Comparison of Multiple Generators in GANs and Analysis of Generated Datasets

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***Abstract*—We propose in this paper a new approach to train the Generative Adversarial Nets (GANs) with a custom mixture of generators to overcome the mode collapsing problem. The main intuition is to employ multiple generators, instead of using a single one as in the original GAN. The idea is simple, yet proven to be extremely effective at covering diverse data modes, easily overcoming the mode collapsing problem and delivering state-of-the-art results. A minimax formulation was able to establish among a classifier, a discriminator, and a set of generators in a similar spirit with GAN. Generators create samples that are intended to come from the same distribution as the training data, whilst the discriminator determines whether samples are true data or generated by generators, and the classifier specifies which generator a sample comes from. The distinguishing feature is that internal samples are created from multiple generators, and then one of them will be randomly selected as final output similar to the mechanism of a probabilistic mixture model. In order to achieve this we introduce a custom training loop in our training method to the Mixture Generative Adversarial Nets (MGAN). We develop theoretical analysis to compare the effect of different stacks of generators, their architecture and effect from their enumeration .We conduct extensive experiments on synthetic 2D data of breast cancer cells to demonstrate the superior performance of our custom built MGAN in achieving state-of-the-art Inception scores over latest baselines, generating diverse and appealing recognizable objects at different resolutions, and specializing in capturing different types of objects by the generators.**

Keywords—MGAN ,breast cancer, analysis, performance, generators (*key words****)***

I. Introduction

Generative Adversarial Nets (GANs) (Goodfellow et al., 2014) are a recent novel class of deep generative models that are successfully applied to a large variety of applications such as image, video generation, image inpainting, semantic segmentation, image-to-image translation, and text-to-image synthesis, to name a few (Goodfellow, 2016). From the game theory metaphor, the model consists of a discriminator and a generator playing a two-player minimax game, wherein the generator aims to generate samples that resemble those in the training data whilst the discriminator tries to distinguish between the two as narrated in (Goodfellow et al., 2014). Training GAN, however, is challenging as it can be easily trapped into the mode collapsing problem where the generator only concentrates on producing samples lying on a few modes instead of the whole data space (Goodfellow, 2016). Many GAN variants have been recently proposed to address this problem. They can be grouped into two main categories: training either a single generator or many generators. This was the problem the previous implementation tried to solve using an ensemble of generators. In this case we take their results, introduce a custom training loop proven to be more efficient and provide an analysis on the images produced by these generators, and decipher their correlation with accuracy on each iteration.

In short, our main contributions are: (i) a custom training loop for the adversarial model to efficiently train a mixture of generators; (ii)) a comprehensive evaluation on the performance of our method on generating real world-scale datasets of diverse cancer cells by using a separate classifier.

II. Generative Adversarial Networks

A. Introduction

Given the discriminator D and generator G, both parameterized via neural networks, training GAN can be formulated as the following minimax objective function: min G max D Ex~Pdata(x) [log D (x)] + Ez~Pz [log (1 − D (G (z)))] (1) where x is drawn from data distribution Pdata, z is drawn from a prior distribution Pz. The mapping G (z) induces a generator distribution P model in data space. GAN alternatively optimizes D and G using stochastic gradient-based learning. As a result, the optimization order in 1 can be reversed, causing the minimax formulation to become maximin. G is therefore incentivized to map every z to a single x that is most likely to be classified as true data, leading to the mode collapsing problem.

B. Proposed Evaluation

The images after being generated by the different sets of Gan's will then be formatted into a dataset and further tested on a separate classifier to confirm which set will yield the most accurate results.

III. Datasets

The breast cancer dataset from breakhis has been used in this paper. The dataset contains a training set and a testing set each containing subdivisions of different levels of magnifications of the cells, for eg. 40X, 100X etc. For efficiency and time related issues, we chose to make use of the 40X magnification folder for both training and testing. The data needed to be cleaned and pickled into a numpy array to be fed into the MGAN. Within the chosen magnification lies sub-labels for benign and malignant samples. Hence two pickle files need to be created to train the model separately. Due to the target images being detailed cells, the necessity of high accuracy and precision needed to be met, hence the data was appropriately segregated and chosen for training and testing purposes. To replicate an original dataset after all, takes quite a lot of effort to make

sure almost no visible difference remains between the faux and original.

