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| **Keywords:** | Infectious disease prediction, deep neural network, artificial neural network, long short-term memory, deep learning, social media big data |
| **Abstract:** | Infectious disease trends are variable and means prediction is not easy. This article predicts infectious diseases outbreak by optimizing the parameters of deep learning algorithms, considering big data including social media data. The performance of the deep neural network (DNN) and long-short term memory (LSTM) learning models were compared with the autoregressive integrated moving average (ARIMA) when predicting three infectious diseases one week into the future. The results show that the DNN and LSTM models perform better than ARIMA. When predicting chickenpox, the top-10 DNN and LSTM models improved average performance by 24% and 19%, respectively. The DNN model performed stably and the LSTM model was more accurate when infectious disease was spreading.We believe that these findings can help eliminate reporting delays in existing surveillance systems and minimize costs to society. |

**Introduction:**

Infectious disease occurs when a person is infected by a pathogen from another person or an animal. It not only harms individuals, but also causes harm on a macro scale and, therefore, is regarded as a social problem [[1](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B1-ijerph-15-01596)].

Infectious disease surveillance is a comprehensive process in which information on infectious disease outbreaks and vectors are continuously and systematically collected, analyzed, and interpreted. Moreover, the results are distributed quickly to people who need them to prevent and control infectious disease.

In the conventional reporting system, some medical organizations’ infectious disease reports are incomplete and delays can occur in the reporting system. For instance, in the traditional influenza surveillance system, around two weeks elapses between when a report is made and when it is disseminated [[2](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B2-ijerph-15-01596)].

In medical organizations using the conventional infectious disease reporting system, a large number of missing and delayed reports can occur, which hinders a prompt response to infectious disease. As such, it is necessary to create a data-based infectious disease prediction model to handle situations in real time. Furthermore, if this model can understand the extent of infectious disease trends, the costs to society from infectious disease can be minimized. In medical organizations using the conventional infectious disease reporting system, a large number of missing and delayed reports can occur, which hinders a prompt response to infectious disease. As such, it is necessary to create a data-based infectious disease prediction model to handle situations in real time. Furthermore, if this model can understand the extent of infectious disease trends, the costs to society from infectious disease can be minimized.

An increasing number of researchers recognize these facts and are performing data-based infectious disease surveillance studies to supplement existing systems and design new models [[3](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B3-ijerph-15-01596),[4](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B4-ijerph-15-01596),[5](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B5-ijerph-15-01596),[6](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B6-ijerph-15-01596),[7](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B7-ijerph-15-01596),[8](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B8-ijerph-15-01596),[9](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B9-ijerph-15-01596)]. Among these, studies are currently being performed on detecting infectious disease using big data such as Internet search queries [[10](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B10-ijerph-15-01596),[11](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B11-ijerph-15-01596),[12](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B12-ijerph-15-01596),[13](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B13-ijerph-15-01596),[14](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B14-ijerph-15-01596),[15](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B15-ijerph-15-01596)]. The Internet search data can be gathered and processed at a speed that is close to real time. According to Towers et al., Internet search data can create surveillance data faster than conventional surveillance systems [[16](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B16-ijerph-15-01596)]. For example, when Huang et al. predicted hand, foot, and mouth disease using the generalized additive model (GAM), the model that included search query data obtained the best results. As such, it has been reported that new big data surveillance tools have the advantage of being easy to access and can identify infectious disease trends before official organizations [[17](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B17-ijerph-15-01596)]. In addition to Internet search data, social media big data is also being considered. Tenkanen et al. report that social media big data is relatively easy to collect and can be used freely, which means accessibility is satisfactory and the data is created continuously in real time with rich content [[18](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B18-ijerph-15-01596)]. As such, studies have used Twitter data to predict the occurrences of mental illness [[19](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B19-ijerph-15-01596)] and infectious disease [[20](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B20-ijerph-15-01596),[21](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B21-ijerph-15-01596),[22](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B22-ijerph-15-01596),[23](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B23-ijerph-15-01596)] in addition to predictions in a variety of other scientific fields [[24](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B24-ijerph-15-01596),[25](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B25-ijerph-15-01596),[26](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B26-ijerph-15-01596),[27](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B27-ijerph-15-01596)]. In particular, a study by Shin et al. reported that infectious diseases and Twitter data are highly correlated. There is the possibility of using digital surveillance systems to monitor infectious disease in the future [[20](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B20-ijerph-15-01596)]. When these points are considered, using search query data and social media big data should have a positive effect on infectious disease predictions.

