

Inferring Risks of Coronavirus Transmission from Community Household Data: Tranche 8 Update

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Headline results

This document presents an updated analysis for the following time period:

- **Tranche 8:** 1 September 2021 to 14 October 2021; high prevalence; schools open; Delta variant dominant; over 49 million first and 45 million second doses distributed by end of time period.

Properties of this Tranche are given in Table 1; the histogram and age density plots are in Figure 1; the pair and residual plots are in Figure 2; and the output from the fitted model is shown in Figure 3, Figure 4 and Table 2.

The most striking feature of the new results is the extremely high relative external risks for school-age children, which would be expected given that schools are open and children are largely unvaccinated. Another change from Tranches 6 and 7 is that those working in patient-facing roles no longer experience significant reduction of external infection risk compared to baseline, and that as alpha becomes negligible, the OR+N gene positivity pattern is no longer associated with significantly reduced transmission.

							Tranche 8	All
Number of participants							339057	441051
Number of households							177552	217738
Number of positive individuals							4757	33468
Households with 1+ positive							3617	24443
Children <12							23377	34700
Children 12–16							18806	24201
OR+N+S positives							4384	18582
OR+N positives							75	9156
Patient-facing participants							10962	16655

Table 1: Tranche 8 sample properties.

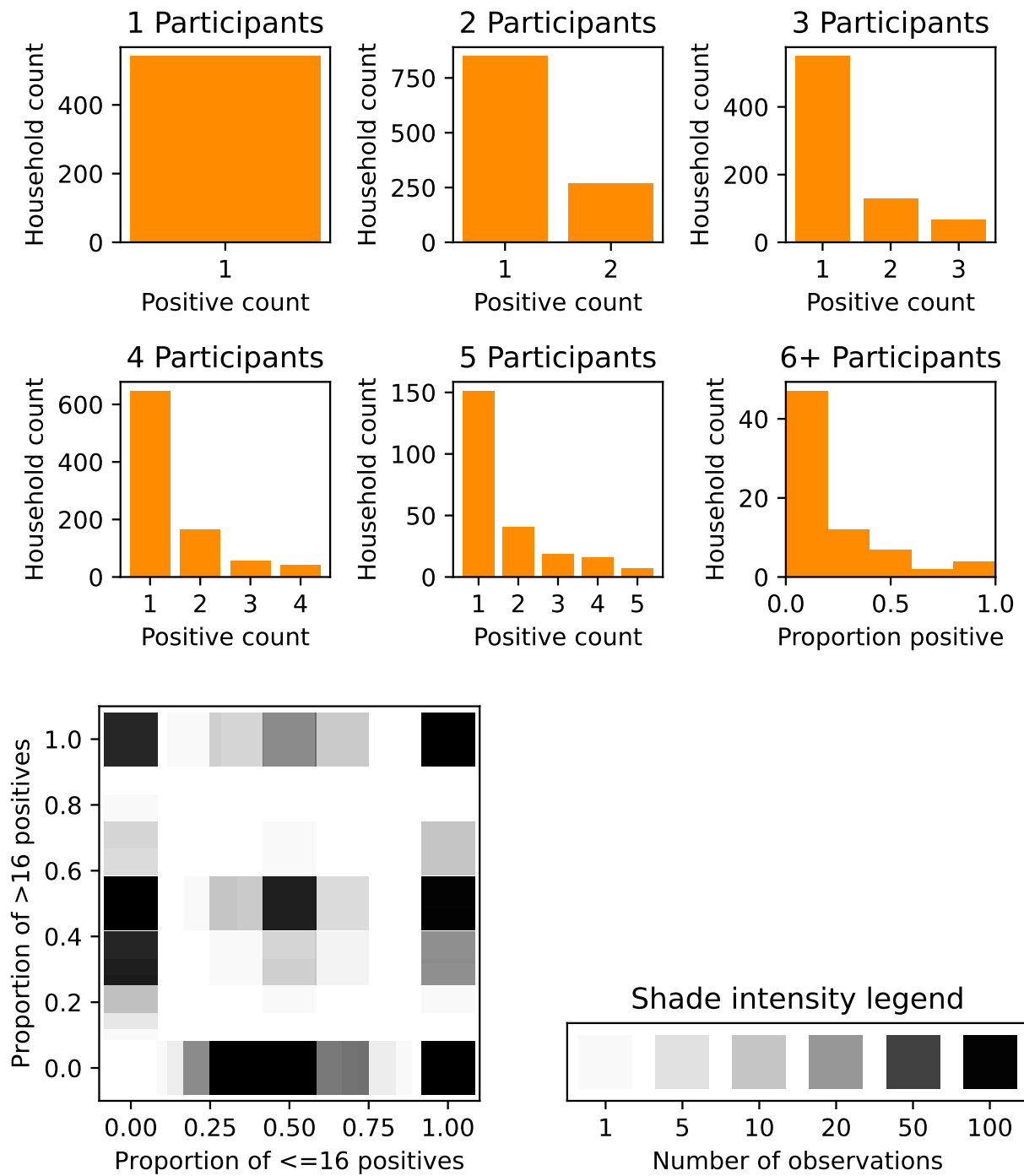


Figure 1: Top: histogram and Bottom: density plot for Tranche 8 data

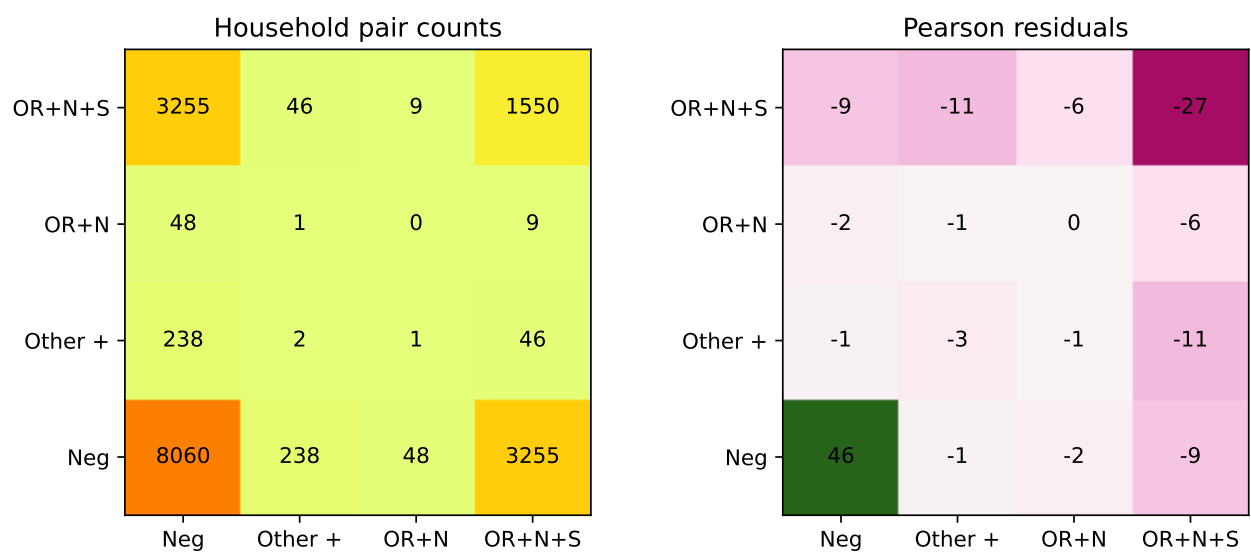


Figure 2: Left: pair count and Right: Pearson residual plots for Tranche 8 data

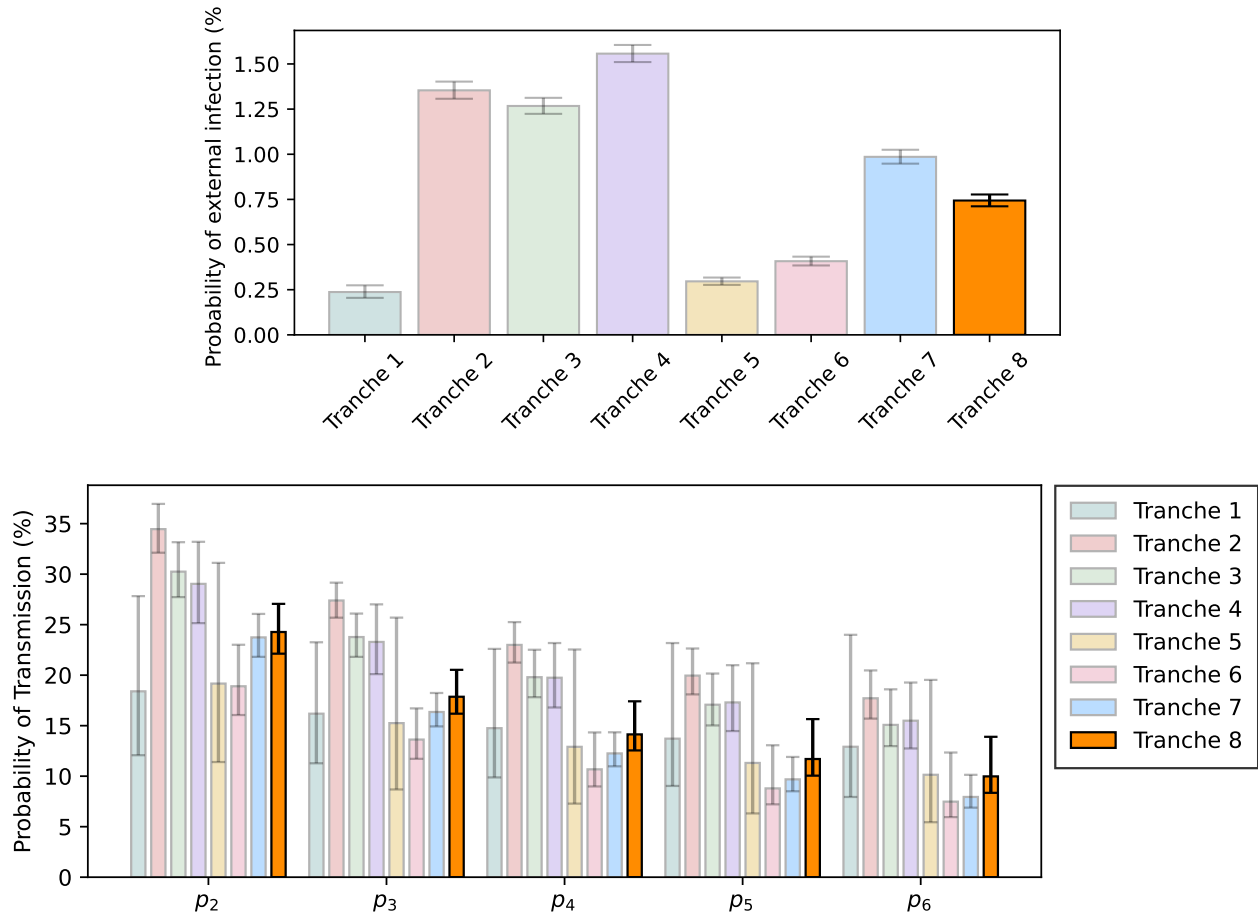


Figure 3: Visualisation of the fitted model. Top: Baseline probability of infection from outside. Bottom: Per-pair baseline probabilities of secondary transmission within the household, not including tertiary transmission effects.

