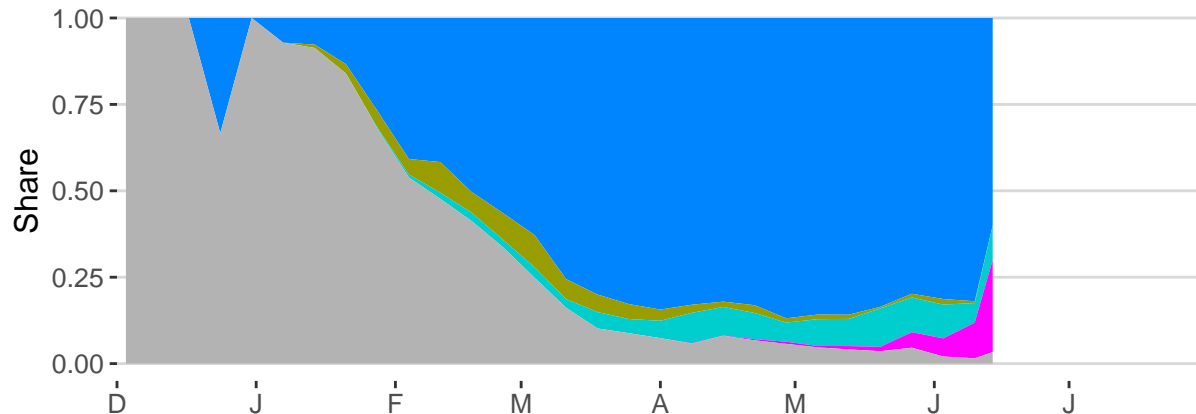


Spread of SARS-CoV2 variants of concern in Belgium
(baseline surveillance, whole genome sequencing+VOC PCR)



Multinomial fit

