

S6 Text. Boosted Regression Trees (BRTs)

Boosted Regression Trees (BRTs) are particularly effective for mapping mosquito distribution and mosquito-borne diseases due to their ability to model complex, non-linear relationships between predictors [1–3]. These models iteratively refine regression trees using gradient boosting, minimizing the unexplained variation in the response variable with each new tree.

BRTs were fitted using the `gbm.step()` function from the `dismo` package in R version 4.0, with default hyperparameters (tree complexity = 4, learning rate = 0.005, bag fraction = 0.75, step size = 10, and cross-validation folds = 10).[4,5] Each model underwent ten-fold cross-validation, where the dataset was divided into ten subsets. Nine subsets were used for training, and predictive accuracy was assessed on the remaining data based on predictive deviance. A total of 100 cross-validated models were fitted, and the mean of these models was calculated to account for variability.

The trained BRT model was then used to project *Ae. aegypti* occurrence probability at a 5 km² resolution. Population projections and urban accessibility data were adjusted to estimate occurrence probabilities across different time periods and SSPs, with all covariates extracted at a 5 km² resolution. For future projections, climatic variables were not used to estimate *Ae. aegypti* occurrence probability; instead, temperature was fixed at 26°C to isolate the effects of anthropogenic variables. This allowed the BRT model to assess the impact of human-driven factors on mosquito distribution, while temperature-induced changes in *Ae. aegypti* density were already accounted for in the life-history model.

References

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