

Overview of the ImageCLEF 2017 Tuberculosis Task — Predicting Tuberculosis Type and Drug Resistances

Yashin Dicente Cid^{1,2}, Alexander Kalinovsky³, Vitali Liauchuk³,
Vassili Kovalev³, and Henning Müller^{1,2}

¹ University of Applied Sciences Western Switzerland (HES-SO), Sierre, Switzerland;

² University of Geneva, Switzerland;

³ United Institute of Informatics Problems, Minsk, Belarus

`yashin.dicente@hevs.ch`

Abstract. ImageCLEF is the image retrieval task of the Conference and Labs of the Evaluation Forum (CLEF). ImageCLEF has historically focused on the multimodal and language-independent retrieval of images. Many tasks are related to image classification and the annotation of image data as well as the retrieval of images. The tuberculosis task was held for the first time in 2017 and had a very encouraging participation with 9 groups submitting results to these very challenging tasks. Two tasks were proposed around tuberculosis: (1) the classification of the cases into five types of tuberculosis and (2) the detection of drug resistances among tuberculosis cases. Many different techniques were used by the participants ranging from Deep Learning to graph-based approaches and best results were obtained by a large variety of approaches. The prediction of tuberculosis types had relatively good performance but the detection of drug resistances remained a very difficult task. More research into this seems necessary.

Keywords: Tuberculosis, Computed Tomography, Image Classification, Drug Resistance, 3D Data Analysis

1 Introduction

ImageCLEF⁴ is the image retrieval task of CLEF (The Cross Language Evaluation Forum). ImageCLEF was first held in 2003 and since 2004 a medical task has been added [1, 2]. More information on the other tasks organized in 2017 can be found in [3] and the past editions are described in [4–6].

About 130 years after the discovery of *Mycobacterium tuberculosis*, the disease remains a persistent threat and a leading cause of death worldwide. The greatest disaster that can happen to a patient with tuberculosis (TB) is that the organisms become resistant to two or more of the standard drugs. In contrast to drug sensitive (DS) tuberculosis, its multi-drug resistant (MDR) form is

⁴ <http://www.imageclef.org/>

much more difficult and expensive to recover from. Thus, early detection of the drug resistance (DR) status is of great importance for effective treatment. The most commonly used methods of DR detection are either expensive or take too much time (up to several months). Therefore there is a need for quick and at the same time cheap methods of DR detection. One of the possible approaches for this task is based on Computed Tomography (CT) image analysis, where many details can be seen. In many countries X-ray imaging is used for disease detection and CT images are only taken when required. The detection of TB subtypes is another important task for tuberculosis analysis, as different types of tuberculosis can be treated in different ways.

This article first describes the two tasks proposed around tuberculosis in 2017. Then, the data sets, evaluation methodology and participation are detailed. The results describe the submitted runs and results obtained for the two subtasks and a discussion and conclusion ends the paper.

2 Tasks, Data Sets, Evaluation, Participation

2.1 The Tasks in 2017

Two subtasks were organized in 2017:

- multi-drug resistance detection (MDR task);
- tuberculosis type classification (TBT task).

This section gives an overview of each of the two subtasks.

Multi-drug resistance detection The goal of the MDR subtask is to assess the probability of a TB patient having resistant form of tuberculosis based on the analysis of a chest CT scan. The training data were given as binary cases even though several levels of resistances exist.

Tuberculosis type classification The goal of the tuberculosis type subtask is to automatically categorize each TB case into one of the following five types: Infiltrative, Focal, Tuberculoma, Miliary, and Fibro-cavernous. The distribution of cases among the classes is not fully equal but distributions are similar in the training and the testing data.

2.2 Datasets

For both subtasks 3D CT images were provided with slice size of 512×512 pixels and number of slices varying from about 50 to 400. All images are part of a tuberculosis screen program in Belarus, which has a high percentage of tuberculosis cases compared to other countries. All the CT images were stored in NIFTI file format with *.nii.gz* file extension (g-zipped *.nii* files). This file format stores raw voxel intensities in Hounsfield units (HU) as well as the corresponding image

metadata such as image dimensions, voxel size in physical units, slice thickness, etc.