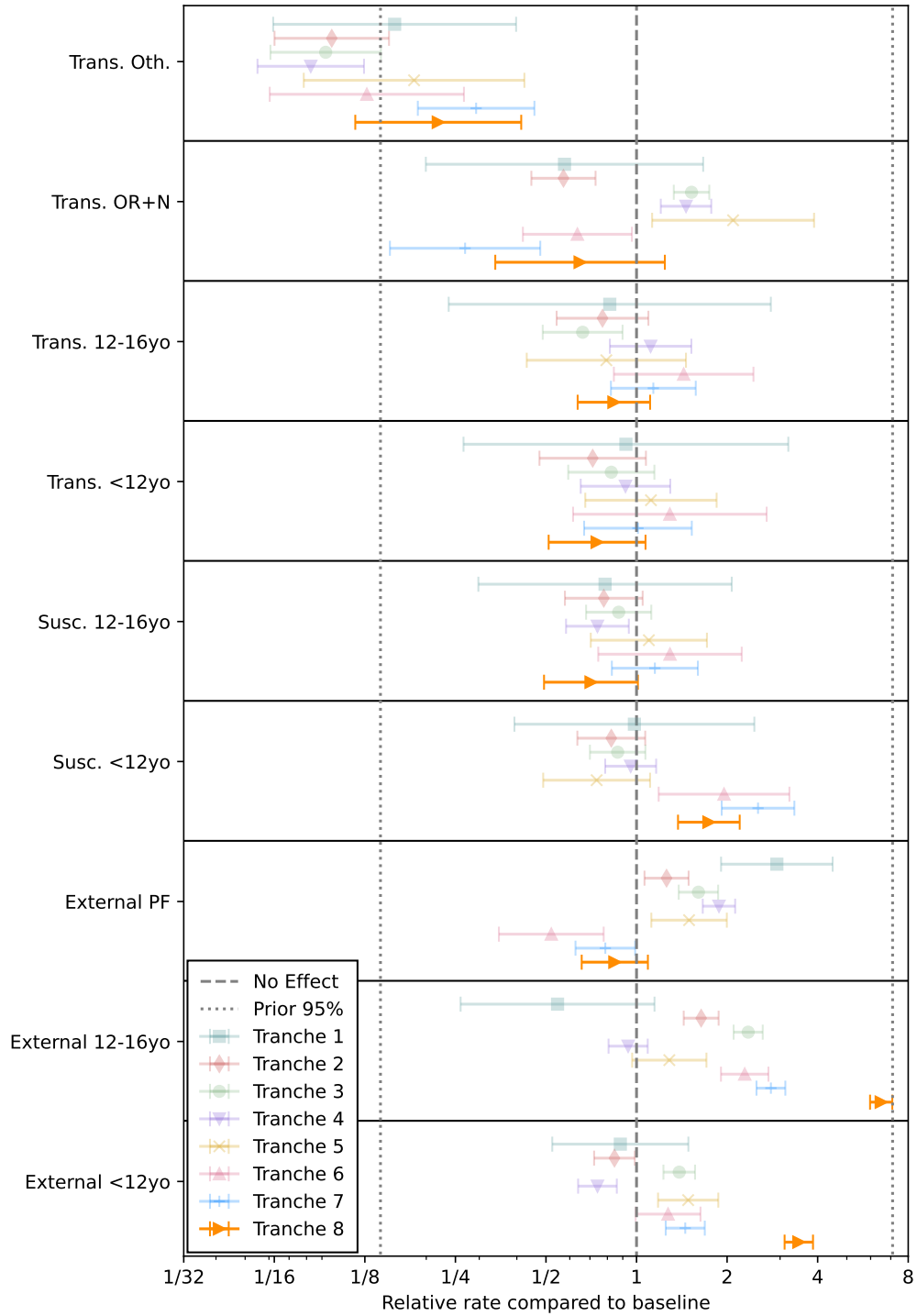


Figure 4: Visualisation of the fitted model. Relative effects on transmission, susceptibility and external exposure compared to baseline of an adult not working in a patient-facing role with OR+N+S maximal PCR gene positivity pattern if positive. ‘Trans.’ stands for relative transmissibility, ‘Susc.’ for relative susceptibility, and ‘External’ for relative external exposure.

								Tranche 8
$1 - q$								0.744 (0.712,0.777) %
p_2								24.3 (22.1,27.1) %
p_3								17.9 (16.2,20.5) %
p_4								14.1 (12.5,17.4) %
p_5								11.7 (10.1,15.6) %
p_6								9.98 (8.35,13.9) %
$\exp(\alpha_{2-11})$								3.46 (3.11,3.86)
$\exp(\alpha_{12-16})$								6.5 (5.97,7.08)
$\exp(\alpha_{\text{PF}})$								0.847 (0.657,1.09)
$\exp(\beta_{2-11})$								1.74 (1.37,2.2)
$\exp(\beta_{12-16})$								0.706 (0.493,1.01)
$\exp(\gamma_{2-11})$								0.739 (0.51,1.07)
$\exp(\gamma_{12-16})$								0.841 (0.637,1.11)
$\exp(\gamma_{\text{OR+N}})$								0.649 (0.339,1.24)
$\exp(\gamma_{\text{CT-oth}})$								0.219 (0.116,0.414)

Table 2: Tranche 8 parameter point estimates and CIs.