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Contribution - Predicting OCT biological marker localization from weak annotations

Javier Gamazo Tejero

ARTORG Center for Biomedical Engineering Research - AIMI

Javier.gamazo-tejero@artorg.unibe.ch

Abstract

Optical Coherence Tomography (OCT) plays a critical role in diagnosis and managing chronic eye conditions such as Age-Related Macular Degeneration and Diabetic Retinopathy, as it is well known that a number of biological markers present in OCT scans correlate to these chronic conditions. As the world's aging population continues to grow and, with it, the number of patients that suffer from such diseases increases over time, the necessity to automatically identify if and where markers are located in scans is becoming paramount. Here, we propose a simple approach that only requires OCT slice-wise binary marker annotations to train, instead of approaching this as a segmentation task that would require extensive and costly training data. We introduce a novel loss function and network structure to incorporate domain knowledge, geometrically constraining the output of our network with biologically plausible solutions. We show in our experiments that our framework significantly outperforms methods that use the same amount of training information.