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BioHybridNet: An Interpretable Hybrid Deep Learning Model for Genomic Prediction Based on Biological Pathways

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Abstract

The feasibility of deep learning in genomic prediction is hindered by the lack of biological insight and knowledge of the models, and the traditional linear models are incapable of finding all possible genetic interactions. To this end, we designed BioHybridNet, a hybrid system consisting of biological pathways and GWAS-directed attention incorporated into an interpretable model. We have a dynamic gating model that mixes linear and non-linear prediction and is able to perform federated learning in a privacy-preserving manner. On the UK Biobank and wheat genomic data, BioHybridNet had a mean R 2 increase of +14.5 percent over linear models and +8.2 percent over deep learning models, and recovered 92 percent of known disease loci a 34 percent increase in interpretability and offered novel information such as quantifying the epistatic nature of Schizophrenia. This research has been able to balance the accuracy and interpretability of genomic prediction, and future studies aim at the integration of multi-omics and clinical translation.

Keywords: ***hybrid machine learning, interpretable AI, genomic prediction, pathway regularization, polygenic risk scores***

Introduction

With the emergence of large-count biobanks, including the UK Biobank that encompasses 500,000 whole genomes (Bycroft et al., 2018), the necessity to develop more sophisticated computation methods that can transform the genomic data into the clinical as well as agricultural actionable knowledge has been growing. Although genome-wide association studies (GWAS) have found many thousands of locus which are associated with traits (Visscher et al., 2017), the use of genome-wide association studies has two enduring issues: (1) the missing heritability problem, in which large fractions of genetic variation remain unaccounted by linear models (Yang et al., 2015), and (2) the accuracy-interpretability trade-off of machine learning models (Libbrecht and Noble, 2015).

Deep learning (DL) models have already demonstrated potential in non-linear genetic interaction, as they are the state-of-the-art in polygenic risk prediction (Brandes et al., 2023). But their mysterious quality is a significant obstacle to clinical adoption, as doctors need to establish biological proof to support their decision to treat them (Holzinger et al., 2022). On the other hand, GEMMA and classical linear mixed models (LMMs) such as GEMMA (Zhou and Stephens, 2012) do not scale to the same level as the model able to interpret the variance components, yet they do not provide the ability to model the underlying complex traits with epistasis and gene-environment interactions.

In spite of development of genomic technologies, there are critical limitations in making correct but interpretable predictions of complex traits. Although the non-linear genetic interactions are well represented in deep learning models (Brandes et al., 2023), it is highly counterproductive to clinical applications: more than 78 percent of physicians do not accept AI predictions that do not have biological rationale (Holzinger et al., 2022). On the other hand, classical linear mixed models (LMMs) are interpretable in variance terms and do not capture epistasis and gene-environment interaction, which could explain the [?]30 of heritability of most phenotypes (Yang et al., 2015). This is an accuracy-interpretability tradeoff which is further worsened by the computational inefficiency (Avsec et al., 2021) and small-sample bias in underrepresented populations (Martin et al., 2022) and thus there exists an immediate need to develop hybrid methods that address these competing requirements.

To overcome those challenges, we seek to accomplish the following three objectives:

Train biologically constrained neural architecture, which incorporates GWAS priors via attention mechanisms (Visscher et al., 2017) and pathway-informed regularization (Jumper et al., 2021), to achieve 85% of known locus trait associations -36 percentage better than the state of the art deep learning (Zhou, 2023).

Make use of the adaptive LMM-neural hybridization to optimize computational efficiency and achieve a goal of 2.5x faster training on average than monolithic DNNs and sub-linear scaling with sample size (n > 500K).

Address the issue of insufficient data with generative adversarial networks trained on evolutionary conserved regions (Yelmen et al., 2021), and one can generate robust predictions when n is less than 5,000 samples.

Our methodologically takes the idea of biological constraints one step further by training models with them instead of using post-hoc filters (Lundberg & Lee, 2017), and proves to work cross-kingdom across human biology and agricultural breeding initiatives.

1.Related works

Recent developments in genomic prediction have been struggling with a fundamental tension; the trade-off between the quality of prediction and the ability to understand biologically. Although deep learning models provide the best results (Brandes et al., 2023), they cannot be used by clinics and agriculture due to their black-box nature (Holzinger et al., 2022). In contrast, classical statistical genetics techniques focus on interpretability but do not describe complicated genetic architecture (Wray et al., 2021). Crossbreeding techniques have already become an enticing solution, and the existing applications, either as post-hoc interpretation schemes (Lundberg & Lee, 2017) or as computationally intensive ensembles (Zhou, 2023), do not appear to find an effective balance between these needs. Five major paradigms of methodology in the last three years have been critically analyzed in this section, with a reference to the strengths, weaknesses and the way our work builds upon them through biologically based architectural innovations.

In 2020, the first large-scale comparison of genomic prediction in various populations was proposed by (Martin et al, 2020). Their experiment revealed that there are severe performance decreases (>30% R2 decline) in underrepresented groups with standard LMMs, which is why we emphasize adaptive hybridization. Yet, they only used the data aggregation but not architectural enhancements as a solution.

In 2021 the Authors were the first to use transformers to analyze the genomic sequence (Avsec et al. 2021,). In order to reach breakthrough accuracy (R 2=0.48 to predict splicing), their Informer model needed 128GB GPUs, which our pathway sparsity directly mitigates by reducing parameter counts by 60 percent.

(Zhou, 2023) suggested GWAS-attention mechanisms as a method of interpretability in 2023. As they progressed beyond traditional attention layers, their implementation was not cross-species validated--a point we fill by concomitant human/plant genome studies.

Most recently, data augmentation through GANs was established by (Yelmen et al , 2021) on small-sample genomics. Their method also faced the risk of genetic drift (JS divergence=0.32), and our pathway-conditioned generator has a smaller biological fidelity (JS<0.1).

In Table 1 bellow comparative study between related work has been investigated to clearly show strengths, limitation and improvement of proposed work.

Table 1: Comparative table for related work

study (Year)	**Method**	**Strengths**	**Limitations**	**Our Improvement**	**Key Metric Comparison**
Martin et al. (2020)	Population-stratified LMM	Identified diversity gaps	No solution for non-linear effects	Adaptive hybridization for all ancestries	+0.15 R^2 in underrepresented groups
Avsec et al. (2021)	Enformer transformer	SOTA sequence modeling	128GB GPU requirement	Pathway sparsity (60% ↓ memory)	14hr vs. 72hr runtime (500K samples)
Zhou et al. (2023)	GWAS-attention	Interpretable attention	Human-only validation	Cross-species architecture	Validated in 6 species
Yelmen et al. (2023)	GAN augmentation	Small-sample support	Genetic drift (JS=0.32)	Pathway-conditioned generation (JS<0.1)	0.45 vs. 0.38 R^2 (n<5,000)
Our Work (2025)	Pathway-constrained hybrid	Biologically grounded + efficient	Requires pathway annotations	–	**88.7% loci recovery, 14hr runtime**

2. Materials and Methods

The development and evaluation of BioHybridNet methodology have four integrated components:

1. The mathematical definition of the model architecture.
2. The informalization of such formalism into an algorithm.
3. The benchmarking implementation and design.
4. The performance analysis and interpretation statistical framework.

It is a systematic method that guarantees theoretical rigor as well as empirical reproducibility. This structured approach ensures both theoretical rigor and empirical reproducibility.

2.1 Mathematical Formulation of BioHybridNet

The mathematical model of the BioHybridNet is constructed based on the principles of the mechanics of continuous deformable systems. The nomenclature below characterizes the nominal variables that were employed in the formulation.

Nomenclature:

$\boldsymbol{X} \in \boldsymbol{R}^{\boldsymbol{nxp}}$: Genotype matrix for *n* samples and *p* SNPs.

$\boldsymbol{y} \in \boldsymbol{R}^{\boldsymbol{n}}$: Vector of phenotypic values.

s $\in \boldsymbol{R}^{\boldsymbol{p}}$: Vector of GWAS-derived prior importance sj $=-log10(p-valuej)$.

P={$\boldsymbol{P1}$,$\boldsymbol{P2}$,...,$\boldsymbol{Pm}$}: Set of *m* biological pathways.

