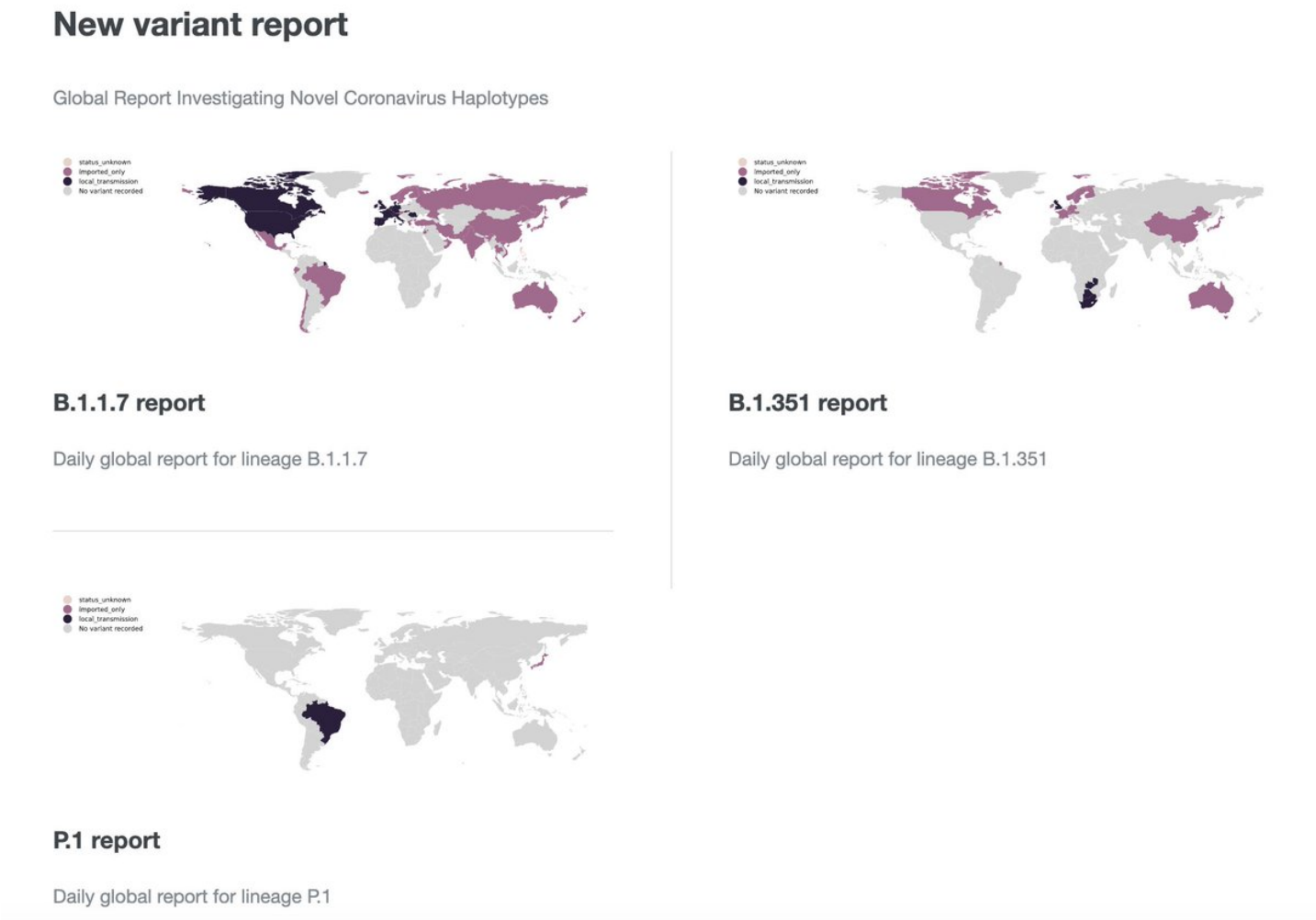
Twitter Thread by Áine O'Toole



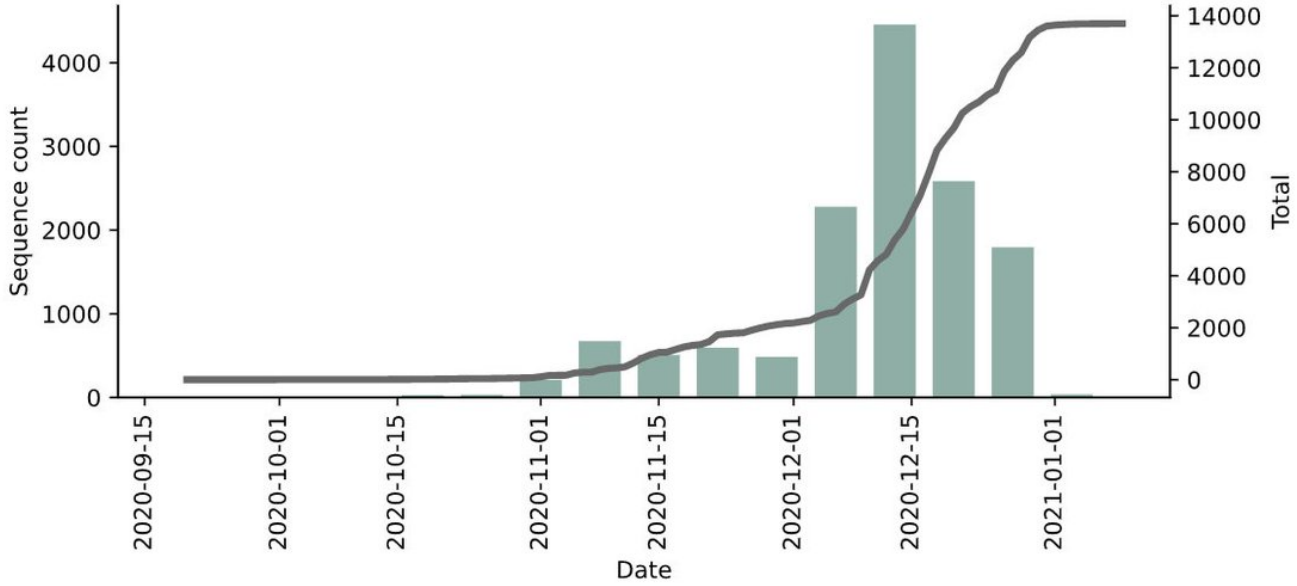
Áine O'Toole
@AineToole

Latest 'lineage of concern' report now available for 2021-01-13. Today we report on lineages B.1.1.7, B.1.351 /501Y.V2 and lineage P.1. @arambaut @viralverity @nmrfaria @MOUGK @Tuliodna



