Boosting Classification Accuracy of Fertile Sperm Cell Images leveraging cDCGAN

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Introduction

Drawing inferences from a spermatozoon (Sperm Cell) image based on its morphology is ubiquitous, challenging, and of substantial practical interest. In the present study, we endeavour to deconstruct and demonstrate a framework to distinguish between the binary classes, which constitutes 'Good' (Fertile) and 'Bad' (Infertile) Sperm Cell images. We have selected the DenseNet121 architecture to train our model for this task. Furthermore, Conditional Deep Convolutional Generative Adversarial Networks (cDCGAN) was used to tackle the minority Class imbalance problem, which was heavily prominent in the dataset chosen for this task. We have hand-picked numerous statistical inferential tests and metrics to validate our model to accentuate the reliability of the obtained results, thus finally formulating and delineating a table based on the respective 'Quality Scores' of the test samples provided. With the cDCGAN training data augmentation, the test-set accuracy was recorded to be 86.2%, while the model without cDCGAN scored only 24.3%.

Background of the study

It is estimated that infertility affects 48.5 million couples globally. Males are found to be solely responsible for 20-30% of infertility cases and contribute to 50% of cases overall. Visually analyzing the sperm is a very sophisticated evaluation tool of human fertility and is a strong indicator of a man's physical and, thus, reproductive health.

Methodology

Data Redistribution

Data Preparation

Data Augmentation using cDCGAN

Training the architecture (DenseNet121)

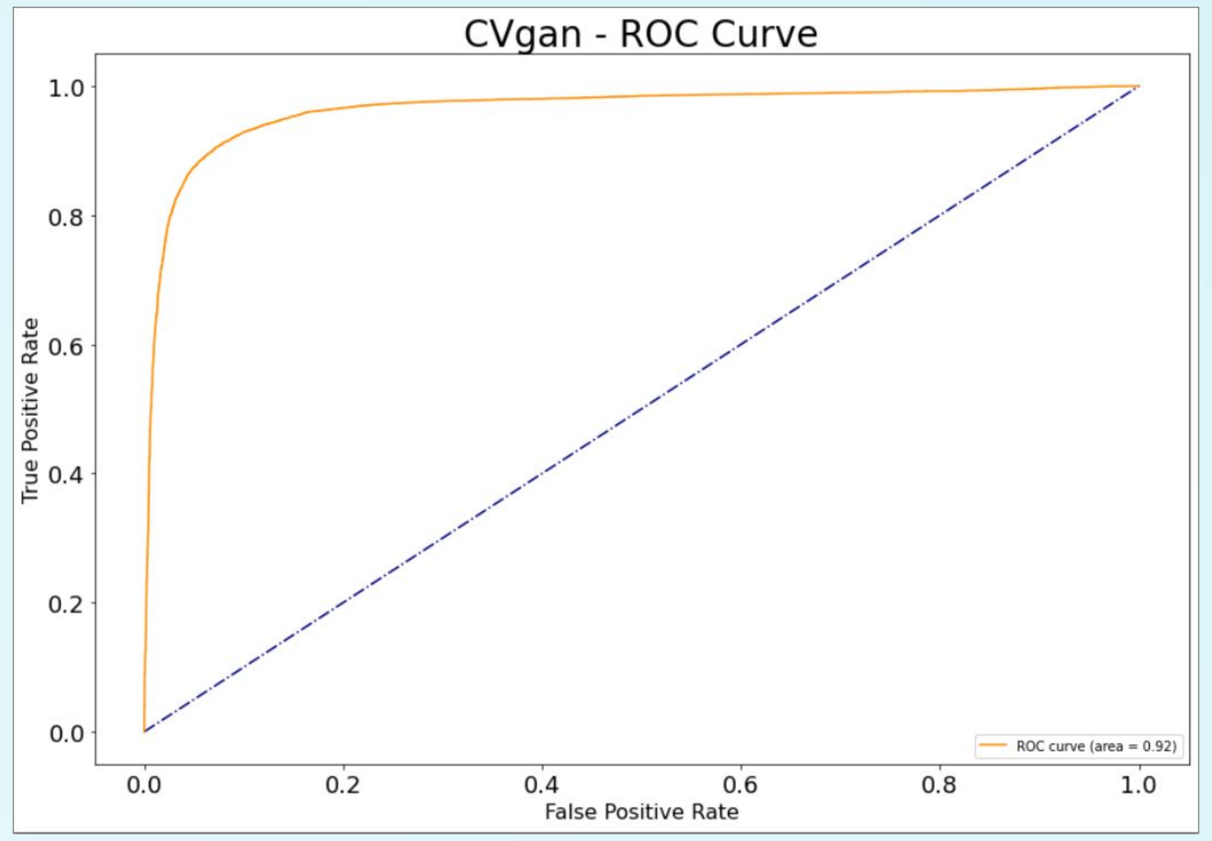
Model Validation

Employment of the Threshold Technique

Evaluation of Quality Scores on Test Set

Results

CV#	F1-Score	roc_auc Score	best_thr	Test Accuracy
CV_{GAN}	0.602±0.02	0.922±0.03	0.715±0.02	0.862±0.02
CV_{RAW}	0.452±0.05	0.512±0.03	0.185±0.04	0.243±0.06



Test Samples	Quality Scores
D926	0
E883	35
E902	0
E914	27
E919	17
E950	34
E952	10
E979	46
E986	38
E998	60

Conclusion

We present a method by virtue of which we could exhibit the task of classifying Sperm Cell images based on morphology. However, this method also encompasses a real-world approach to train an architecture on high-quality annotated images and using the same architecture to draw inferences on low-quality annotated unlabelled images. We explored the efficacy of our method through the means of various statistical tests. In light of this proposition, we have also made meticulous efforts to make our model learn to classify and validate the results using a different distribution (with greater variance) than the former.