



## GAN-Based Metaphase Image Enhancement

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### ABSTRACT:

Medical images like metaphase imaging can be effectively visualized thanks to machine learning's success in medicine. First and foremost, before training the data (pictures), any redundant or irrelevant information, such as noise, artefacts, or incorrect data, must be removed. The staining noises, uniformity, and blurring frequently occurring in chromosomal images meaningfully impact the karyotyping procedure. In this study, chromosomal image processing was done using transfer learning on a Generative Adversarial Network (GAN). The automated karyotyping approach produces promising results that are effectively employed for segmentation. Natural Image Quality Evaluator (NIQE) and Perception-based Image Quality Evaluator (PIQE) scores have been used to quantify the performance of the suggested method. On average, 1000 images used for testing and perfect in removing noise, blurriness and contrast have been obtained.

### Introduction:

Karyotyping is the scientific term that is used for the study of chromosomes. Cytogenetics mainly focuses on chromosome analysis and cell activity study to diagnose early-stage genetic disease. A smaller number or a higher number of chromosomes than the standard pair of chromosomes caused several congenital abnormalities like Down syndrome, chronic myelogenous leukemia and Edwards's syndrome. Over the decades, the intelligence in machines has been embedded such that devices can compute the problems of daily life. The manual process of karyotyping computer-aided methods is introduced so that the tediousness, laboriousness, error-proneness, and more time-consuming problems can be solved. The booming research created an automated karyotyping system (AKS). AKS undergoes pre-processing, segmentation, feature extraction and classification[1].

Automatic karyotyping systems face challenges with the quality of input images. The input metaphase images or chromosome images prone to staining noise, blurriness and in homogeneous illumination. Moreover, the contrast has been lacking in the banding patterns, which

provides a poor study of chromosome structure. When the analysis of chromosomes is not appropriate, predicting genetic abnormalities during the classification phase of AKS is complex. These are the challenges faced during the first stage of AKS, known as pre-processing [2].

The quality of the image is affected and results in degradation due to blurring, motion artifact and environmental disturbance. Image Quality Assessment model (IQA) perfectly assess the quality of images in comparison with human judgement. The models are classified into two classes: Subjective approach and Objective approach model. Subjective approach has been highly accurate and required physical judgement time consuming and laborious. Second approach is objective based on logical concept. The image quality has been predicted with an automatic process. Image Quality Assessment model follows three methods Reduced Reference (RR), Full Reference (FR) and No-Reference (NR). Reference images has been predicting the quality of test images using some features set. The image is not appropriate for real-world applications because in some conditions the availability of reference



image has not been much in all imaging condition. So, the preference is testing the dataset with non-reference (NR) techniques are preferred. The non-reference (NR) techniques are also called blind-IQA model. The Non-Reference model does not prefer initial knowledge of reference images for assessing quality of test images. The perception beneath these model Natural Scene Statistics (NSS) and Human Visual System (HVS). The natural scene statistics, features are statistics regular and vary with level of distortion. However, HVS based model prefers perceptual features to imitate the visual content present in human being vision physiology[3].The paper enclosing technique for enhancing metaphase images using machine learning approach. The literature in relation to pre-processing has been included in the paper in Section II,

## I. Literature Survey

Pre-processing of metaphase images require removal of inhomogeneity, blurriness and noises (sensor and staining) for designing better automated karyotyping system. The literature based on various image preparation techniques based on machine learning for image's quality enhancement of metaphase images.

