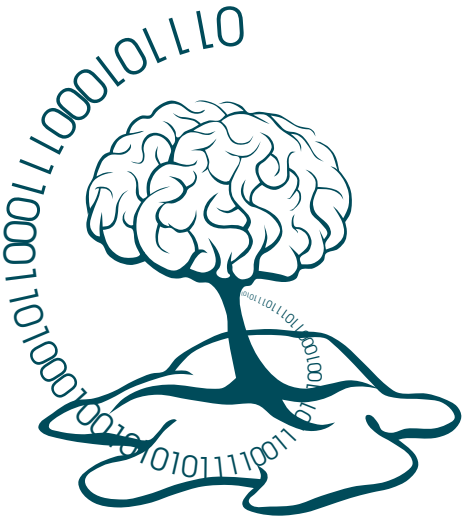

Ischemic Stroke Lesion Segmentation

www.isles-challenge.org

Proceedings

5th October 2015

Munich, Germany

UNIVERSITÄT ZU LÜBECK

Technische Universität München

UNIVERSITÄT BERN

MICCAI'15 MUNICH

Preface

Stroke is the second most frequent cause of death and a major cause of disability in industrial countries. In patients who survive, stroke is generally associated with high socioeconomic costs due to persistent disability. Its most frequent manifestation is the ischemic stroke, whose diagnosis often involves the acquisition of brain magnetic resonance (MR) scans to assess the stroke lesion's presence, location, extent, evolution and other factors. An automated method to locate, segment and quantify the lesion area would support clinicians and researchers alike, rendering their findings more robust and reproducible.

New methods for stroke segmentation are regularly proposed. But, more often than desirable, it is difficult to compare their fitness, as the reported results are obtained on private datasets. Challenges aim to overcome these shortcomings by providing (1) a public dataset that reflects the diversity of the problem and (2) a platform for a fair and direct comparison of methods with suitable evaluation measures. Thus, the scientific progress is promoted.

With ISLES, we provide such a challenge covering ischemic stroke lesion segmentation in multi-spectral MRI data. The task is backed by a well established clinical and research motivation and a large number of already existing methods. Each team may participate in either one or both of two sub-tasks:

SISS Automatic segmentation of ischemic stroke lesion volumes from multi-spectral MRI sequences acquired in the sub-acute stroke development stage.

SPES Automatic segmentation of acute ischemic stroke lesion volumes from multi-spectral MRI sequences for stroke outcome prediction.

The participants downloaded a set of training cases with associated expert segmentations of the stroke lesions to train and evaluate their approach, then submitted a short paper describing their method. After reviewing by the organizers, a total of 17 articles were accepted and compiled into this volume. At the day of the challenge, each teams' results as obtained on an independent test set of cases will be revealed and a ranking of methods established.

For the final ranking and more information, visit WWW.ISLES-CHALLENGE.ORG.

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August 2015

Version: 2015-09-30

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Version: 2015-09-30

Input Data Adaptive Learning (IDAL) for sub-acute Ischemic Stroke Lesion Segmentation

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Abstract. In machine learning larger databases are usually associated with higher classification accuracy due to better generalization. In some medical applications with highly variable expressions of pathologies exactly this generalization may lead to non-optimal classifiers. Here approaches incorporating these varying manifestations of a disease in a flexible way to improve the classification are needed. This paper therefore presents a method to learn from a large training base consisting only of sparsly annotated data, adaptively selecting optimal training samples for given input data. This way heterogeneous databases are supported two-fold. First, by being able to deal with sparsely annotated data allows a quick inclusion of new data sets. Secondly, by adapting the classifiers according to the input data the heterogeneity of the database is further exploited.

Keywords: Adaptive Learning, Lession Segmentation, Machine Learning, Random Forest

1 Motivation

Learning from large datasets becomes more and more important in computer vision. This is also true for machine learning in the context of medical image computing, but poses special challenges. The data, that are used here are usually highly individual – not only because of the variety of imaging modalities and imaging configurations but also because pathological changes have a great variety of appearances. This leads to new challenges for machine learning in medical imaging: a) how do we create large training sets covering the diversity of a pathology and b) how to incorporate such heterogeneity in a beneficial way. We propose a new algorithm that faces these challenges. Building on prior work we use an algorithm that allows learning from sparse and unambiguous regions (SURs) and enhance it with a new method were classifiers are only trained on similar data. We call this approach 'Input Data Adapted Learning' (IDAL).

