Forecasting infectious disease epidemics via weighted density ensembles

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Accurate and reliable predictions of infectious disease dynamics can be valuable to public health organizations that plan interventions to decrease or prevent disease transmission. Generally seen as the most robust type of predictive models, ensemble-based methodologies combine outputs from individual models to create a combined prediction for a target of interest. We have implemented ensemble methods that form a predictive density for a target of interest as a weighted sum of the predictive densities from component models. In the simplest case, equal weight is assigned to each component model; in more complex cases, the weights can vary with the location, prediction target, week of the season when the predictions are made, a measure of component model uncertainty, recent observations of disease incidence, and other observed covariates.

In this talk, I will describe the methods used to estimate the component model weights for these weighted density ensembles. For simple settings we use the degenerate EM algorithm, and in more complex settings we use gradient tree boosting to estimate penalized weights as functions of covariates. Additionally, I will describe our evaluation of these methods in two applications of forecasting influenza in the US. In one application, we combined 21 models from 4 different research groups to create real-time ensemble forecasts of influenza in the US in the 2017/2018 winter flu season.