Risk of Training Diagnostic Algorithms on Data with Demographic Bias

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Abstract. One of the critical challenges in machine learning applications is to have fair predictions. There are numerous recent examples in various domains that convincingly show that algorithms trained with biased datasets can easily lead to erroneous or discriminatory conclusions. This is even more crucial in clinical applications where the predictive algorithms are designed mainly based on a limited or given set of medical images and demographic variables such as age, sex and race are not taken into account. In this work, we conduct a survey of the MICCAI 2018 proceedings to investigate the common practice in medical image analysis applications. Surprisingly, we found that papers focusing on diagnosis rarely describe the demographics of the datasets used, and the diagnosis is purely based on images. In order to highlight the importance of considering the demographics in diagnosis tasks, we used a publicly available dataset of skin lesions. We then demonstrate that a classifier with an overall area under the curve (AUC) of 0.83 has variable performance between 0.76 and 0.91 on subgroups based on age and sex, even though the training set was relatively balanced. Moreover, we show that it is possible to learn unbiased features by explicitly using demographic variables in an adversarial training setup, which leads to balanced scores per subgroups. Finally, we discuss the implications of these results and provide recommendations for further research.

Keywords: Computer-aided diagnosis · Demographic bias · Fairness

1 Introduction

In medical image analysis, machine learning (ML) algorithms can be on par with or even exceed the performance of experts. However, for reliable generalization, large datasets are needed, which is often not the case [5,12]. A further requirement is that the properties of the training data are similar to the test data, which is sometimes overlooked. For example, some patient groups (based on age, sex, ethnicity among others) can be overrepresented in the data, biasing the model. Besides the notorious discriminatory face recognition example [4], detrimental effects of such bias have been demonstrated in various domains, varying from
predictions of recidivism, to job offer or loan decisions. For medical imaging, the problem seems relatively unexplored, despite the potentially harmful consequences.

We aim to quantify whether and how bias is addressed in medical imaging papers focusing on the diagnosis. We first survey proceedings from a recent conference. For selected papers, we report the sample size, whether any demographic measures are available, whether these are used by the algorithm and whether demographics/bias are discussed in the paper. Using a dataset of skin lesions, we then demonstrate that a classifier trained on a relatively balanced dataset in terms of age and sex already shows biased results on the held-out test set. Finally, we provide some guidelines for evaluating algorithms with regard to this important topic.

1.1 Related work

One form of dataset bias refers to a distribution shift between datasets, such that models trained on one dataset, show a drop in performance on the other. This idea has been studied in computer vision [14, 25]. In medical imaging, such drops in performance can be experienced in datasets collected at different centers [2, 20, 26]. Such differences are often addressed with transfer learning [5] techniques, which either align the data distributions or learn dataset-independent representations.

A more specific case of dataset bias is when the bias is based on the demographics of the training subjects including differences in ages, sexes, diets, habits, genetics and so on. As an example, it has been demonstrated that face recognition algorithms can discriminate based on e.g. skin color and perform poorly on under-represented groups [4]. In medical imaging, similar factors might influence the data, thus have an impact on the incidence of disease too, as shown in some studies. For instance, [7, 16] describe that signs of brain aging as a biomarker of aging can be predicted from brain neuroimaging and retinal images; or the work by [8] demonstrates the relation between the human immunodeficiency virus and the aging process of the brain [8]. Thus it is essential to include the demographics in the data analysis.

Various algorithms to mitigate this type of bias have been proposed. The first set of approaches focuses on preventing this bias in the first place i.e., creating a balanced set in the data preparation step [22]. However, this is not always an option especially for medical data which is rare and where new acquisitions are often costly. Therefore, recent studies have focused mainly on learning representations that are not only predictive of the actual outputs but also invariant to the extraneous factors [1, 9, 21, 28]. In most cases, by including the additional available demographic information during training, their predictive power is mitigated by an adversarial loss and the features become invariant to them.

