Abstract

Metabolism describes the set of all enzyme-catalyzed reactions that transform nutrients into molecules that support biological function. Stable-isotope tracing is a method of measuring intracellular metabolic pathway utilization (metabolic flux) by feeding a tracer nutrient consisting of a heavy isotope into a cellular system and tracking the subsequent downstream pathway utilization. In this study, we present a novel deep-learning model that predicts metabolic fluxes in the form of relative isotopologue abundances from bulk unlabeled metabolomics data. Our model was trained on a large dataset of stable-isotope tracing experiments using MALDI-MSI and is able to accurately predict the proportions of isotopologue counts in the absence of labeled tracers. By leveraging the power of deep learning, our model is able to capture complex relationships between metabolites and predict isotope tracing data with state-of-the-art accuracy. We demonstrate the effectiveness of our approach by comparing our model's predictions to those obtained through traditional stable-isotope tracing experiments. Our method has the potential to revolutionize the field of metabolomics by providing both a cost-effective and time-effective alternative to traditional stable-isotope tracing methods for predicting metabolic fluxes.