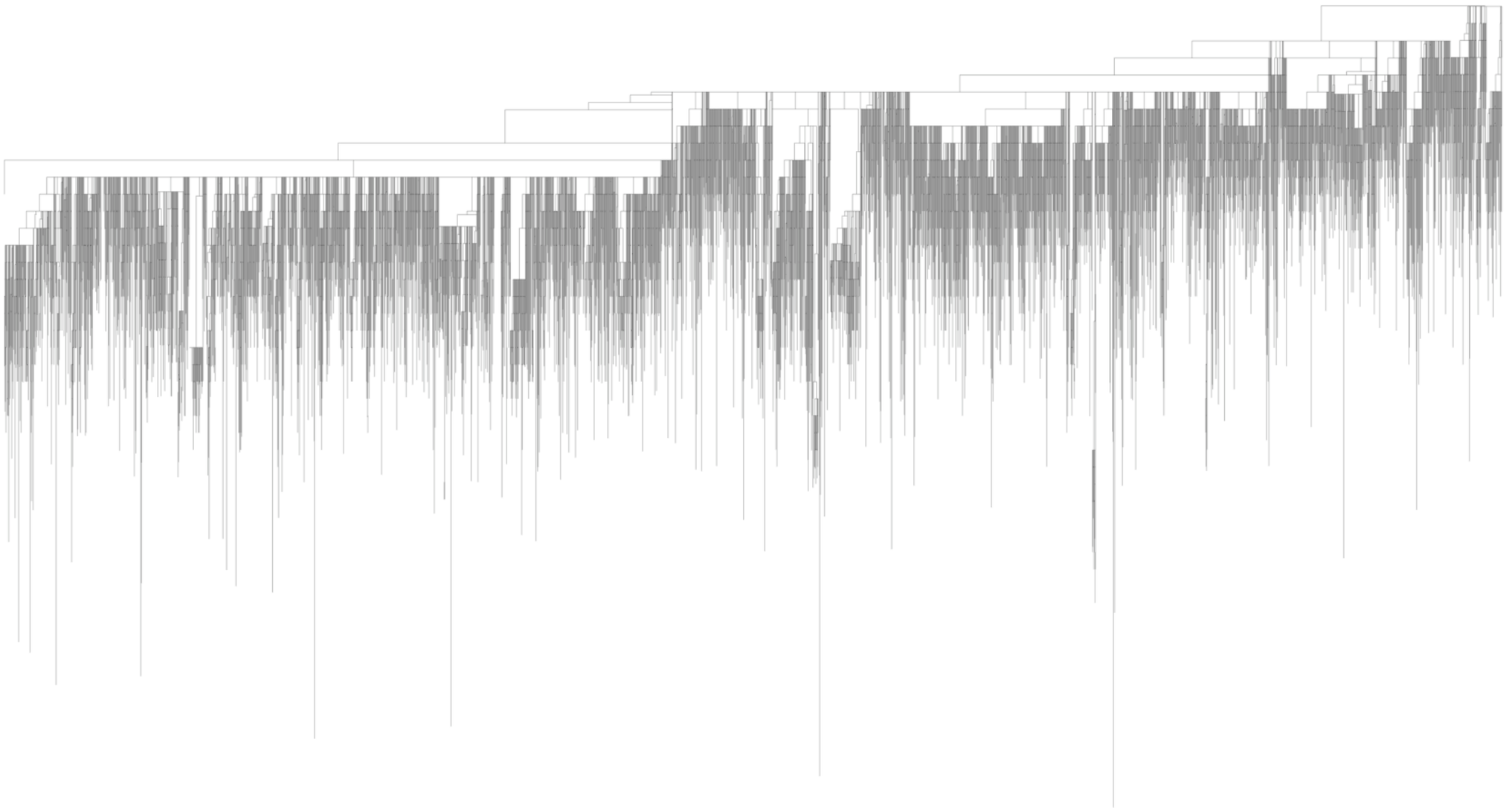


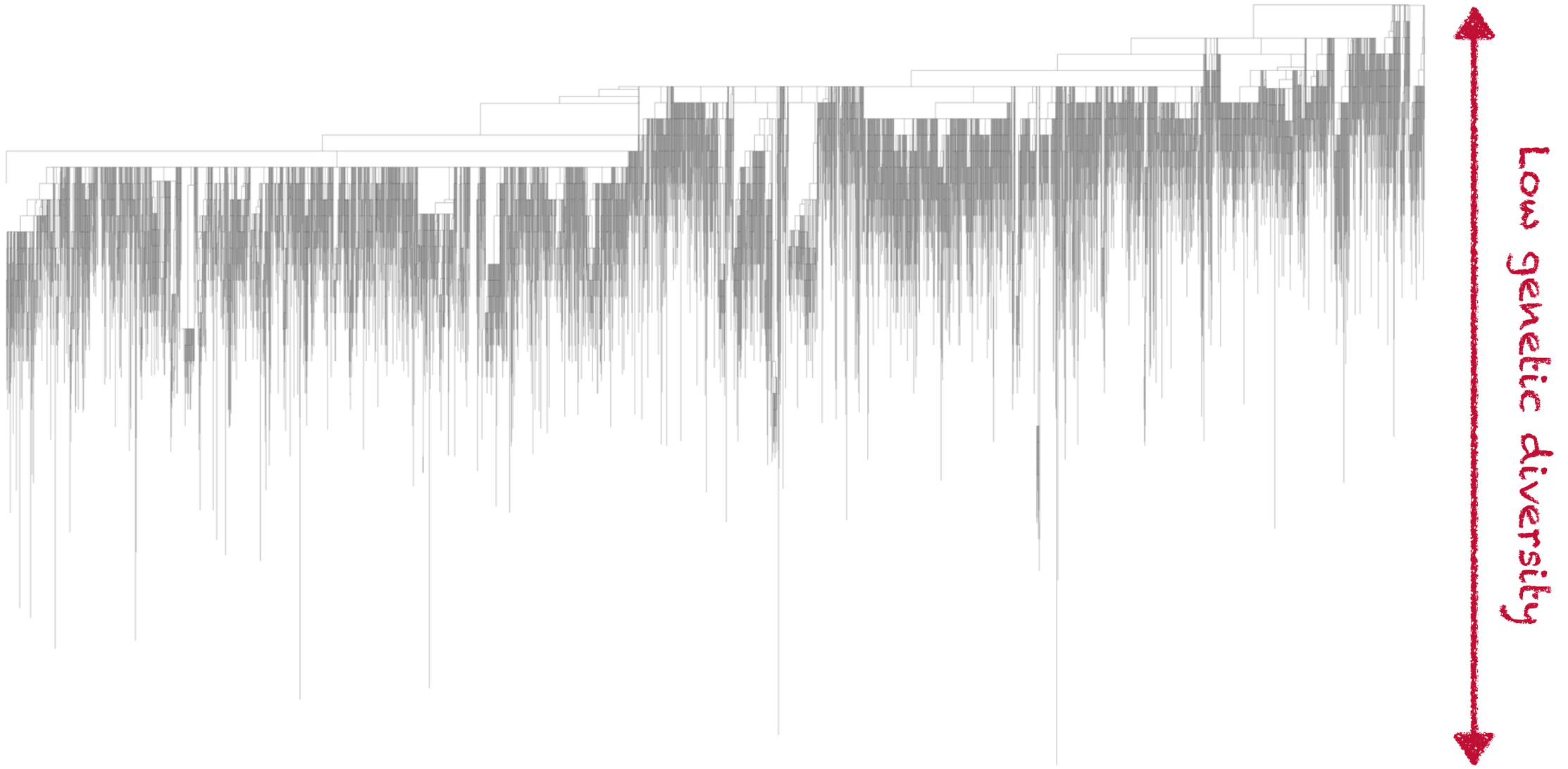
ESTABLISHMENT & LINEAGE DYNAMICS OF THE SARS-COV-2 EPIDEMIC IN THE UK

LOUIS DU PLESSIS



~88,000 SARS-CoV-2 genomes

https://microreact.org/project/cogconsortium-2020-09-24



~88,000 SARS-CoV-2 genomes

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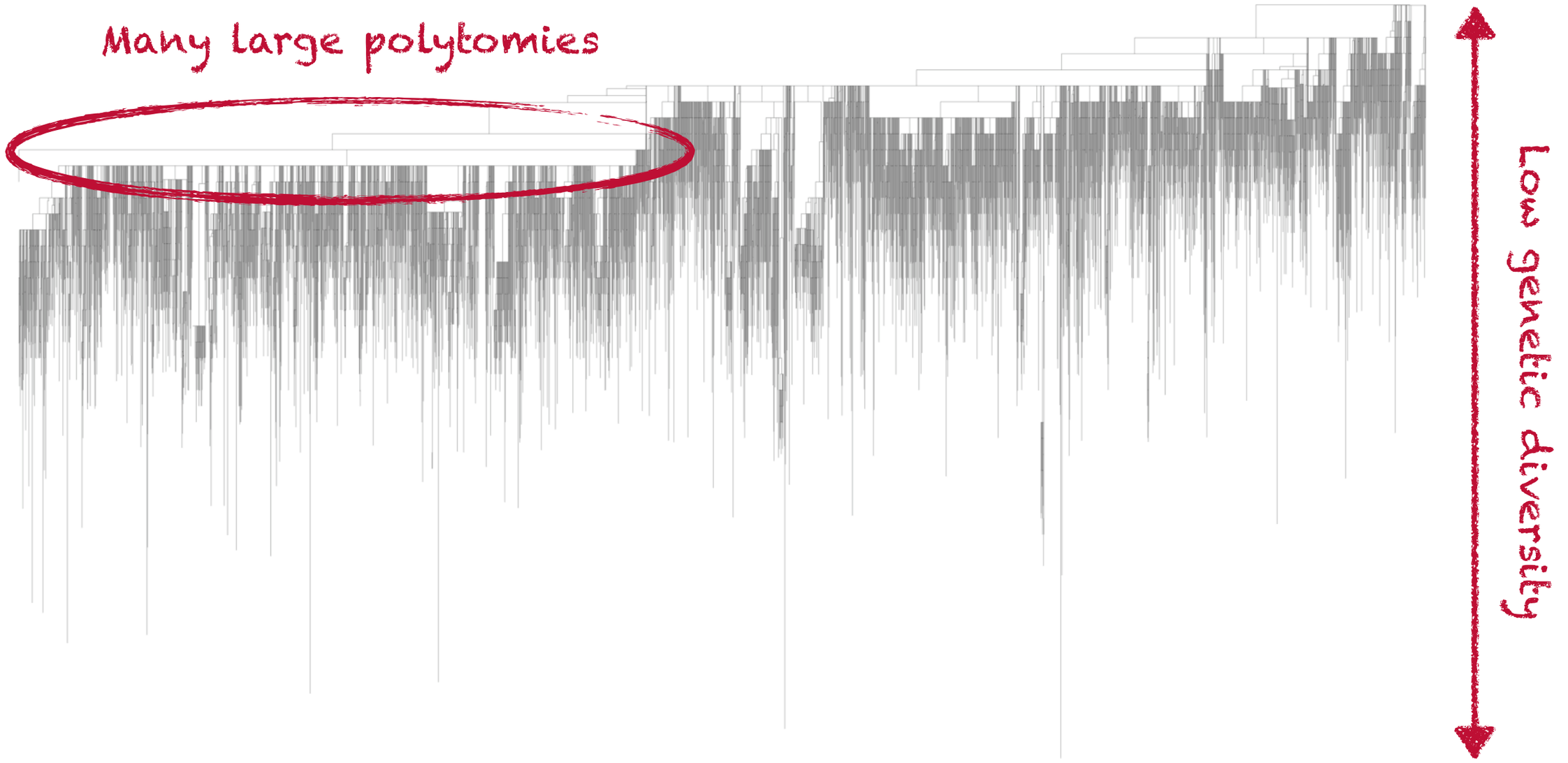
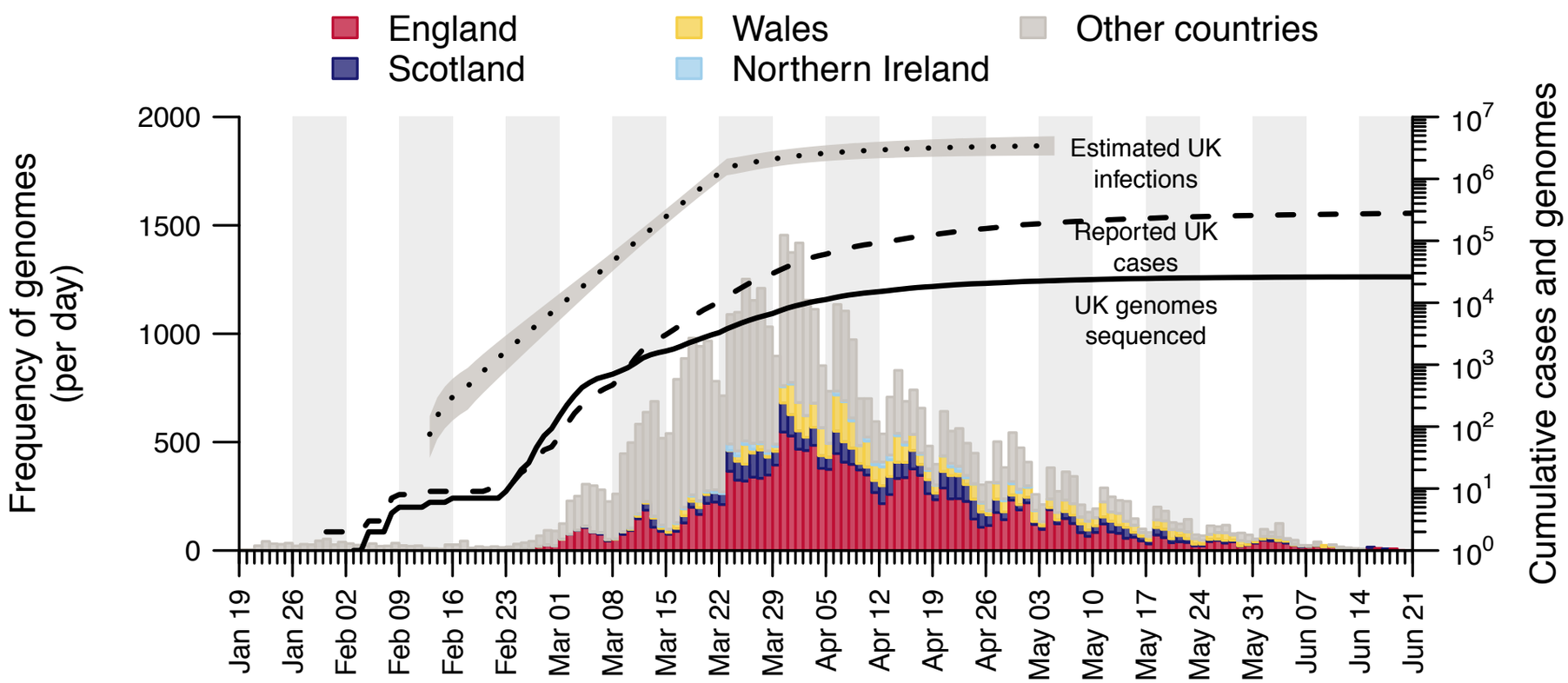


