

# SARS-CoV2 qPCR positivity (%)

Environmental swabs, binomial GLMM tensor spline fit  
 $\text{brm}(\text{SARS.CoV.2.qPCR.positive} \mid \text{trials}(\text{nsamples}) \sim (1 \mid \text{stall}) + \text{t2}(x, y, \text{by}=\text{Sample.type}), \text{family}=\text{binomial}(\text{logit}))$