The researchers aid in analyzed the input images for better representation. The pre-processing methods removed the noise. The non-linear operation-based approach of median filtering with window of 5x5 has been used and freed chromosome images from surrounding noises [4].Next authors proposed a method for denoising and image enhancement of chromosome images .The strategy follows quantitatively modelled with subjective and objective criteria [5].The study investigate chromosome image enhancement for extracting the features using deep learning network [6].The proposal of (NR)/blind method for evaluating the quality of distorted images without using reference image. The Divine Identification -based Image Verity and Integrity Evaluation (DIVINE) a two-stage architecture includes distortion recognition and distortion -specific quality evaluation[7].A local binary pattern (LBP) is employed in the NR-IQA model to gather textural information before being changed to extract structural information[8].The Super-Resolution Generative Adversarial Network (SRGAN) for sharp visual perception with a realistic texture of chromosome images .The Residual-in-Residual Dense Block (RRDB),has a batch normalization network for

forecasting the relative realness rather than absolute value. The authors proposed ESRGAN for enhancements of chromosome images with producing a higher visual quality and natural textures than the SRGAN[9].The study uses a deep learning-based technique called Transfer GAN to enhancing the resolution of multimodal CT images while reducing the required radiation dose. The method follows an extensive tests using an approach of transfer learning for improves visualization and quantity[10].Futher,images of chromosomes are enhanced using novel approach defending against adversarial attacks called Chained Dual-GAN (CD GAN). CD GAN uses iterative under-sampling and oversampling to minimize the perturbations of the hostile image[11].Area of single image super resolution(SISR) has been improved using a GAN-based model called SRGAN.A deep residual network (ResNet) with skip links is the SRGAN generator that enhancing chromosome images The augmented perceptual loss function that consists of adversarial loss and content loss. The scientists used feature maps from the VGG network to build a content loss that more precisely assesses perceptual similarity. Adversarial loss was used to create images that were more realistic and organic. Compared to earlier models, the SRGAN model produces images with higher perceptual quality. The results of this approach, however, frequently have undesirable artifacts[12].

## II. Proposed Method

The chromosome images are affected with staining, imaging conditions and sample defects that need to be enhanced for better analyzing chromosome band features. The upcoming subsections focus on repository and technique behind the proposed model. Interest in deep learning-based computer systems to support medical diagnosis is high. However, public contributions cannot accelerate the development and enhancement of these systems because of restrictions on data access arising from proprietary and privacy constraints. The dataset used in the proposed model has been fine tune using the concept of transfer learning. The fine tuning will be performed on the basis of two factors: quality of images and volume of the dataset. Artificial intelligence (AI) uses GANs to augment data. Artificial neural networks (ANNs) generate synthetic images and simultaneously learn to identify them as real photographs. The robust suggested ESRGAN model



,will train the large dataset images in the significant amount of time. Transfer learning in this work refers to the process of retraining the ESRGAN model that had been trained for general image super-resolution for a second related task (medical image pre-processing) on datasets of metaphase images. The transfer learning method is beneficial in amending the medical-based images.

This method can enhance the model's performance by utilizing insights from natural-picture datasets. Transfer learning also speeds up the model's convergence. We apply the transfer learning technique[13] to address these difficulties.

## A) Dataset

Chromosomes are intracellular aggregates that house genes, which are the primary focus of biological cytogenetics research. Each of the 5,000 metaphase cell photos in the database has 46 chromosomes (23 pairs) and 5,000 photographs in total. The dataset also includes three distinct categories of annotations: 1) 2,000 annotations for each chromosome, 2) 229,852 object annotations (bounding boxes) for 24 separate chromosomes, and 3) 5000 pixel-level labels for a single chromosome segmentation.

## B) Method

A deep learning-based model called ESRGAN, or Enhanced Super-Resolution Generative Adversarial Network, is employed for challenges involving the super-resolution of images. The process of enhancing an image's resolution, usually from a lower-resolution to a higher-resolution one, is known as super-resolution. The goal of ESRGAN is to produce realistic, high-quality images from low-resolution ones.

The Super-Resolution Generative Adversarial Network (SRGAN) was improved upon by ESRGAN. It makes use of the discriminator network and generator network of a Generative Adversarial Network (GAN) architecture. An image with low resolution is fed into the generator network, which outputs an image with high resolution. The goal of the discriminator network is to differentiate between the images produced by the generator and actual high-resolution pictures.