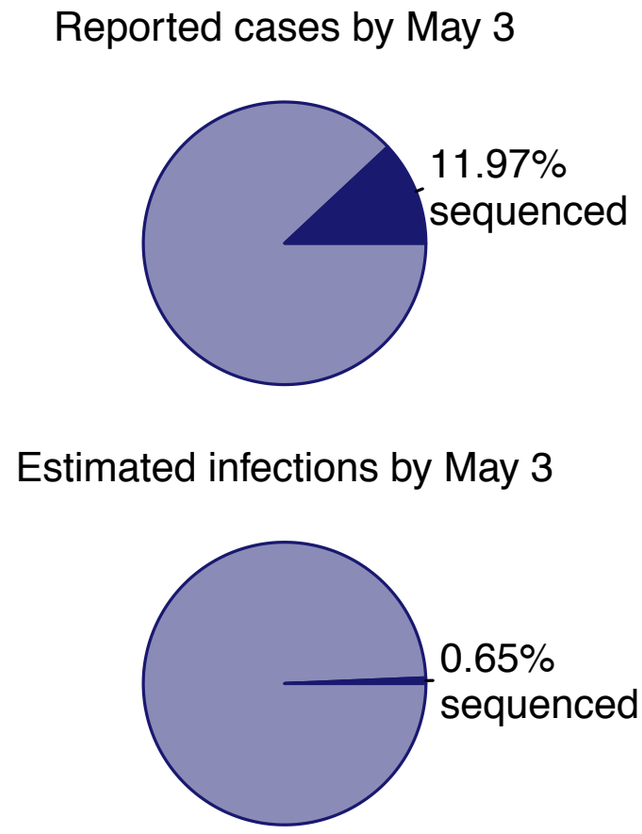
~88,000 SARS-CoV-2 genomes

https://microreact.org/project/cogconsortium-2020-09-24

Sampling of SARS-CoV-2 genomes

First 6 months of the pandemic





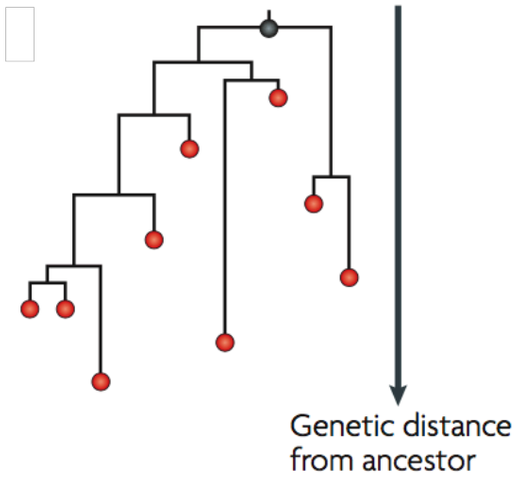
- **50,887** SARS-CoV-2 genomes
- **26,181** from the UK (51.5%)

Flaxman et al. (2020) *Nature*

Efficiently analysing huge datasets in BEAST

Genetic distance tree

(subst/site)



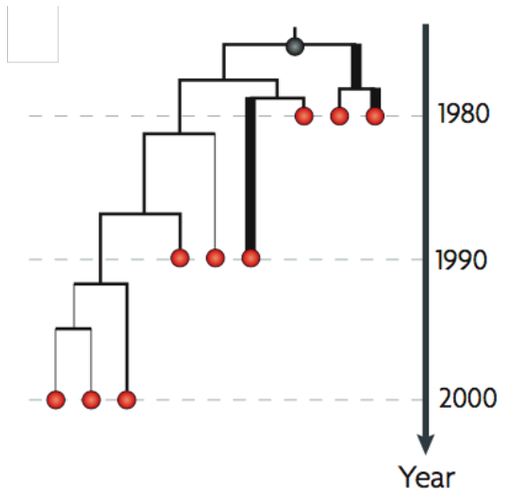
Clock rate

(subst/site/year)

$= \mu \times$

Time tree

(year)



Pybus and Rambaut (2009) *Nat Rev Genet*

Efficiently analysing huge datasets in BEAST

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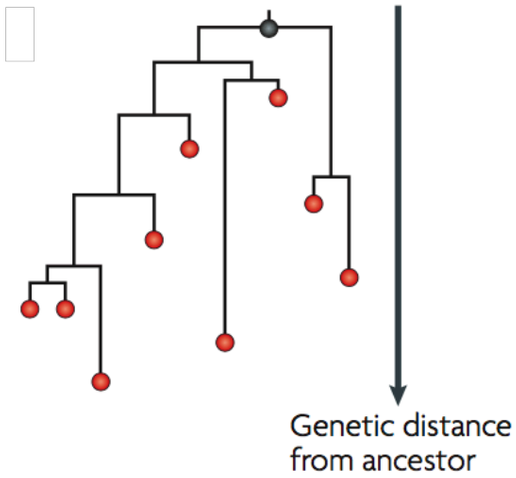

Clock rate

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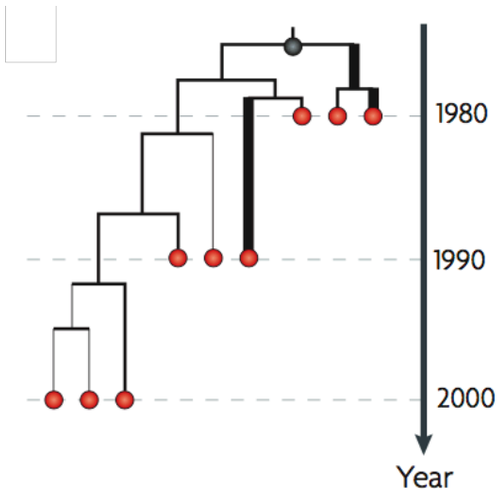
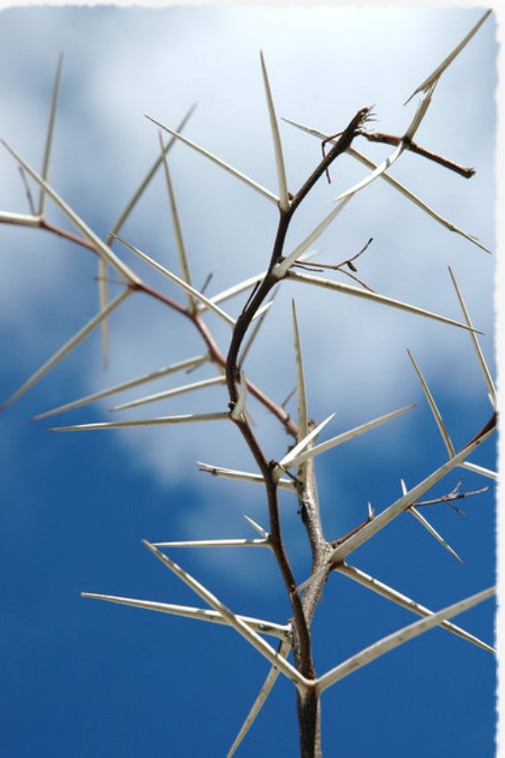
$= \mu \times$

Time tree

(year)





Thorney BEAST (by JT McCrone & Andrew Rambaut)

- Scale branches on a guide tree
- Only integrate over polytomy resolutions
- More efficient data structures

https://beast.community/thorney_beast

Pybus and Rambaut (2009) *Nat Rev Genet*

Definition: UK transmission lineages

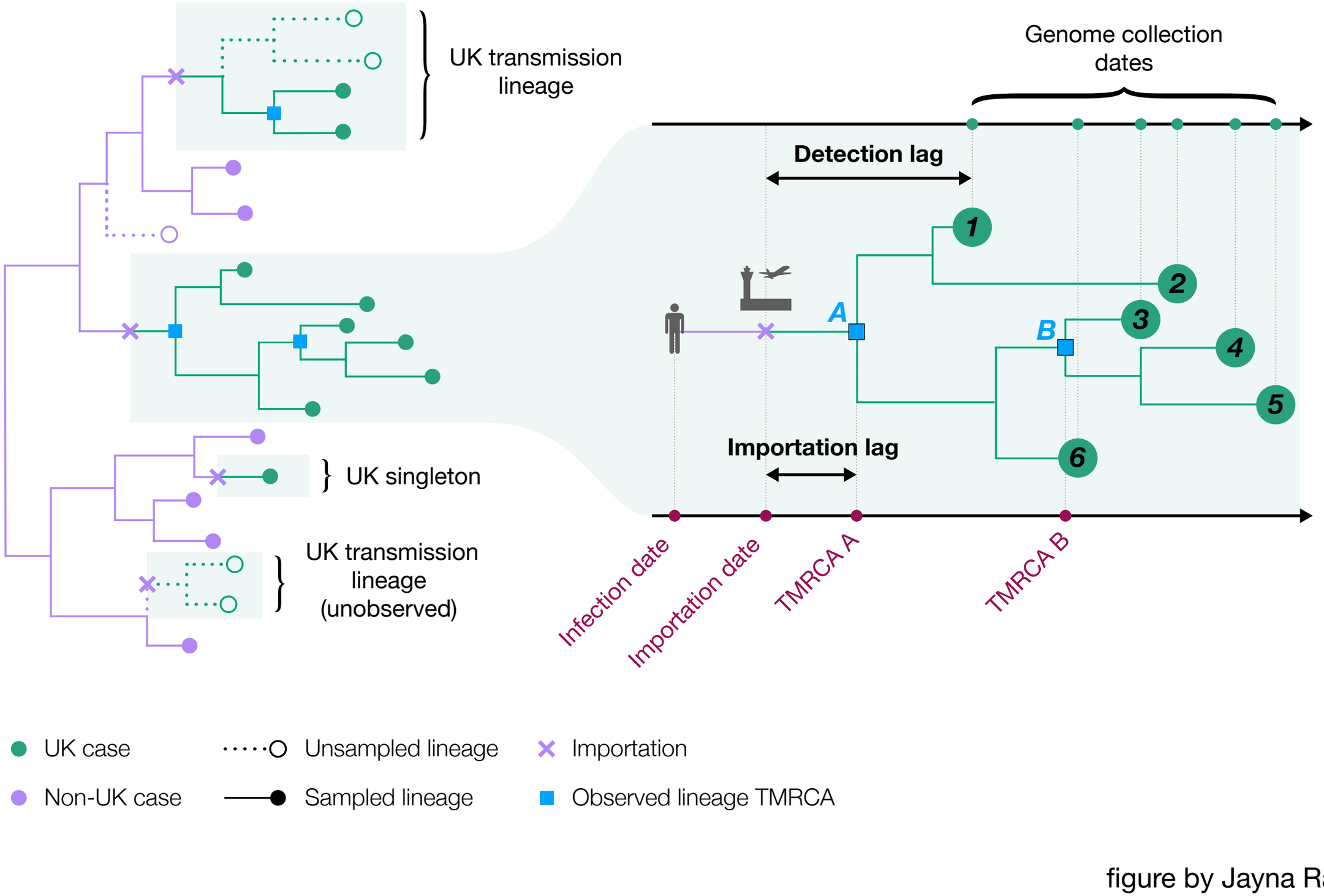


figure by Jayna Raghwani

Definition: UK transmission lineages

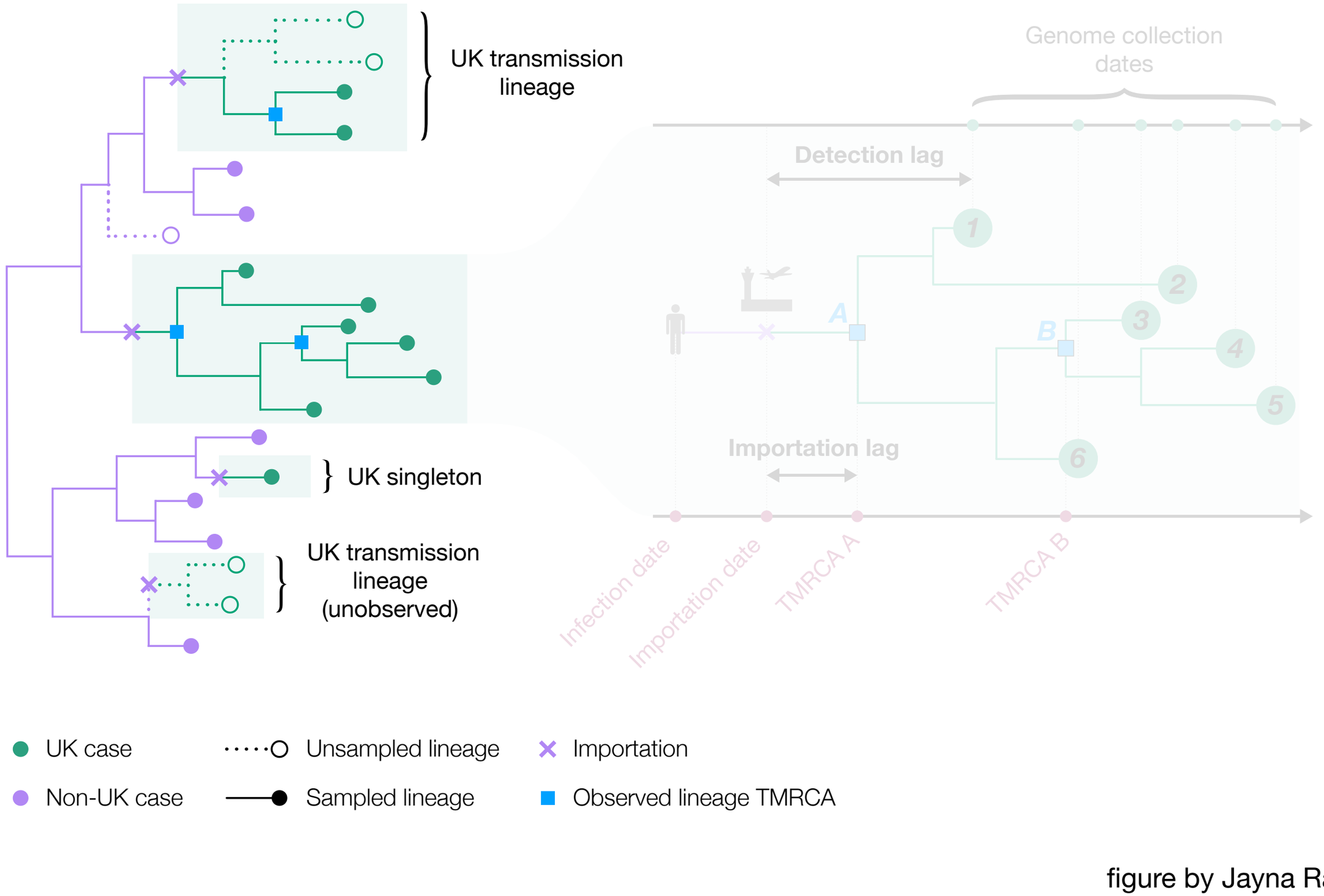
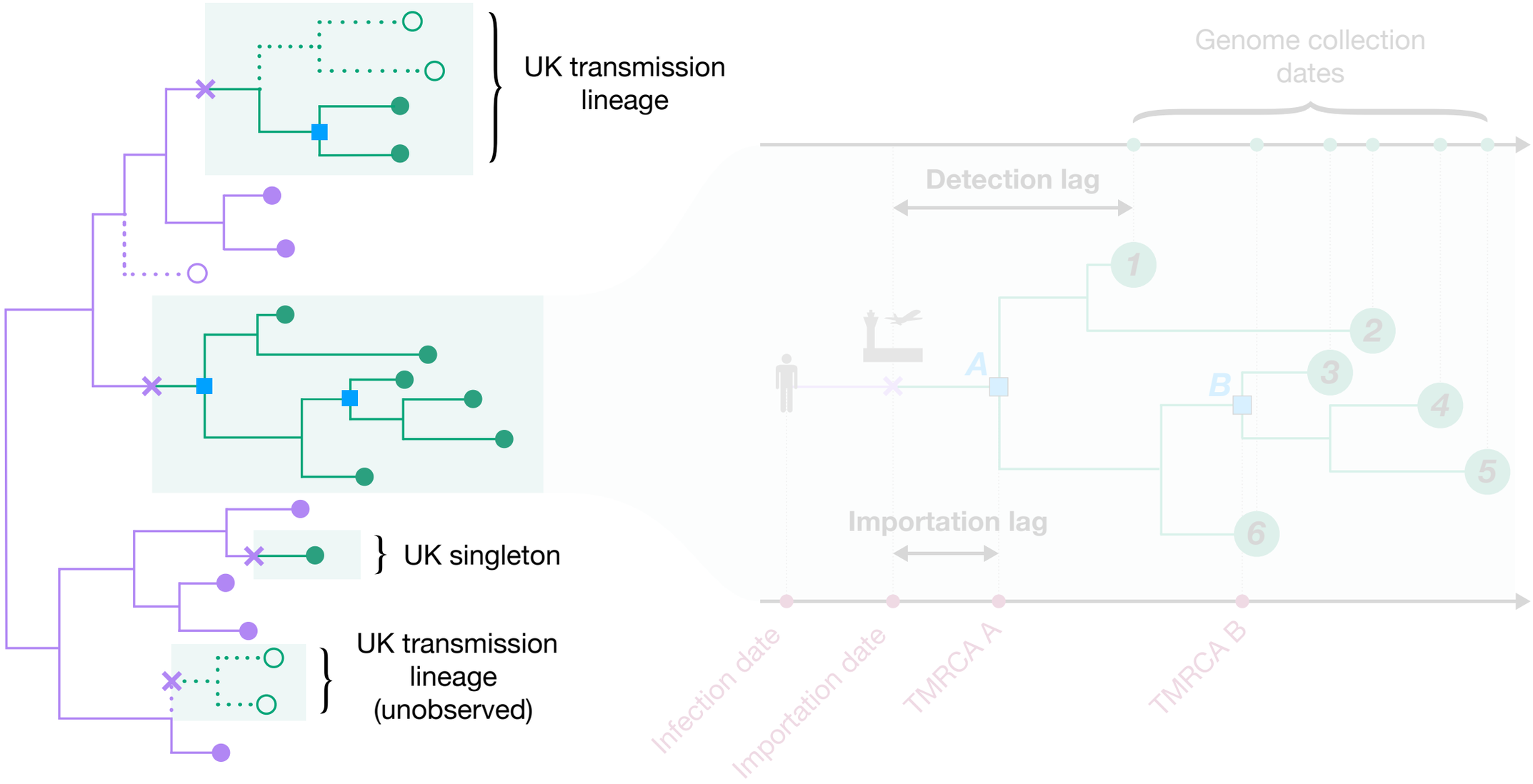


