Multi-Domain Balanced Sampling Improves Out-of-Distribution Generalization of Chest X-ray Pathology Prediction Models

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Abstract

Learning models that generalize under different distribution shifts in medical imaging has been a long-standing research challenge. There have been several proposals for efficient and robust visual representation learning among vision research practitioners, especially in the sensitive and critical biomedical domain. In this paper, we propose an idea for out-of-distribution generalization of chest X-ray pathologies that uses a simple balanced batch sampling technique. We observed that balanced sampling between the multiple training datasets improves the performance over baseline models trained without balancing. Code for this work is available on Github.[1]

1 Introduction

Pathology detection or classification in medical imaging using deep learning [5], [4] continues to be an open research challenge. Although the field of computer vision has progressed significantly owing to advances in model architecture, optimization techniques, and data augmentation, learning relevant feature representations from visual data still remains a challenge [2] [9]. The field of medical imaging using deep learning suffers from the same issues, since they rely mostly on the same deep learning approaches inspired by studies on general purpose datasets, like ImageNet [13]. The issue becomes more challenging when test data is subject to distribution shifts [12]. When confronted with chest X-rays from different datasets, a straightforward approach, followed by [2], is to merge these datasets and form mini-batches by sampling uniformly from the merged dataset.

The question is: can we find a more robust and efficient way of learning representations from medical images by accounting for which dataset each example came from?

In this work, we examine how balanced batch sampling from each training dataset can improve a model's generalization on out-of-distribution (OoD) chest X-ray datasets. We compare this to [2] and a baseline model trained without balanced batching.

Our work shows that, by training vision algorithms on chest X-rays using balanced mini-batches, we may achieve performance gains during inference on out-of-distribution chest X-ray datasets.

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[1] https://github.com/etetteh/OoD_Gen-Chest_Xray

2 Experiment

We aim to classify 4 chest X-ray pathologies, namely Cardiomegaly, Consolidation, Edema, and Effusion. We compare our approach to two baselines that follow SOTA medical image classification approaches. We describe the baselines in 2.1.

This choice of pathologies is strictly because all the datasets in this experiment include labels for all of these pathologies, and not for any other particular reason. The training, validation and test datasets all come from different distributions. This is to ensure that test and validation datasets are out-of-distribution with respect to the training data. For example, when training on ChestX-ray8 and CheXpert datasets, we validate on MIMIC-CXR dataset and test on PadChest.

Datasets We consider four publicly available chest X-ray image datasets for this experiment: ChestX-ray8 [14], CheXpert [6], MIMIC-CXR-JPG [7], and PadChest [1]. Table 1 displays the details of our datasets.

Table 1: Details of datasets in this work.

Datasets	# Samples Total (unique patients)	# Samples Used	# Pathologies	Geo. Region
ChestX-ray8 dataset (NIH)	67,310	27,520	14	Northeast USA
MIMIC-CXR Dataset (MIMIC)	96,155	27,520	13	Northeast USA
PadChest Dataset (PC)	91,658	27,520	27	Spain
CheXpert Dataset (CHEX)	29,420	27,520	13	Western USA

We use a subset of 27,520 images from each dataset for training, 11,008 for validation, and 13,760 for inference. We end up with training samples of 55,040 images, since we use two datasets as the train set. The training data is sampled sequentially from the original dataset. On the other hand, the entire validation and test datasets are sampled from the data loaders as batches. We use the TorchXRayVision [2, 3] library, which is specialized in handling chest X-ray images, to load the raw data.

2.1 Training

In order to increase the diversity of the training dataset to improve the robustness of the trained model [15], we perform the following basic augmentation techniques: we resize all images to 112x112 resolution (this is done to speed up the experiments), rotate the images by up to 45 degrees, translate by up to [-0.15, 0.15], and scale by [0.85, 1.15].

We perform a leave-a-dataset-out cross validation, and perform training using a DenseNet-121 architecture from the torchvision library. The model is fine-tuned [10, 16] using ImageNet weights, and without any modification to its architecture except the input channel is changed to 1 (for gray-scale images).

We use an Adam [8] optimizer with a fixed learning rate of 1e-03, weight decay of 1e-05, and amsgrad set to true. We run all our experiments for 200 epochs with a batch size of 64, using a binary cross-entropy with logits as our loss function. We perform early stopping [11], and use the final best validation model state, for our inference.

We run the experiments with three different seeds and report the average. Unless otherwise stated, all results are on the test datasets.

2.2 Models compared

We compare with 2 different baselines, one taken from previous work and one which we train following [2], a state-of-the-art method, on our specific datasets:

Baseline XRV is a DenseNet-121 model, from the TorchXRayVision library [3] that is trained on 8 chest X-ray datasets (including all the datasets we use in our experiments), and tasked to classify 18 chest X-ray pathologies. We only performed inference using this model for comparison with our models.

