

Results - B.1.351, “South Africa variant”

4/14/2021

Phylogeographic mapping

Ancestral character estimation was performed on a dated phylogeny exported from NextStrain. Each isolate was assigned to one of two binary categories: “Norway” or “Rest of the world (RoW)”. The output is presented in Fig.1.

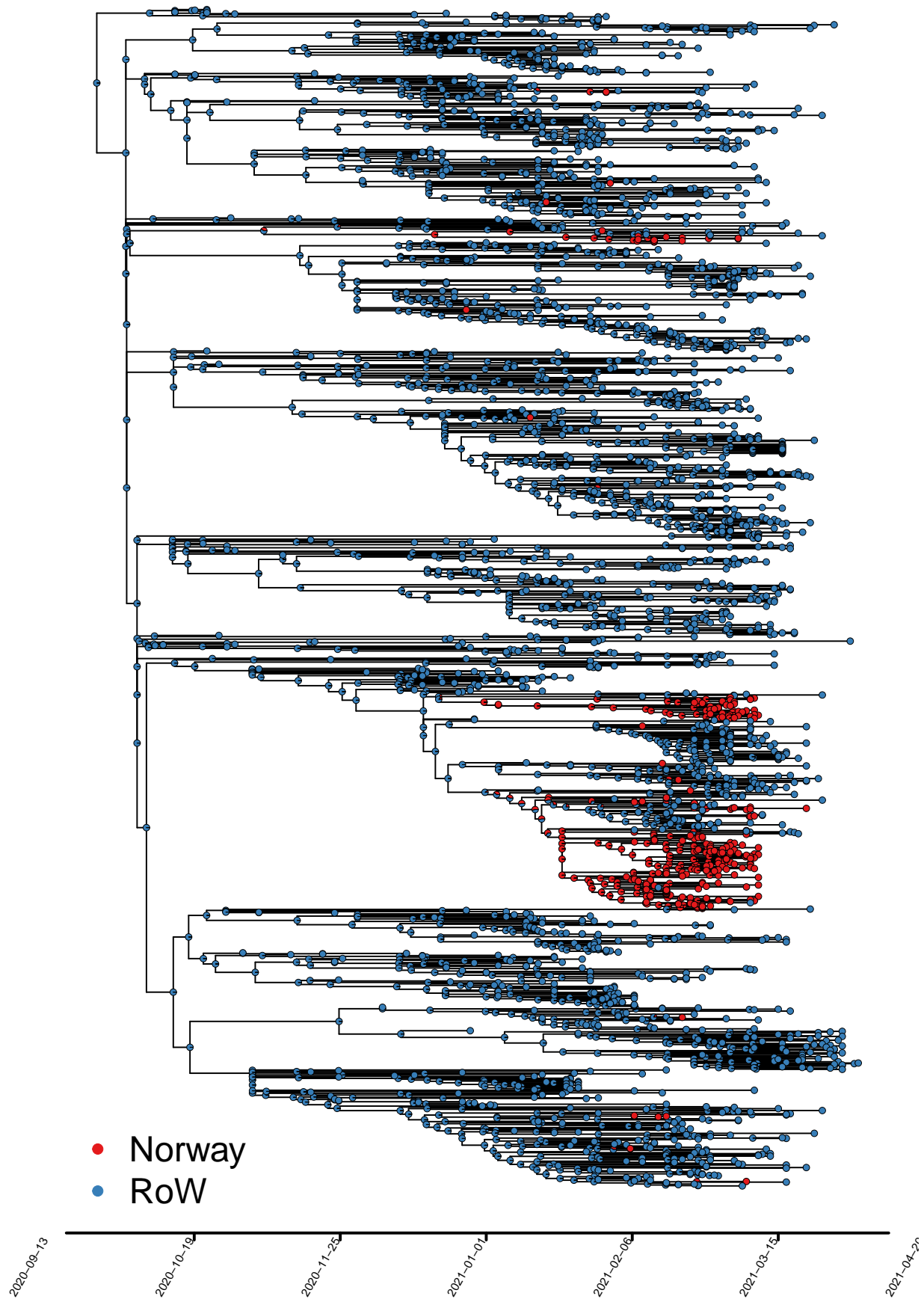


Fig. 1. B.1.351 phylogeny colored by binary geographic mappings (Norway, rest of the world [RoW]). The number of Norwegian isolates resulting from local transmission vs introductions from abroad were estimated from the tree and is summarized in Table 1.

