A Comparison of Infectious Disease Forecasting Combinations Methods

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Forecast combinations have prospered remarkably in recent years, being very useful for predicting the evolution of infectious diseases such as the flu or Covid-19, among many others. Within the framework of the Covid-19 pandemic and at the initiative of the Spanish Mathematics Committee (CEMat), a web tool was developed to show the evolution of indicators of interest in the pandemic together with short-term daily predictions of them (ForeCoop project, https://covid19.citic.udc.es). The predictions were actually cooperative predictions (meta-predictions), since they were built by combining predictions submitted by a wide range of research groups from all over Spain. Following these ideas, this work will try to compare ForeCoop implementation with other procedures available in R packages such as ForecastComb, Opera, ForecastCombinations and ForecastHybrid. Different multivariate and functional regression models will be used as individual predictors, trying to improve the accuracy of the predictions by integrating information collected from different sources (surveillance services, IoT platforms, social networks,...) and with different temporal or spatial level aggregation (day/week, region/country, other). Finally, aspects such as the automation of the process, CPU time, evaluation metrics, the difficulties inherent to the process and some conclusions about the usefulness of the work developed will be discussed.

Keywords: Forecast combinations, infectious diseases.