figure by Jayna Raghwani

Definition: UK transmission lineages

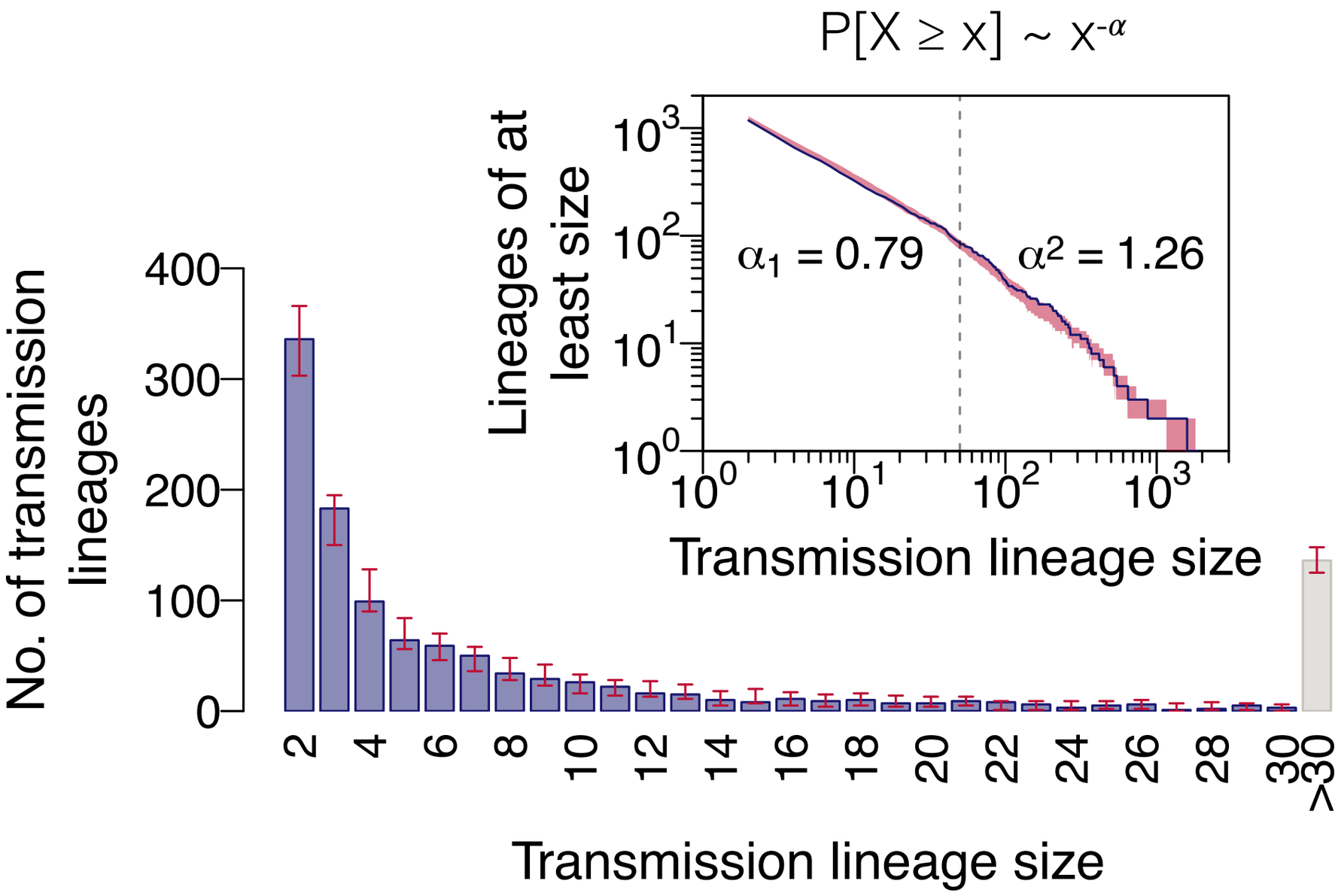


UK transmission lineages ≠ Pango lineages

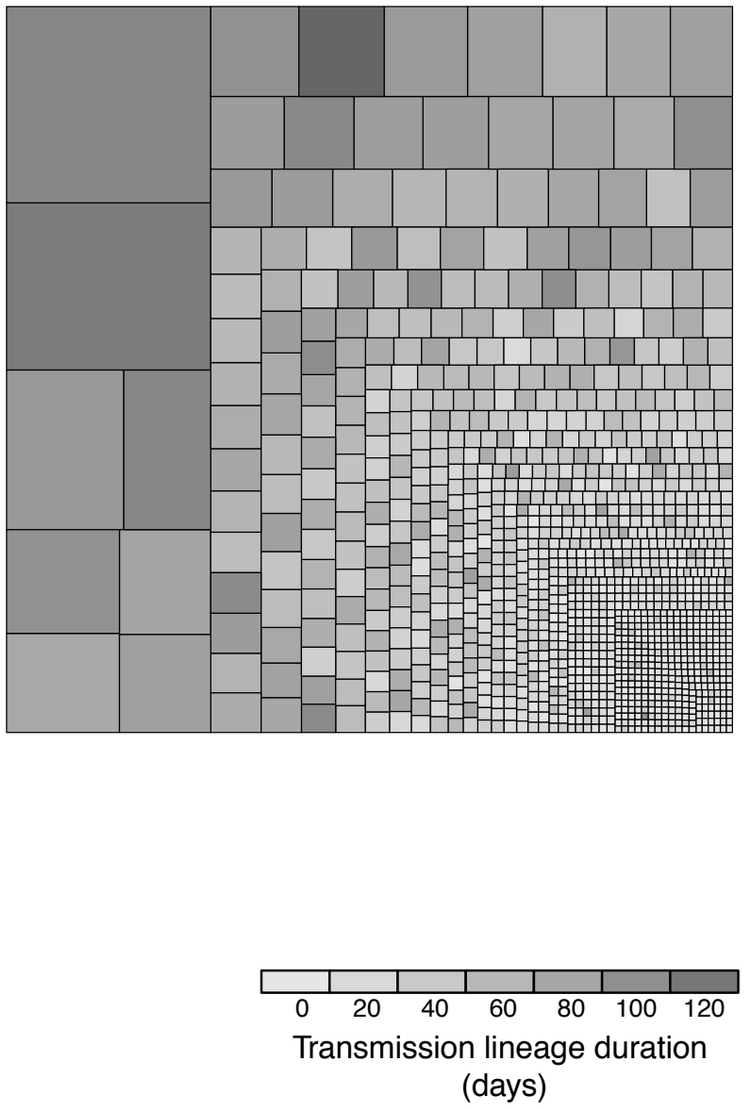
figure by Jayna Raghwani

Sizes of UK transmission lineages

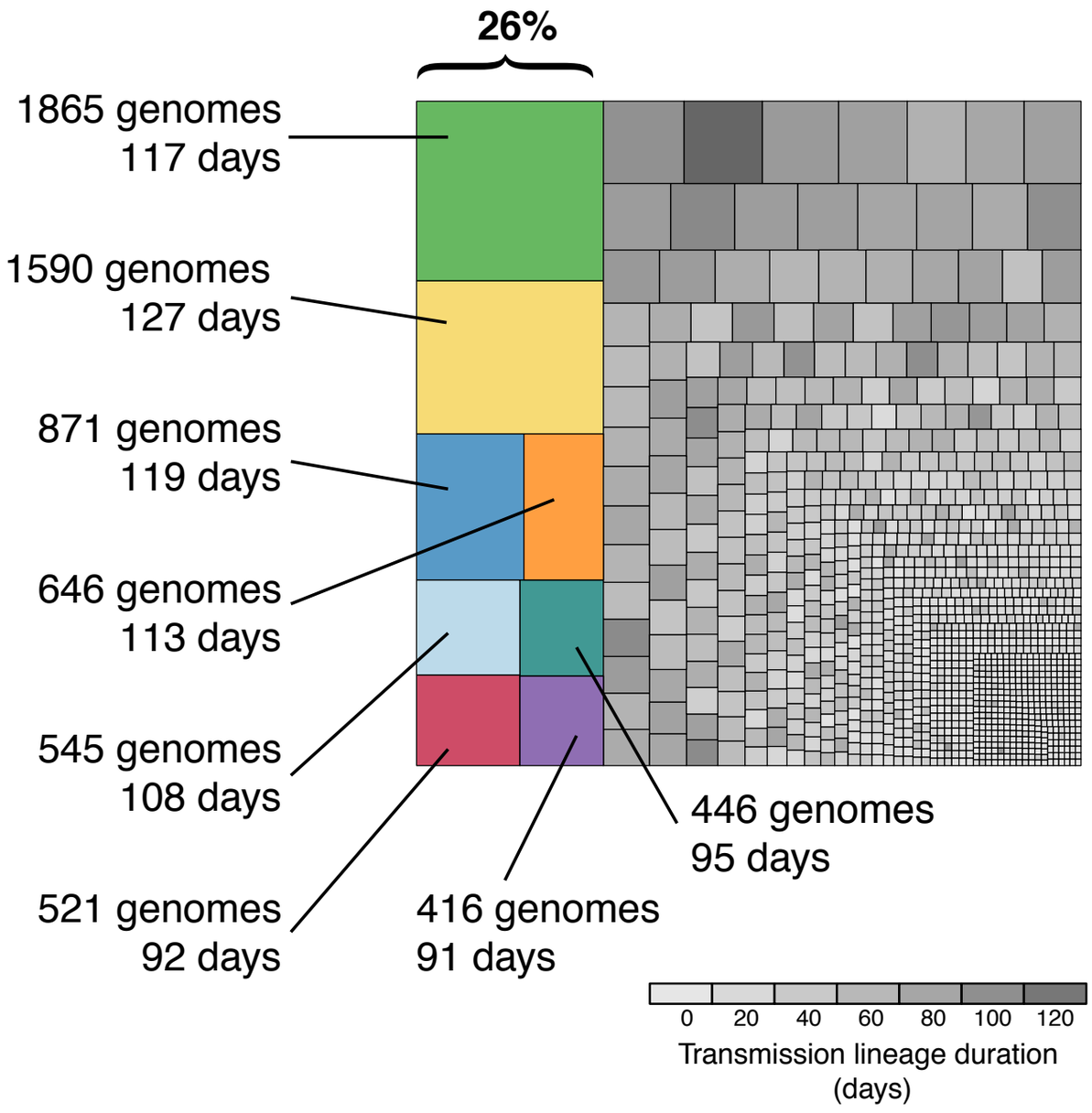
26,181 UK genomes into **1179** lineages and **1650** singletons