Table 1. Estimated number of Norwegian infections that are caused by import and local transmission in geographically mapped phylogeny in Figure 1.

	2.5%	50%	97.5%
Import	20.0000	22.0000	23.0000
Local transmission	167.0000	168.0000	170.0000
Import / Total	0.1053	0.1158	0.1211

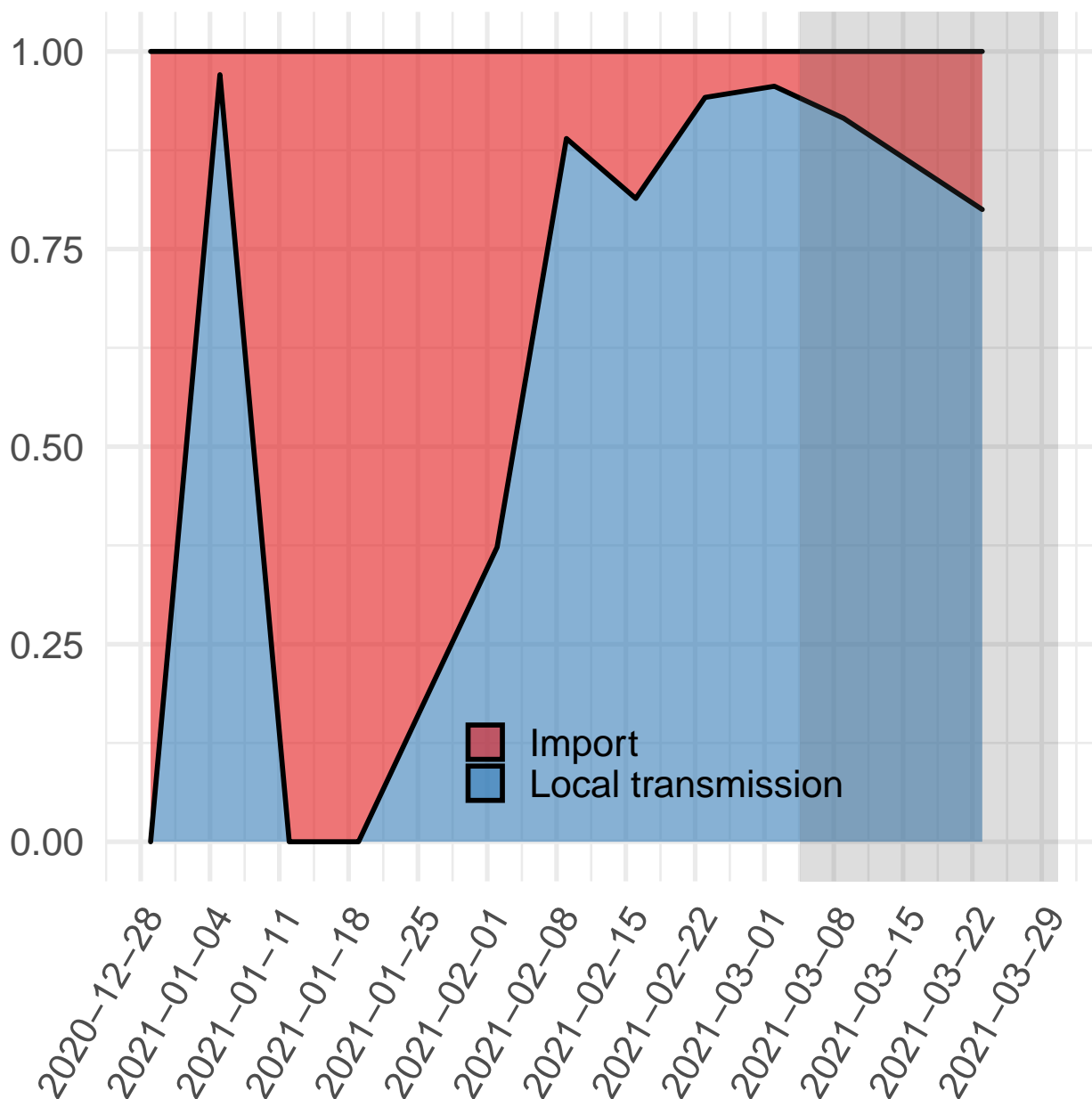


Fig. 2. Forhold mellom import og lokaltransmisjon av B.1.351 over tid i Norge. OBS, ingen sekvenserte

isolater som er nyere enn 10. mars.

