

Inferring Risks of Coronavirus Transmission from Community Household Data: Tranche 9 Update

Thomas House Heather Riley Lorenzo Pellis Koen B. Pouwels
Sebastian Bacon Arturas Eidukas Kaveh Jahanshahi
Rosalind M. Eggo A. Sarah Walker

Headline results

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

- **Tranche 9:** 15 October 2021 to 3 December 2021; high prevalence; schools open; Delta variant dominant; over 50 million first, 46 million second and 19 million third 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.

These results continue the previously seen patterns of elevated external infection risk for children of school age, and reduced risk for those working in patient-facing roles, which is consistent with the expected impact of vaccination policy. More difficult to interpret is that less reduction in transmission is now associated with PCR gene positivity pattern, and more is associated with being in the 12-16 age group. This would be consistent with the hypothesis that there is some reduction of transmission from children, which is mainly mediated via viral load, but testing this hypothesis requires additional analysis.

								Tranche 9	All
Number of participants								351092	447983
Number of households								183719	221181
Number of positive individuals								6817	40938
Households with 1+ positive								5107	29616
Children <12								23900	35252
Children 12–16								19708	24669
OR+N+S positives								6373	25482
OR+N positives								144	9463
Patient-facing participants								11626	17358

Table 1: Tranche 9 sample properties.