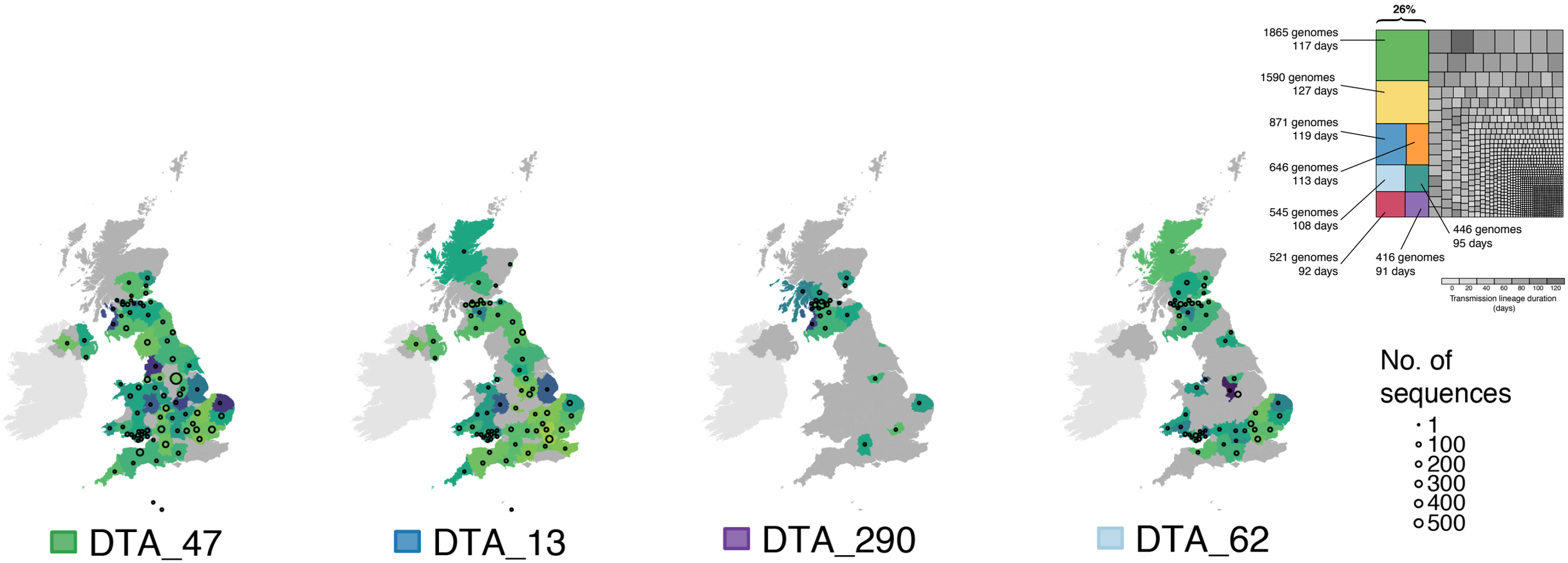
UK transmission lineage breakdown



UK transmission lineage breakdown

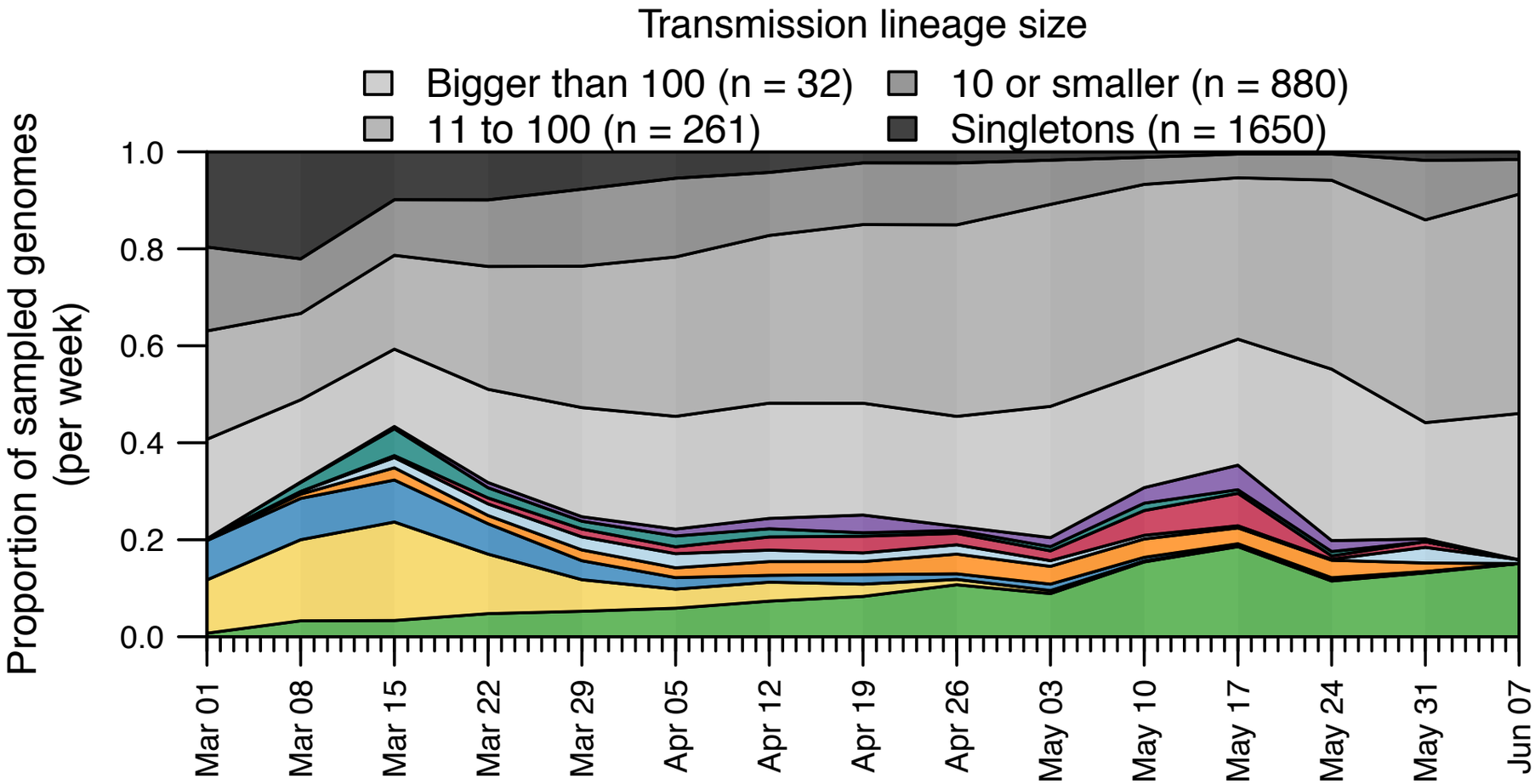


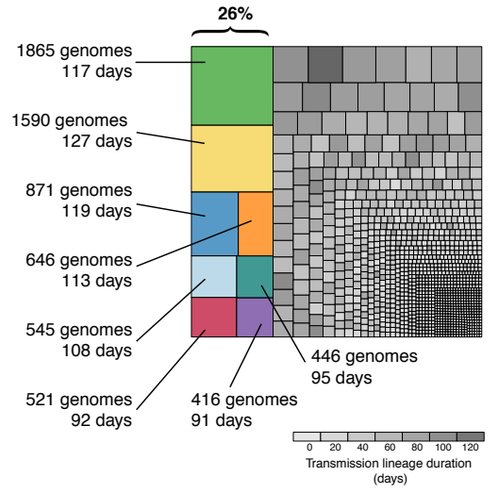
Geographic spread of transmission lineages