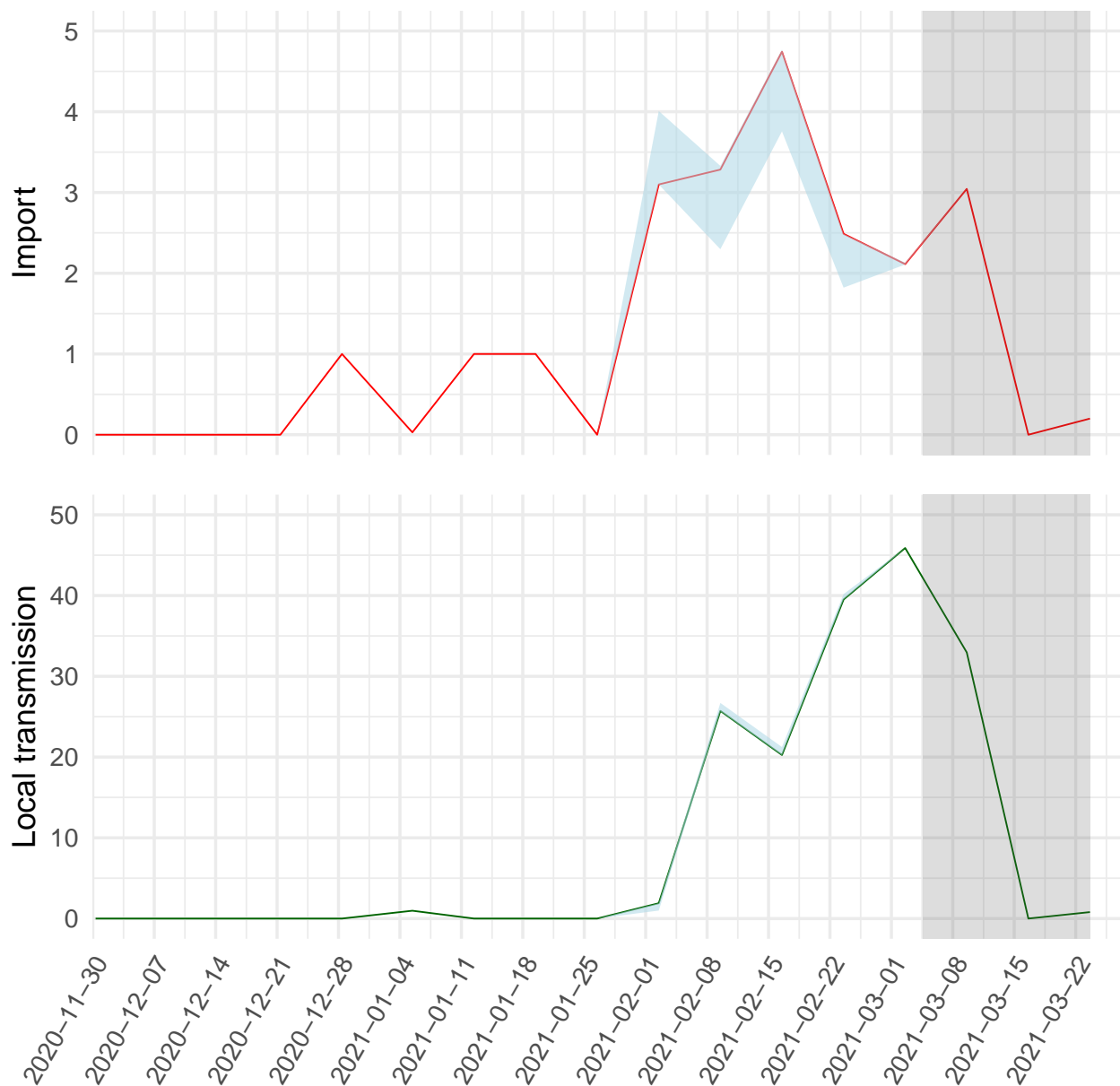


Fig. 3. Import og transmisjon av B.1.351. Estimert antall import-hendelser (øverst) og lokale transmisjoner (nederst) per uke. Det er knyttet stor usikkerhet rundt estimater i perioden skravert i grått.

