



Figure 4: Comparison between NUTS and our samplers for SIR model with diagonal metric adaptation (tuned by `Rstan`'s default setting): The x-axis in each plot corresponds to the desired accept probability δ of the primal-dual averaging algorithm. In the first row, y-axis is the ESS per gradient for the parameters $(\beta, \gamma, \xi, \phi)$. ESS of samples of NUTS, eHMC, eHMCq and eHMCu is estimated by `effectiveSize` of R package `coda`.