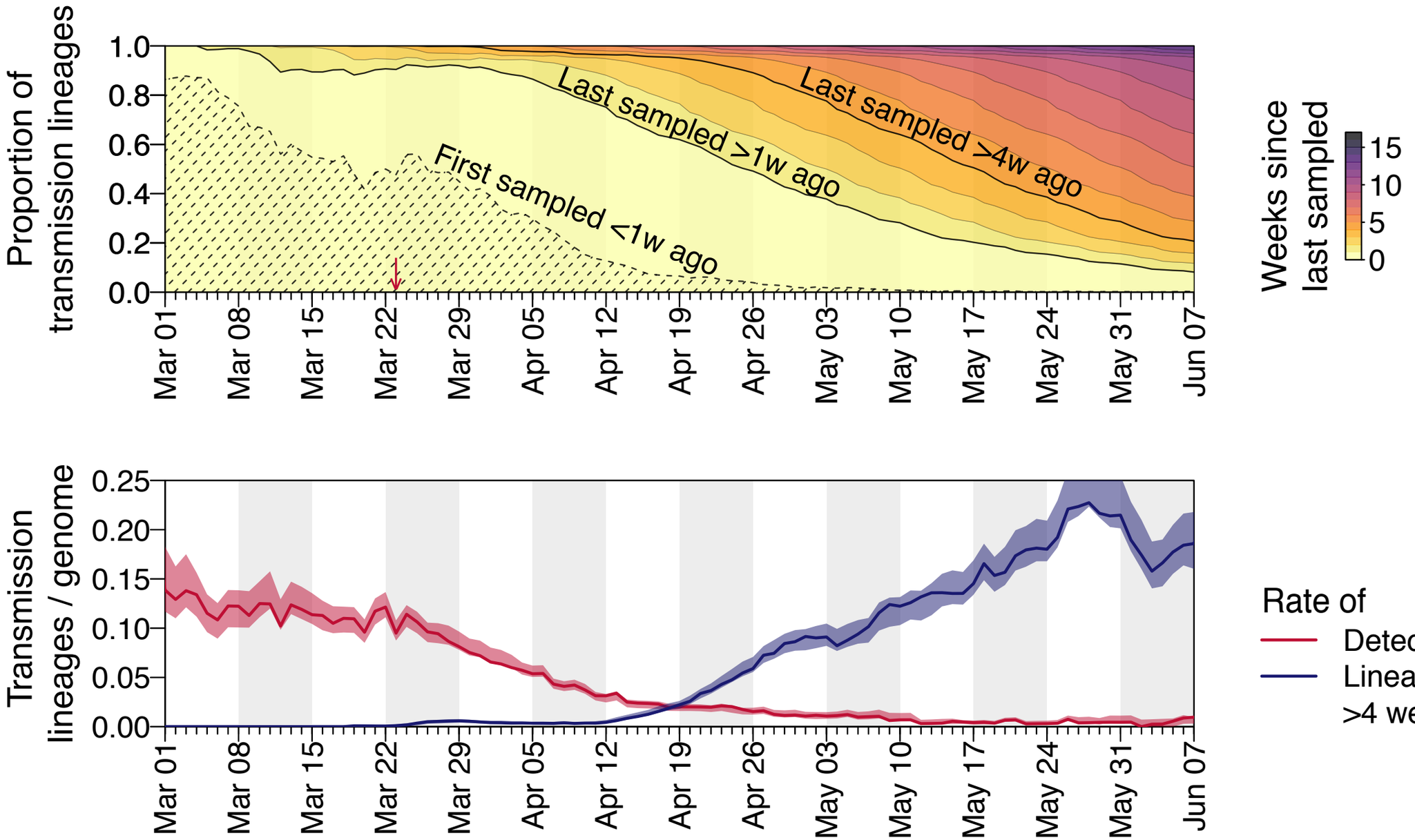
work by Chris Ruis

Sample breakdown by UK transmission lineage

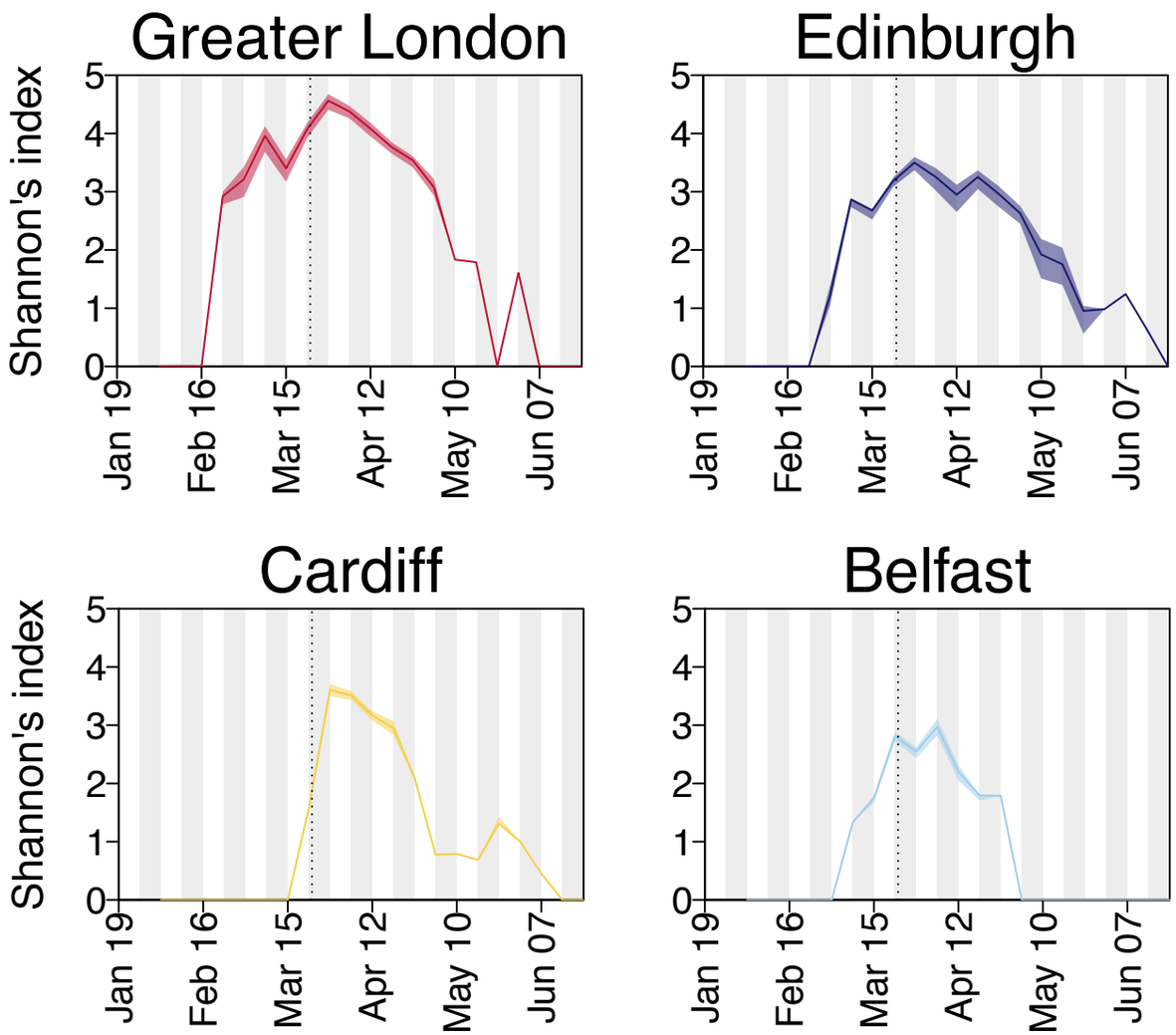


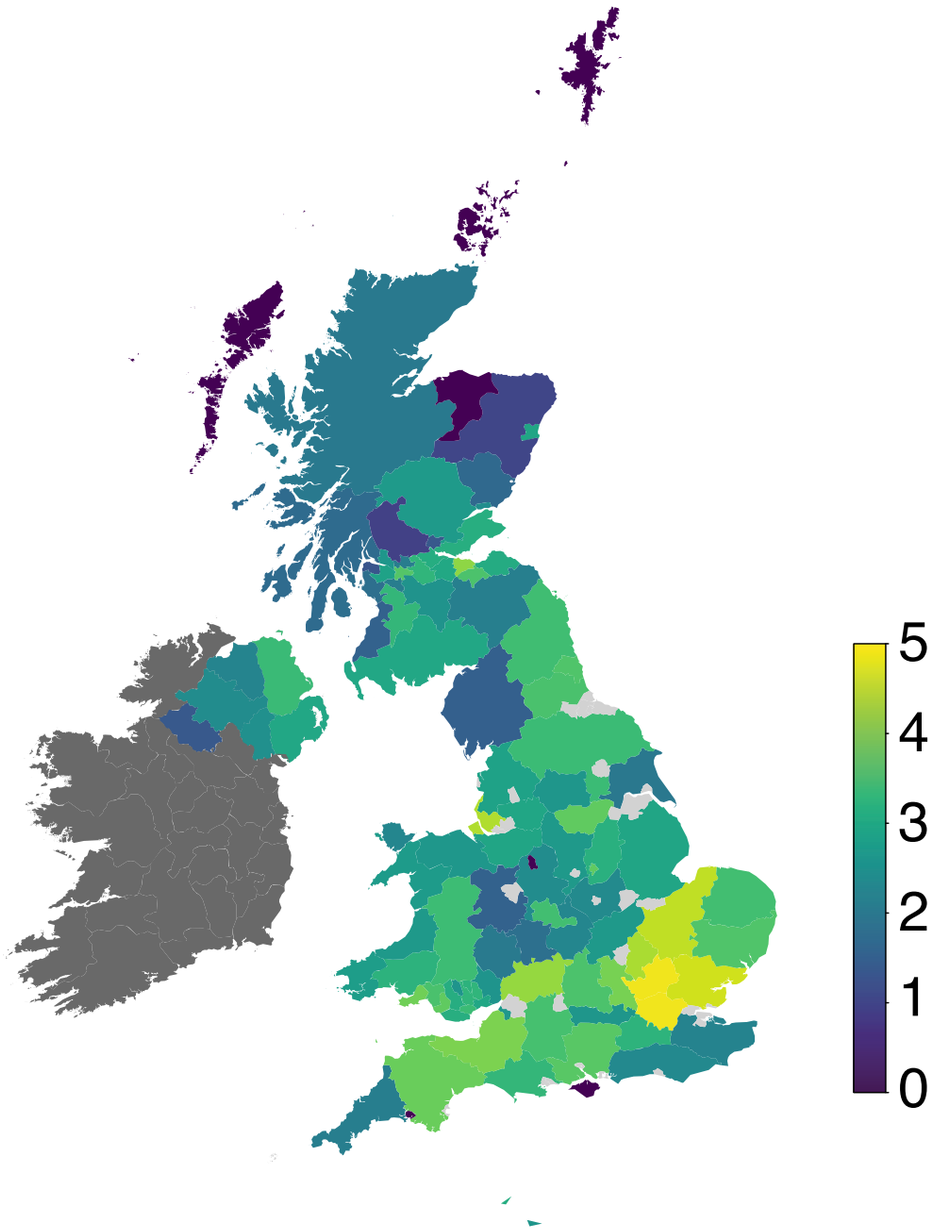


Detection of UK transmission lineages



Shannon’s index for lineage diversity





work by Verity Hill

Definition: TMRCA and importation lag

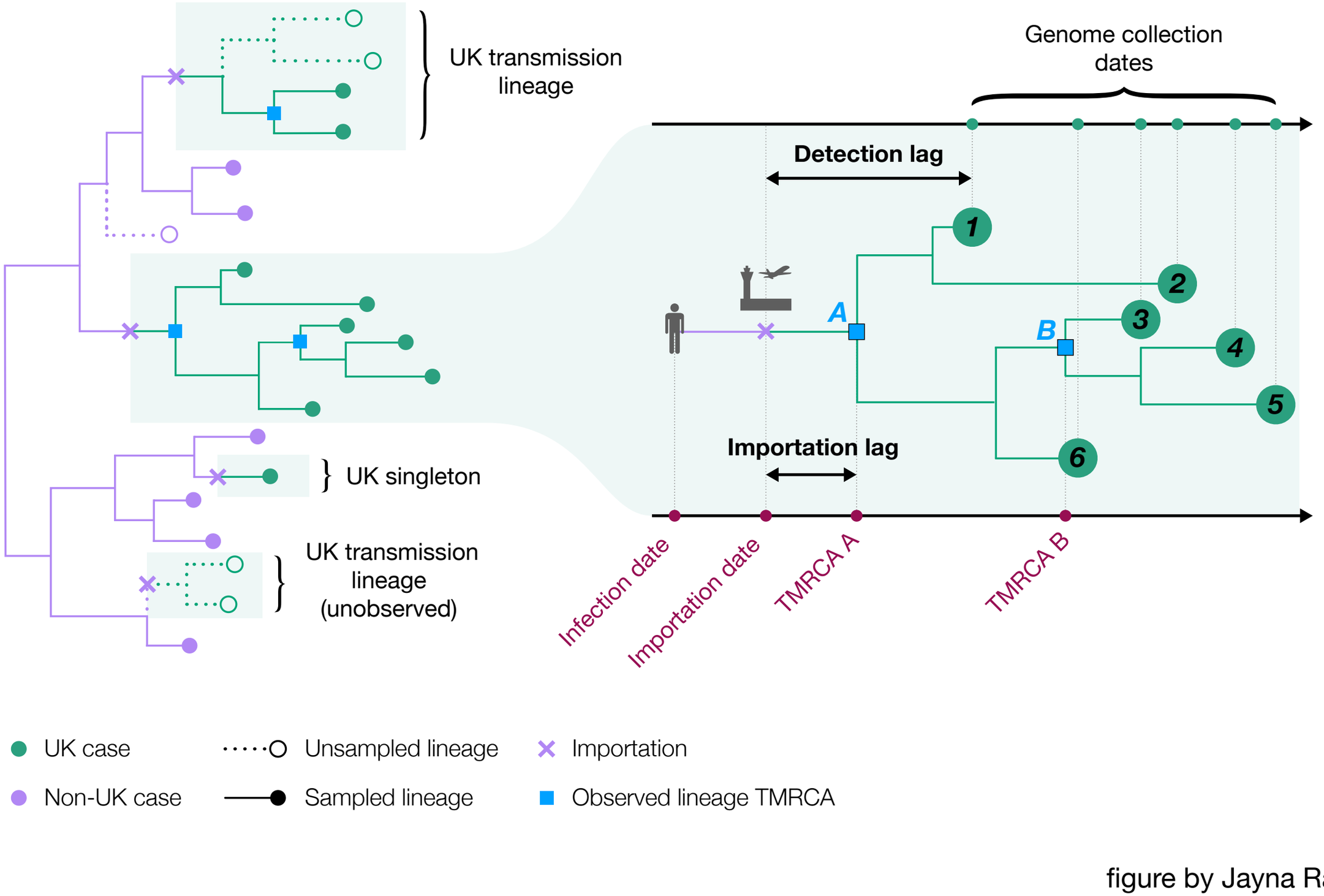


figure by Jayna Raghwani

Definition: TMRCA and importation lag

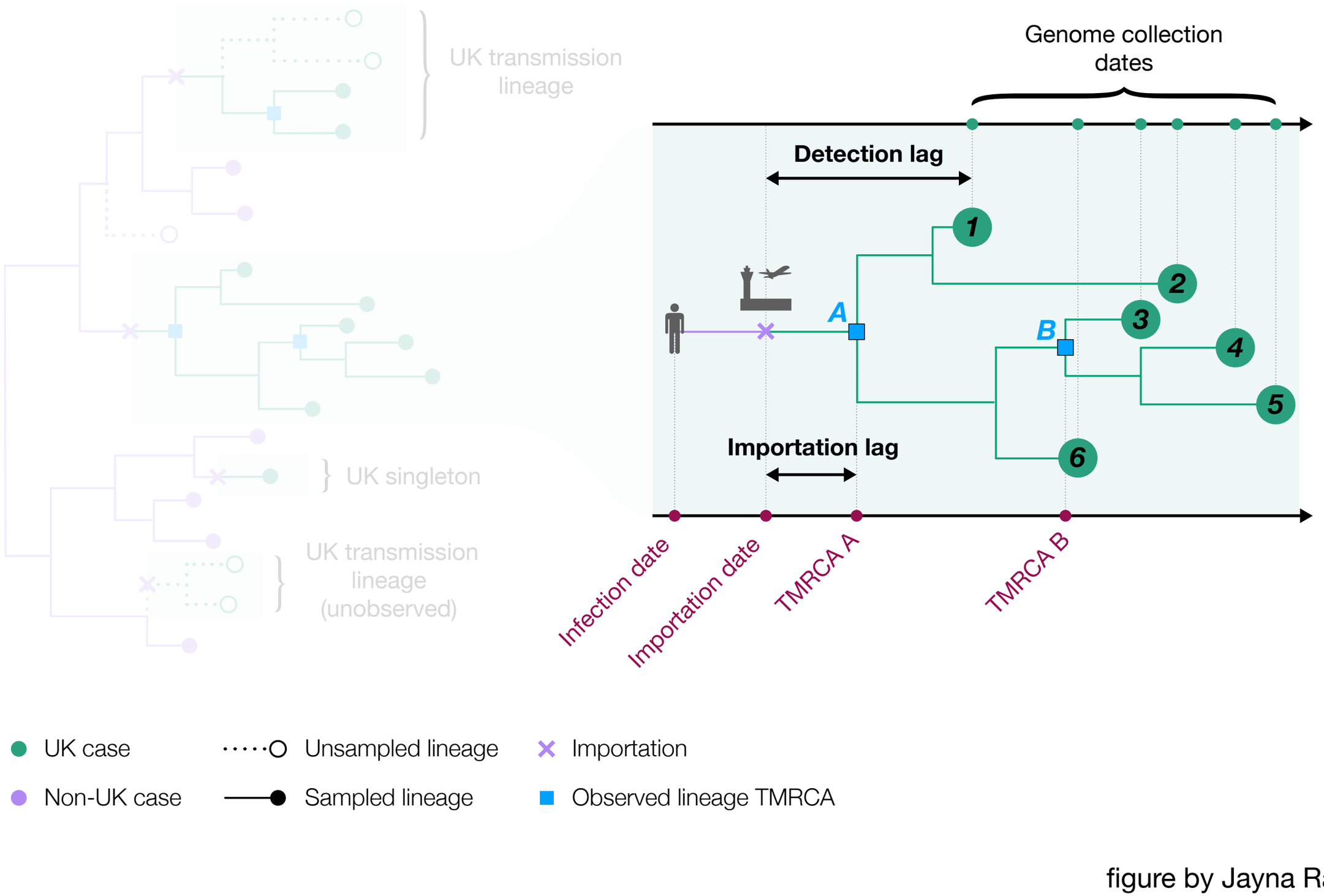


figure by Jayna Raghwani

Definition: TMRCA and importation lag