All lung tuberculosis data including CT images and associated annotations were provided by Republican Research and Practical Center for Pulmonology and Tuberculosis which is located in Minsk, Belarus. The data were collected in framework of several projects aimed at creation of information resources on lung tuberculosis and drug resistance problem. The projects were conducted by a multi-disciplinary team and funded by the National Institute of Allergy and Infectious Diseases, National Institutes of Health (NIH), U.S. Department of Health and Human Services, USA through the Civilian Research and Development Foundation (CRDF). The dedicated web-portal⁵ developed in framework of the projects stores information on more than 940 tuberculosis patients from five countries: Azerbaijan, Belarus, Georgia, Moldova and Romania. The information includes CT scans, X-ray images, genome data, clinical and social data.

Moreover, for all patients in both subtasks we provided automatically extracted masks of the lungs to make further processing easier. These masks were extracted using the method described in [7]. Figure 1 shows one CT example with the provided mask as overlay.

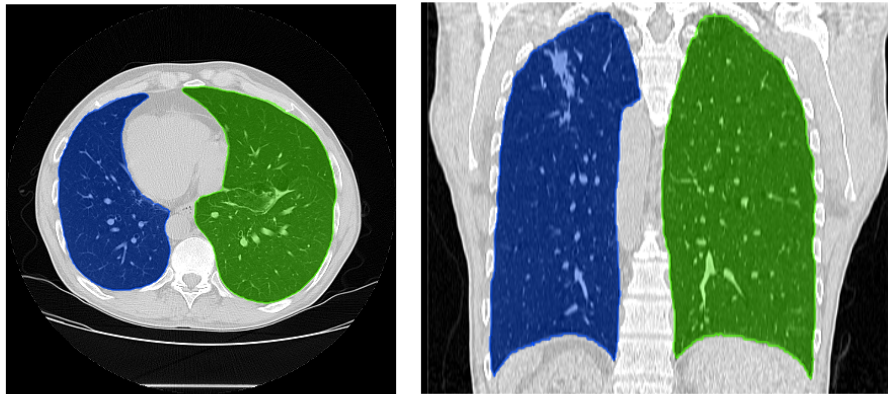


Fig. 1. Example of a CT scan and mask provided. Right and left lungs are colored in green and blue, respectively.

Multi-drug Resistance Detection For this subtask, a dataset of 3D CT images was used along with a set of clinically relevant metadata. The dataset includes only HIV-negative patients with no relapses. Each patient was classified into one of the two classes: drug sensitive (DS) or multi-drug resistant (MDR) cases.

⁵ <http://tbportals.niaid.nih.gov/>

A patient was considered DS if tuberculosis bacteria were sensitive to all the anti-tuberculosis drugs tested. In case of MDR tuberculosis the corresponding drug susceptibility tests showed resistance to at least Isoniazid and Rifampicin – the two most powerful anti-TB drugs. In reality there are several levels of resistances but to make the task as easy as possible only these two most representative classes were retained.

Table 1. Dataset for the MDR subtask.

# Patients	Train Test	
DS	134	101
MDR	96	113
Total patients	230	214

Tuberculosis Type Classification The dataset used in this subtask includes chest CT scans of TB patients along with the TB type. Figure 2 shows one example for each of the five TB types.

Table 2. Dataset for the TBT subtask.

# Patients	Train Test	
Type 1 (T1) – Infiltrative	140	80
Type 2 (T2) – Focal	120	70
Type 3 (T3) – Tuberculoma	100	60
Type 4 (T4) – Miliary	80	50
Type 5 (T5) – Fibro-cavernous	60	40
Total patients	500	300

2.3 Evaluation Measures and Scenario

The participants were allowed to submit up to 10 runs to the tuberculosis task for each of the two sub tasks. In the case of the MDR tasks, participants had to provide, for each patient in the test set, the probability between 0 and 1 of belonging to the MDR class. These probabilities were used to build Receiver Operating Characteristic (ROC) curves. Since the MDR dataset was not perfectly balanced and had a relative small size, we decided to use the Area Under the ROC Curve (AUC) to rank the participant runs. Moreover, we provided the accuracy of the binary classification using a standard threshold of 0.50.