The use of a perceptual loss function that combines adversarial loss with content loss is the main novelty of

ESRGAN. More realistic and aesthetically pleasing high-resolution photos are produced with this method. In order to collect picture information more effectively, ESRGAN additionally includes a feature extraction network.

ESRGAN, a kin to other GAN-based models, has been extensively employed in many applications, such as enhancing the quality of low-resolution photos and videos and upscaling images in photography. It has addressed the difficulty of producing high-quality super-resolved images, which has benefited the fields of computer vision and image processing.

Based on a Generative Adversarial Network (GAN) structure, the architecture of ESRGAN (Enhanced Super-Resolution Generative Adversarial Network) offers certain improvements over SRGAN. An overview of ESRGAN's architecture is as follows:

- Grid of Generators (G):

Using a low-resolution image (LR) as input, the generator network in ESRGAN seeks to produce a high-resolution image (HR).

Usually arranged in a deep neural network architecture, it is composed of several convolutional layers.

The design might have residual blocks, where residual connections support the preservation of details and aid in the training of deeper networks.

A feature extraction network, also known as the Feature Pyramid Network (FPN), is frequently used by ESRGAN to extract features from the generator's intermediate layers. To calculate perceptual loss, one can use these features.

- Network Discriminator (D):

The discriminator network's job is to distinguish between high-resolution images produced by the generator and actual high-resolution photos (false images).

A convolutional neural network (CNN) is commonly used as the discriminator. It produces a single value that indicates the likelihood that the input image is a genuine high-resolution image.

- Functions of Loss:



To train the network, ESRGAN employs a variety of loss functions:

**Perceptual Loss:** Using a pre-trained network such as VGG, this loss quantifies the difference between generated feature representations and actual high-resolution images.

**Adversarial Loss:** This loss motivates the generator to create pictures that are more identical to real-world high-resolution pictures and more realistic. It is predicated on the discriminator's output.

**Content Loss:** The generator is prompted to create images that accurately reflect the content of the low-resolution input by the content loss.

- Training:

In a GAN scenario, when the generator attempts to produce images that the discriminator is unable to discern from actual high-resolution images, ESRGAN is trained.

Up until convergence is reached, the generator and discriminator networks are updated iteratively throughout training.

### C) Proposed Model

In our suggested method, the dataset is loaded to the pre-trained generator and discriminator networks of the ESRGAN model[14]. The loaded networks are refined using datasets of medical images in the following stage. We fine-tune the pre-trained ESRGAN model separately on the chromosome of the metaphase images. The model has been trained using four NVIDIA V100 GPUs. The relatively modest amount of data in most medical datasets is one of the major obstacles in the field of super-resolution for medical images. However, most medical datasets do not feature photos with a high spatial resolution. The main steps in the model's fine-tuning process are shown in Figure 1. For the fine-tuning of the dataset, we used 2000 examples, with input being a noise image and output being a clean image.