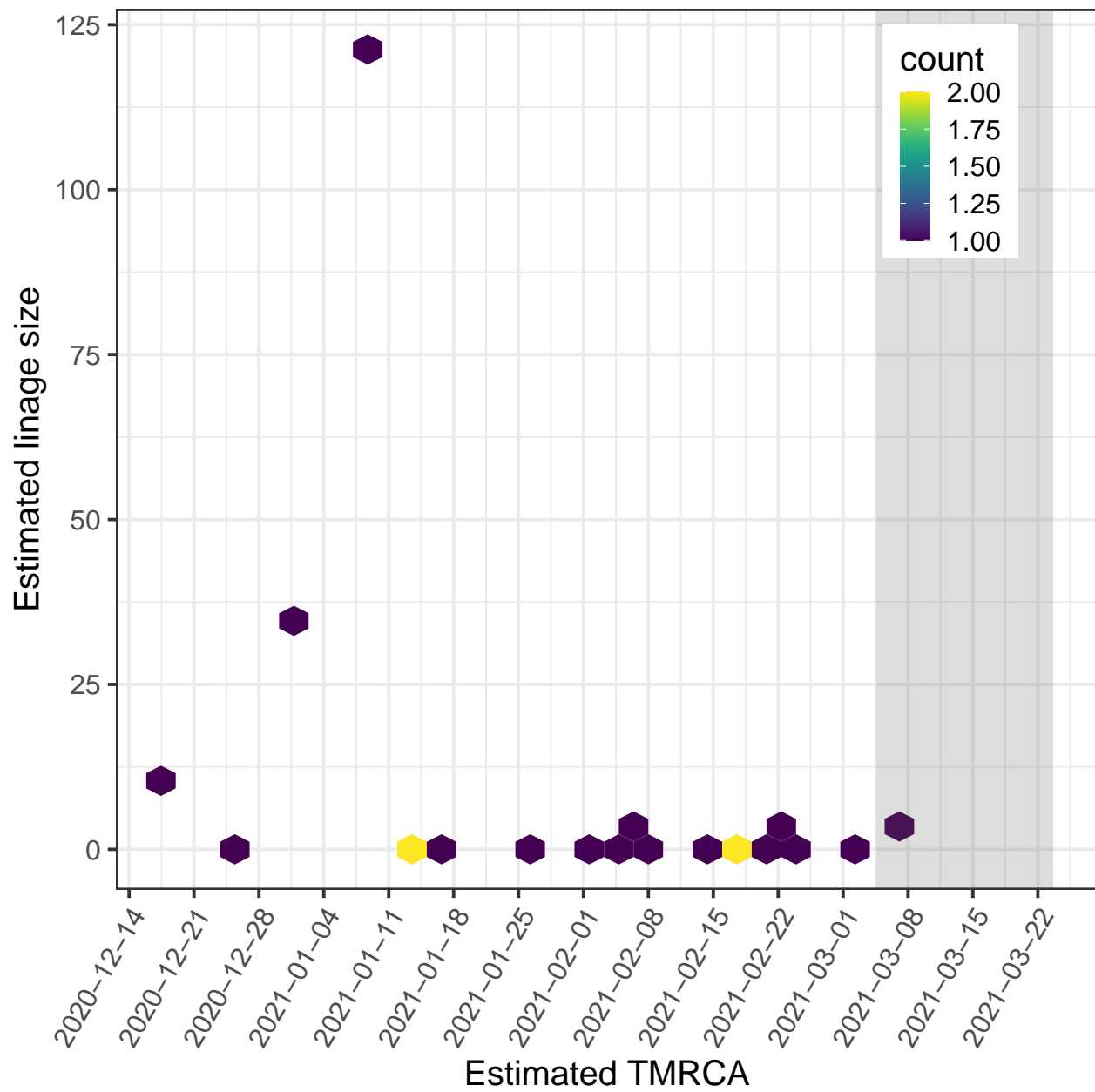


Fig. 4. Klyngestørrelser som funksjon av importtidspunkt, B.1.351 “TMRCA” = time of most recent common ancestor, og indikerer estimert tidspunkt for hver enkelt import. Den store klyngen som skiller seg ut her tilsvarer Bodø-utbruddet.