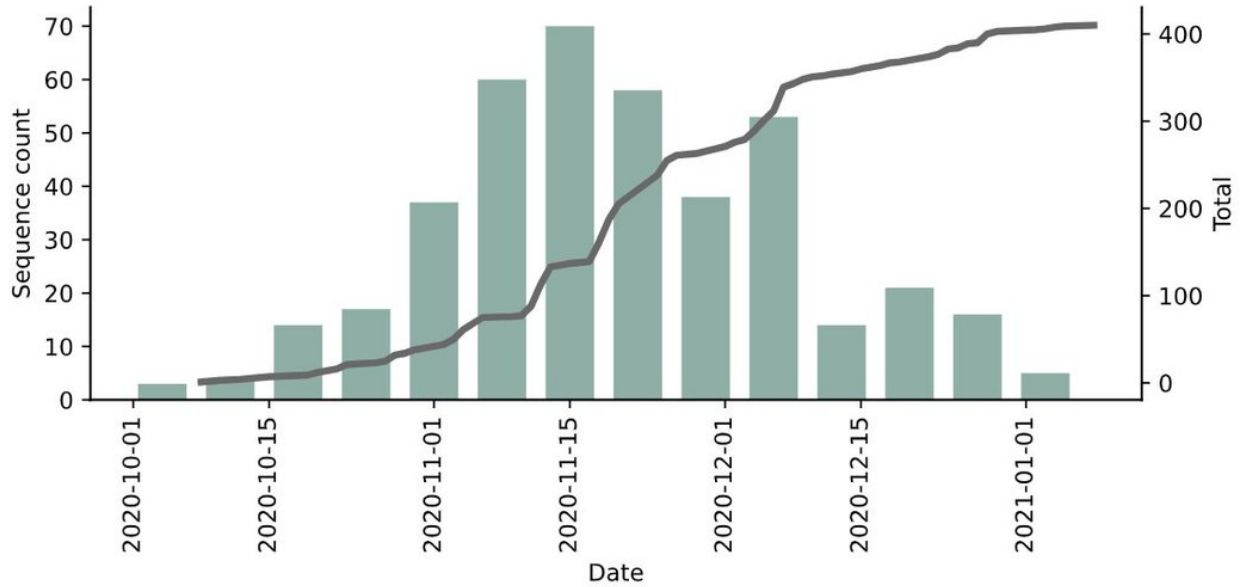
Today, 13,699 sequences on GISAID from 35 different countries were assigned lineage B.1.1.7.

Figure 1 | Cumulative sequence count over time B.1.1.7



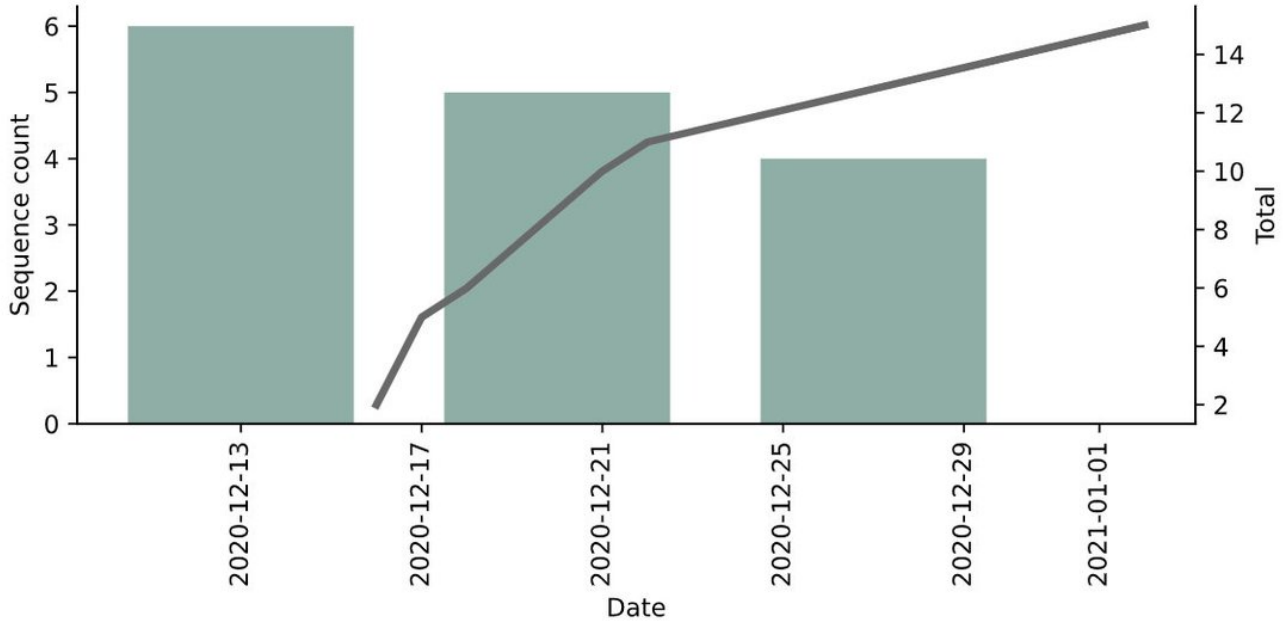
410 sequences from 12 different countries across the globe were assigned lineage B.1.351/ 501Y.V2. @Tuliodna @houzhou