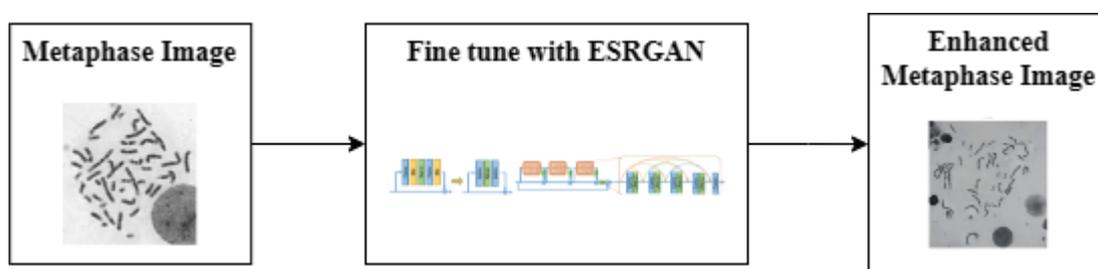
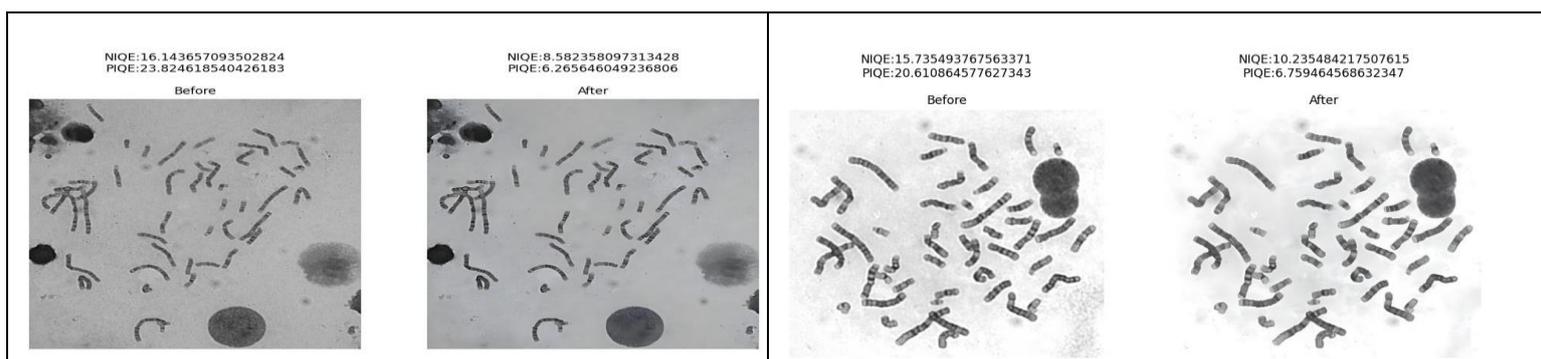


Figure 1: Proposed work for pre-processing the images

### III. Experimental Result Analysis

In this section, we performed the ESRGAN on the non-reference image and analysis using the parameters PIQE

and NIQE. We have done the sample analysis on the 1000 random samples and plotted four images at random images for visual comparison. The image results before and after are shown in the Figure 2.