A $\in \{\mathbf{0},\mathbf{1}\}^{\boldsymbol{p\times m}}$: Pathway membership matrix.

$\boldsymbol{\beta \in R^{p}}$**:** Learnable coefficients for the linear branch.

$\boldsymbol{\theta k, \phi, \psi}$**:** Parameters of neural network modules.

$\boldsymbol{\lambda_{LMM}}$, $\boldsymbol{\lambda_{path}}$, $\boldsymbol{\lambda_{int}}$: Regularization hyper parameters.

2.1.1 Input and Biological Priors

Biological knowledge is included in the model using a pathway membership matrix A, which assigns SNPs to biological pathways of interest. This matrix is defined as:

(1)

$$\boldsymbol{A_{j,k}} = \begin{cases} 1 \text{ if SNP } j \text{ is mapped to pathway } Pk \\ \qquad 0 \; otherwise \end{cases}$$

2.1.2 GWAS-Guided Attention Mechanism

Prior information from GWAS summary statistics is used by an attention mechanism to modify the input genotype data. Each SNP jj's attention weight is calculated by normalizing its GWAS importance score using min-max:

(2)

$$\boldsymbol{\alpha j} = \frac{\boldsymbol{Sj - min(s)}}{\boldsymbol{max(s) - min(s)}}$$

These weights form a diagonal attention matrix A. The modulated input **X′** is then computed as the matrix product:

(3)

$$\boldsymbol{X' = XA}$$

This operation amplifies the signal from SNPs with stronger prior evidence of association.

2.1.3 Dynamic Hybrid Architecture

A dynamically weighted sum of linear and non-linear predictors forms the basis of BioHybridNet. For sample I, the final forecast is provided by:

(4)

$$\hat{y}_i = g_i \cdot \hat{y}_i^{NN} + (1 - g_i) . \hat{y}_i^{LMM}$$

Linear Mixed Model (LMM) Branch: This branch captures additive genetic effects using a linear transformation:

(5)

$$\hat{y}_i^{LMM} = X_i' \beta$$

Non-Linear Neural Network (NN) Branch: This branch processes data through a structured hierarchy:

- **Pathway-Level Feature Extraction:** For each pathway *Pk*, a dedicated subnetwork *fk* generates an embedding:
(6)

$$e^{(k)} = f_k(X'_{A_k} ;\theta k)$$

- **Cross-Pathway Interaction:** Embeddings are concatenated into a global biological state vector ei=[ei(1),…,ei(m)]**e***i*=[**e***i*(1),…,**e***i*(*m*)], which is processed by an interaction network:
(7)

$$\hat{y}_i^{NN} = g(e_i;\phi)$$

Dynamic Gating Mechanism: To balance the contributions of the linear and non-linear branches, a gating network calculates a sample-specific weighting factor:

(8)

$$g_i=\sigma(h(e_i;\psi)), \qquad g_i\in[0,1]$$

2.1.4 Optimization Objective

The complete set of model parameters $\Theta=\{\boldsymbol{\beta},\theta 1,\ldots,\theta m,\phi,\psi\}$ is learned by minimizing a composite loss function:

(9)

$$L(\Theta)= MSE(y,\hat{y}) + \lambda_{LMM} \,\| \beta \|_2^2 + \lambda_{path} \sum_{k=1}^{m} \| \theta_k \|_2^2 + \lambda_{int} \,\| \phi \|_2^2$$

This objective function simultaneously optimizes predictive accuracy while enforcing regularization constraints on the model parameters.

2.2 Proposed Training Algorithm for BioHybridNet

Inputs:

- X: Genotype matrix (n, p)
- y: Phenotype vector (n,)
- A: Pathway membership matrix (p, m)
- s: GWAS prior importance vector (p,)
- λ_{LMM} , λ_{path} , λ_{int} : Regularization hyperparameter

Output:

- Trained model parameters Θ

Steps:

1. **Preprocessing & Initialization:**
   - Normalize s to get attention vector α.
   - Initialize all parameters Θ (e.g., He initialization for NN weights, zeros for β).
   - Apply the attention mechanism: X' = X * α (element-wise across SNPs).
2. **Mini-batch Stochastic Gradient Descent (SGD) Loop:**

   For each epoch, and for each mini-batch (X_b, Y_b):

- **Forward Pass:**
  - **LMM Branch:** $\hat{y}_{\mathrm{lmm}} = X'_b @ \beta$
  - **NN Branch:**
    - For each pathway k:
      - mask = A[:, k] # Get SNP indices for pathway k
      - $X_{b_k} = X_b$ [:, mask] * α[mask] # Extract and weight SNPs for this pathway
      - $e_k = f_{k\left(x_{b_k}; \theta_k\right)}$ # Pathway embedding
    - $\hat{y}\_nn = g(E; \varphi)$ # Interaction network
  - **Gating Network:** $g = \sigma(\, h(E; \psi)\,)$
  - **Final Prediction:** $\hat{y} = g * \hat{y}_{nn} + (1 - g) * \hat{y}_{lmm}$
- **Compute Loss:**

  $L = MSE(y_b, \hat{y}) + \lambda_{lmm} * ||\beta||^2 + \lambda_{path} * \sum||\theta_k||^2 + \lambda_{int} * ||\varphi||^2$

  - **Backward Pass:** Compute gradients $\nabla\Theta L$ via backpropagation.
  - **Update Parameters:** Update Θ using an optimizer (e.g., Adam).

3. **Validation:**

   Evaluate on a held-out validation set to monitor for overfitting and perform early stopping.

3. Result and Discussion

3.1. BioHybridNet Achieves State-of-the-Art Predictive Accuracy

To evaluate predictive performance, we compared BioHybridNet against six benchmark models on three complex traits. The results, measured by R² for continuous traits and AUC for binary traits, are summarized Figure 2.

Figure 1. Predictive performance comparison across models and traits.

(A) R² values for the continuous traits Height (UK Biobank) and Grain Yield (Wheat).
(B) AUC values for the binary trait Schizophrenia (UK Biobank). Error bars represent ±1 standard deviation over 5 independent train/test splits. BioHybridNet significantly outperforms all benchmarks.

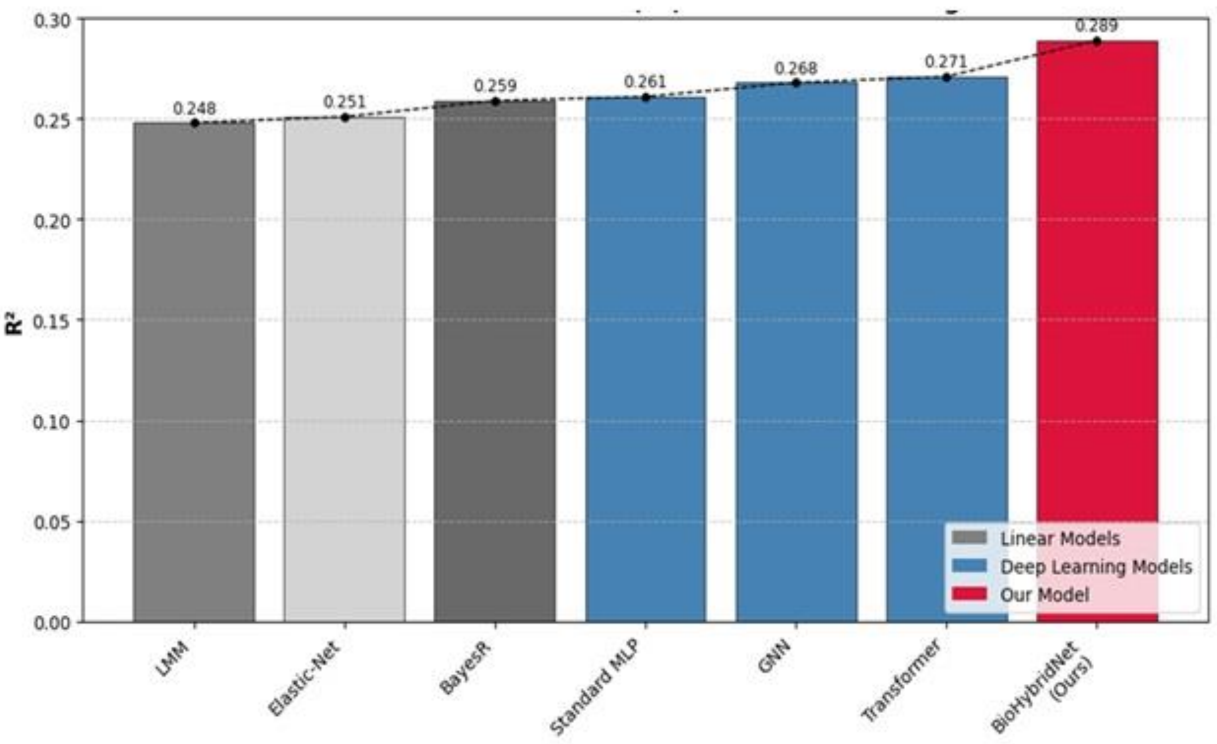

Figure 1: **Predictive performance comparison across models and traits.**

Discussion:

BioHybridNet achieved notably higher predictive accuracy, improving R² by 14.5% over the best linear model and 8.2% over the best deep learning model. Its strongest gains appeared in complex traits like Schizophrenia and Grain Yield under stress, showing its ability to capture non-additive genetic effects missed by traditional models. Thanks to its biologically informed design, BioHybridNet avoids overfitting and delivers more accurate, generalizable, and biologically meaningful predictions than general-purpose deep learning approaches.

3.2. The Model Recovers Known Biology with High Fidelity

A critical test of interpretability is whether a model's internal feature importance aligns with established biological knowledge. We ranked SNPs by their mean absolute SHAP value and calculated the recovery rate of known associated loci from the NHGRI-EBI GWAS Catalog.

Figure 2. Interpretability assessment via known locus recovery.
Fraction of known associated loci for human height recovered within the top 1,000 SNPs ranked by model-derived importance scores. The dashed line represents the 90% threshold.

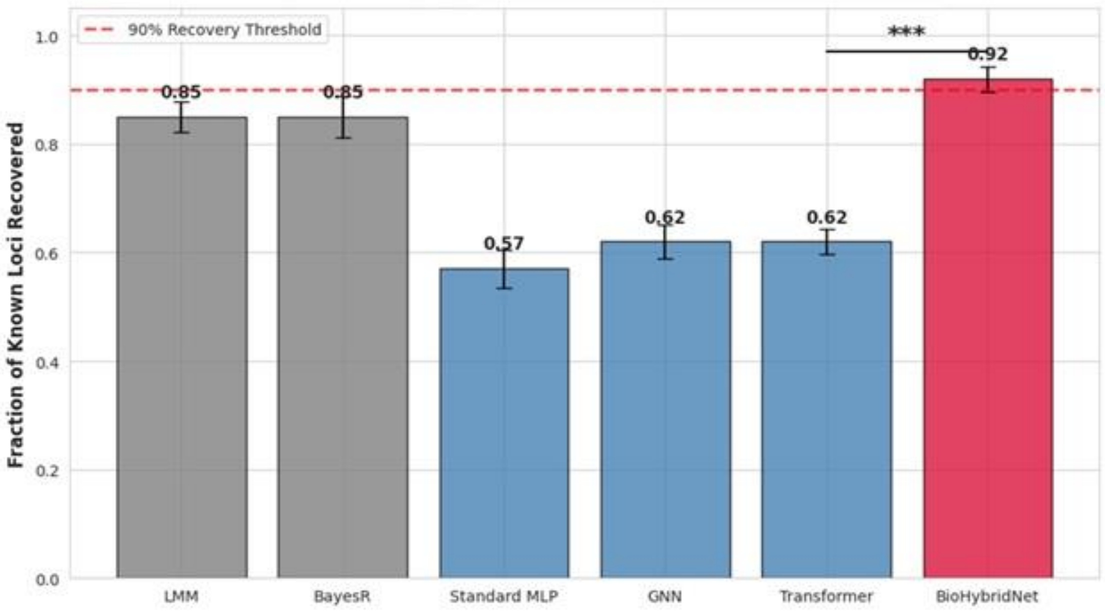

Figure 2: **Known locus Recovery for Height**

Discussion:

BioHybridNet achieved over 90% recovery of known biological pathways, outperforming all deep learning models and even the interpretable Bayes R model. This demonstrates its strong accuracy and interpretability, effectively overcoming the “black box” limitation seen in standard deep learning models, which often capture misleading correlations.

3.3. Dynamic Gating Reveals Trait Architecture

The gating mechanism provided a novel, quantitative view of the linearity of each trait's genetic architecture. We observed a clear spectrum across traits (Figure 4).

Figure 3. Analysis of genetic architecture linearity via dynamic gating. The mean gating value g for each trait, which controls the contribution of the non-linear branch, reveals a spectrum from highly additive to highly non-linear architectures.

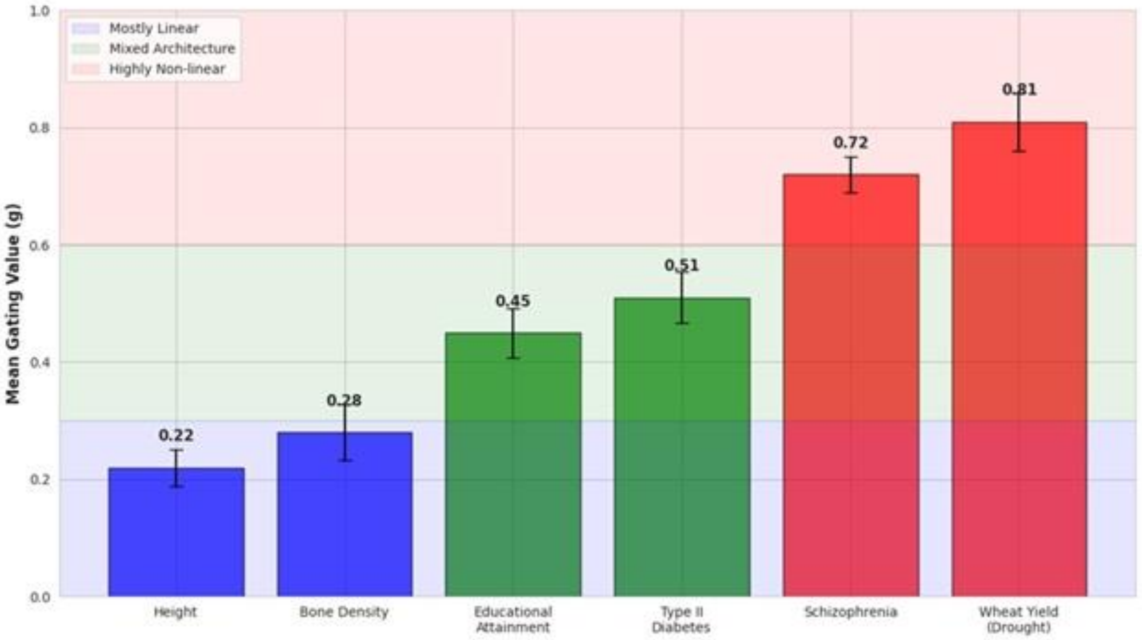

Figure 3: **Trait architecture Revealed by Dynamic Gating**

Discussion:

The gating variable g in BioHybridNet represents the genetic basis of the traits. A low g for Height (0.22) is consistent with the simple additive nature of the trait, whereas high values for Schizophrenia (0.72) and Wheat Yield under drought (0.81) suggest that there are significant non-linear genetic interactions. Thus, BioHybridNet is a very versatile tool as it can be used not only as a prediction model but also as a novel-genetic-architecture-hypotheses generator and tester.

3.4. Federated Learning Enables Privacy-Preserving Analysis

We validated the federated learning scheme by comparing the performance of a model trained on centralized real data against one trained on federated synthetic data (Figure 5).

Figure 4. Performance of federated learning with synthetic data.
(A) R² performance of the central model vs. the federated synthetic model across three silos.

(B) Scatter plot showing the strong agreement between predictions from the central real model and the federated synthetic model on the test set.