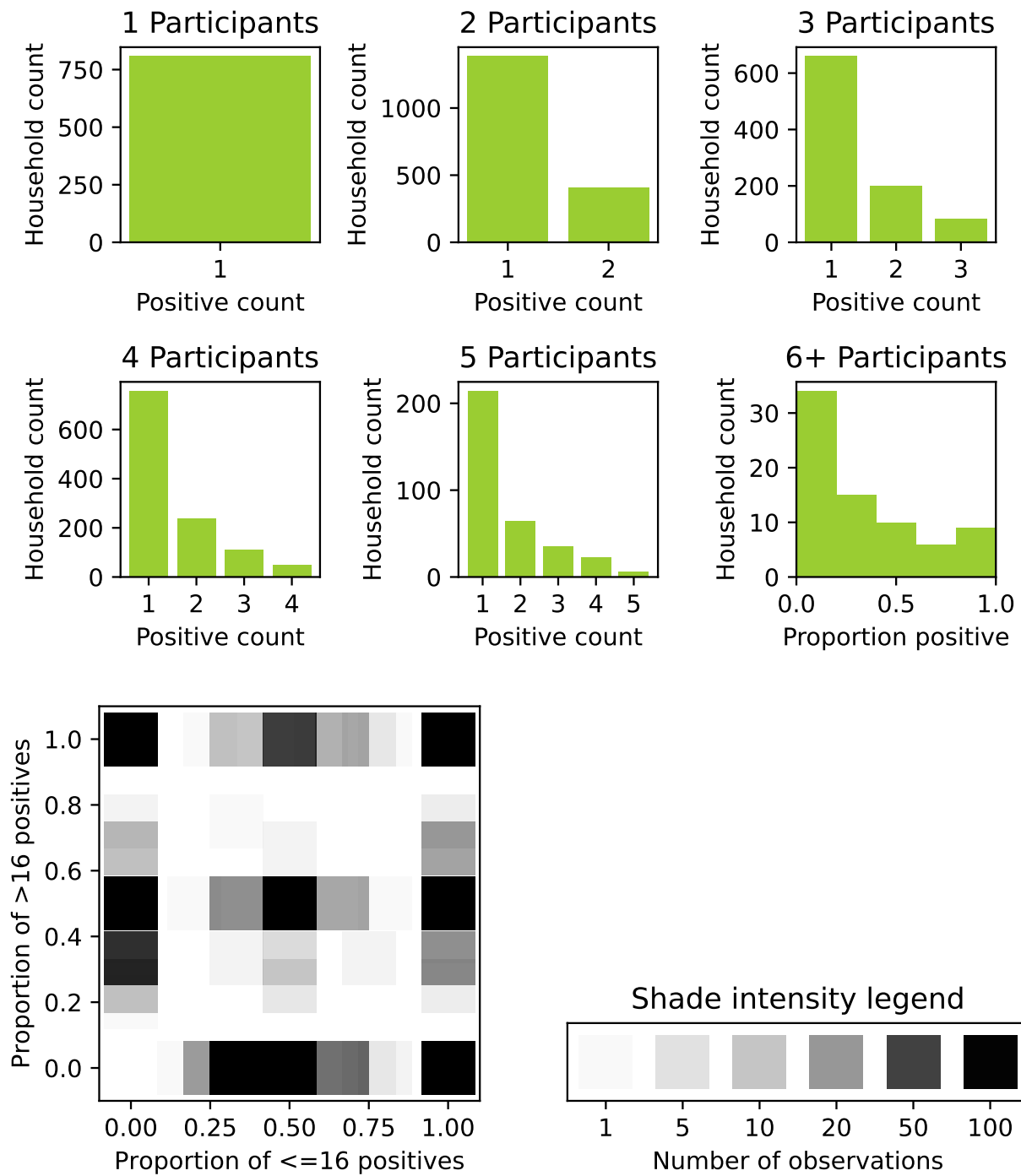


Figure 1: Top: histogram and Bottom: density plot for Tranche 9 data

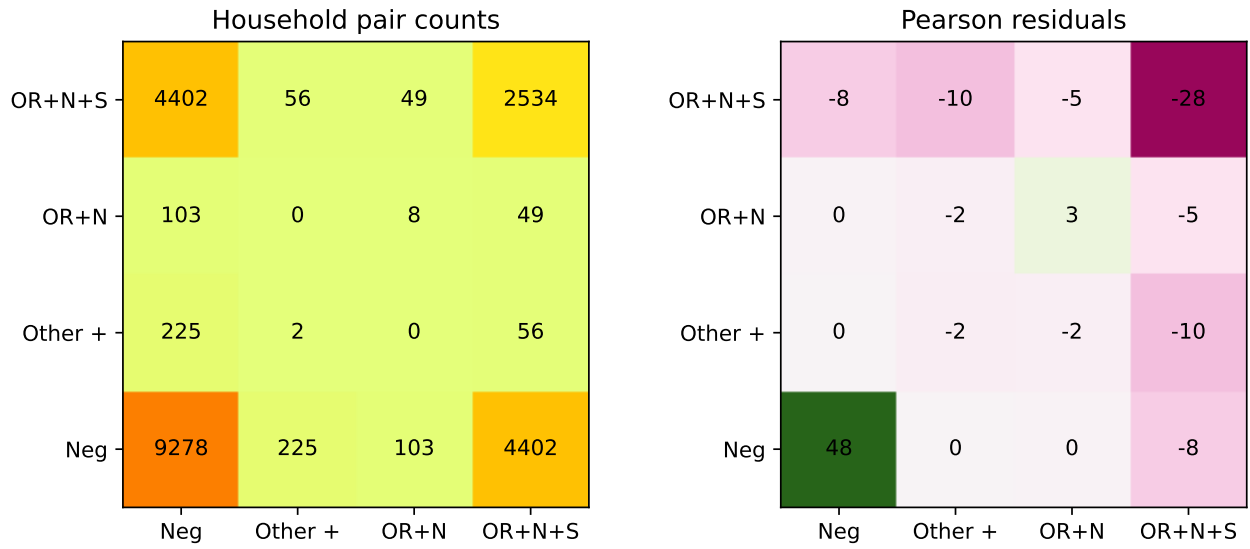


Figure 2: Left: pair count and Right: Pearson residual plots for Tranche 9 data

