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ATOMIC : A graph attention neural network for ATOpy dermatitis prediction on human gut MICrobiome

Hyunsu Bong[1], Songhyeon Kim[1], Young Her[2], Joonhong Min[3], and Minji Jeon[1,4,5*]

[1]Department of Medicine, Korea University College of Medicine
[2]Department of Dermatology, School of Medicine, Kangwon National University
[3]Department of Dermatology, Kangwon National University Hospital, Kangwon National University College of Medicine
[4]Department of Biomedical Informatics, Korea University College of Medicine
[5]Biomedical Research Center, Korea University Anam Hospital
**Corresponding author: mjjeon@korea.ac.kr*

Atopic dermatitis (AD) is a common chronic allergic disease characterized by intense itching and eczema. AD is known to be influenced by genetics, various environmental factors, and particularly alterations in the gut microbiome. Recent advances in metagenomic sequencing technology have led to an increase in the number of studies that have identified a link between the gut microbiome and AD. However, due to the diverse types, distributions, and complex correlations of microbiomes, it is challenging to fully understand the patterns in microbiome data using existing statistical methods. Therefore, it is necessary to develop deep learning models that can effectively consider and analyze these relationships and diagnose diseases.

A lot of machine learning and deep learning research has been proposed to diagnose diseases based on microbiome. However, existing studies do not fully account for the interactions between microbes. Moreover, most studies utilize benchmark datasets, and lack disease-specific models, especially for AD and they do not use clinical information. Therefore, it is necessary to develop a new model that utilizes large-scale microbiome data specific to AD, accounts for complex interactions between microbes, and utilizes real-world clinical information.

In this study, we proposed a graph attention model called ATOMIC that predicts AD using large-scale microbiome data. We collected and preprocessed publicly available AD microbiome data. ATOMIC is pre-trained on the large-scale multinational microbiome abundance data. In the process, graphs were constructed to account for correlation between microbes. Afterwards, it is fine-tuned on the additional microbiome data and clinical information collected at Kangwon National University Hospital. Our model demonstrates superior performance compared to existing models that utilize

machine learning and deep learning techniques. The results show that our model can identify the key microbes that contribute to AD and elucidate the relationships between the microbes.