Guided interactive image segmentation using machine learning and color-based image set clustering.

Info

PUBLISHED DATE
2022-09-30

JOURNAL
Bioinformatics

LINK
https://www.ncbi.nlm.nih.gov/pubmed/35976110

Authors

A. Friebel T. Johann **D. Drasdo** **S. Hoehme**

Abstract

MOTIVATION: Over the last decades, image processing and analysis have become one of the key technologies in systems biology and medicine. The quantification of anatomical structures and dynamic processes in living systems is essential for understanding the complex underlying mechanisms and allows, i.e. the construction of spatio-temporal models that illuminate the interplay between architecture and function. Recently, deep learning significantly improved the performance of traditional image analysis in cases where imaging techniques provide large amounts of data. However, if only a few images are available or qualified annotations are expensive to produce, the applicability of deep learning is still limited. RESULTS: We present a novel approach that combines machine learning-based interactive image segmentation using supervoxels with a clustering method for the automated identification of similarly colored images in large image sets which enables a guided reuse of interactively trained classifiers. Our approach solves the problem of deteriorated segmentation and quantification accuracy when reusing trained classifiers which is due to significant color variability prevalent and often unavoidable in biological and medical images. This increase in efficiency improves the suitability of interactive segmentation for larger image sets, enabling efficient quantification or the rapid generation of training data for deep learning with minimal effort. The presented methods are applicable for almost any image type and represent a useful tool for image analysis tasks in general. AVAILABILITY AND IMPLEMENTATION: The presented methods are implemented in our image processing software TiQuant which is freely available at tiquant.hoehme.com. SUPPLEMENTARY INFORMATION: Supplementary data are available at Bioinformatics online.