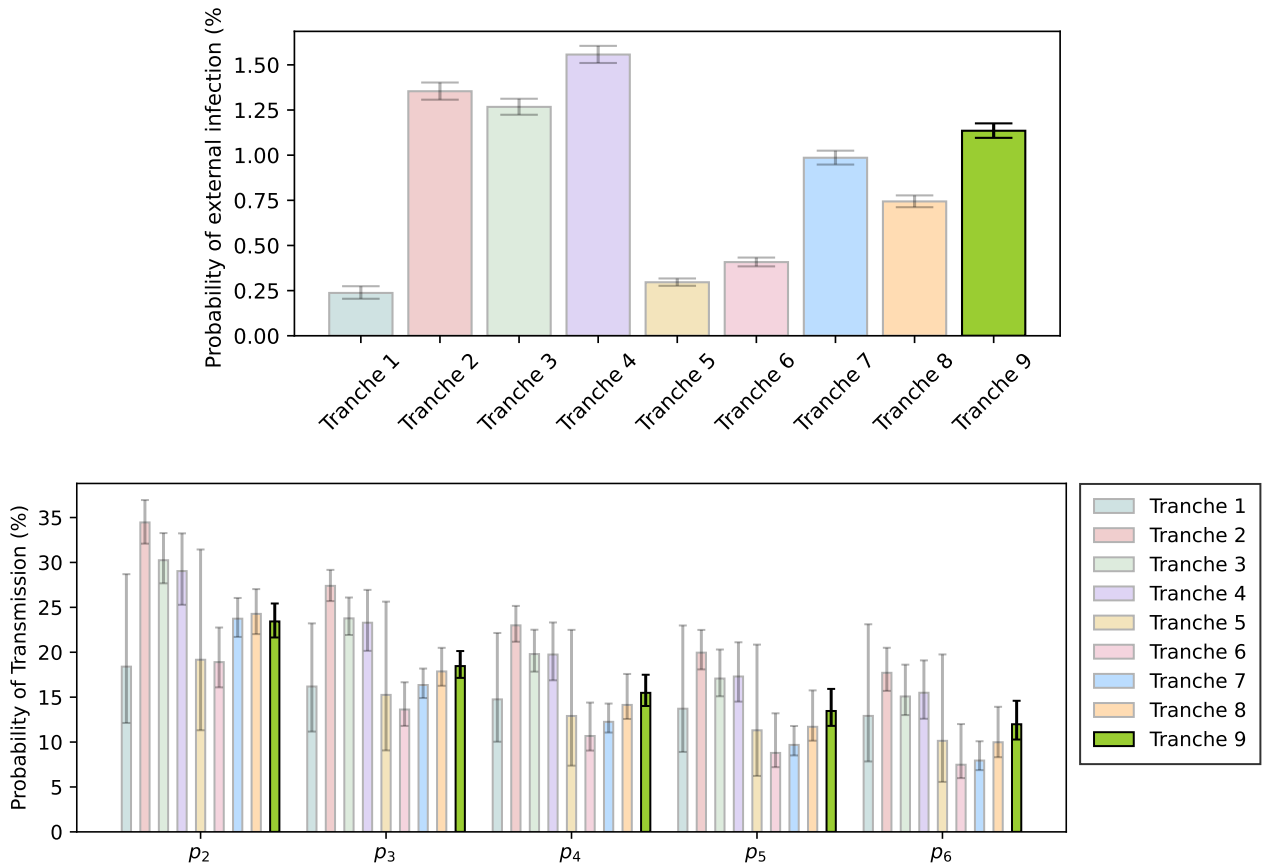


Figure 3: Visualisation of the fitted model. Top: Baseline probability of infection from outside. Bottom: Per-pair baseline probabilities of secondary transmission within the household, not including tertiary transmission effects.