In the case of the TBT task, the participants had to predict the TB type of each patient, and submit a run containing a categorical label in the set $\{1, 2, 3, 4, 5\}$. For this task Cohen’s Kappa was provided for each run along with the

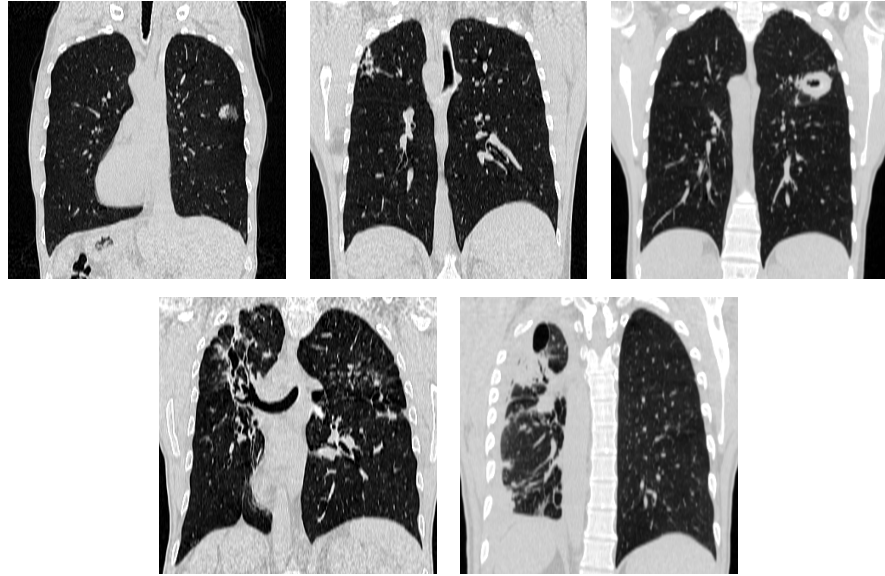


Fig. 2. Examples of the TB types. First row, from left to right: Infiltrative, Focal, and Tuberculoma types. Second row: Miliary, and Fibro-cavernous types.

weighted average accuracy along the classes. The former measure is not sensitive to unbalanced datasets as in this task.

2.4 Participation

94 teams registered for the tuberculosis task and 48 signed the end user agreement. Finally, 9 teams from 9 countries submitted a run for at least one of the two subtasks. Table 3 shows the list of participants and the task(s) where they participated.

3 Results

This section provides the results obtained by the participants in each of the subtasks.

3.1 MDR Detection

Table 4 shows the results obtained for the MDR detection subtask. The runs were evaluated on the test set of images using ROC curves produced from the probabilities provided by participants. The results in the table are sorted by AUC in descending order. Figure 3 shows the ROC curve for the best run of each participant. Moreover, the best operating point in the curve is highlighted. The accuracy is given in the table as well.

Table 3. List of participants submitting a run to at least one subtask.

Group Name	Main institution	Country	Submission	
			MDR	TBT
Aegean Tuberculosis	University of the Aegean	Greece	×	–
BatmanLab	University of Pittsburgh	USA	×	×
BioinformaticsUA	Institute of Electronics and Informatics Engineering of University of Aveiro	Portugal	×	×
HHU DBS	Heinrich-Heine-Universität Düsseldorf, Institut für Informatik	Germany	×	–
Image Processing	Department of Computer Science, Middlesex University	United Kingdom	–	×
MedGIFT	University of Applied Sciences Western Switzerland (HES-SO)	Switzerland	×	×
MEDGIFT UPB	University Politehnica of Bucharest	Romania	×	×
SGEast	ISTD Pillar, Singapore University of Technology and Design	Singapore	×	×
UIIP	United Institute of Informatics Problems	Belarus	×	×

It should be noticed that the task of image-based recognition of MDR for tuberculosis is very difficult and challenging. It was not clear from the start whether this task is actually possible with visual data alone. There are several studies dedicated to this problem that reported presence of statistically significant links between drug resistance status and various features of the patient lungs [8–11]. However, none of the studies reported any precise classification of drug resistance with accuracy far beyond the level of statistical significance.

