Individual-level models (ILMs), fitted in a Bayesian MCMC framework, are a class of discrete time models used to model the spread of infectious diseases. They can account for spatial and temporal disease dynamics by modelling the infectious pressure exerted by infected individuals of a population on each susceptible individual. Unfortunately, for large populations, quantifying this infectious pressure can be computationally burdensome leading to a time-consuming likelihood calculation. Here, we introduce sampling methods in order to estimate the infectious pressure on each susceptible and, thus, speed-up the likelihood calculation.