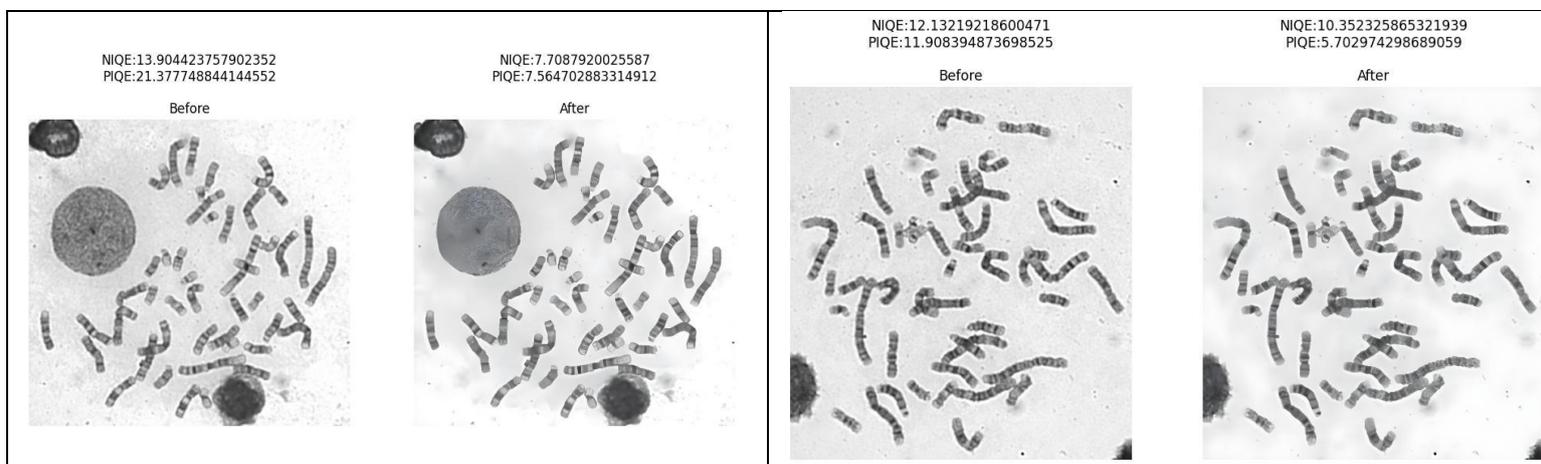


Figure 2: Pre-processed images

The following bar plot visualizes the results of the pre-processing of 1000 sample random images. It shows the minimum, first quartile, median, third quartile, and maximum values (also outliers) for NIQE and PIQE scores before and after the pre-processing.

It can be seen that all the numbers have reduced, thus indicating a gain/increase in quality shown in Figure 3.

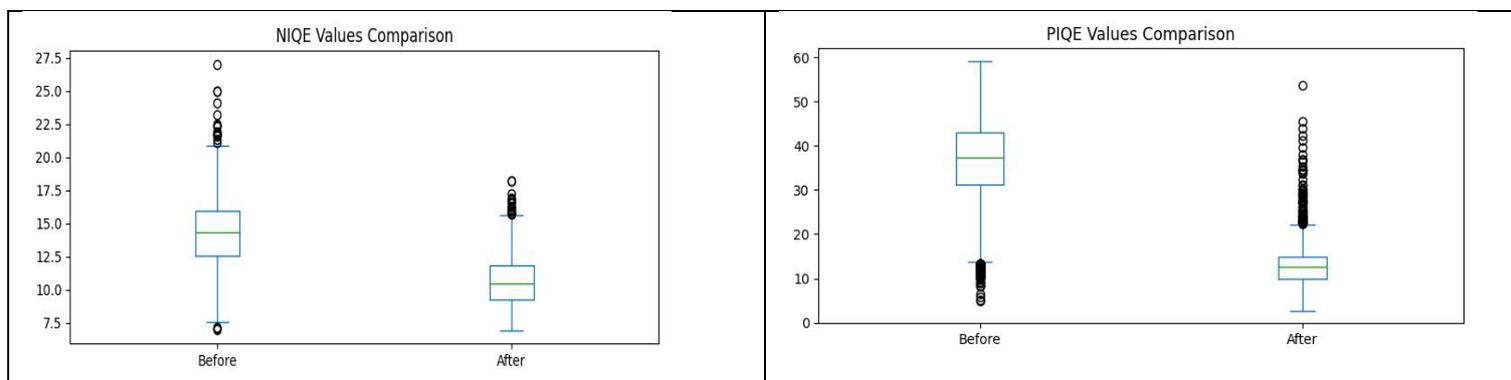


Figure 3: Performance measure

#### IV. Conclusion

In this work, we have successfully developed, tested, and evaluated a technique to improve the image quality of metaphase chromosome images using a transfer learning approach on ESR-GAN. It can be determined visually that the contrast and clarity of images have improved, blurriness reduced, and noise artifacts minimized, improving the subjective quality of images. It is also clear, using IQA measurements, that the objective quality of images has also improved significantly.

#### V. Future scope

We can use our pre-processing techniques to replace pre-processing in existing/future AKS[15] solutions to evaluate the comparative performance of our pre-processing flow vs. other pre-processing methods concerning results as part of full AKS flow.

