Multimodal artificial intelligence measuring skeletal muscle index from combined chest X-ray and clnical metadata.

Primary Researcher: Kosuke Kita
Doctoral Course Student, Osaka University
Co-researchers: Yu Moriguchi
Project Lecturer, Osaka University

・Introduction

Sarcopenia is a condition characterized by the progressive loss of skeletal muscle mass, strength, and function. It is commonly associated with aging, but can also be influenced by other factors such as physical inactivity, poor nutrition, and certain chronic diseases. According to Asian Working Group 2019 guideline, height-adjusted muscle mass has been adopted as one of the indicators to diagnose sarcopenia. Specifically skeletal muscle mass index (SMI) has been used as height-adjusted muscle mass, which is the appendicular skeletal muscle mass divided by the square of the height. DXA (Dual-energy X-ray Absorptiometry) and bioimpedance analyses are recommended as a tool measuring muscle mass in the guideline. Although DXA is more reliable tool than bioimpedance in terms of accuracy, patients do not have easy access to DXA due to the limited number of hospitals where it has been implemented. Considering this limited access to DXA, more convenient and accurate tool for measuring muscle mass is expected. We aim to develop an artificial intelligence that measures muscle mass from blood test, and chest X-ray images, which are commonly examined in hospitals.

・Methods

Data of participants who visited health check clinic at Japan Community Heath care Organization Osaka Hospital, Osaka, Japan, between January 2016 and June 2023 were used as split to train set and test set (80:20). We established a multi modal model combining a convolutional neural network (CNN) model and a gradient boosting decision tree (GBDT) model. A CNN model was trained to predict muscle mass each appendicular muscle mass and bone mineral density from chest X-ray images; then a GBDT model was trained to predict SMI from the integrated feature which combined blood test data, patient information, and the feature from chest X-ray images extracted through the CNN. We evaluated our model's performance with five-fold cross validation. We revealed important predictors of SMI among the integrated feature processed by GBDT based on SHapley Additive exPlanations (SHAP) values, which represents each features' importance. We used DXA to measure targeted SMI.

・Results

Mean age of the collected dataset (n = 3295; women n = 968, 29.3%; low muscle mass n = 991, 30.1%; average height = 1.65 ± 0.09 m) was 61.9 years. In the test set (n = 628) the pearson correlation coefficient for SMI prediction was 0.91 with an average difference of 0.40 ± 0.09 kg/m^2. The accuracy for predicting low or normal SMI calculated based on a guideline threshold was 0.84. Among the GBDT model features, body mass index, creatinine, and muscle mass in left leg are the most important predictors of SMI.

・Discussion and Conclusion

The average difference between targeted and predicted SMI was 0.40 ± 0.09 kg/m^2. Considering the average height was 1.65 ± 0.09 m, the average difference in appendicular skeletal muscle mass was 1.09 ± 0.39 kg. A past study comparing DXA and bioimpedance analysis has reported that the bioimpedance overestimated appendicular skeletal muscle mass by 1.97kg, which means our multimodal model is supposed to outperform the bioimpedance analysis. Our chest X-ray and blood test based multimodal model improved measuring appendicular skeletal muscle mass, which merits further investigation.