Random Batch Sampling follows previous approaches of studies performed on chest X-ray pathology classification using different data distributions, which involves merging multiple datasets into a larger one for training. We merge two datasets for training, and the remaining two are use for validation and inference respectively.

Balanced Batch Sampling We create two training environments, one for each of our training datasets. At each training step, we sample data from each of the environments, compute the individual losses and back-propagate using the sum of the losses from the environments.

3 Results and Discussion

In this section, we present and discuss the findings of our work. Table 2 shows the results of our experiments.

Our results suggest that out-of-distribution generalization performance may be improved by using a balanced batching technique - sampling data from each environment/dataset equally and computing the sum of the losses.

Table 2: Comparison of balanced batch sampling to not balanced and an existing pre-trained model.

Model	Seed / TRAIN / VALID / TEST	0 NIH_CHEX MIMIC PC	42 NIH_PC MIMIC CHEX	99 CHEX_MIMIC PC NIH	1 NIH_MIMIC CHEX PC	2 CHEX_PC NIH MIMIC	3 MIMIC_PC CHEX NIH	MEAN
*Baseline XRV (no training, using pre-trained 'all' model from [3])	*Best Valid AUC*	-	-	-	-	-	-	-
	Avg Test AUC	**0.91**	**0.92**	**0.82**	**0.91**	**0.92**	**0.82**	**0.88 ±0.05**
	Cardiomegaly	0.92	0.90	0.91	0.92	0.90	0.91	0.91 ±0.01
	Effusion	0.94	0.95	0.86	0.94	0.95	0.86	0.92 ±0.04
	Edema	0.95	0.92	0.76	0.95	0.92	0.76	0.87 ±0.09
	Consolidation	0.85	0.90	0.75	0.85	0.90	0.75	0.83 ±0.07
Random Batching (finetuned from ImageNet model)	*Best Valid AUC*	0.85	0.84	0.89	0.81	0.79	0.88	0.84 ±0.04
	Avg Test AUC	**0.89**	**0.80**	**0.74**	**0.87**	**0.89**	**0.76**	**0.82 ±0.07**
	Cardiomegaly	0.92	0.81	0.79	0.92	0.88	0.78	0.85 ±0.07
	Effusion	0.90	0.85	0.80	0.89	0.93	0.81	0.86 ±0.05
	Edema	0.94	0.78	0.70	0.91	0.90	0.74	0.83 ±0.10
	Consolidation	0.79	0.77	0.66	0.77	0.86	0.69	0.76 ±0.07
Balanced Batching (finetuned from ImageNet model)	*Best Valid AUC*	0.91	0.89	0.91	0.89	0.81	0.89	0.88 ±0.04
	Avg Test AUC	**0.90**	**0.86**	**0.79**	**0.91**	**0.89**	**0.80**	**0.86 ±0.05**
	Cardiomegaly	0.90	0.87	0.83	0.92	0.88	0.87	0.88 ±0.03
	Effusion	0.92	0.92	0.83	0.93	0.93	0.84	0.89 ±0.05
	Edema	0.95	0.85	0.79	0.95	0.90	0.79	0.87 ±0.07
	Consolidation	0.84	0.82	0.72	0.85	0.86	0.71	0.80 ±0.07

*Trained using a superset of data compared to models trained in our work. Best Valid AUC is not reported, because the model was used off-the-shelf for inference only.

From Table 2, we can observe performance gains from the balanced batch sampling model over the random batch sampling model. By using balanced batching, we are able to outperform the random sampling approach in all six experimental settings, in this work.

Randomly sampling mini-batches from a merged dataset may result in data bias, because the sampled data may come from only one of the multiple distributions available or there may be fewer samples from some distributions than the other. This may result in a model biased towards a certain distribution. On the other hand, the balanced batch sampling uses a stratified sampling approach, which ensures the algorithm sees data from each distribution at every iteration during training. The model in this case is less/not biased towards any of the distribution. The training datasets themselves were balanced for both balanced and random batch sampling. So it appears the overall balancing is not as impactful as the balancing of the mini-batches passed to the algorithm. The challenge of sample imbalance for each task is taken care of by computing a weighted loss.

Also, although the Baseline XRV model is trained on a much larger data, and overlaps the test data, the average AUC of our model trained with balanced batching is as almost good as the XRV model.

Potential negative societal impact

This research uses only previously public data, so there are no privacy concerns. We do not foresee any negative societal impact as a result of the research described in this work.

Acknowledgments

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