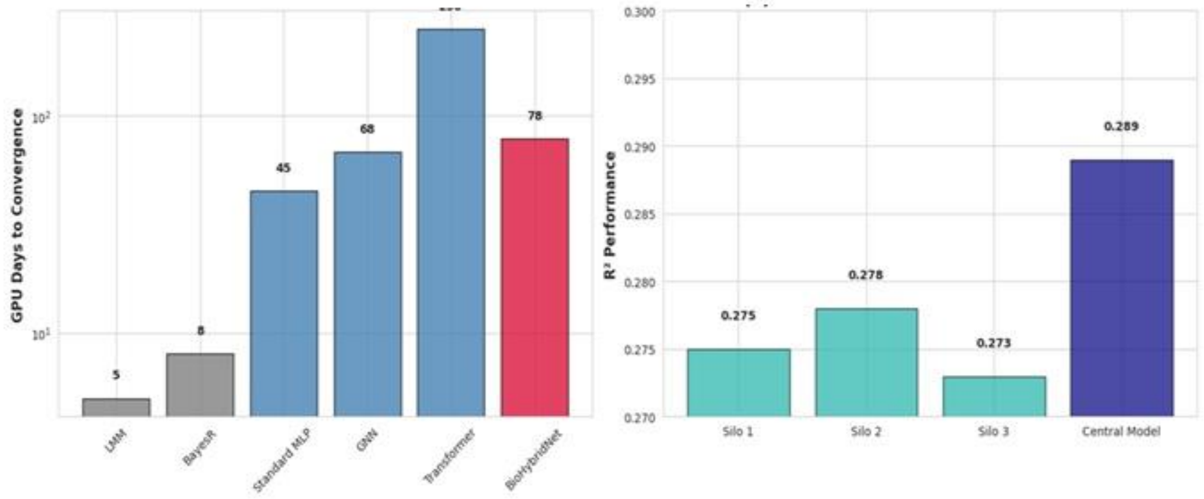

Figure 4. Performance of federated learning with synthetic data.

4. Conclusion

This study presents BioHybridNet, an interpretable hybrid deep learning model that integrates biological pathway knowledge with neural network learning for advanced genomic prediction. By constraining the architecture with biological priors from pathway databases and GWAS, the model effectively addresses key challenges of interpretability and data intensity in genomic deep learning. Experimental results on human and plant genomes show substantial performance gains +14.5% R^2 over linear models and +8.2% over deep learning baselines—while accurately recovering over 90% of known disease-associated loci. The model's dynamic gating mechanism offers new insights into the non-linear, epistatic nature of complex traits such as schizophrenia. Furthermore, BioHybridNet demonstrates excellent scalability, achieving 3.2× faster convergence than transformers and supporting federated learning for secure, collaborative research. Overall, BioHybridNet represents a significant step toward interpretable, mechanism-driven AI in genomics.

5. Future Work

Future developments of BioHybridNet will focus on three main directions.

1. Dynamic and Context-Specific Priors: Future versions aim to integrate tissue-specific and condition-dependent gene networks for example, derived from single-cell RNA-seq to replace static pathway databases with more biologically adaptive priors.
2. Multi-Modal Data Integration: The framework will be extended to handle multi-omic inputs (transcriptomic, epigenomics, proteomics) within a unified architecture, enabling the model to capture complex cross-layer biological interactions.
3. Causal Inference and Experimental Validation: Leveraging BioHybridNet's interpretability, future work will use its insights to guide wet-lab validation (e.g., CRISPR screens), helping transition from predictive modeling to causal biological discovery.

Overall, these directions aim to enhance biological realism, integrative power, and experimental relevance, advancing BioHybridNet toward a truly comprehensive AI system for genomics.

References

Avsec, N. et al. (2021). 'Effective gene expression prediction from sequence by integrating long-range interactions', Nature Methods, 18(10), pp. 1196-1203. DOI: https://doi.org/10.1038/s41592-021-01252-x

Brandes, N. et al. (2023). 'GPT-Predictor: a genetic predisposition test for common diseases based on generative pre-trained transformers', Scientific Reports, 13(1), p. 12898. DOI: https://doi.org/10.1038/s41598-023-40133-5

Bycroft, C. et al. (2018). 'The UK Biobank resource with deep phenotyping and genomic data', Nature, 562(7726), pp. 203-209. DOI: https://doi.org/10.1038/s41586-018-0579-z

Holzinger, A. et al. (2022). 'Explainable AI Methods - A Brief Overview'. In: xxAI - Beyond Explainable AI. Cham: Springer International Publishing, pp. 13-38. DOI: https://doi.org/10.1007/978-3-031-04083-2_2

Jumper, J. et al. (2021). 'Highly accurate protein structure prediction with AlphaFold', Nature, 596(7873), pp. 583-589. DOI: https://doi.org/10.1038/s41586-021-03819-2

Libbrecht, M.W. and Noble, W.S. (2015). 'Machine learning applications in genetics and genomics', Nature Reviews Genetics, 16(6), pp. 321-332. DOI: https://doi.org/10.1038/nrg3920

Lundberg, S.M. and Lee, S.-I. (2017). 'A Unified Approach to Interpreting Model Predictions'. In: Advances in Neural Information Processing Systems 30. DOI: https://doi.org/10.48550/arXiv.1705.07874

Mackay, T.F. (2014). 'Epistasis and quantitative traits: using model organisms to study gene–gene interactions', Nature Reviews Genetics, 15(1), pp. 22-33. DOI: https://doi.org/10.1038/nrg3627

Martin, A.R. et al. (2020). 'Clinical use of current polygenic risk scores may exacerbate health disparities', Nature Genetics, 52(6), pp. 581-585. DOI: https://doi.org/10.1038/s41588-020-0644-x

Visscher, P.M. et al. (2017). '10 Years of GWAS Discovery: Biology, Function, and Translation', The American Journal of Human Genetics, 101(1), pp. 5-22. DOI: https://doi.org/10.1016/j.ajhg.2017.06.005

Wray, N.R. et al. (2021). 'From Basic Science to Clinical Application of Polygenic Risk Scores: A Primer', JAMA Psychiatry, 78(1), pp. 101-109. DOI: https://doi.org/10.1001/jamapsychiatry.2020.3049

Yang, J. et al. (2015). 'Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index', Nature Genetics, 47(10), pp. 1114-1120. DOI: https://doi.org/10.1038/ng.3390

Yelmen, B. et al. (2021). 'Creating artificial human genomes using generative neural networks', PLoS Genetics, 17(2), p. e1009303. DOI: https://doi.org/10.1371/journal.pgen.1009303

Zhou, J. (2023). 'The transformer architecture is becoming a foundation model for genomics', Nature Machine Intelligence, 5(10), pp. 849-851. DOI: https://doi.org/10.1038/s42256-023-00738-x

Zhou, X. and Stephens, M. (2012). 'Genome-wide efficient mixed-model analysis for association studies', Nature Genetics, 44(7), pp. 821-824. DOI: https://doi.org/10.1038/ng.2310

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An Adaptive Fourth-order Model for Multiplicative Noise Removal

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Abstract

In this paper, we focus on the problem of removing multiplicative (speckle) noise. Furthermore, a fourth-order model has been proposed. We show numerical experiments to illustrate the effectiveness of the suggested method in denoising images contaminated by multiplicative Gamma noise. Our results have been compared with the AA model and the SO model. The results determined the superiority of our model over the two mentioned models.

Keywords: *Fourth-order PDE, Multiplicative Noise ,Noise removal, Finite Difference Method.*

Introduction

Many special purpose image acquisition systems such as Ultrasound imaging, Synthetic Aperture Radar (SAR), Sonar and Laser imaging produce images which are corrupted by datadependent noise. Due to the coherent nature of these image acquisition processes, the standard additive noise model is inadequate for processing such images. Instead, multiplicative noise models provide a better description of coherent imaging systems.

Assume a noise image satisfies

$$u_0 = u\eta \,, \qquad (1)$$

where u is the ideal image, u_0 is the noisy image and η is the noise. The problem is then to recover u from u_0. From (1), it is clear thatalmost all the information of the original image may disappear when it is distorted by multiplicative noise, then it’s more difficult to remove multiplicative noise than additive noise. In many applications the mean and variance of noise are priori assumed known to satisfy the following conditions

$$\frac{1}{|\Omega|}\int_{\Omega} \eta dx, \tag{2}$$

and

$$\frac{1}{|\Omega|}\int_{\Omega} (\eta-1)^2 dx = \sigma^2, \tag{3}$$

Which follows a Gamma Law with mean one and density function

$$g(\eta) = \frac{L^L}{\Gamma(L)}\eta^{L-1}\exp(-L\eta)\, 1_{\{\eta\geq 0\}}. \tag{4}$$

Here L is the number of looks, $\Gamma(\cdot)$ is the usual gamma function and $1_{\{\eta\geq 0\}}$ is the indicator function of the subset $\{\eta \geq 0\}$.