IV. METHODS

A. *Working of the MGAN*

The idea here is to use a mixture of many distributions rather than a single one as in the standard GAN, to approximate the data distribution. Simultaneously we enlarge the divergence of those distributions so that they cover different data modes.

Taking an analogy to a game among K generators G1:K, a discriminator D and a classifier C can be formulated. Each generator Gk maps z to x = Gk (z), thus inducing a single distribution PGk ; and K generators altogether induce a mixture over K distributions, namely P model in the data space. An index u is drawn from a multinomial distribution Mult(π), where π = [π1, π2, ..., πK] is the coefficients of the mixture; and then the sample Gu (z) is used as the output. Here, we use a predefined π and fix it instead of learning. The discriminator D aims to distinguish between this sample and the training samples. The classifier C performs multi-class classification to classify samples labeled by the indices of their corresponding generators. We term this whole process and our model the Mixture Generative Adversarial Nets (MGAN).

B. *Dataset Generation*

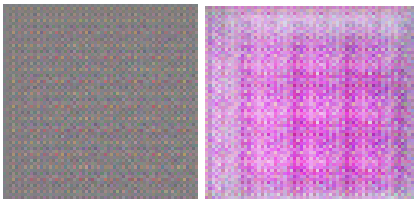
The basic intuition here is to generate multiple unique data samples for our model, as well as minimizing the problem of modal collapse. We reused the experimental design proposed in (Metz et al., 2016) to investigate how well our MGAN can explore and capture multiple data modes. The training data is sampled from a 2D mixture of 8 isotropic Gaussian distributions with a covariance matrix of 0.02I and means arranged in a circle of zero centroid and radius of 2.0. Our purpose of using such small variance is to create low density regions and separate the modes. We employ 4 generators, each with a simple architecture of an input layer with 256 noise units drawn from isotropic multivariate Gaussian distribution N (0, I), and two fully connected hidden layers with 128 ReLU units each. For the discriminator and classifier, one hidden layer with 128 ReLU units is used. The diversity hyperparameter β is set to 0.125.

C. *Evaluation*

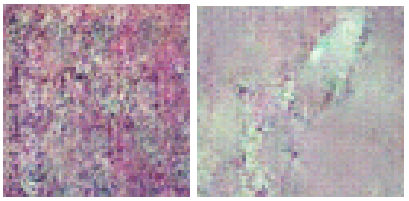
We present samples randomly generated by our proposed model trained on the 2 datasets (one benign and one malignant) for qualitative assessment. Our dataset contains a wide range benign and malignant colored microscopic images consisting of training dataset and a testing dataset each containing subdivisions of different levels of magnifications of the cells such as 40X, 100X etc. Images generated from our custom dataset each with a resolution 64×64, are diverse with some recognizable objects pink hue, cancer generated mass and our the MGAN is capable of generating visually appealing images with complicated details. However, many samples are still incomplete and unrealistic which can be inferred from closer inspection of the dataset generated

V. RESULTS

VI. BENIGN:

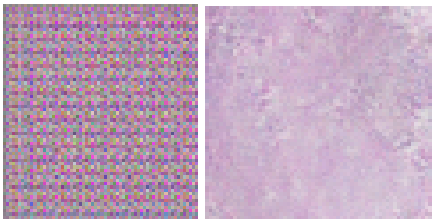


a)1st epoch b)350th epoch

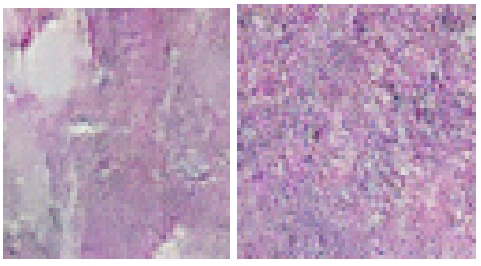


c)750th epoch d)1000epoch

VII. MALIGNANT:



a) 1st epoch b) 350th epoch



c)750th epoch d)1000th epoch

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