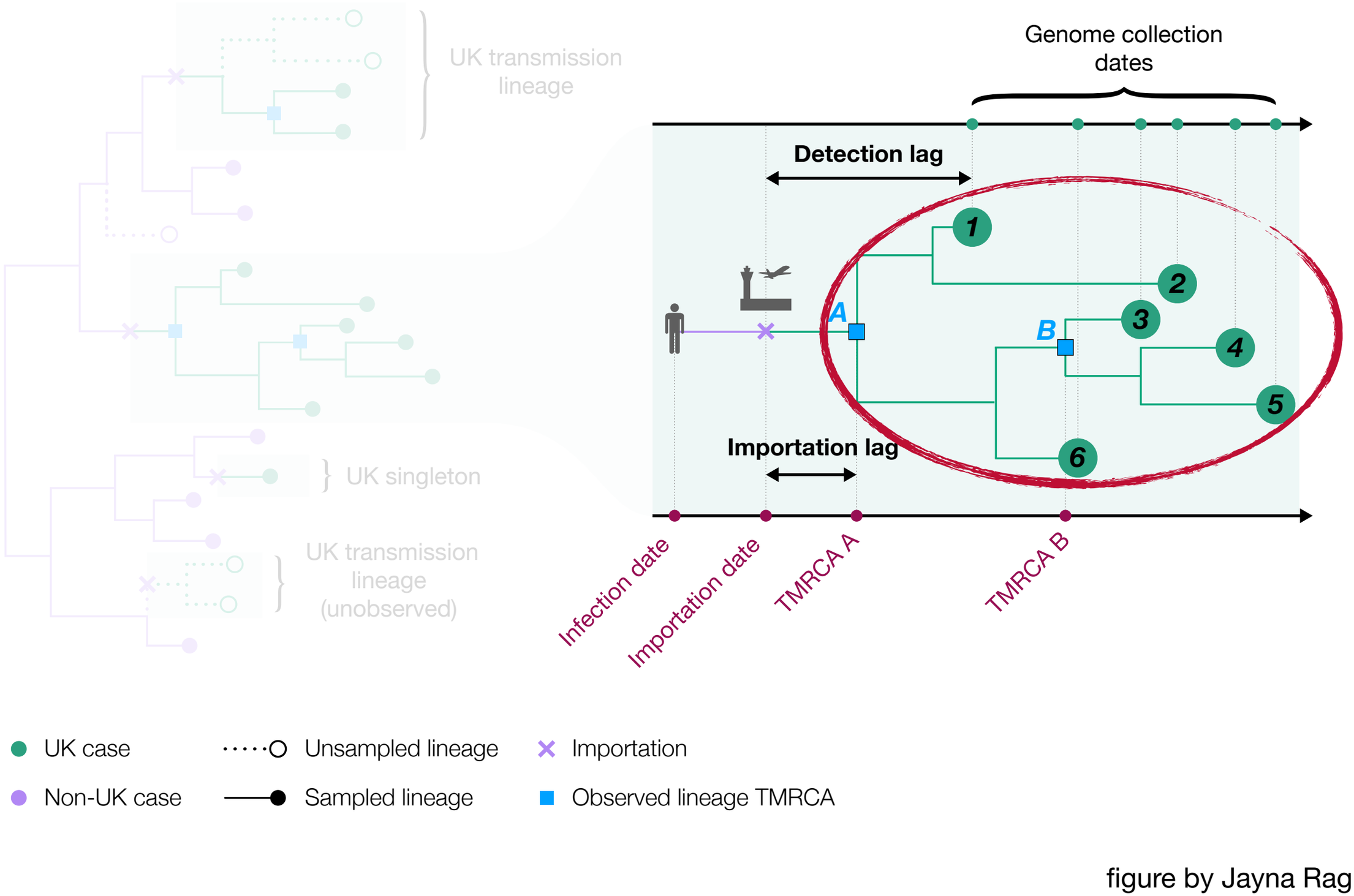


figure by Jayna Raghwani

Definition: TMRCA and importation lag

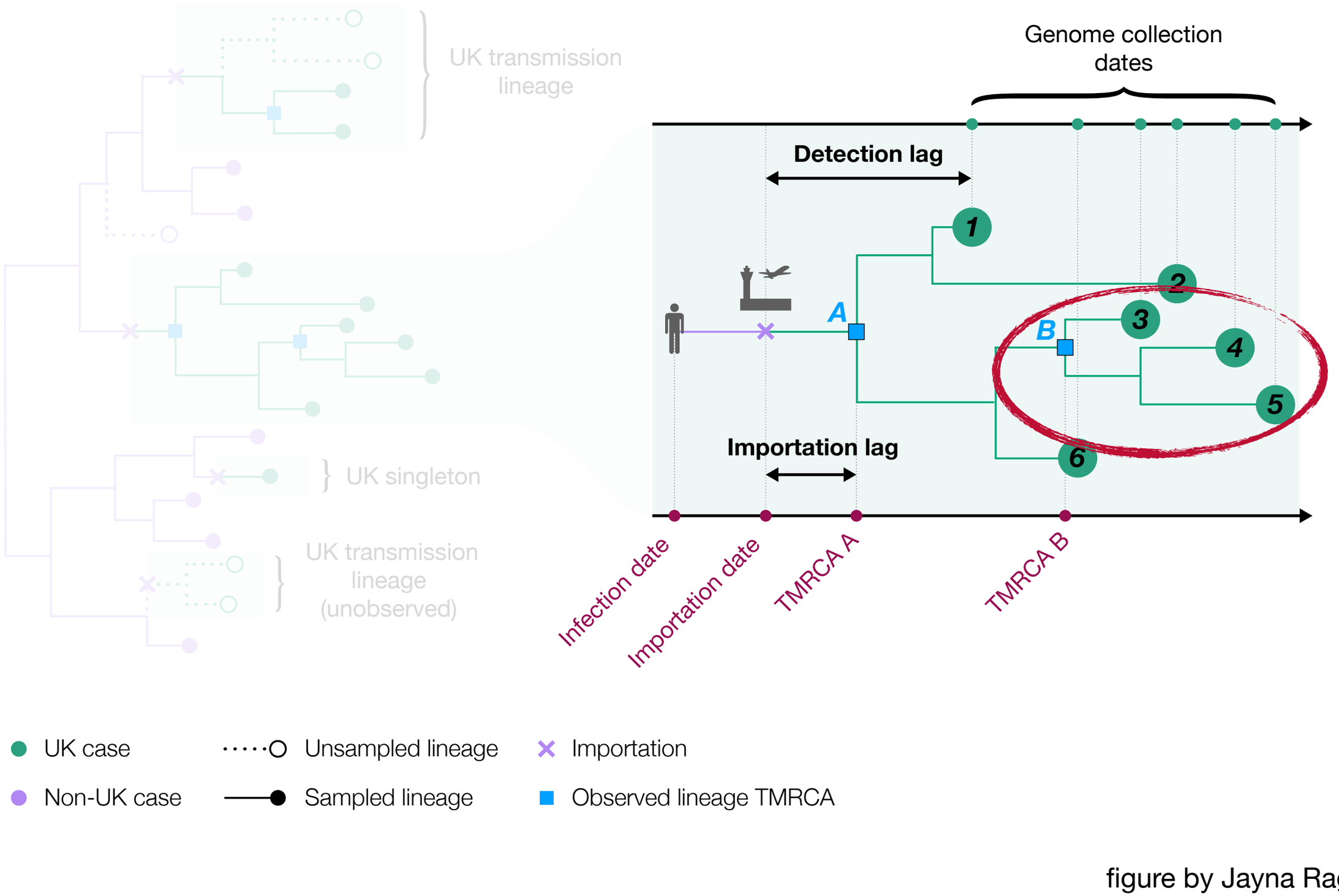


figure by Jayna Raghwani

Definition: TMRCA and importation lag

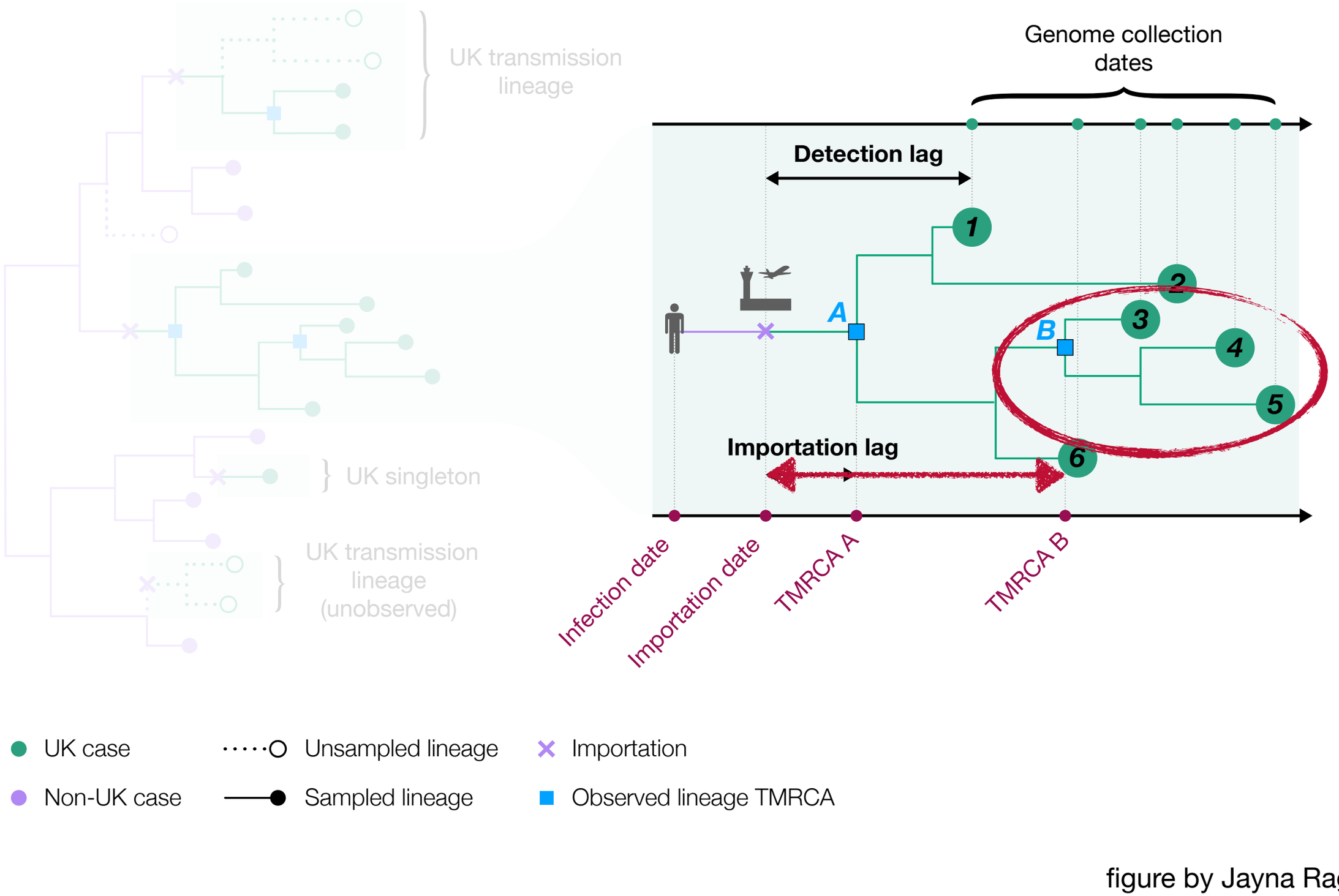
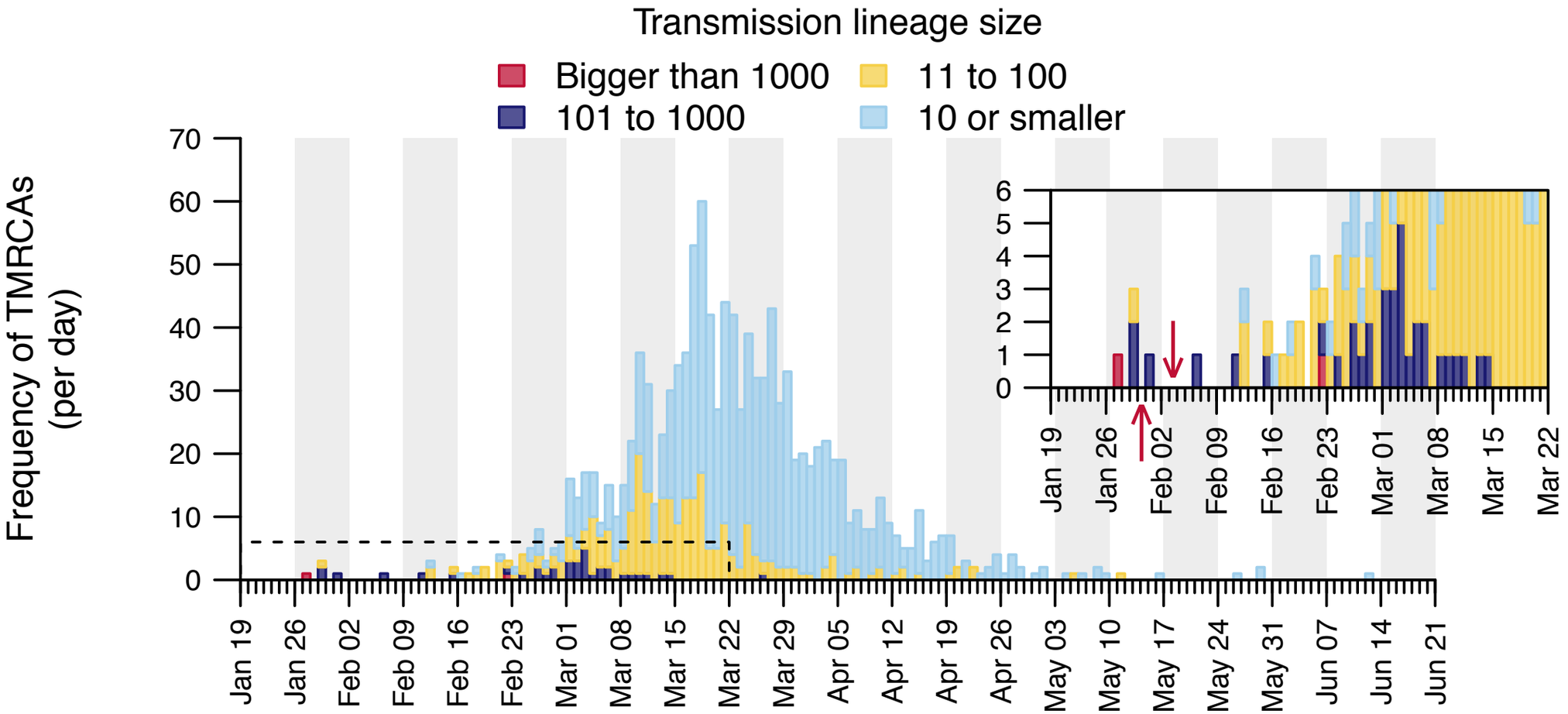


figure by Jayna Raghwani

Estimated TMRCAs of UK transmission lineages



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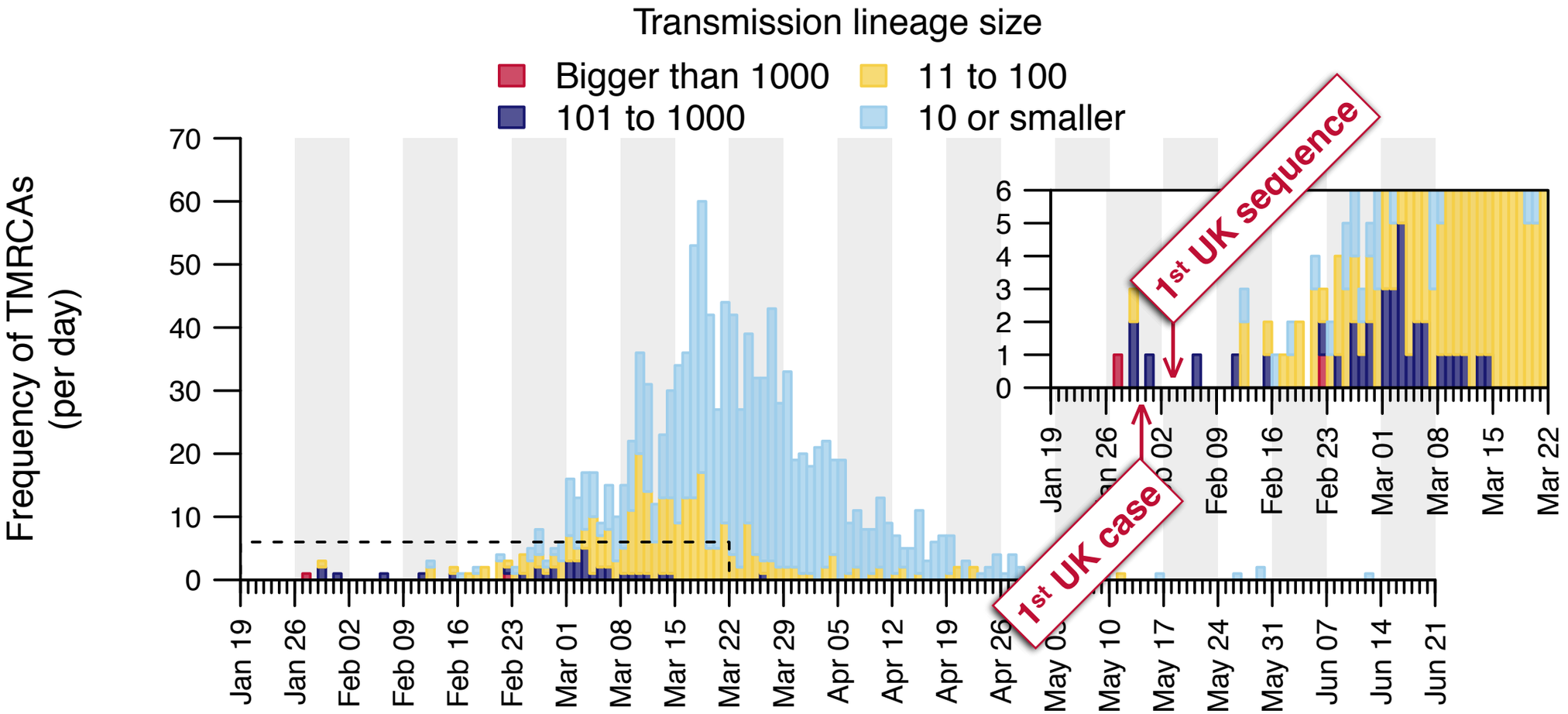
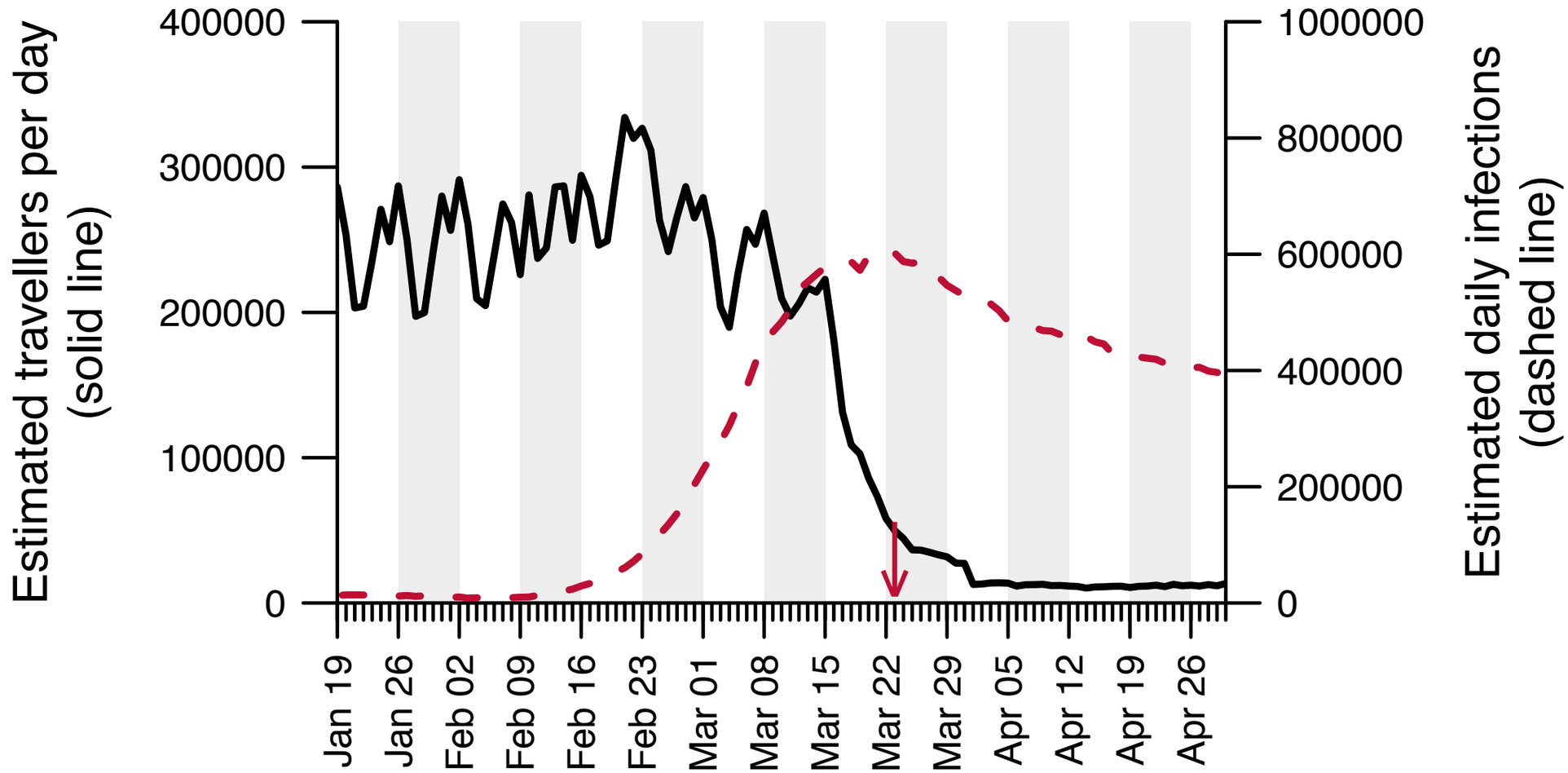
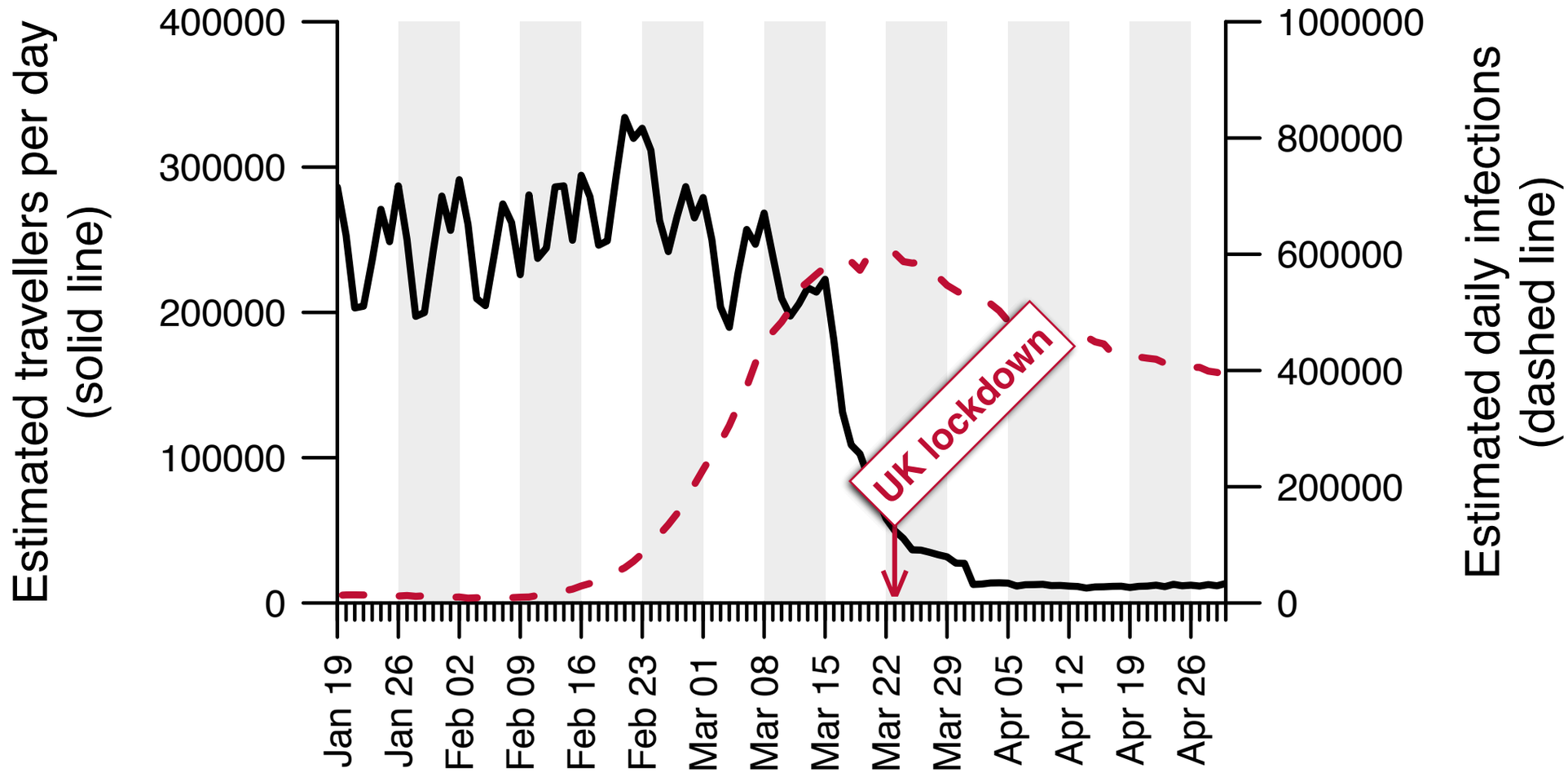