2 Overview

Instead of training a single classifier that is used to predict all unseen images we propose to adaptively train a new classifier for every new image. This allows to

use only few, but similar images during training. While such an approach makes a classifier less general, we expect that the so-trained classifier is better suited to deal with the afore mentioned heterogeneity.

We realized this approach with a three-staged algorithm (Fig. 1). During the first stage, that is performed offline like traditional classifier training, we train an similarity classifier (SC) which can group similar images based on a similarity measure.

The offline trained SC is used in the second stage – the online training – to find images that are similar to the new, unlabeled images. Based on this individual, input-dependent subset of training images, a new voxel-based classifier (VC) is trained. For this, we used the approach presented in [5] which allows to train a voxel-based classifier (VC) from sparsely and unambiguously labeled regions (SURs). This VC is then used in the last stage to label each voxel of the new image, leading to the prediction mask.

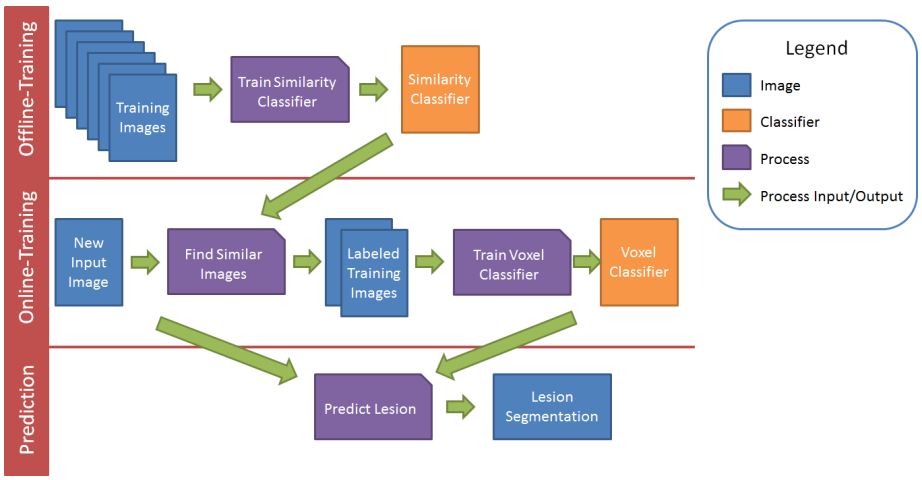

Fig. 1. Overview of the three stages used for our algorithm.

3 Preprocessing

A simple preprocessing is applied before the images where used for training or prediction. Our brainmask includes all voxels for which neither T1 nor T2 are zero.

We normalize all MR-images to a CSF-mode of 0 and an overall brain matter mode of 1. We found that using the mode instead of mean provides a more robust normalization since the mode is less affected by the size of the lesions. We obtained the CSF-area by training a simple classifier using only the pure voxel intensities.

4 Similarity Classifier (SC)

The main idea of our work is to find similar images which are then used to train a voxel classifier. Therefore, the similarity between two images is defined by the ability to successfully use them to train a classifier. Accordingly, we define the similarity $\rho(I_0, I_1)$ of two image I_0 and I_1 as the Dice score that a voxel classifier trained with I_0 scores if the mask for I_1 is predicted.

While it is possible to directly calculate the similarity of two images with known voxel labels, it needs to be estimated for new images with unknown voxel labels. We chose Neighbourhood approxing Forests (NAF) for this task [1]. NAF are trained to find the most similar images based on a high-dimensional representation by training trees that group the training data in a way that maximizes the similarity within each leaf node. For the prediction, the new images are then passed below each tree and for every sample the number of leaf nodes that had been reached and contains this sample type is returned. A high number of samples therefore indicates a high similarity between a training sample and the sample that is used to predict.