Among the submitted runs, the three best results were achieved by the MedGIFT team. Methods based on a graph-model of the lungs were used for the description of lung CT appearance [12]. For different variations of the method the AUC calculated over the test set varied from 0.5112 to 0.5825. The SGEast team employed deep learning in both subtasks. Two-dimensional convolutional neural networks were used for describing the CT scans and recurrent neural networks were used for image classification [13]. Combined with preprocessing procedures such as image slicing and data augmentation the method resulted in 0.5620 AUC value for their best run. The UIIP team used an image description method based on the calculation of co-occurrence matrices of 3D supervoxels which allowed to achieve an AUC of 0.5415 [14]. The best performing result in terms of classification accuracy was achieved by the HHU DBS team by using deep convolutional networks which operate directly in 3D [15]. The method demonstrated a classification accuracy of 56.8% with an AUC of 0.5297 for the best run. The Batmanlab used a 3D intensity-based supervoxel image representation and various texture

Table 4. Results obtained by the participants in the MDR task.

Group Name	Run	AUC	ACC	Rank
MedGIFT	MDR_Top1_correct.csv	0.5825	0.5164	1
MedGIFT	MDR_submitted_topBest3_correct.csv	0.5727	0.4648	2
MedGIFT	MDR_submitted_topBest5_correct.csv	0.5624	0.4836	3
SGEast	MDR_LSTM_6_probs.txt	0.5620	0.5493	4
SGEast	MDR_resnet_full.txt	0.5591	0.5493	5
SGEast	MDR_BiLSTM_25_wcrop_probs.txt	0.5501	0.5399	6
UIIP	MDR_supervoxels_run_1.txt	0.5415	0.4930	7
SGEast	MDR_LSTM_18_wcrop_probs.txt	0.5404	0.5540	8
SGEast	MDR_LSTM_21_wcrop_probs.txt	0.5360	0.5070	9
MedGIFT	MDR_Top2_correct.csv	0.5337	0.4883	10
HHU DBS	MDR_basecnndo_212.csv	0.5297	0.5681	11
SGEast	MDR_LSTM_25_wcrop_probs.txt	0.5297	0.5211	12
BatmanLab	MDR_submitted_top5.csv	0.5241	0.5164	13
HHU DBS	MDR_basecnndo_113.csv	0.5237	0.5540	14
MEDGIFT UPB	MDR_TST_RUN_1.txt	0.5184	0.5352	15
BatmanLab	MDR_submitted_top4_0.656522.csv	0.5130	0.5024	16
MedGIFT	MDR_Top3_correct.csv	0.5112	0.4413	17
HHU DBS	MDR_basecnndo_132.csv	0.5054	0.5305	18
HHU DBS	MDR_basecnndo_182.csv	0.5042	0.5211	19
HHU DBS	MDR_basecnndo_116.csv	0.5001	0.4930	20
HHU DBS	MDR_basecnndo_142.csv	0.4995	0.5211	21
HHU DBS	MDR_basecnndo_120.csv	0.4935	0.4977	22
SGEast	MDR_resnet_partial.txt	0.4915	0.4930	23
BatmanLab	MDR-submitted_top1.csv	0.4899	0.4789	24
BatmanLab	MDR_SuperVx_Hist_FHOG_rf_0.648419.csv	0.4899	0.4789	25
Aegean Tuberculosis	MDR_DETECTION_EXPORT2.csv	0.4833	0.4648	26
BatmanLab	MDR_SuperVx_FHOG_rf_0.637994.csv	0.4601	0.4554	27
BioinformaticsUA	MDR_run1.txt	0.4596	0.4648	28