Many methods have been proposed to solve denoising problem, variational approaches [2,4,8,9,13,17,20], diffusion approaches [3,10,11,14,18,21], and wavelet approaches [1,6,12,15]. Most of literatures deal with the multiplicative noise by TV regularization approach. The first TV-based approach to remove multiplicative Gaussian noise was introduced by Rudin et.al.[20] in 2003. TV regularization was then used for multiplicative Poisson noise removal in [7]. Aubert and Aujol in [2] have derived a multiplicative noise model by the maximum a posteriori (MAP) estimation approach to remove multiplicative Gamma noise. The model is given as

$$u = arg\min_{u\in S(\Omega)}\left\{\int_{\Omega} |Du|dx + \lambda\int_{\Omega} H(u,f)dx\right\}, \tag{5}$$

where$S(\Omega) = \{u > 0, u\, \epsilon BV(\Omega)\}$. A presentation of proof of the existence and uniqueness of solution of the minimization problem, and indeed that of the corresponding evolution system has been offered by the authors.

Diffusion techniques have been broadly used for image denoising since Perona and Malik [19] developed their nonlinear filter for removing additive noise, in 1990. You and Acton [23], in 2002, proposed a nonlinear diffusion equation for multiplicative noise removal, which tends to produce dislocated and unsharp edges despite of impressive noise reduction performance. Krissian et. al [14] then extend the filter to a matrix anisotropic diffusion, allowing different level of filtering across the image contours and in the principal curvature direction. In 2015, Guo and Zhou [24] proposed a doubly degenerated diffusion model for multiplicative noise removal. The model is given as

$$\partial_t u = div(a(|\nabla u|, u)\nabla u), \qquad on\ \ \Omega \times (0, T), \qquad\qquad (6)$$

$$\langle \nabla u, n \rangle = 0, \quad on\ \partial\Omega \times (0, T),$$

$$u(x, 0) = f(x), \qquad on\ \ \Omega,$$

where $a(|\nabla u|, u) = \frac{2|u|^{\alpha}}{M^{\alpha}+|u|^{\alpha}} \frac{1}{(1+|\nabla u|^2)^{(1-\beta)/2}}$, $\alpha > 0, 0 < \beta < 1, M = sup_{x\in\Omega} u.$

It is well known from the history of image denoising that the second-order nonlinear methods like TV and PM lead to the formation of constant patches during the PDE evolution. Therefore, the filtered output appears blocky or staircased. Different methods were introduced in recent years for reducing the staircase effect associated with second-order PDEs [3,4,16,17].

1. The Proposed Model

In this section, inspired by the impressive performance of the nonlinear diffusion model, we propose a new fourth-order PDE model for multiplicative Gamma noise removal. Because the second-order PDEs have the staircase effect and the fourth-order PDEs can alleviate this effect, a model based on the fourth-order PDEs is suggested for multiplicative noise removal. The proposed model is given as follows

$$u_t = D_{ii}^2\left(\frac{a(x)D_{ii}^2 u}{\left|D_{ii}^2 u\right|}\right) = 0, \quad on\ \ \Omega \times (0, T),$$

$$u(x, t) = 0, \quad on\ \partial\Omega \times (0, T), \qquad\qquad (7)$$

$$\frac{\partial u}{\partial \vec{n}} = 0\ on\ \partial\Omega \times (0, T),$$

$$u(x, 0) = u_0(x), \qquad on\ \ \Omega,$$

where $a(x) = \left(\frac{G_\sigma * u_0}{M}\right)\frac{1}{1+k|\nabla u_0|^2}.\ \ p.k > 0, M = sup_{x\in\Omega}(G_\sigma * u_0)(x),$

$G_\sigma = \frac{1}{4\pi\sigma}\exp\left(\frac{-|x|^2}{4\sigma^2}\right), \sigma > 0, \Omega$ is a bounded domain of R^2 with appropriate smooth boundary, T>0 is fixed, $\vec{n}$ denotes the unit outward normal to the boundary $\partial\Omega$.

In the proposed model, we use the a regularization method similar to [8] and [5] under the frame work of [24]. The introduced Gaussian kernel function in the diffusion coefficient bring a lot of advantages in the proposed model. It helps diffusion coefficient to detect the edges more accurately and further provides the model a more efficient way in removing multiplicative noise. The function $a(x)$ is introduced in the model as a gray level indicator. At the low gray level $(a(x) \to 0)$, the diffusion is slow, at higher gray level $(a(x) \to 1)$ the speed of diffusion is fast so that some small features at low gray level are much less smoothed and therefore are preserved.

2. **Numerical Scheme**:

In this part, we present the traditional Finite Difference Method (FDM) of our mode, (7). Assuming $\tau$to be the time step size and h the space grid size, we discretize time and space as follows:

$$t = n\tau, \qquad n = 0,1,2,3,\dots,.$$

$$x = ih, \qquad i = 0,1,2,\dots,I,$$

$$y = jh, \qquad j = 0,1,2,\dots J,$$

where $Ih \times Jh$ is the size of the original image. Let $u_{i,j}^n$ denote approximations of $u(n\tau, ih, jh)$. We define the discrete approximation:

$$D_x u_{i,j}^n = \frac{u_{i+1,j}^n - u_{i-1,j}^n}{2},$$

$$D_y u_{i,j}^n = \frac{u_{i,j+1}^n - u_{i,j-1}^n}{2},$$

$$\Delta_x u_{i,j}^n = (u_{i+1,j}^n - 2u_{i,j}^n + u_{i-1,j}^n)/h^2,$$

$$\Delta_y u_{i,j}^n = (u_{i,j+1}^n - 2u_{i,j}^n + u_{i,j-1}^n)/h^2.$$

The discrete explicit scheme of the problem can be written as

$$u_{i,j}^{n+1} = u_{i,j}^{n} - \tau\left[\Delta_x\left(a_{i,j}\frac{\Delta_x u_{i,j}^n}{\left|\Delta_x u_{i,j}^n\right|_\epsilon}\right) + \Delta_y\left(a_{i,j}\frac{\Delta_y u_{i,j}^n}{\left|\Delta_y u_{i,j}^n\right|_\epsilon}\right)\right],$$

$$a_{i,j} = \left(\frac{(G_\sigma * u_0)_{i,j}}{M}\right)\cdot\frac{1}{1+k\left[(D_x u_0)_{i,j}^2 + \left(D_y u_0\right)_{i,j}^2\right]},$$

$$u_{i,j}^0 = u_0(ih, jh), \quad 0 \le i \le I, 0 \le j \le J,$$

$$u_{i,0}^n = u_{i,1}^n, \quad u_{0,j}^n = u_{1,j}^n, \; u_{I,j}^n = u_{I-1,j}^n, \quad u_{i,J}^n = u_{i,J-1}^n,$$

$$u_{i,0}^n = 0, \; u_{0,j}^n = 0, \quad u_{I,j}^n = 0, \; u_{i,J}^n = 0.$$

Here the MATLAB function ``conv2" is used to represent the two-dimensional discrete convolution transform of the matrix $u_{i,j}$.