#### Statements and Declarations

- **Competing Interests:**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

**References**

- [1] T. Arora and R. Dhir, "A review of metaphase chromosome image selection techniques for automatic karyotype generation," *Medical and Biological Engineering and Computing*, vol. 54, no. 8. Springer Verlag, pp. 1147–1157, Aug. 01, 2016. doi: 10.1007/s11517-015-1419-z.
- [2] E. Poletti, E. Grisan, and A. Ruggeri, "A modular framework for the automatic classification of chromosomes in Q-band images," *Comput Methods Programs Biomed*, vol. 105, no. 2, pp. 120–130, Feb. 2012, doi: 10.1016/j.cmpb.2011.07.013.
- [3] J. Rajavelthala and V. H. Gaidhane, "An efficient approach for no-reference image quality assessment based on statistical texture and structural features," *Engineering Science and Technology, an International Journal*, vol. 30, Jun. 2022, doi: 10.1016/j.jestch.2021.07.002.
- [4] C. College of Engineering, Cherthala. D. of C. S. and E. College of Engineering, Institute of Electrical and Electronics Engineers. Kerala Section, and IEEE Xplore (Online service), 2016 International Conference on Information Science (ICIS) : proceedings : August 12-13, 2016, College of Engineering Cherthala.
- [5] R. S. Remya, H. Prasad, S. Hariharan, and C. Gopakumar, "Chromosome Image Enhancement for Efficient Karyotyping," in 2022 International Conference on Innovative Trends in Information Technology, ICITIIT 2022, Institute of Electrical and Electronics Engineers Inc., 2022. doi: 10.1109/ICITIIT54346.2022.9744195.
- [6] Q. Li, L. Wang, IEEE Engineering in Medicine and Biology Society, and Institute of Electrical and Electronics Engineers, Proceedings, 2019 12th International Congress on Image and Signal Processing, BioMedical Engineering and Informatics: CISP-BMEI 2019: 19-21 October 2019, Huaqiao, China.
- [7] A. K. Moorthy and A. C. Bovik, "Blind image quality assessment: From natural scene statistics to perceptual quality," *IEEE Transactions on Image Processing*, vol. 20, no. 12, pp. 3350–3364, Dec. 2011, doi: 10.1109/TIP.2011.2147325.
- [8] T. Ojala, M. Pietika, and T. Ma, "Multiresolution Gray-Scale and Rotation Invariant Texture Classification with Local Binary Patterns."
- [9] Institute of Electrical and Electronics Engineers, IEEE Engineering in Medicine and Biology Society, and IEEE Signal Processing Society, IEEE ISBI 2020 International Symposium on Biomedical Imaging: 2020 symposium proceedings : April 3-7, 2020, Iowa City, Iowa.
- [10] A. B. Singh, "Chained Dual-GAN: A Generalized Defense against Adversarial Attacks," 2022, doi: 10.21203/rs.3.rs-1623864/v2.
- [11] L. Liu, P. Fieguth, Y. Guo, X. Wang, and M. Pietikäinen, "Local binary features for texture classification: Taxonomy and experimental study," *Pattern Recognit*, vol. 62, pp. 135–160, Feb. 2017, doi: 10.1016/j.patcog.2016.08.032.
- [12] T. Zhou, Q. Li, H. Lu, Q. Cheng, and X. Zhang, "GAN review: Models and medical image fusion applications," *Information Fusion*, vol. 91, pp. 134–148, Mar. 2023, doi: 10.1016/j.inffus.2022.10.017.
- [13] K. Weiss, T. M. Khoshgoftaar, and D. D. Wang, "A survey of transfer learning," *J Big Data*, vol. 3, no. 1, Dec. 2016, doi: 10.1186/s40537-016-0043-6.
- [14] J. Shao, Q. Wang, A. Wijesinghe, and E. Rahm, "ErGAN: Generative Adversarial Networks for Entity Resolution," Dec. 2020, [Online]. Available: <http://arxiv.org/abs/2012.10004>
- [15] N. Meenakshisundaram and G. Ramkumar, "A Combined Deep CNN-LSTM Network for Chromosome Classification for Metaphase Selection," in 5th International Conference on Inventive Computation Technologies, ICICT 2022 - Proceedings, Institute of Electrical and Electronics Engineers Inc., 2022, pp. 1005–1010. doi: 10.1109/ICICT54344.2022.9850651.