Due to the rise of machine learning diagnostic applications in the medical image analysis domain, we conduct a survey of the published techniques in MICCAI 2018 [10] to investigate the inclusion of demographics in addition to the medical images. Our results show that even though the demographics might impact the
outcome of the models, it is not a widely discussed topic in medical imaging. Not only most of the datasets do not include the demographic information, but also the proposed techniques rarely propose to correct for potential biases in their models. Additionally, we use a relatively balanced dataset of skin lesions [6] and highlight the importance of correction for age and sex biases in this dataset. The closest study to this analysis is [15], where they show that skin lesion datasets over-represent lighter skin, but do not find large differences in performance for different skin types.

2 Methods

2.1 Paper analysis

We screened the MICCAI 2018 proceedings [10] for papers on diagnosis using macroscopic images. We, therefore, focused on the chapters “Machine Learning in Medical Imaging”, “Optical and Histology Applications”, “Cardiac, Chest and Abdominal Applications” and “Neuroimaging and Brain Segmentation Methods: Neuroimaging”. Papers were included if they focused on the diagnosis or detection of abnormalities. For each selected paper, one of the authors quantified the following: number of public or private datasets used, number of subjects, whether demographic information was given, and whether demographics were discussed.

2.2 Classifier analysis

To understand potential differences in the performance of a classifier for different demographic groups, we set up a baseline binary classification experiment. We used the ISIC 2017 skin lesion dataset [6] for the diagnosis of melanoma skin cancer since the age and sex were available for over 75% of the subjects. We included only the subjects for which both variables were available in our analysis. Age was provided to the nearest 5 years. To create large enough subgroups for evaluation, we split the subjects by calculating the median age in the training set (equal to 60) and using that as a threshold. The numbers of subjects in each group are provided in Table 1.

| ISIC subset | Total | Included | Male | Female | $< 60$ | $\geq 60$ |
|-------------|-------|----------|------|--------|-------|----------|
| Train       | 2000  | 1744     | 886  | 858    | 1087  | 657      |
| Validation  | 150   | 149      | 90   | 59     | 87    | 62       |
| Test        | 600   | 553      | 283  | 270    | 302   | 251      |

**Baseline network.** We trained an Inception-v4 [24] network as our baseline model using the training procedure from [19], which has outperformed the
top result (0.874) from the ISIC 2017 challenge. The network uses data augmentation based on adjusting the color (saturation, contrast, brightness, hue) and geometry (affine transformations, flips, random crops) of the image. The network is initialized with ImageNet weights, and then further trained on randomly augmented training images resized to $299 \times 299$. Training is then done with stochastic gradient descent with a momentum factor of 0.9, batch size of 40, and learning rate of 1e-3 which is reduced to 1e-4 after the 10th epoch. Early stopping is used if the validation area under the curve (AUC) does not improve after 8 epochs. At test time, an image is randomly augmented 32 times, and the predictions are averaged. All parameters are used as defined by [19] and not specifically optimized for the subset of data that we used. We evaluated the classifiers with AUC for the following groups: all subjects, male, female, young ($< 60$) and old ($\geq 60$).

**Bias-aware network.** To evaluate whether the learned representation has any relation to the available demographics, we use the method proposed by [1]. Thus we employ an ensemble network with a shared feature encoder (the same as the baseline model) and two classifier heads. One classifier is in charge of classifying the skin cancer and it consists of a fully connected layer followed by average pooling and softmax layers (similar to the baseline model). The other head is supposed to predict the confounding parameter and it consists of a fully connected layer followed by an average pooling layer. Parameters of the encoder, cancer classifier and bias predictor are denoted by $\theta_e$, $\theta_c$, $\theta_{bp}$ respectively. Three losses are used for training the network. For training the skin cancer classifier head and encoder a cross-entropy loss ($L_c$) is used. While for optimizing the bias predictor head, a bias prediction loss ($L_{bp}$) is defined as the negative-squared Pearson correlation coefficient ($-\text{Corr}^2$). By minimizing $-\text{Corr}^2$, the correlation between the predicted and true confounding parameter should increase. Since sex is a binary parameter, in some experiments we define $L_{bp}$ as a binary cross-entropy loss ($BCE$). The third loss is defined as $L_{br} = -\lambda L_{bp}$ and is used to optimize the encoder adversarially to reduce the predictive power of the encoded features for the confounding parameter. $\lambda$ determines how much the encoder is penalized for leading to correct predictions of the target demographic parameter.