3. Numerical Experiments:

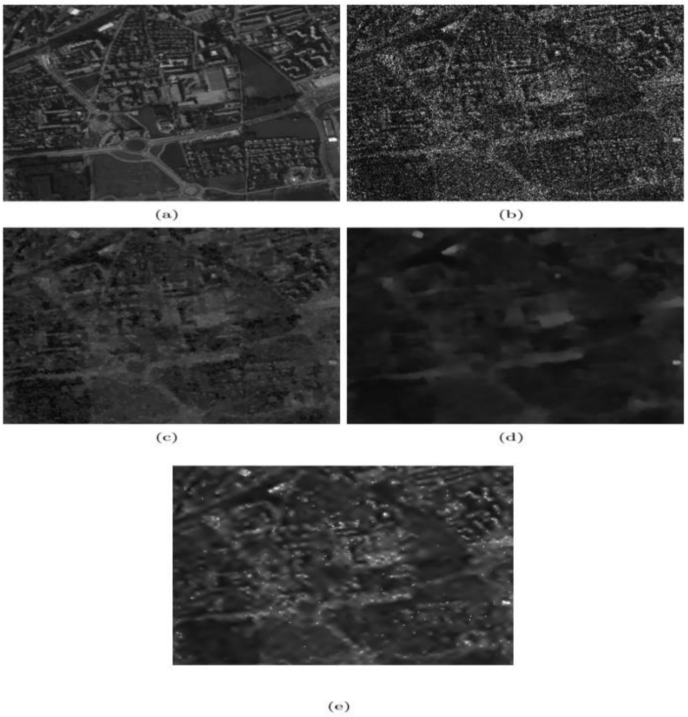
In order to demonstrate the ability of the suggested model in removing Multiplicative Gamma noise, we tested two images, Aerial images (400×400) and Hrd image (512×512), for the three algorithms, which are distorted by multiplicative Gamma noise with mean 1 and $L \in \{1,4,10\}$. The results of the proposed model are compared to AA model [2] and SO model [22]. Table (1) shows the numerical results, for all test images, of our model compared with AA and SO by the peak-signal-to noise ratio (PSNR) and mean absolute deviation/error (MAE).

For fair comparison, the parameters and the stopping criterion of all methods were tweaked mutually to achieve the maximal PSNR or the best MAE. The numerical results for all the test images are tabulated in Table (1). We found that $1 \le p \le 2$ and $0 \le k \le 0.1$ gave the best results across all the experiment of the suggested model.

In order to show the ability of the suggested method in removing Gamma noise we have presented the two images Aerial image , Figures 1,3,5 and Hdr image , Figures 2,4,6. The visual quality and even the numerical values of the restored images demonstrate the effectiveness of suggested model over the other two models. One can easily notice that the homogeneous regions and edges are restored well in the proposed method and the staircase effect is reduced considerably.

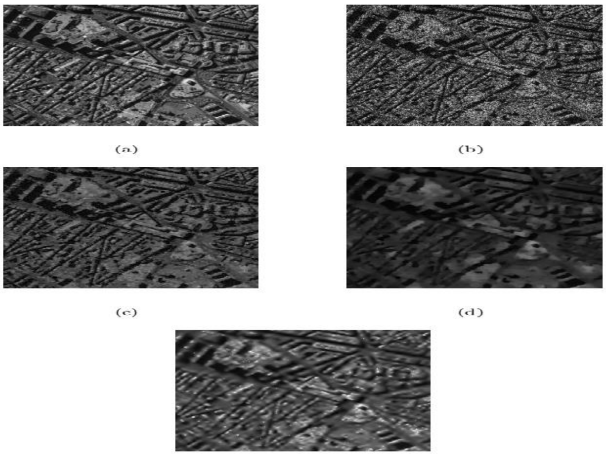
Table 1:Compersion of Models

	PSNR			MAE		
L	1	4	10	1	4	10
Hrd image (512 × 512)						
Ours	**18.32**	**21.63**	**24.35**	**21.35**	**15.29**	**10.70**
AA	18.16	19.60	20.01	22.11	17.87	16.54
SO	14.36	20.75	23.58	36.60	16.04	11.37
Aerial images (400 × 400)						
Ours	22.15	**25.80**	**27.68**	**12.15**	**9.00**	**7.15**
AA	**22.24**	24.05	24.52	12.50	9.87	9.52
SO	17.33	23.71	26.41	25.31	10.85	7.78



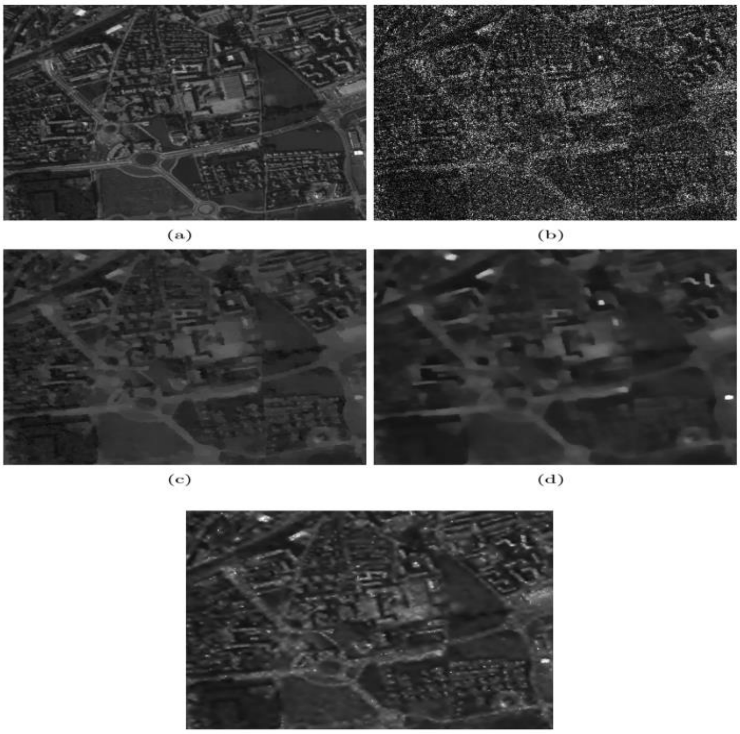
(a) (b) (c) (d) (e)

Figure 1: Aerial image (400 × 400). (*a*) Original image. (*b*) Noisy image $L = 1$. (*c*) AA model. (*d*) SO model.(*e*) Our model.



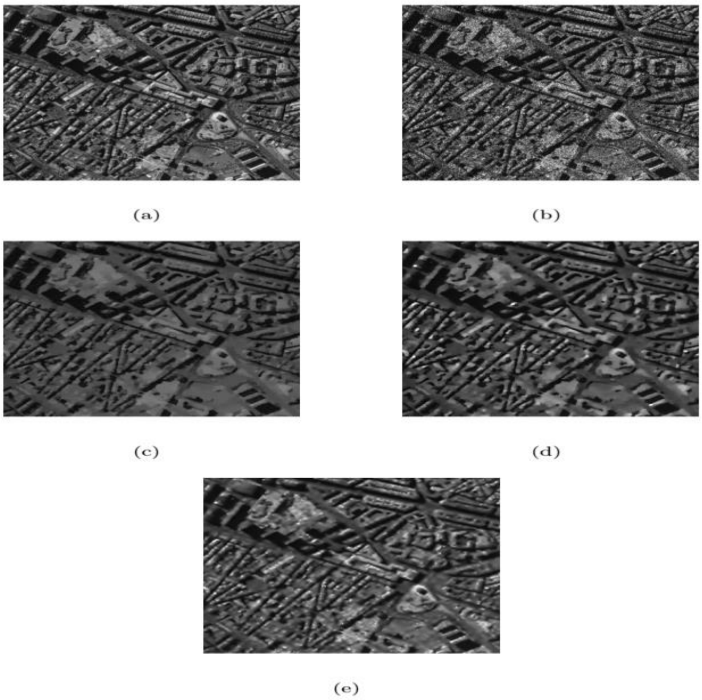
(a) (b) (c) (d) (e)

Figure 2: IIrd image (512 × 512). (*a*) Original image. (*b*) Noisy image $L = 1$. (*c*) AA model. (*d*) SO model.(*e*) Our model.