In addition to these studies, there are also studies that have used techniques from the field of deep learning to predict infectious disease [[22](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B22-ijerph-15-01596),[23](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B23-ijerph-15-01596),[28](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B28-ijerph-15-01596),[29](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B29-ijerph-15-01596)]. Deep learning is an analysis method and, like big data, it is being actively used in a variety of fields [[30](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B30-ijerph-15-01596)]. Deep learning yields satisfactory results when it is used to perform tasks that are difficult for conventional analysis methods [[31](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B31-ijerph-15-01596),[32](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B32-ijerph-15-01596),[33](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B33-ijerph-15-01596)]. In a study by Xu et al., a model that used deep learning yielded better prediction performance than the generalized linear model (GLM), the least absolute shrinkage and selection operator (LASSO) model, and the autoregressive integrated moving average (ARIMA) model [[28](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B28-ijerph-15-01596)]. As such, methods of predicting infectious disease that use deep learning are helpful for designing effective models.

There are also examples of infectious disease prediction based on environmental factors such as weather [[34](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B34-ijerph-15-01596),[35](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B35-ijerph-15-01596),[36](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B36-ijerph-15-01596),[37](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B37-ijerph-15-01596)]. Previous studies have confirmed that weather data comprises a factor that has a great influence on the occurrence of infectious diseases [[38](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B38-ijerph-15-01596),[39](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B39-ijerph-15-01596),[40](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B40-ijerph-15-01596)]. Liang et al. showed that rainfall and humidity are risk factors for a hemorrhagic fever with a renal syndrome [[41](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B41-ijerph-15-01596)]. In addition, a study by Huang et al. reported that trends in dengue fever show a strong correlation with temperature and humidity [[42](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6121625/#B42-ijerph-15-01596)]. Previous studies indicate that infectious disease can be predicted more effectively if weather variables, Internet big data, and deep learning are used.

**Conclusion:**

Infectious disease is a social problem in that it can cause not only personal damage but also widespread harm. For this reason, research is being conducted to minimize social losses by predicting the spread of infectious diseases. The aim of this study was to design an infectious disease prediction model that is more suitable than existing models by using various input variables and deep learning techniques. Therefore, in this study, the optimal parameters were set using a variable selection method based on OLS. The relationship between actual instances of disease occurrence and the Internet search query data tends to have a time lag, which means a lag was added to each infectious disease’s dataset to find the future trend. Next, an analysis of ARIMA, DNN, and LSTM was performed with optimal parameters.

The results of OLS analysis using optimal parameters showed that the regression models for each infectious disease had significant results. Of the four input variables, the Naver search frequency had a significant relationship with all three infectious diseases. The performance of the OLS and ARIMA analysis was used to evaluate the deep learning models. Looking at the results for DNN and LSTM, both the deep learning models made much better predictions than the OLS and ARIMA models for all infectious diseases. Moreover, the DNN models had the best performance on average, but the LSTM models made more accurate predictions when infectious diseases were spreading. However, in the case of malaria, there were few occurrences of the disease compared to other infectious diseases, which means the predictions were not comparatively accurate.

This study was also able to reveal special characteristics of the DNN and LSTM models. The DNN model produced smaller values than the LSTM model on average when predicting infectious diseases. Suitable predictions can be made using the DNN model when predicting the minimum value for disease occurrence and using the LSTM model when predicting the maximum value.

## Supplementary Materials:

The following are available online at <http://www.mdpi.com/1660-4601/15/8/1596/s1>, Table S1: The root mean squared error (RMSE) and prediction graphs of top 10 deep neural network (DNN) and long-short term memory (LSTM) models for chickenpox. The seasonal autoregressive integrated moving average (ARIMA) model is denoted as ARIMA(p, d, q)(P, D, Q)S. where p is the order of the autoregressive part, d is the order of the differencing, q is the order of the moving-average process, and S is the length of the seasonal cycle. (P, D, Q) is the seasonal part of the model. The numbers in parentheses indicate each deep learning model’s optimizer, activation, and number of epochs, respectively. (optimizer) 1: Adadelta, 2: Adagrad, 3: Adam, 4: Adamax, 5: Nadam, 6: RMSProp, and 7: SGD, (activation function) 1: ELU, 2: ReLU, 3: SELU, and 4: SoftPlus, (number of epochs) 1: 400, 2: 600, 3: 800, and 4: 1000, Table S2: The RMSE and prediction graphs of the top 10 DNN and LSTM models for scarlet fever, Table S3: The RMSE and prediction graphs of top 10 DNN and LSTM models for malaria.

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