features in each supervoxel and achieved their maximum performance at 0.5241 AUC [16]. 2D deep learning techniques were used by MEDGIFT UPB along with CT image slicing and data augmentation, which resulted in an AUC of 0.5184 for their best run [17]. The Aegean Tuberculosis group obtained an AUC of 0.4833 with their single run. However, no details on their technique were provided. Finally, the Bioinformatics UA team also used 3D convolutional neural networks in their study and achieved 46.0% of classification accuracy with an AUC of 0.4648 in the MDR subtask [18]. The authors believe that using data augmentation and weight regularization may potentially improve the results.

3.2 Tuberculosis Type Classification

Table 5 shows the results obtained for the tuberculosis type subtask. The runs were evaluated on the test set of images using the unweighted Cohen’s Kappa coefficient and classification accuracy. The results are sorted by Cohen’s Kappa

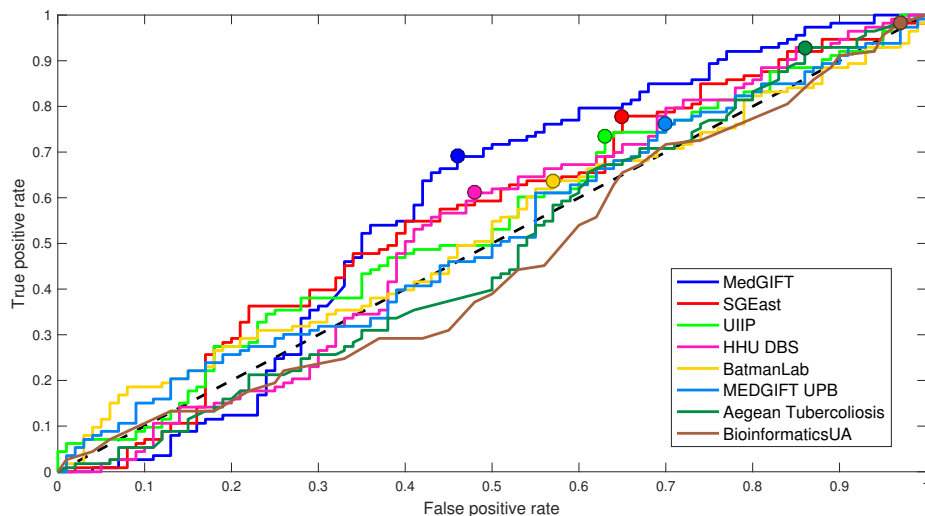


Fig. 3. ROC curves of the best run per participant. The dot on each curve corresponds to best operating point.

coefficient in descending order. In addition, Figure 4 contains the confusion matrices of each team’s best run. These matrices show the percentage of patients from each class classified in each TB type. When analyzing these matrices, we found that the best performance per TB type is found in the first 4 teams (SGEeast, MEDGIFT UPB, Image Processing, and UIIP). These methods seem to be complementary, being expert each one in classifying a different TB type. Thus, the organizers of the task have performed a late fusion with the best run from these 4 best teams. The results of the corresponding fusion are included at the end of both Table 5 and Figure 4. In the tuberculosis type subtask, most of the teams used the same set of methods as they used for MDR detection subtask. The best results were achieved by the SGEeast and MEDGIFT UPB groups with Cohen’s Kappa of 0.2438 and 0.2329 respectively for their best runs. The Image Processing group used a technique based on splitting CT images into sets of small 2D patches followed by classification of image patches via convolutional neural networks [19]. The corresponding submitted run scored 0.2187 for Cohen’s Kappa. The UIIP team used a different approach for TB type classification that uses extended multi-sort co-occurrence matrices of voxels in 3D images. The only submitted run resulted in a Kappa score of 0.1956. The best runs of MedGIFT, BatmanLab and BioinformaticsUA groups achieved Cohen’s Kappa values of 0.1623, 0.1533, and 0.0222, respectively. Finally, the fusion of the best runs of the 4 best teams achieved a 0.3263 Cohen’s Kappa value. This result is an important improvement with respect the best participant run and shows how complementary the approaches of these four participants are. However, when analyzing its confusion matrix in Figure 4, this fusion method mainly improved

Table 5. Results obtained by the participants in the TBT task. Last row includes the results of a late fusion performed by the organizers using the best run file from the 4 groups achieving highest kappa.