Figure 1 | Cumulative sequence count over time B.1.351

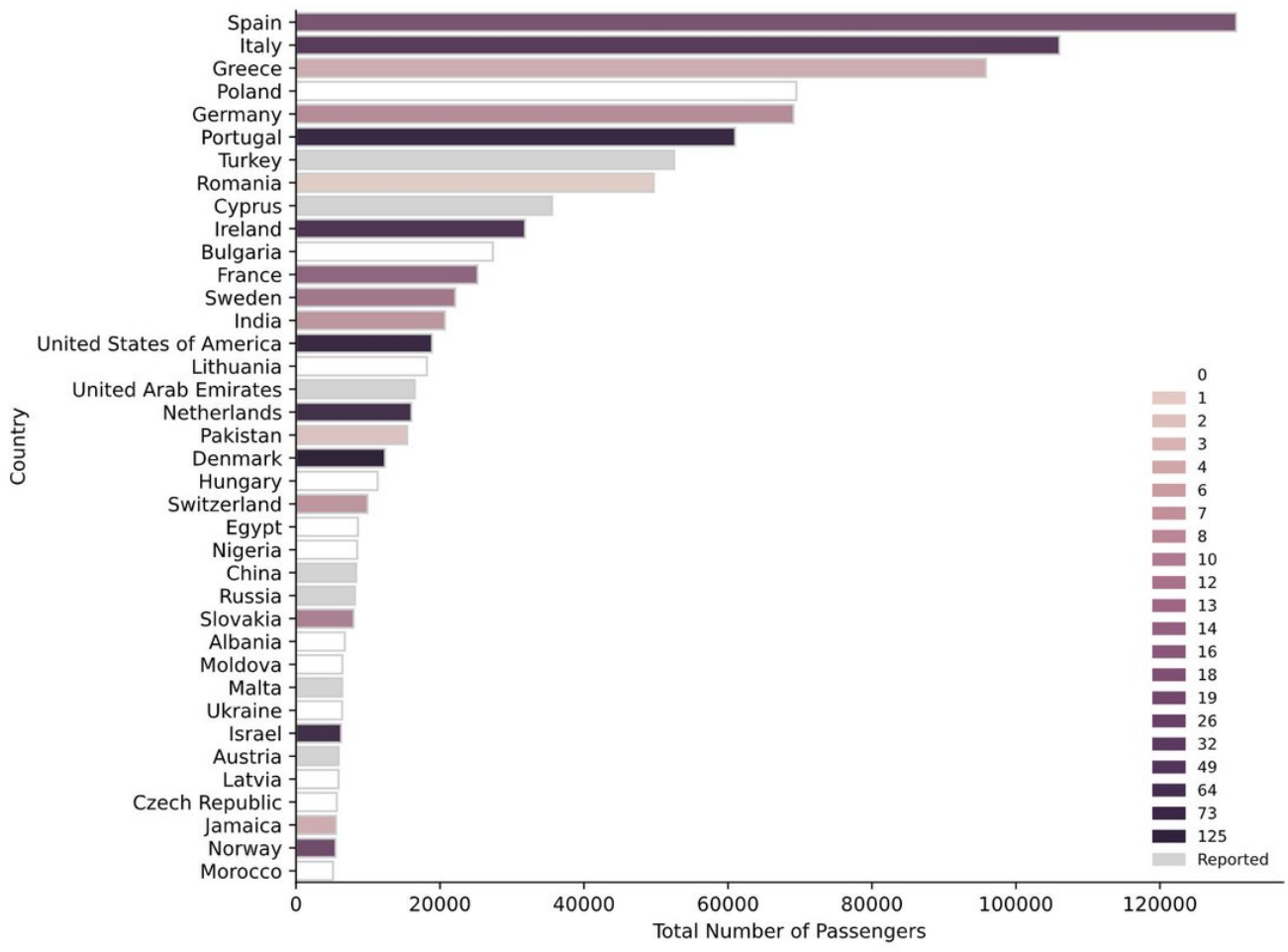


We also newly present data tracking lineage P.1, referred to on virological by @nmrfaria et al (https://t.co/cbOeQULIGS). This lineage