The ensemble network is trained iteratively with three main steps: (a) updating $\theta_e$ and $\theta_c$ based on the $L_c$ loss; (b) updating only the $\theta_{bp}$ parameters based on $L_{bp}$ loss; (c) and finally updating $\theta_e$ adversarially based on $L_{br}$ loss. Note that the encoder weights are not updated in the second step, and the bias predictor weights are not updated in the third step. The updates are done one-by-one iteratively. The learning rates and optimizers of the three update steps are the same as the baseline model. It is worth mentioning that for the steps involving the bias prediction, we only use the control data to make sure that the confounding parameters are reliably estimated from healthy subjects. Multiple experiments are performed to see whether it is possible to weaken the potential relationship between the encoded features from images and the confounding parameters, in our case age or sex.
3 Results

3.1 Paper analysis

A total of 65 papers fit our inclusion criteria. Several statistics of the datasets used, and the inclusion of demographic information by the papers are shown in Fig. 1. In total there were 52 papers using 1 dataset, 11 papers using 2 datasets, and 2 papers using 3 or more datasets. Nearly half (32 papers) did not use any public datasets. The sizes of the datasets varied between 10 subjects and 112K subjects, with 217 subjects as the median size.

In this set of 65 papers, 12 papers described at least age or sex. Notably, 10 of these were neuroimaging papers. Of the 12 papers, only 3 also evaluate or discuss their results with respect to the demographics. [18] test whether their glaucoma risk index differs significantly between the healthy and patient groups, while also checking whether these groups have statistically different age and sex distributions. [11] stratify their results of detecting brain malformations by age group (children vs adults). Finally [13] corrects their Alzheimer’s score estimation for brain images, with a factor based on linear regression of cognitively normal subjects.

3.2 Classifier analysis

The AUC performances on the test set across different subgroups and all the subjects are shown in Table 2. For each experiment, we have specified the $L_{bp}$, demographic, and $\lambda$ parameters used during training. The baseline model achieves an overall AUC of 0.83 that is slightly lower than the AUC of 0.88 reported in [19] because we only use the subset of subjects with known demographics and we do only half of the test time augmentations used by [19]. Moreover, the ensemble networks achieve the same performances as the baseline model when $\lambda$ is set to 0 (experiments 2, 4 and 6) because there is no back-propagation from
Table 2: An overview of the AUCs obtained in each experiment. The most balanced performances after correction for the bias are bolded.

| Experiment | Confounder | $\lambda$ Lbp | All   | Young | Old | Male | Female |
|------------|------------|----------------|-------|-------|-----|------|--------|
| 1. Baseline| N/A        | N/A            | 0.83  | 0.76  | 0.84| 0.76| 0.90   |
| 2. Ensemble| age        | 0 Corr$^2$     | 0.83  | 0.78  | 0.83| 0.77| 0.90   |
| 3. Ensemble| age        | 5 Corr$^2$     | 0.80  | 0.77  | 0.80| 0.73| 0.90   |
| 4. Ensemble| sex        | 0 Corr$^2$     | 0.83  | 0.77  | 0.84| 0.76| 0.91   |
| 5. Ensemble| sex        | 5 Corr$^2$     | 0.72  | 0.64  | 0.75| 0.78| 0.78   |
| 6. Ensemble| sex        | 0 BCE          | 0.84  | 0.77  | 0.85| 0.78| 0.90   |
| 7. Ensemble| sex        | 0.5 BCE        | 0.83  | 0.78  | 0.84| 0.77| 0.91   |