Group Name	Run	Kappa	ACC	Rank
SGEast	TBT_resnet_full.txt	0.2438	0.4033	1
SGEast	TBT_LSTM_17_wcrop.txt	0.2374	0.3900	2
MEDGIFT UPB	TBT_T_GNet.txt	0.2329	0.3867	3
SGEast	TBT_LSTM_13_wcrop.txt	0.2291	0.3833	4
Image Processing	TBT-testSet-label-Apr26-XGao-1.txt	0.2187	0.4067	5
SGEast	TBT_LSTM_46_wcrop.txt	0.2174	0.3900	6
UIIP	TBT_iiggad_PCA_RF_run_1.txt	0.1956	0.3900	7
MEDGIFT UPB	TBT_..._GoogleNet_10crops_at_different_scales_.txt	0.1900	0.3733	8
SGEast	TBT_resnet_partial.txt	0.1729	0.3567	9
MedGIFT	TBT_Top1_correct.csv	0.1623	0.3600	10
SGEast	TBT_LSTM_25_wcrop.txt	0.1548	0.3400	11
MedGIFT	TBT_submitted_topBest3_correct.csv	0.1548	0.3500	12
BatmanLab	TBT_SuperVx_Hist_FHOG_lr_0.414000.csv	0.1533	0.3433	13
SGEast	TBT_LSTM_37_wcrop.txt	0.1431	0.3333	14
MedGIFT	TBT_submitted_topBest5_correct.csv	0.1410	0.3367	15
MedGIFT	TBT_Top4_correct.csv	0.1352	0.3300	16
MedGIFT	TBT_Top2_correct.csv	0.1235	0.3200	17
BatmanLab	TBT_submitted_bootstrap.csv	0.1057	0.3033	18
BatmanLab	TBT_submitted_top3_0.490000.csv	0.1057	0.3033	19
BatmanLab	TBT_SuperVx_Hist_FHOG_Reisz_lr_0.426000.csv	0.0478	0.2567	20
BatmanLab	TBT_submitted_top2_0.430000.csv	0.0437	0.2533	21
BioinformaticsUA	TBT_run0.txt	0.0222	0.2400	22
BioinformaticsUA	TBT_run1.txt	0.0093	0.1233	23
Fusion of best 4 methods		0.3263	0.4867	-

the performance for T1. In all the other classes, the performance is below the best performance achieved in the corresponding class by at least one of the fused methods. In any case, the average accuracy obtained it is also superior (0.4867) to all submitted runs by an important margin.

4 Discussion and Conclusions

The results obtained by the participants confirm the difficulty of the MDR task. Independently of the technique applied, all runs remained relatively close to the performance of a random classifier, meaning that there is likely a high potential for improvements. One explanation is that it is not possible to detect MDR patients based on images alone, and maybe additional data on the patients need to be combined with visual information. The results above random encourage to find and add more cases to this dataset and continue exploring the detection of drug resistance based on images, as a much larger training data set can maybe better cover the different subtypes, as can potentially the addition of multi-modal information. On the other hand, there are other existing forms of TB

