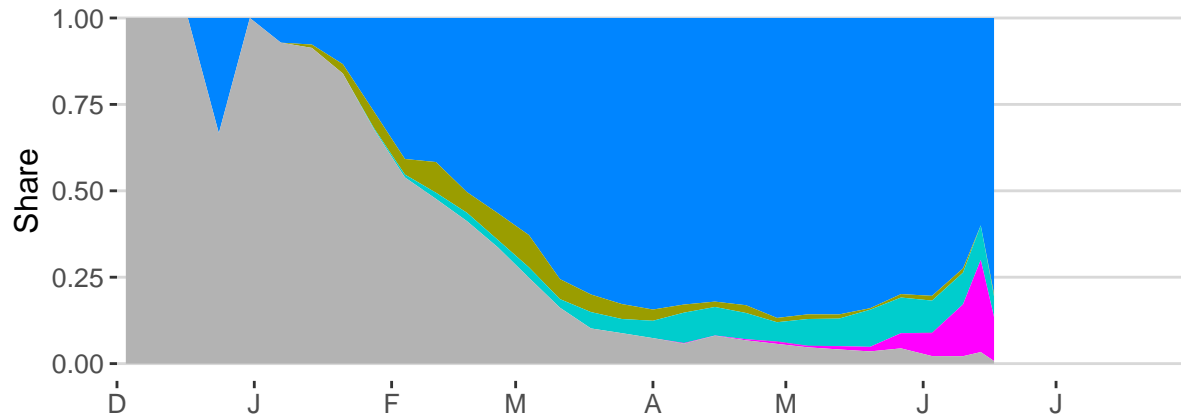


Spread of SARS-CoV2 variants of concern in Belgium (baseline surveillance, whole genome sequencing+VOC PCR)



Multinomial fit