has been detected in Brazil and Japan so far, with 15 sequences on GISAID, but has a number of biologically significant mutations. @arambaut

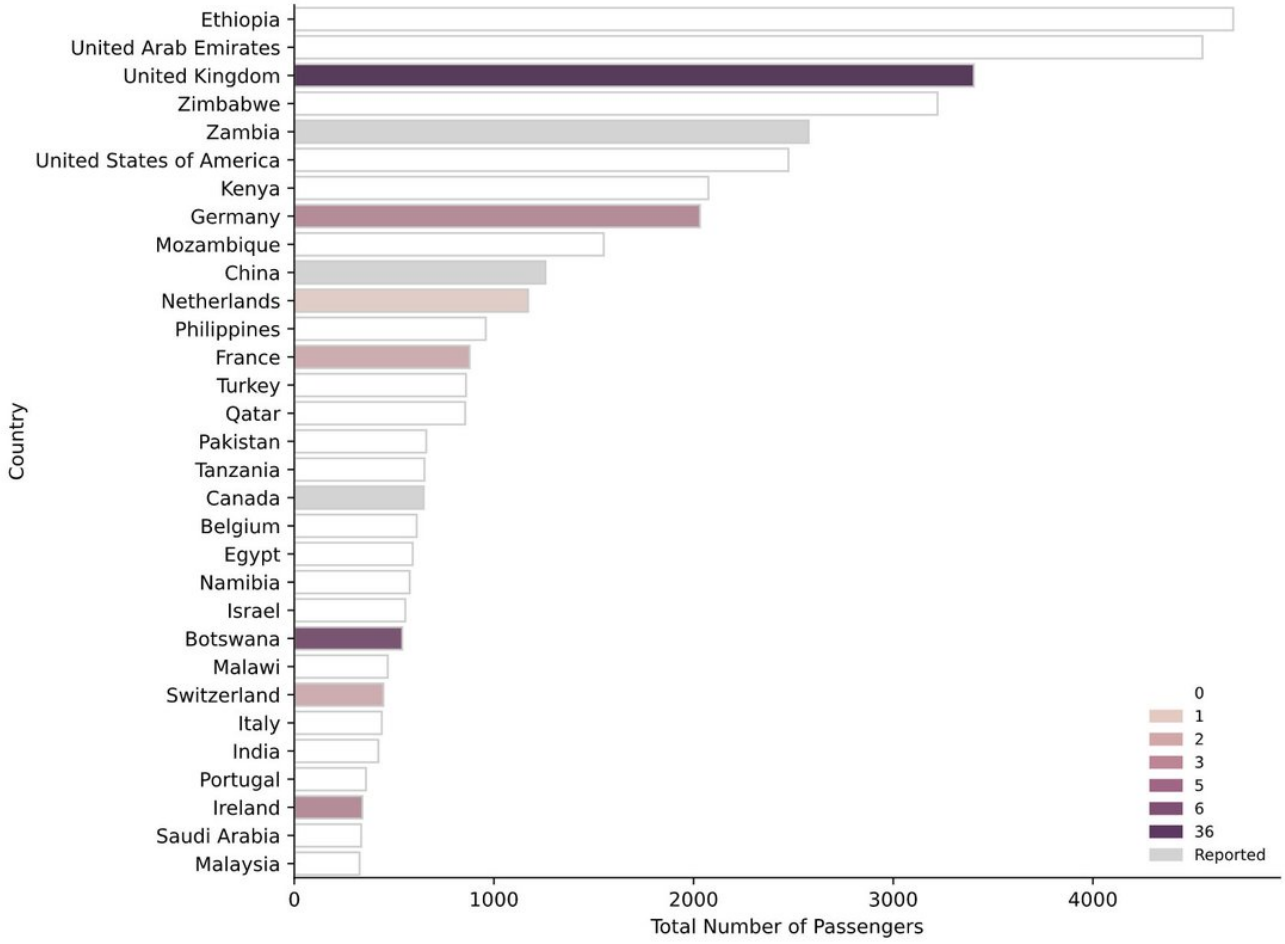
Figure 1 | Cumulative sequence count over time P.1