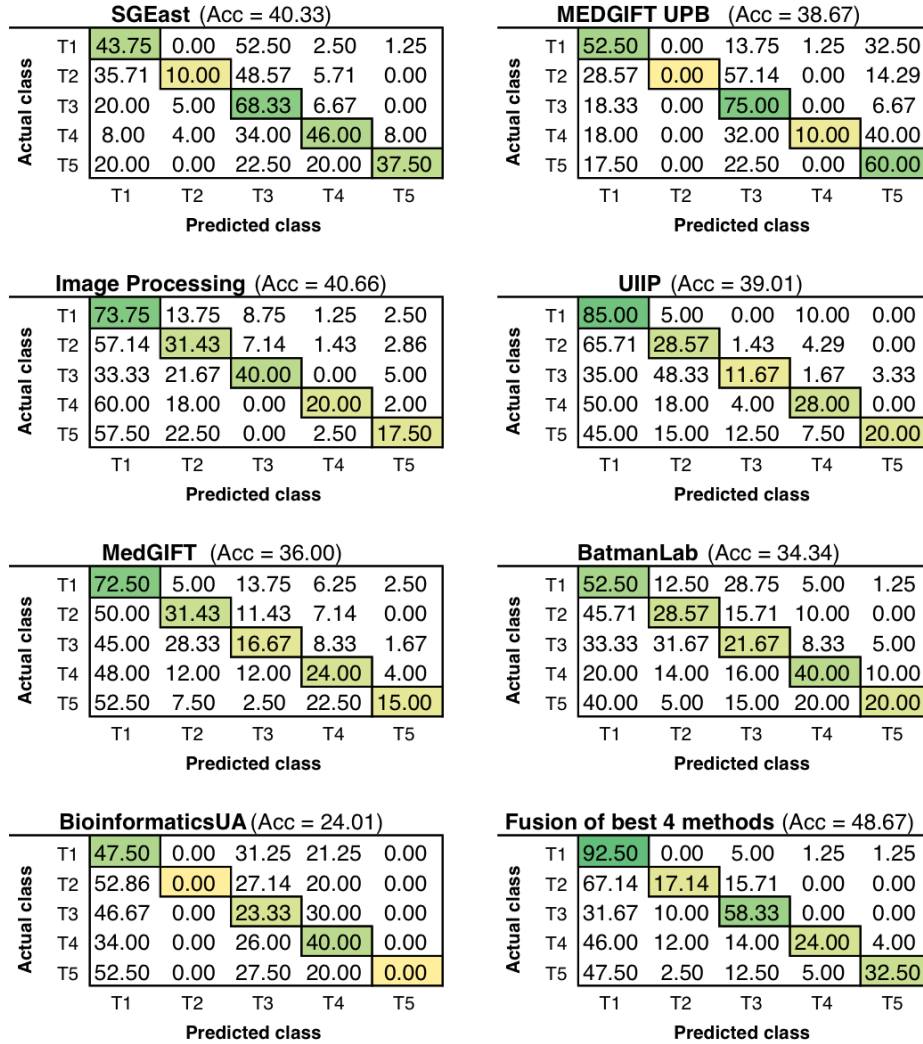


Fig. 4. Confusion matrices of the best run per group and the fusion of the best 4 groups. The values are expressed in %. Acc refers to the weighted average accuracy.

drug resistance which are not considered with this study. For example, quick detection of Extensively drug-resistant (XDR) tuberculosis is also of a great scientific and practical interest.

The TB subtask results are clearly based on the suitability of the imaging techniques for a specific task. The best runs seem to exploit quite different aspects and each of them is best for one specific class. This complementarity is highlighted by the very good results of a simple late fusion of the four best runs. However, there is still room for improvement, especially in the types Focal (T2), Tuberculoma (T3), Miliary (T4), and Fibro-cavernous (T5). For this particular task, deep learning methods worked better than other approaches, obtaining the 6 best results. Nonetheless, the late fusion performed by the organizers combining the prediction of three deep learning techniques and one based on 3D texture features surpassed the best participant run. This suggests that different TB types may need to be described by different approaches and such an approach can lead to optimal results.

2017 was the first year of the ImageCLEF TB task. The number of registered participants and the results obtained show the interest of the community in this task, and encourages the inclusion of the TB task in the upcoming editions of ImageCLEF. There is still much to be learned and a detailed analysis of the results should help with this.

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