Fig. 2: Left: The $L_{bp}$ loss of the ensemble network with $\lambda = 0$ (experiments 2 and 4 in Table 2); right: The $L_{bp}$ and $L_{br}/\lambda$ losses when $\lambda > 0$ (experiments 3 and 5).

the bias predictor head to the encoder i.e., $L_{br} = 0$. In these experiments, both subgroup splits show large differences between them: depending on age, the AUC varies between 0.76 and 0.85 (9%), and depending on sex, between 0.76 and 0.91 (15%). The obtained $L_{bp}$ values for experiment 2 and 4 ($\lambda = 0$) are also shown in Fig. 2 (left). As seen in this figure, there exist some correlations between the predicted and true confounding parameter when the encoder is only optimized for classifying skin cancer. This correlation is stronger for age than sex.

When we use the ensemble network to predict the age of the control subjects in an adversarial setting (experiment 3), we see that the differences between the performances of young and old subgroups decrease (only 3%), while that is not the case for male/female subgroups. Similarly, when the sex is used as the confounding parameter (experiment 5), the AUC of male/female subgroups get closer (5% difference), while the difference between young/old subgroups remains large (11%). The values of $L_{bp}$ and $L_{br}/\lambda$ for experiments 3 and 5 are visualized in Fig. 2 (right). Since the training is a min-max optimization problem, compared to the left figure, the correlation does not increase during training i.e., $L_{bp}$ does not decrease. Additionally, the training stops much earlier resulting in a drop in the overall AUC of the skin cancer classifier.
Since sex is a binary parameter unlike age, the $BCE$ loss is used in experiments 6 and 7. As depicted by results, the $BCE$ loss is not as effective as the $-Corr^2$ and the AUCs are almost the same as the baseline model. Note that $\lambda$ is determined heuristically based on the ratio between $L_c$ and $L_{bp}$ loss in order to have an effective penalty in updating the encoder weights.

4 Discussion and conclusions

Our paper analysis showed that demographics are rarely discussed and used in diagnostic algorithms. A possible way to address this problem would be to standardize what information about the data needs to be included in a research paper. This could be inspired by model cards [17], which describe what situations a model is trained to deal with (or not). Enforcing such standards would require large-scale collaboration between journals and conferences, but researchers could already include such model cards to increase awareness in the community as a whole. Although this type of measure does not remove bias, it can show that a bias potentially might exist. The exact sources of this bias could then be quantified, for example following the framework proposed by [23].

Another important direction is building bias-aware algorithms and evaluating them. Once an algorithm is designed to be sensitive to bias, we need to evaluate whether it is successful at this. Therefore, we need ways to quantify what performance gap is evidence of bias or not.

Our classifier analysis results showed large differences in performance between male and female subjects, and between different groups of age for the baseline model. The male/female difference is somewhat surprising, given that the training data was relatively balanced. This suggests that these factors might influence how difficult a skin lesion is to diagnose. For example, men and women have different distributions of melanoma subtypes [3], some of these could be over or underrepresented in the data. Additionally, we demonstrated the possibility to correct for the potential bias in predictions to some extent by using an adversarial training setting.

Our results indicate that age, sex and possibly other characteristics might bias the results differently. There might be some correlations between different confounders, or a case of Simpson’s paradox [27]. Moreover, there might be additional unknown factors (for instance the skin color or the hairs on the skin) that need to be identified and treated appropriately. In general, correction is more effective, when all confounding parameters are known and used simultaneously along with training for the main target task. Additionally, we treated the age as a continuous parameter, but the evaluation was done for two subgroups (young and old). The fairness of this evaluation strategy needs to be investigated in future works.

In conclusion, we highlighted the importance of fairness in medical datasets and diagnostic algorithms, since ignoring it could affect the generalization across different demographic subgroups. We believe that this is an important point of attention for researchers working in medical image analysis community.
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