# D GOODNESS OF FIT OF MIXED EFFECTS MODELS

Figure D1 provides two graphical displays of the goodness of the model fit: the quantile-quantile plot of the standardized estimated random effects compared to a normal distribution and the plot of residuals; both are shown for the risk difference (identity link) model, but are similar for the odds ratio (logit link) model.

These figures suggest violations of the model assumptions, including potential non-normality of the random effects. The Mahalanobis distance from the estimated random effects to the normal distribution,[59] however, is not significant at the 0.05 level. Common goodness-of-fit tests applied to this distribution, such as the Kolmogorov-Smirnov, Anderson-Darling, and Cramér-von Mises tests,[60] also yield non-significant results (all with p-values above 0.65). The power of these tests to detect violations of the assumptions with a small number of clusters can be quite low, however.[61]
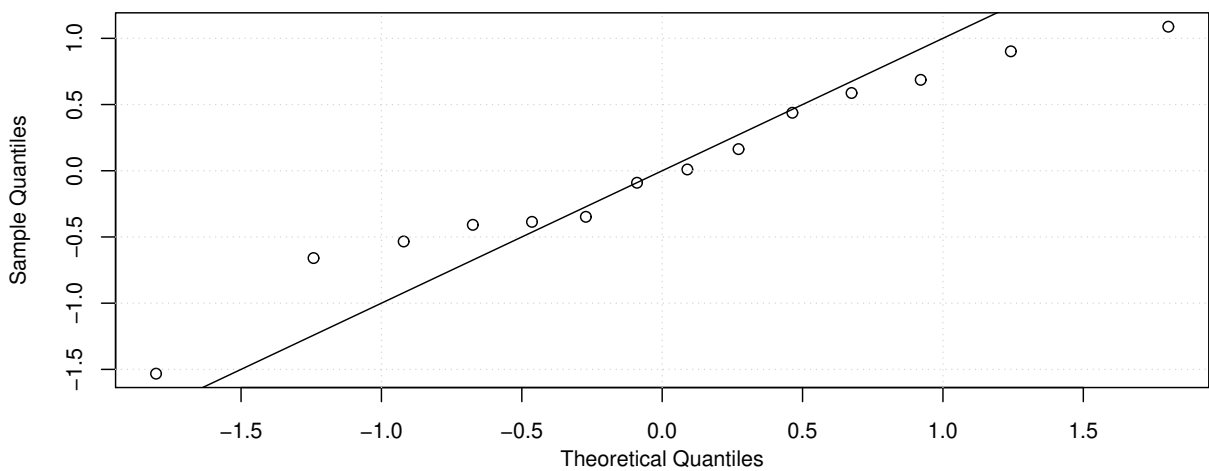
(a) Quantile–Quantile Plot of the Standardized Estimated Random Effects for the Mixed Effects Model with an Identity Link vs. Standard Normal Distribution
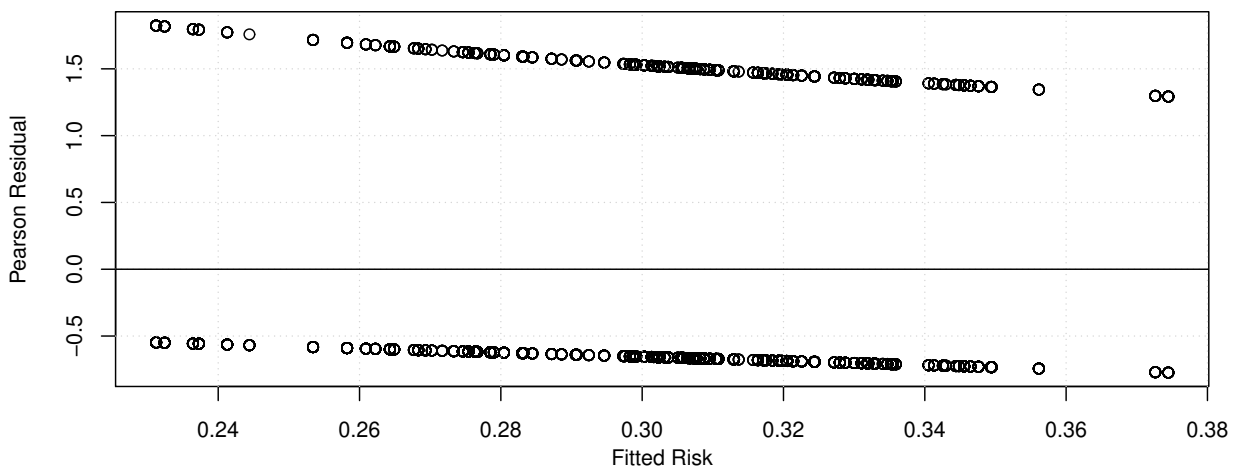
(b) Pearson Residuals vs. Fitted Risk Values for the Mixed Effects Model with an Identity Link

FIGURE D1 Diagnostics for Mixed Effects Models for Tuberculosis SW-CRT