Summary of "SODA: Detecting Covid-19 in Chest X-rays with Semi-Supervised Open Set Domain Adaptation"

The purpose of the study is to effectively support the traditional PT-PCR testing and increase the speed of diagnosis of COVID-19 in patients from their chest X-rays. These methods are necessary due to the long time taken for the PT-PCR test results and the lower sensitivity of the PT-PCR test. Moreover, medical imaging is easily performed across most hospitals in the world.

The authors have approached the chest x-ray image classification problem in a semi-supervised open set domain adaptation setting and have proposed a novel Semi-Supervised Open Set Domain Adversarial network (SODA) that helps to address the overfitting problem when training on a very small dataset of COVID-19 and to reduce the domain shift.

SODA mainly comprises of 4 parts:

- 1. A feature extractor G_f , to extract the features of the image. It is DenseNet121 network that is pre-trained on ChestXray-14 dataset.
- 2. A multi-label classifier G_y , which is a binary classifier to predict the probability for the label l. It is implemented in the form of a one layer MLP with sigmoid activation.
- 3. Domain alignment component inspired from Domain adversarial training that consists of two discriminators D_G and D_C that finds the probability that image x belongs to the source domain for general images and images with common labels respectively. D_G helps to find the domain invariant features of the image. D_C helps to differentiate between the domains of images with common labels to learn the common labels present in the source and target domain and thus avoid negative transfer,
- 4. Common Label Recognizer R, that determines if the unlabeled image x consists of a label that is common to both the source and target domains. This component is used as most of the images in the target domain is unlabeled which makes it difficult for D_C to check if the unlabeled image has label that is common to both domains.

The probability r is used as a weight in calculation of loss for D_C in case of unlabeled images and in D_G to highlight the alignment of common labels.

 D_G , D_C and R are implemented in the form of an MLP consisting of 2 hidden layers of dimensions 1024 with ReLU activation. They are trained using the cross entropy loss.

SODA is trained as a min-max game amongst G_y , D_G , D_C , and R. The objective function for SODA is as follows:

$$\min_{G_y,R} \max_{D_g,D_c} L_{G_y} + \lambda_R L_R - \lambda_{D_g} L_{D_g} - \lambda_{D_c}^{label} L_{D_c}^{label} - \lambda_{D_c}^{un} L_{D_c}^{un}$$

$$\tag{1}$$

Where L_R , L_{DG} , L_{DC}^{label} and L_{DC}^{un} are respectively loss functions for the Common Label Recognizer R, discriminator D_G , and discriminator D_C for label and unlabeled images. L_{Gy} denotes the crossentropy loss for multi-label classifier G_y while γ denotes the loss function coefficient.

As in the case of traditional unsupervised domain adaptation, the authors have employed the large scale ChestXray-14 dataset as the source domain and the newly published COVID-19 x-ray images as the target domain. The COVID-19 x-ray images consist of only two labels – Covid-19 positive and Pneumonia. The authors compare SODA with the following models:

- 1. Models that are pre-trained on ChestXray-14 dataset and then fine-tuned using transfer learning on COVID-19 x-ray images. For this they have selected DenseNet121 and ResNet50
- 2. Domain adaption models such as Domain Adversarial Neural Networks (DANN) and Partial Adversarial Domain Adaptation (PADA)

Following are some key points related to the performance of SODA:

- The proposed SODA outperform all 4 models on the basis of the AUC-ROC scores for both labels COVID-19 and Pneumonia.
- To investigate the ability of the models to extract domain invariant features, Proxy Adistance (PAD) is calculated. SODA outperforms both DANN and PADA by scoring a lower PAD value.
- On projecting the features extracted from the feature extractor G_Y using t-SNE, it can be seen that SODA separates the label 'Pneumonia' and 'Covid-19' present in the target domain in the best manner as compared to DANN and PADA.
- From the Grad-CAM visualization, it was seen that SODA was more accurately able to detect the locations of pathogens present in chest x-ray images.