Trends in inbound travel and COVID-19 cases



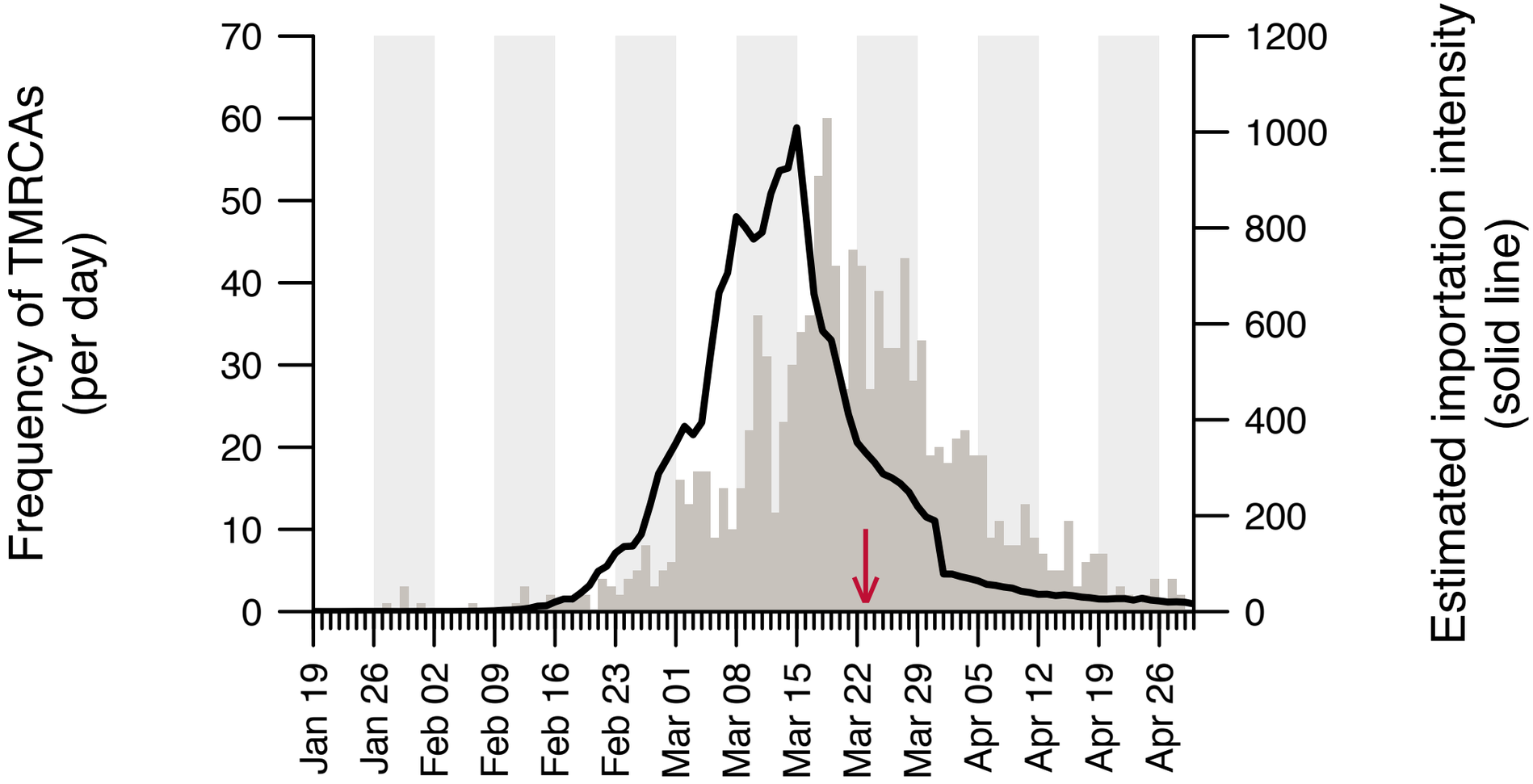
work by Alex Zarebski

Trends in inbound travel and COVID-19 cases



work by Alex Zarebski

Estimated Importation Intensity



work by Alex Zarebski

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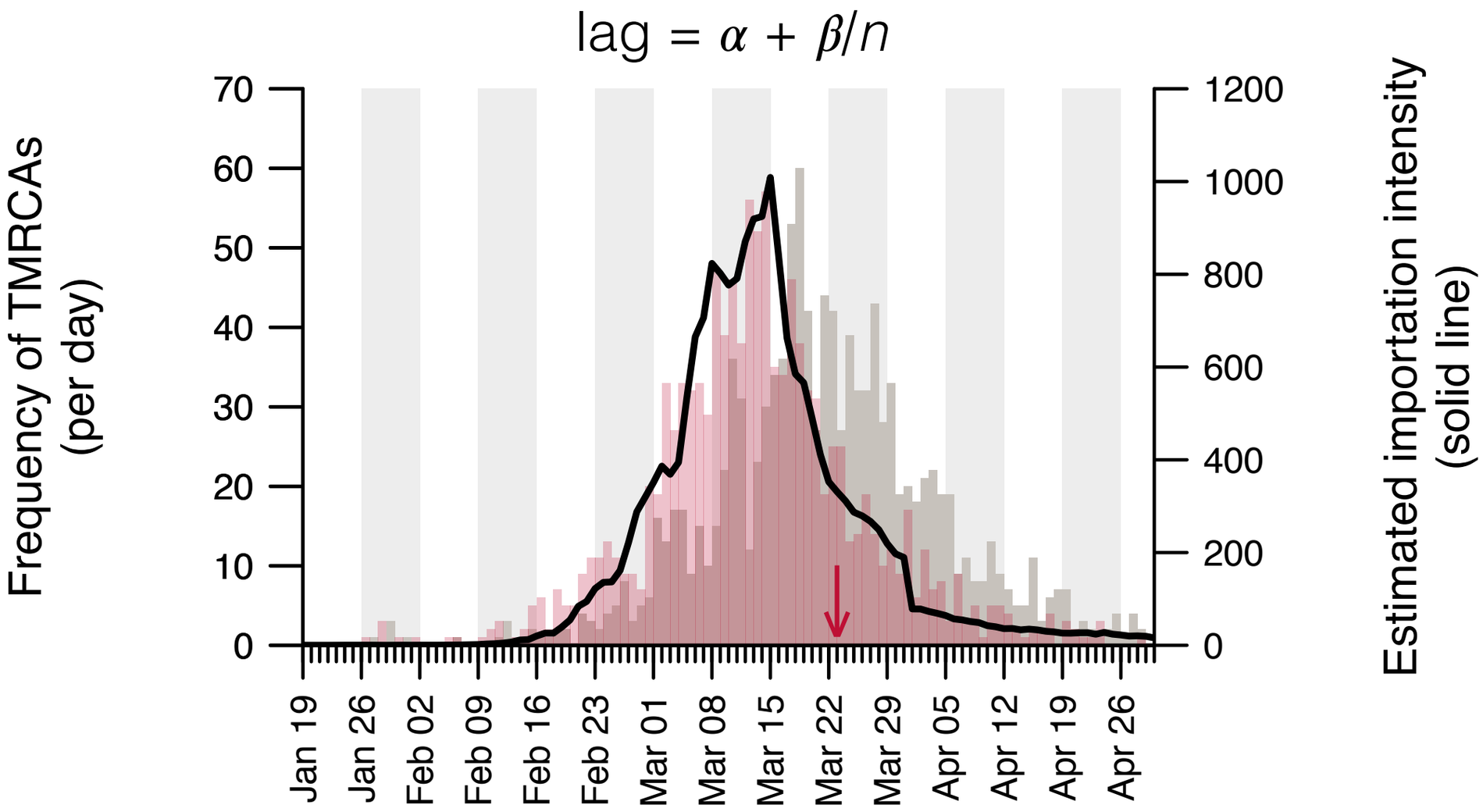
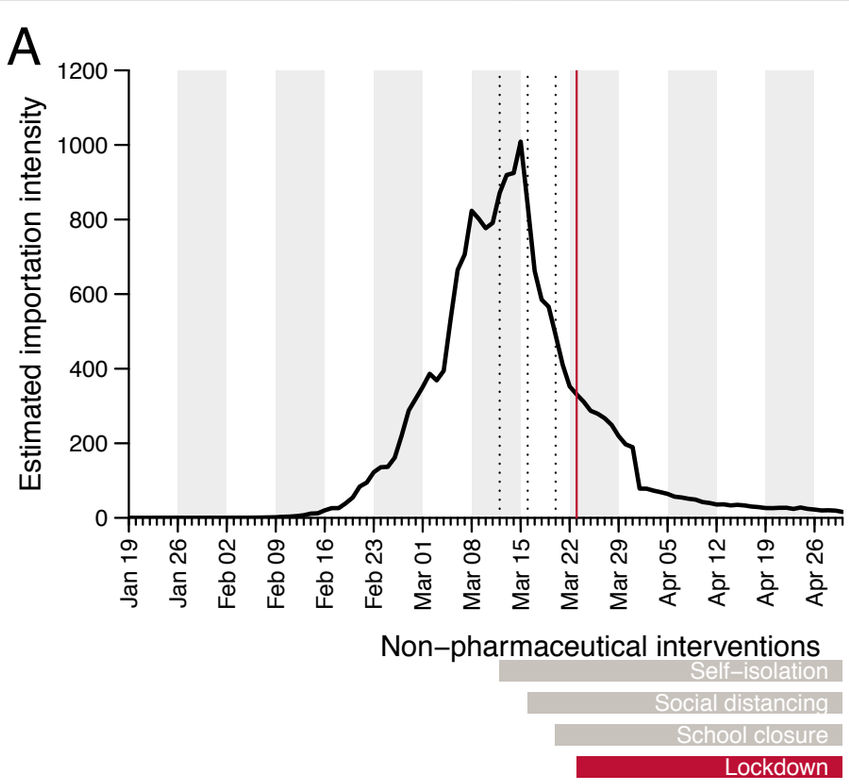
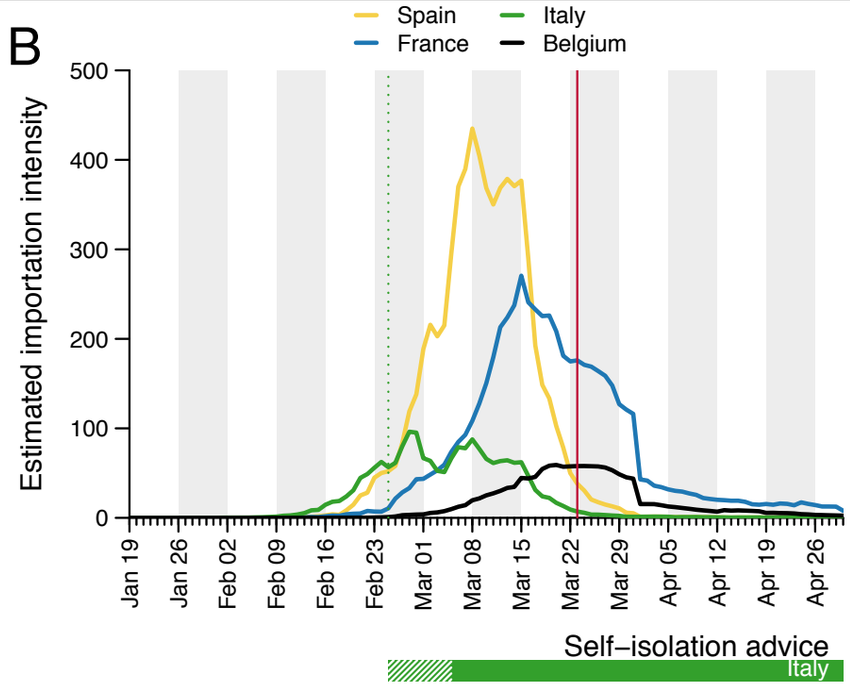
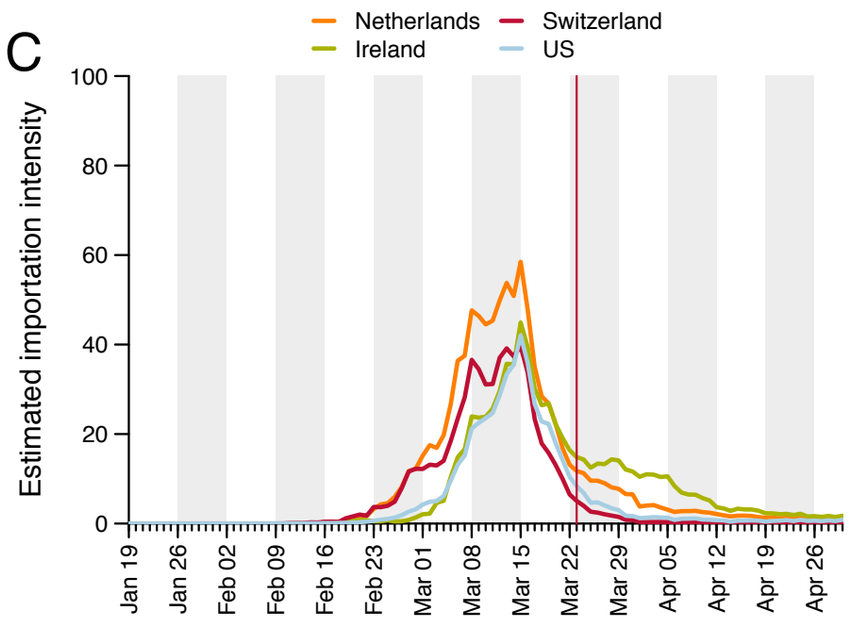