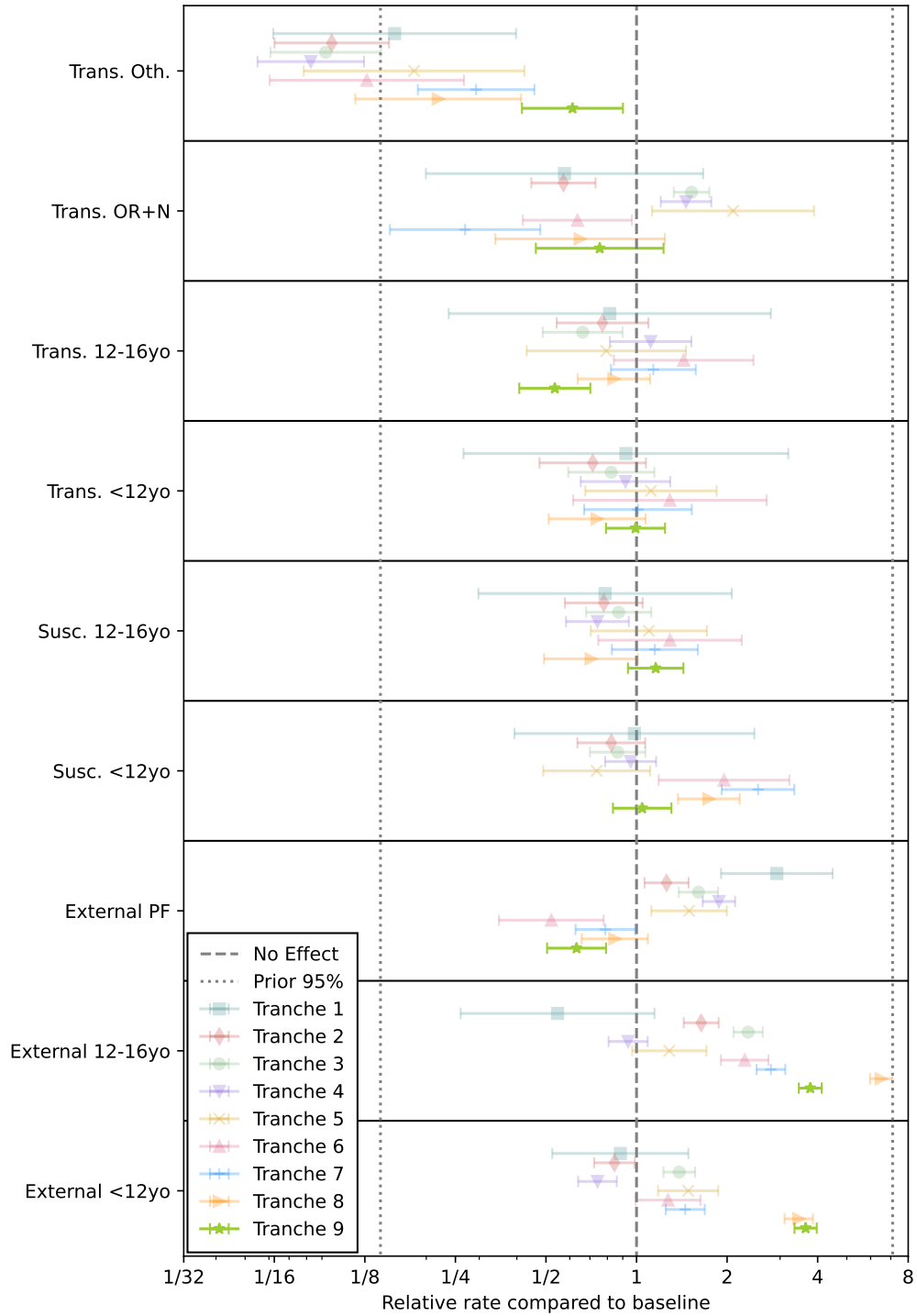


Figure 4: Visualisation of the fitted model. Relative effects on transmission, susceptibility and external exposure compared to baseline of an adult not working in a patient-facing role with OR+N+S maximal PCR gene positivity pattern if positive. ‘Trans.’ stands for relative transmissibility, ‘Susc.’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

								Tranche 9
$1 - q$								1.14 (1.1,1.18) %
p_2								23.4 (21.6,25.4) %
p_3								18.5 (17.1,20.1) %
p_4								15.5 (14.0,17.5) %
p_5								13.5 (11.8,15.9) %
p_6								12.0 (10.3,14.6) %
$\exp(\alpha_{2-11})$								3.65 (3.35,3.97)
$\exp(\alpha_{12-16})$								3.78 (3.46,4.13)
$\exp(\alpha_{PF})$								0.632 (0.504,0.792)
$\exp(\beta_{2-11})$								1.04 (0.835,1.31)
$\exp(\beta_{12-16})$								1.16 (0.937,1.43)
$\exp(\gamma_{2-11})$								0.992 (0.792,1.24)
$\exp(\gamma_{12-16})$								0.535 (0.408,0.702)
$\exp(\gamma_{OR+N})$								0.754 (0.463,1.23)
$\exp(\gamma_{CT-oth})$								0.612 (0.416,0.901)

Table 2: Tranche 9 parameter point estimates and CIs.