Unsupervised Identification of Clinically Relevant Clusters in Routine Imaging Data

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Abstract—This abstract is a summary of [3]. Currently, computational image analysis typically relies on well annotated and curated training data. While these kind of data sets enable the creation of accurate and sensitive detectors for specific findings, they are limited, since annotation is only feasible on a relatively small number of cases. We propose unsupervised learning to group patients based on non-annotated clinical routine imaging data. We show that based on learned visual features, we identify population clusters with homogeneous (within clusters) but distinct (across clusters) clinical findings. To evaluate the link between visual clusters and clinical findings, we compare clusters with natural language processing algorithms.

I. IDENTIFICATION OF CLUSTERS

Spatial Normlization We perform spatial normalization to establish spatial correspondences of voxels across the population. For this purpose, we employ a multi-template spatial normalization algorithm that is able to deal with the high variability present in routine imaging data [4].

Feature Extraction We extract features that capture complementary visual characteristics in order to map an image to a visual descriptor representation. We densely sample Haralick [2] features to encode rotation invariant texture and *Shape Features* (3D-SIFT [5]) to encode rotation variant gradient changes. Subsequently we quantize these features to *Bag of visual Words* to summarize local features to global volume descriptors. In advance, we augment the features with their spatial position in the reference space. Finally, we learn a set of 20 latent topics of co-occurring feature settings by using *Latent Dirichlet Allocation* (LDA) [1]. This allows to interpret an image as a mixture of topics represented by its 20 dimensional topic assignment vector.

Clustering We perform clustering of the population to retrieve groups of subjects with (visually) similar properties. Here we interpret the Euclidean distance between two volume descriptors as a measure of visual similarity.

II. EVALUATION

Clustering is performed on the full set of images, while for evaluation only records with a report are considered. Reports are processed by a natural language processing pipeline mapping free text to a set of pathology terms. Aim of the evaluation is to test the hypothesis, that the clustering reflects pathological subgroups in the population. In order to do so



Fig. 1. T-SNE embedding illustrating the routine imaging landscape

we test whether volume label assignments (pathology terms) are associated with cluster assignments. A cell- χ^2 -test is performed for each term and each cluster to test whether its cluster frequency is significantly different from its population frequency.

III. RESULTS

We discovered more than 250 (positive and negative) associations between clusters and terms. We find that combining complementary features improves clustering compared to individual feature sets and show that learning latent topics of commonly occuring feature classes furthermore improve results. We demonstrate that visual features extracted from the lungs have prognostic power for numerous pathological findings.

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