To train the NAF and use it as SC we first calculated the similarity of all training images according to the previously given definition of $\rho(\cdot, \cdot)$. We then built a feature vector for every patient based on the normalized T_1, T_2, DWI, and FLAIR image by calculating the first order statistics for the whole brain (Intensity minimum, maximum, range, mean, variance, sum, median, std. deviation, mean absolute deviation, root means square, uniformity, entropy, energy, kurtosis, skewness and the number of voxels). Although these are all image-derived values, the proposed approach also allows the use of additional information like patient age, diagnosis, etc., which are not included in the challenge data.

We trained the NAF with 100 trees, a minimum of two samples at each leaf, 30 random tests for best split at each node during the training and a maximum tree depth of 12. After predicting a new patient (Online Training stage, see Fig. 1) we chose the three highest ranked training images to train the new VC.

5 Voxel Classifier (VC)

The estimation of voxel labels is done by a voxel-wise classification. For this task extremely randomized trees (ExtraTrees)-based classifiers are used [2]. Previous work showed that ExtraTrees usually perform slightly better than canonical Random Forests [4] and were already successfully applied in lesion segmentation [6]. Voxel features were derived from the normalized MR-images. We used the intensity and the differences between each of the modalities. Additionally, the Gaussian, Difference of Gaussian, Laplacian of Gaussian (3 directions), and Hessian of Gaussian were calculated with Gaussian sigma of 1 mm, 3 mm, and 5 mm, leading to 82 features per voxel.

Instead of training on the given full labels we created sparsely and unambiguous annotated regions (SURs) which allows the fast labeling of new training data [3, 5]. The necessary labeling for the SISS 2015 challenge dataset was done

in less than $2^1/_2$ hours. The sampling error introduced by SUR-based labeling was corrected by using DALSA-learning [5].

For this, every training sample x is weighted with an correction weight w which is selected to ensure that the probability for this sample in the training data equals the probability P for this sample in the complete image, i.e.

$$w(x) = \frac{P_{\text{Complete Image}}(x)}{P_{\text{SURs}}(x)} \tag{1}$$

We estimate the unknown $w(x)$ by training a parameter-less logistic regression that differentiates between voxels that are labeled by SURs and voxels that are within the brain mask. By using the probabilistic output of this method, w can be estimated [5].

Each ExtraTrees classifier was trained with 50 trees and the Gini purity as optimization measurement. The maximum tree depth was not limited. During each training (during similarity calculation and final VC training) the best class weights, and minimum samples at leaf nodes were independently estimated by using cross validation.

Acknowledgment: This work was carried out with the support of the German Research Foundation (DFG) within project I04, SFB/TRR 125 Cognition-Guided Surgery

References

[1] E. Konukoglu, B. Glocker, D. Zikic, A. Criminisi: 'Neighbourhood approximation using randomized forests' Medical Image Analysis, Vol. 17, Issue 7, Pages 790-804, 2013

[2] P. Geurts, D. Ernst, L. Wehenkel: 'Extremely randomized trees', Machine Learning, Vol. 63, Pages 3-42, 2006

[3] M. Goetz, C. Weber, B. Stieltjes, K.H. Maier-Hein: 'Learning from Small Amounts of Labeled Data in a Brain Tumor Classification Task' NIPS 2014 Workshop on Transfer and Multi-task learning: Theory Meets Practice

[4] M. Goetz, C. Weber, J. Bloecher, B. Stieltjes, H.P. Meinzer, K.H. Maier-Hein: 'Extremely randomized trees based brain tumor segmentation' Proceedings of BRATS Challenge-MICCAI, 2014

[5] M. Goetz, C. Weber, F. Binczyk, J. Polanska, R. Tarnawski, B. Bobek-Billewicz, U. Koethe, J. Kleesiek, B. Stieltjes, K.H. Maier-Hein: 'DALSA: Domain Adaptation for Supervised Learning from Sparsely Annotated MR Images', IEEE Transactions on Medical Imaging, vol.PP, 2015 doi: 10.1109/TMI.2015.2463078

[6] O. Maier, M. Wilms, J. Gablentz, U.M. Krämer, T.F. Münte, H.Handels, 'Extra Tree forests for sub-acute ischemic stroke lesion segmentation in MR sequences' Journal of Neuroscience Methods, Volume 240, Pages 89-100, 2015