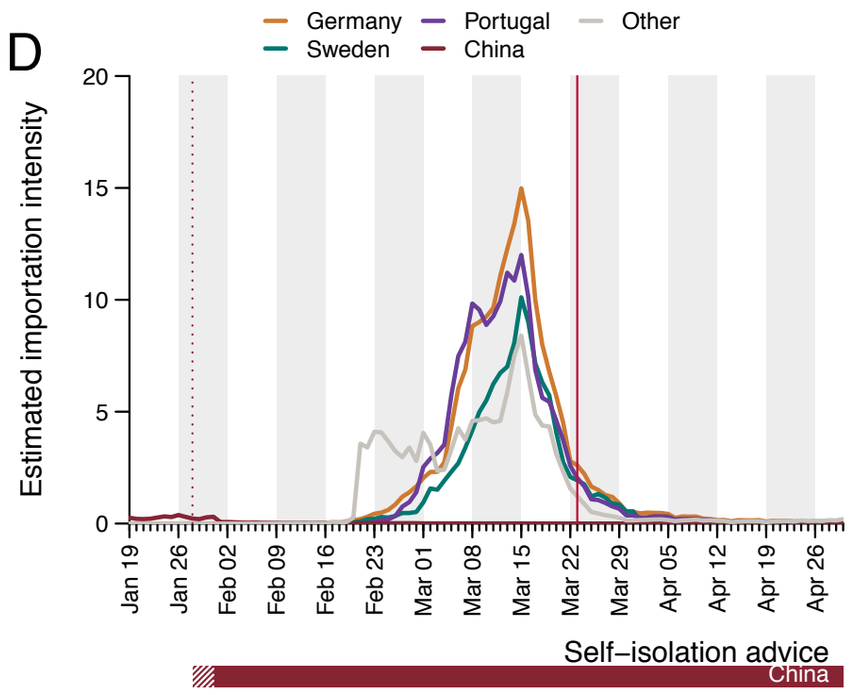
work by Alex Zarebski

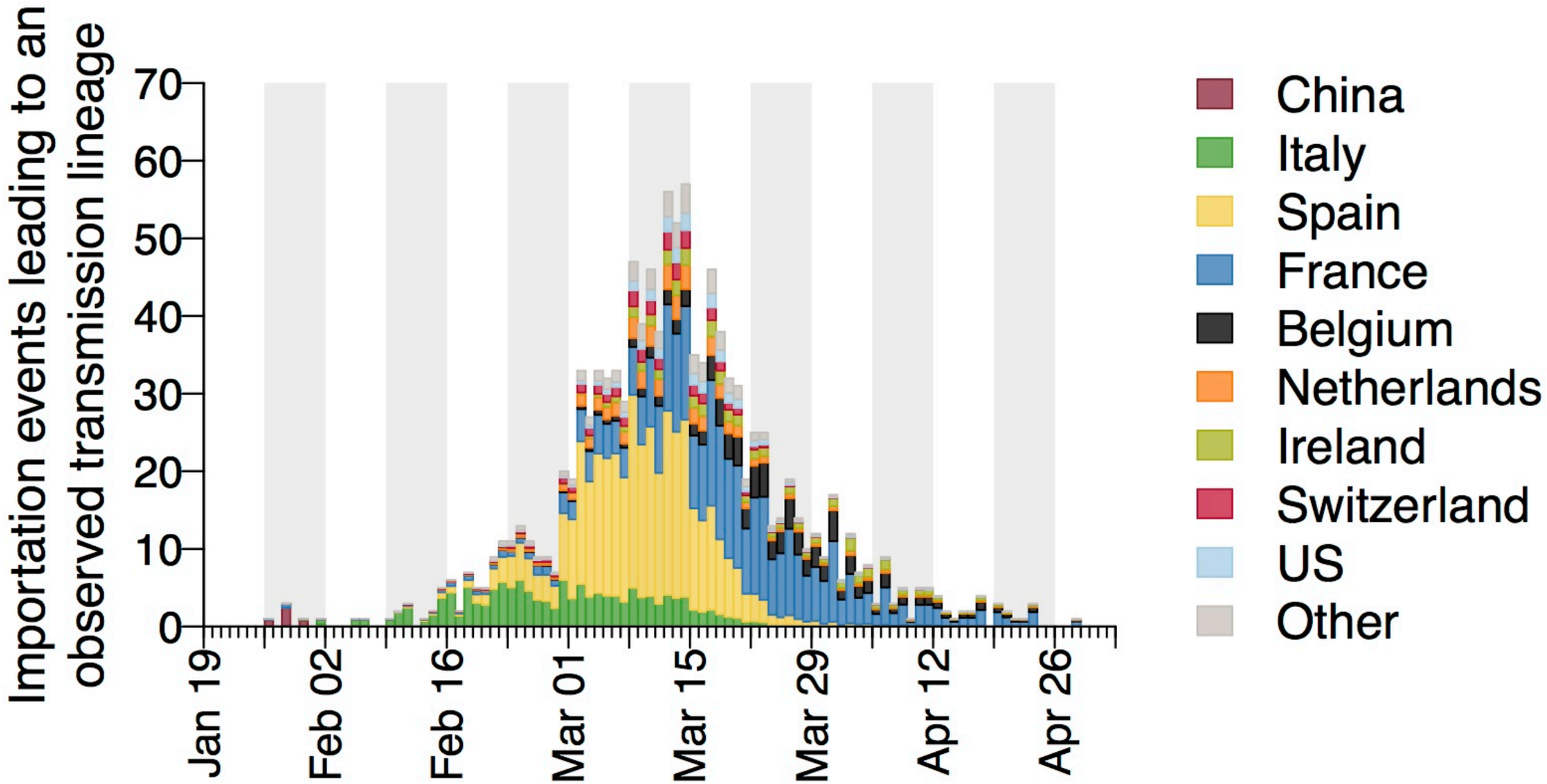
Country-specific importation intensity

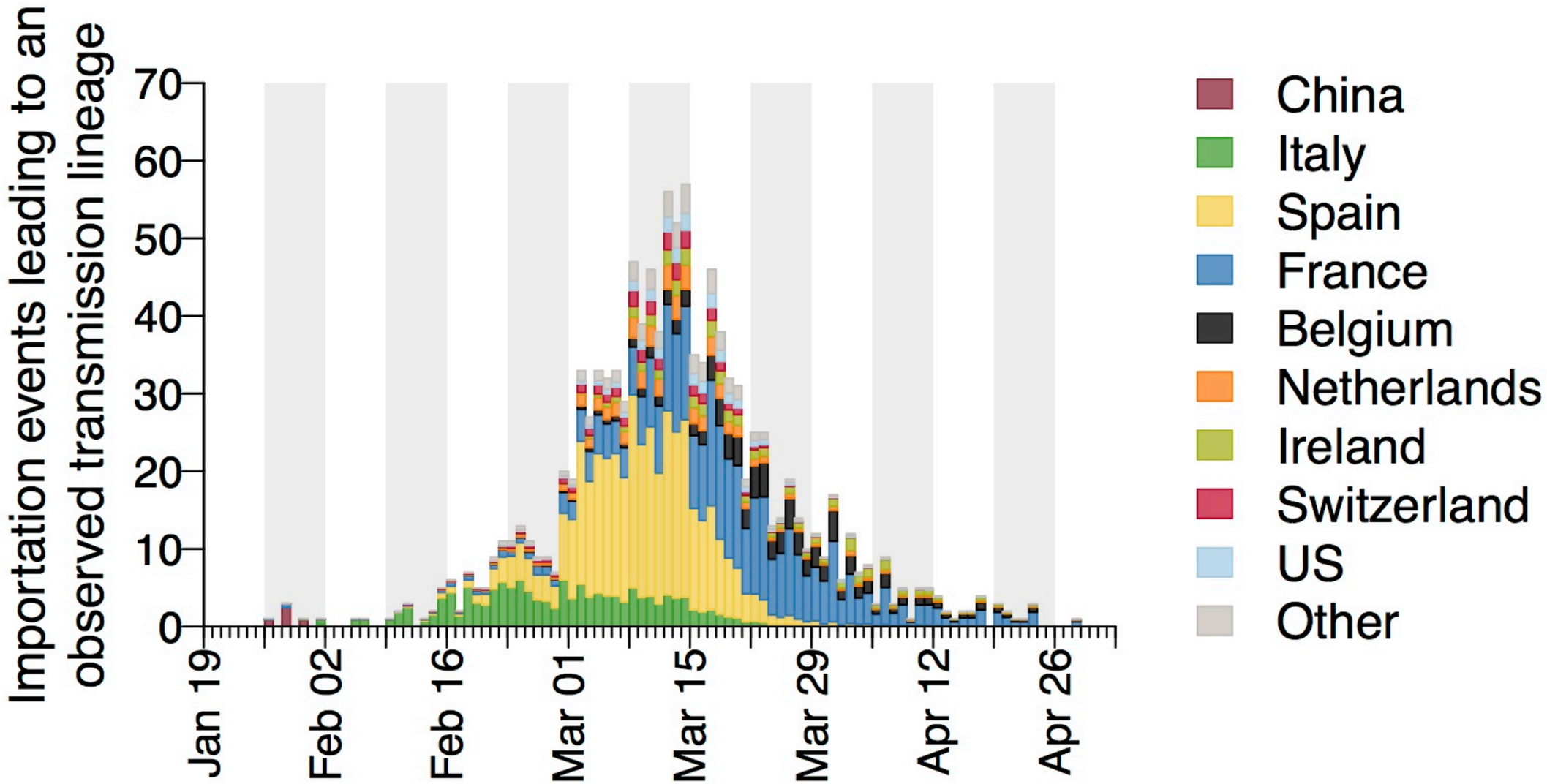









Importation events leading to an observed transmission lineage
0
10
20
30
40
50
60
70
Jan 19
Feb 02
Feb 16
Mar 01
Mar 15
Mar 29
Apr 12
Apr 26
China
Italy
Spain
France
Belgium
Netherlands
Ireland
Switzerland
US
Other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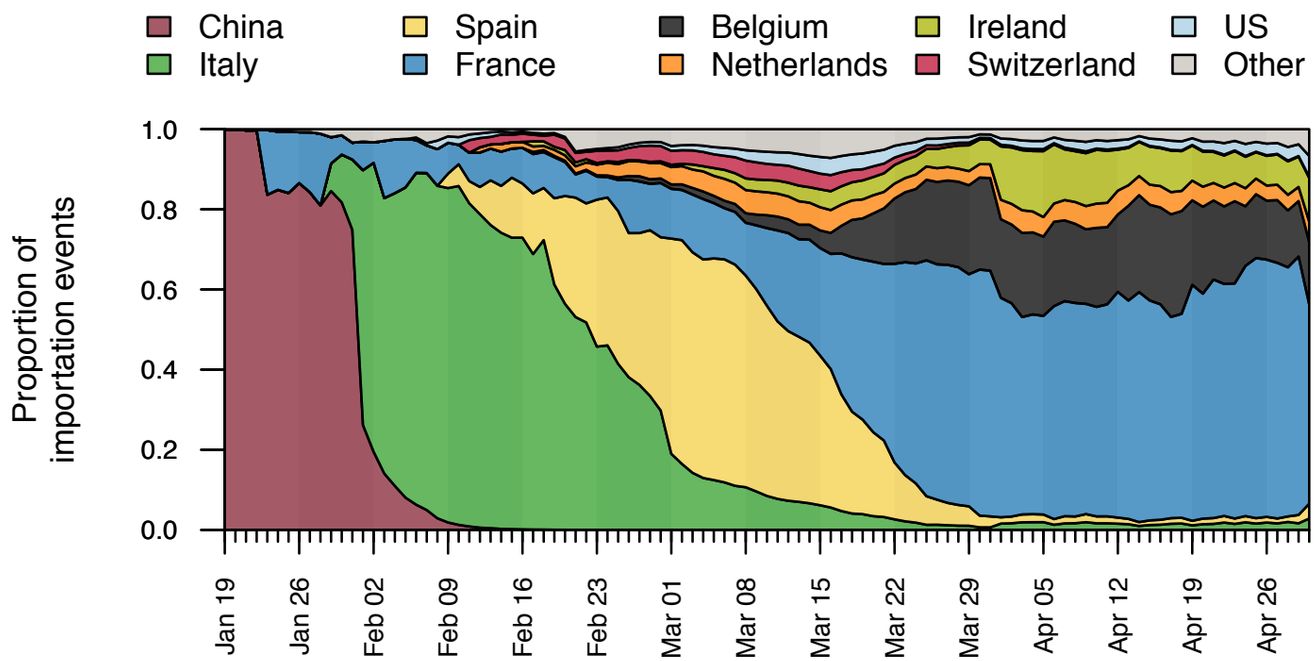
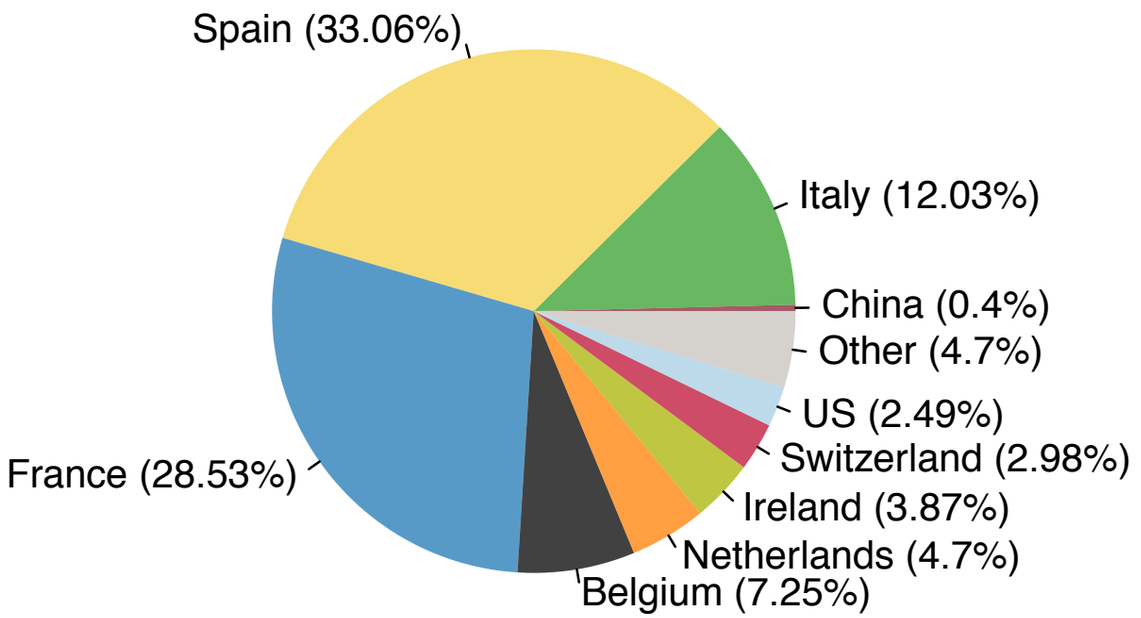

China
Italy
Spain
France
Belgium
Netherlands
Ireland
Switzerland
US
Other
Proportion of importation events
0.0
0.2
0.4
0.6
0.8
1.0
Jan 19
Jan 26
Feb 02
Feb 09
Feb 16
Feb 23
Mar 01
Mar 08
Mar 15
Mar 22
Mar 29
Apr 05
Apr 12
Apr 19
Apr 26


Spain (33.06%)
Italy (12.03%)
China (0.4%)
Other (4.7%)
US (2.49%)
Switzerland (2.98%)
Ireland (3.87%)
Netherlands (4.7%)
Belgium (7.25%)
France (28.53%)

Acknowledgments

University of Oxford
Oliver Pybus
Alex Zarebski
Moritz Kraemer
Bernardo Gutierrez
Jayna Raghwani
Nuno Faria
Tetyana Vasylyeva
David Aanensen

University of Edinburgh
Andrew Rambaut
JT McCrone
Verity Hill
Jordan Ashworth
Rachel Colquhoun
Ben Jackson
Áine O'Toole
Emily Scher

University of Birmingham
Nicholas Loman
Samuel Nicholls

University of Cambridge
Chris Ruis

University of Toronto / BlueDot
Alexander Watts
Isaac Bogoch
Kamran Khan

Imperial College
Kris Parag
Erik Volz

Public Health Wales
Tom Connor

and everyone who sampled, sequenced and shared SARS-CoV-2 genomes!

COG-UK COVID-19 GENOMICS UK CONSORTIUM

https://www.cogconsortium.uk

OXFORD MARTIN SCHOOL

UNIVERSITY OF OXFORD

@laduplessis

RESEARCH

CORONAVIRUS

Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK

Louis du Plessis[1]*, John T. McCrone[2]*, Alexander E. Zarebski[1]*, Verity Hill[2]*, Christopher Ruis[3,4]*, Bernardo Gutierrez[1,5], Jayna Raghwani[1], Jordan Ashworth[2], Rachel Colquhoun[2], Thomas R. Connor[6,7], Nuno R. Faria[1,8], Ben Jackson[2], Nicholas J. Loman[9], Áine O'Toole[2], Samuel M. Nicholls[9], Kris V. Parag[8], Emily Scher[2], Tetyana I. Vasylyeva[1], Erik M. Volz[8], Alexander Watts[10,11], Isaac I. Bogoch[12,13], Kamran Khan[10,11,12], COVID-19 Genomics UK (COG-UK) Consortium†, David M. Aanensen[14,15], Moritz U. G. Kraemer[1]‡, Andrew Rambaut[2]‡§, Oliver G. Pybus[1,16]‡§

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