We present updated reports and sequence counts of B.1.1.7 on flights leaving London in October. A total of 51 countries have reported cases of B.1.1.7. @MOUGK @viralverity



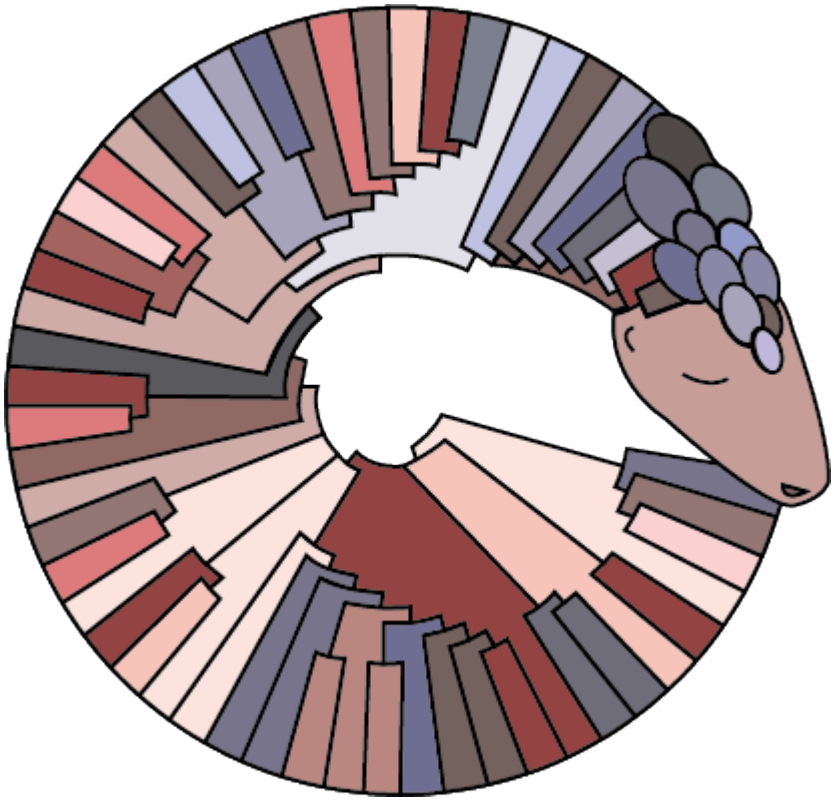
And present updated counts of sequences on GISAID and reports of B.1.351/ 501Y.V2 on flights leaving South African airports in October. To date, 16 countries have reported cases of B.1.351/ 501Y.V2. @Tuliodna @houzhou



Currently all reports of P.1 are represented by sequences on GISAID. @nmrfaria @arambaut



As always, please alert us to any reports of lineages of concern we may not have covered either via Twitter or by PR here: https://t.co/ZYocrrBAXg



Find the full detailed report at https://t.co/e3J9becNTz @arambaut @EvolveDotZoo @MOUGK @viralverity

