

Gastrointestinal disease simulation

The health component of the megadapt model is implemented as two separate regression models that simulate the expected number of incidences of gastrointestinal diseases in the lowland and in the highlands of Mexico City. The two models simulate incidences in the lowland and in the highlands of Mexico City.

For the lowlands, a regression model of the form

$$g_{jT} = \rho W G_T + \beta f_{jT} + \varepsilon_j \quad (14)$$

was used to incorporate the full set of predictors and the spatial dependency observed in the data. G_T is an $J \times 1$ vector of observations of the dependent variable, with one observation for every census-block, f_{jT} is the number of flooding in census-block j , β is a parameter that relates the number of flooding to the risk of gastrointestinal diseases. ε_j is a $J \times 1$ vector of disturbance terms, where ε_j is assumed to be independently and identically distributed for all j , with zero mean and variance σ^2 . This regression is spatial because it captures the spatial dependency observed in the incidence data (*Baeza et al. In review*). The model thus incorporates an additional regressor in the form of a spatially lagged variable, $W G_T$ (Anselin, 2001). This variable captures cross-section dependencies, in which exist a covariance structure in different locations derives from the geographic space (Anselin 1998, Anselin, 2001). The term ρ is the unknown spatial lag coefficient, and W is the $J \times J$ contiguity matrix. For this implementation of Megadapt dynamics model we assumed that $\rho W G_T \sim \rho W G_{T-1}$. This assumption is based on the A new model will be required to calculate a temporal regression.