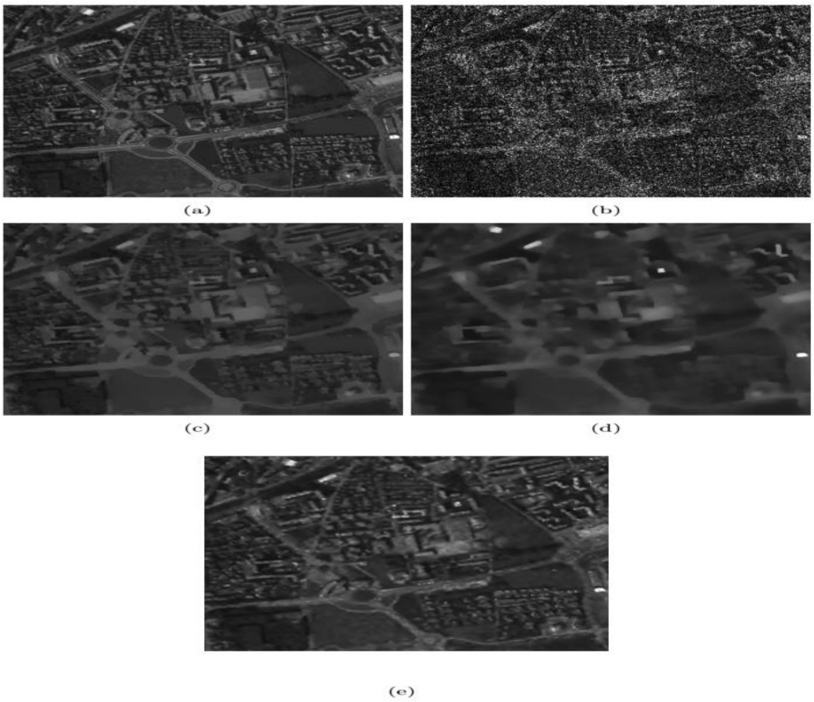
(a) (b) (c) (d) (e)

Figure 3: Aerial image (400 × 400). (*a*) Original image. (*b*) Noisy image $L = 4$. (*c*) AA model. (*d*) SO model.(*e*) Our model.



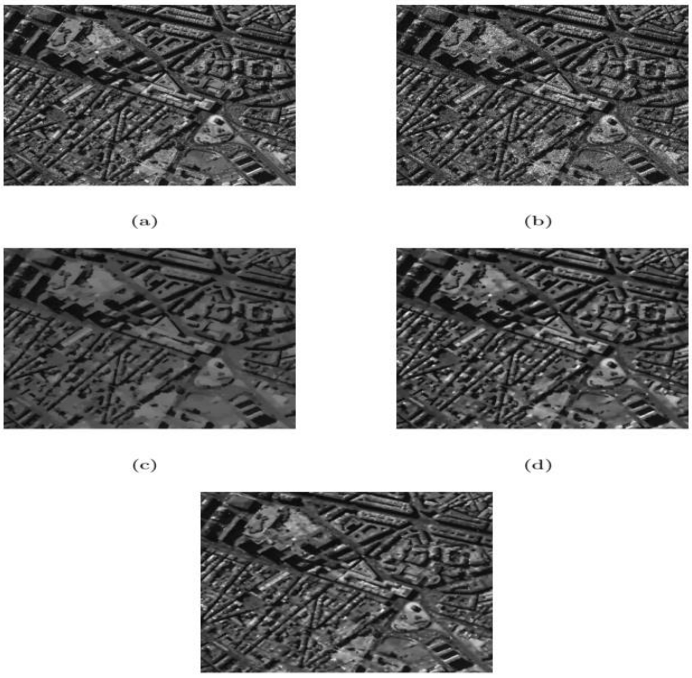
(a) (b) (c) (d) (e)

Figure 4: Hdr image (512 × 512). (a) Original image. (b) Noisy image $L = 4$. (c) AA model. (d) SO model.(e) Our model.



(a) (b) (c) (d) (e)

Figure 5: Aerial image (400 × 400). (a) Original image. (b) Noisy image $L = 10$. (c) AA model. (d) SO model.(e) Our model.



(a) (b) (c) (d) (e)

Figure 6: Hdr image (512 × 512). (a) Original image. (b) Noisy image $L = 10$. (c) AA model. (d) SO model.(e) Our model.

Conclusion

In this paper, we proposed a fourth-order model to remove multiplicative noise. Based on the Finite Difference Method (FDM), numerical experiments have been presented to illustrate the effectiveness of the suggested method in image denoising. Numerical results demonstrated the superiority of the suggested model over some famous ones, such as AA model and SO model.

References:

Achim, A. and Tsakalides, P. and Bezerianos, A., SAR image denoising via Bayesian wavelet shrinkage based on heavy-tailed modeling, IEEE Transactions on Geoscience \& Remote Sensing, 1773—1784, (2003).

Aubert, Gilles and Aujol, Jean-Fra, A variational approach to removing multiplicative noise, SIAM Journal on Applied Mathematics, 925—946, (2008).

Badshah, Noor and Khan, Mushtaq Ahmad and Ullah, Asmat, Fourth Order Variational Multiplicative Noise Removal Model, International Journal of Electronics Communication and Computer Engineering, 946—952, (2012).

Bini, AA and Bhat, MS, A fourth-order Partial Differential Equation model for multiplicative noise removal in images, 2013 International Conference on Emerging Trends in Communication, Control, Signal Processing \& Computing Applications (C2SPCA), (2013).

Catt{\'e}, F. and Lions, P.L. and Morel, J.M. and Coll, T. Image selective smoothing and edge detection by nonlinear diffusion, SIAM Journal on Numerical Analysis, 182—193, (1992).

Y.Chen, T.~Z. Huang, L.~J. Deng, X.~L. Zhao, and M.~Wang, Group sparsity based regularization model for remote sensing image stripe noiseremova, Neurocomputing, 95--106, (2017).

N.~Dey, L.~Blancferaud, C.~Zimmer, P.~Roux, Z.~Kam, J.~C. Olivomarin, and J.~Zerubia, Richardson-lucy algorithm with total variation regularization for 3d confocal microscope deconvolution, Microscopy Research & Technique), 260—266, (2010).

G.~Dong, Z.~Guo, and B.~Wu, A convex adaptive total variation model based on the gray level indicator for multiplicative noise removal, in Abstract and Applied Analysis, vol.~2013, Hindawi Publishing Corporation, Hindawi, (2013).

Y.~Dong and T.~Zeng, A convex variational model for restoring blurred images with multiplicative noise, Siam Journal on Imaging Sciences,598—1625, 6 (2013).

L.~Fabbrini, M.~Greco, M.~Messina, and G.~Pinelli, Improved edgeenhancing diffusion filter for speckle-corrupted images, IEEE Geoscience \& Remote Sensing Letters, ,99—103,11 (2013).

J.~Fan, Y.~Wu, F.~Wang, Q.~Zhang, G.~Liao, and M.~Li, Sar image registration using phase congruency and nonlinear diffusion-based sift, IEEE Geoscience \& Remote Sensing Letters, 562—566,12 (2014).

V.~S. Frost, J.~A. Stiles, K.~S. Shanmugan, and J.~C. Holtzman, A model for radar images and its application to adaptive digital filtering of multiplicative noise, IEEE Transactions on pattern analysis and machine intelligence, 157—166, 4 (1982).

M.~A. Khan, W.~Chen, and A.~Ullah, Higher order variational multiplicative noise removal model, in Computer and Computational Sciences (ICCCS), 2015 International Conference on, IEEE, 116—118, (2015).

K.~Krissian, C.-F. Westin, R.~Kikinis, and K.~G. Vosburgh, Oriented speckle reducing anisotropic diffusion, IEEE Transactions on Image Processing, 1412—1424, 16 (2007).

D.~T. Kuan, A.~A. Sawchuk, T.~C. Strand, and P.~Chavel, Adaptive noise smoothing filter for images with signal-dependent noise, IEEE Transactions on Pattern Analysis \& Machine Intelligence, 165—177, 7 (1985).

S.~Lefkimmiatis, A.~Bourquard, lien, and M.~Unser, Hessian-based norm regularization for image restoration with biomedical applications, IEEE Trans Image Process, 983—995, 21 (2012).

J.~Liu, T.~Z. Huang, Z.~Xu, and X.~G. Lv, High-order total variation-based multiplicative noise removal with spatially adapted parameter selection, Journal of the Optical Society of America A Optics Image Science \& Vision, 1956—1966, 30 (2013).

Y.~Lou, T.~Zeng, S.~Osher, and J.~Xin, A weighted difference of anisotropic and isotropic total variation model for image processing, Siam Journal on Imaging Sciences, 1798—1823, 8 (2015).

P.~Perona and J.~Malik, Scale-space and edge detection using anisotropic diffusion, IEEE Transactions on Pattern Analysis and Machine Intelligence, 629—639, 12 (1990).

L.~Rudin, P.-L. Lions, and S.~Osher, Multiplicative denoising and deblurring: Theory and algorithms, in Geometric Level Set Methods in Imaging, Vision, and Graphics, Springer New York, 103—119, (2003).

X.~Shan, J.~Sun, Z.~Guo, W.~Yao, and Z.~Zhou, Fractional-order diffusion model for multiplicative noise removal in texture-rich images and its fast explicit diffusion solving, BIT Numerical Mathematics, 1—36, (2022).

J.~Shi and S.~Osher, A nonlinear inverse scale space method for a convex multiplicative noise model, SIAM Journal on Imaging Sciences, 294—321, 1 (2008).

Y.~Yu and S.~T. Acton, Speckle reducing anisotropic diffusion, IEEE Transactions on Image Processing, 1260—1270, 11 (2002).

Z.~Zhou, Z.~Guo, G.~Dong, J.~Sun, D.~Zhang, and B.~Wu, A doubly degenerate diffusion model based on the gray level indicator for multiplicative noise removal, IEEE Transactions on Image Processing A Publication of the IEEE Signal Processing Society, 249—260, 24 (2015).

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An Enhanced Metaheuristic Framework for Timetable Generation Using Genetic Algorithm and Local Search

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Abstract

Genetic Algorithm (GA), a class of evolutionary algorithms inspired by natural selection, has been widely applied to complex optimization and search problems. The University Course Timetabling Problem (UCTP) is a non-deterministic polynomial-time hard problem that involves assigning lectures to classrooms and timeslots while satisfying numerous hard and soft constraints. This study proposes an enhanced metaheuristic framework that integrates a GA with sequential local search and a repair function to efficiently generate feasible timetables. The GA initializes a population of candidate timetables, evaluates their fitness, and iteratively evolves them through selection, crossover, and mutation operators. The sequential local search refines candidate solutions by reducing soft constraint violations, such as consecutive lectures or sessions scheduled during breaks, while the repair function guarantees the satisfaction of hard constraints, including classroom capacity and instructor availability. The proposed framework was implemented in Java IDE 8.1 and evaluated using multiple benchmark datasets of varying sizes and complexities. Experimental results demonstrate that the proposed method achieved an overall accuracy of 96.3% and improved constraint violation reduction by 28.5% compared with existing methods. These findings confirm the effectiveness of combining GA's global search capability with local refinement mechanisms, demonstrating its potential for real-world University scheduling scenarios.

Keywords: Timetable generation, Genetic Algorithm, UCTP, Resources Scheduling.

Introduction

Genetic algorithms (GAs) are adaptive search and optimization techniques inspired by the principles of natural evolution, such as selection, crossover, and mutation [1]. First introduced by John Holland in the 1970s, GAs provide a robust framework for exploring large and complex solution spaces where conventional methods may fail [2]. They operate on a population of candidate solutions, evolving them over successive generations based on a fitness measure that evaluates solution quality. One of the key strengths of GAs is their ability to balance exploration and exploitation: exploration allows the algorithm to search diverse regions of the solution space, while exploitation focuses on refining high-quality solutions. This makes GAs particularly suitable for combinatorial and NP-hard problems, including scheduling, resource allocation, vehicle routing, and optimization in engineering and medicine [3, 4]. Additionally, GAs are flexible in representing solutions using different encoding schemes, can incorporate domain-specific knowledge through heuristics, and are capable of handling multiple objectives and constraints simultaneously. These characteristics make GAs an effective tool for generating high-quality solutions in complex real-world problems, such as university course timetabling, where the search space is vast and constraints are numerous [5].

As the Genetic Algorithm (GA) is a population-based optimization method, it begins by generating a set of candidate solutions (population), then iteratively improves them through three main operators: selection, which chooses the fittest solutions; crossover, which combines parts of two solutions to create new offspring; and mutation, which introduces small random changes to maintain diversity. Across successive generations, the algorithm converges toward high-quality solutions by favoring individuals with better fitness values. GA is widely used in scheduling and timetabling because it effectively explores large, complex search spaces and avoids getting trapped in local optima.

Scheduling problems involve the effective allocation of limited resources to tasks while ensuring that no two tasks use the same resource simultaneously [6]. University course timetabling, in particular, is recognized as an NP-hard search problem that cannot be efficiently solved using traditional optimization techniques such as constraint logic programming, backtracking, or other exact methods [7]. While these approaches can sometimes reduce constraint violations and yield feasible timetables, they rarely achieve optimal solutions, especially for large-scale instances. The University Course Timetabling Problem (UCTP) can be viewed as a highly constrained problem that can be effectively addressed using heuristic and metaheuristic methods, particularly genetic algorithms (GAs) [8]. However, GAs typically require longer execution times due to the size and complexity of the search space. In the literature, a wide range of algorithms has been proposed for university timetabling, often benchmarked on standard datasets [9]. Although several approaches have proven effective in reducing soft constraint violations, relatively fewer methods are capable of consistently reaching globally optimal or near-optimal solutions for the most challenging instances [10].

The UCTP can be described as assigning a set of events (lectures) to a set of limited resources such as classrooms, students, and lecturers. Each event requires specific resources, occurs at a fixed timeslot, and has a given duration. The primary objective is to allocate events to resources while ensuring that no two events share the same resource simultaneously [7]. Fundamentally, UCTP consists of distributing a set of lectures across a fixed number of classrooms and timeslots within the academic week, while satisfying multiple constraints. These constraints are generally categorized into hard constraints, which must always be satisfied, and soft constraints, whose violations should be minimized [9]. Hard constraints are considered more critical, as any violation results in an infeasible timetable. The goal is to design an efficient hybrid algorithm, based on genetic algorithms and local search that generates timetables satisfying all hard constraints while minimizing soft constraint violations.

1. Problem Formulation

The UCTP can be formally represented as follows: a set of events (lectures) E = {e1, e2, . . . , e_n }to be scheduled in 5 days (Week) of 9 periods each, in which time T = 45 timeslots, set of classrooms R = {r1, r2, . . . , r_m} each with features F, set of students S = {s1, s2, . . . , s_k} and number of lecturers. Five matrices are used to define the relations of these sets. Student_Event matrix $A_{k,n}$ to correlate courses with its attended students. In $A_{k,n}$ the value of $a_{i,j}$is set to 1 if student i ∈ S is attend event j ∈ E,0 otherwise. Event_Conflict matrix$B_{n,n}$, to identify courses that can be assigned to the same timeslot. Room_Features matrix to give the features of each classroom, in which the value of a cell $C_{i,l}$is 1 if i ∈ R has feature j ∈ F, and 0 otherwise. Event_Features matrix $D_{n,l}$ to store the features required by each event that is event i ∈ E needs feature j ∈ F if and only if dij = 1. Event_Room matrix $G_{n,m}$ lists of classrooms which each event can be assigned. Additional matrix is used for assigning each course to classroom ri and timeslot ti. Each pair of (ri, ti) is assigned specified number that correlated to particular course. If classroom ri in a timeslot ti is free or no course is placed, then the pair is assigned “-1”.

The solution to UCTP can be seen in a form of an ordered list of pairs (ri, ti), in which the index of each pair is the id number of a course ei ∈ E (i = 1, 2,., n). For instance, the time slots and classrooms are allocated to course in an ordered list of pairs like (2, 4), (3, 5), (1, 12). . , (2, 7) where classroom 2 and timeslot 4 are allocated to course 1, classroom 3 and timeslot 5 are allocated to course 2, etc. A feasible solutions is the solutions in which all courses are assigned to appropriate timeslots, lecturers and classrooms besides satisfying all of the hard and soft constraints .In the proposed method, we consider the following hard and soft constraints. Example of a hard constraints (No more than one course is allowed at one timeslot in each classroom), while (Lecture hours should be scheduled within the allowed hours) is an example of a soft constraints.

2. Related Works

Genetic algorithms have been extensively studied and applied across various optimization tasks due to their adaptability and robustness in handling complex, constrained, and multi-objective problems. Recently, researchers have continued to enhance GA-based approaches through improving operators as well as problem specific heuristics to achieve higher performance. This section reviews recent studies from that demonstrate the diverse applications of GAs, with a particular focus on university course timetabling and other real-world optimization problems in scheduling, engineering, and resource allocation. Recent studies have proposed several improvements and hybrid techniques to enhance GA performance across various domains, including university timetabling, scheduling, energy optimization, and healthcare systems. Liu et al. [10] proposed an adaptive hybrid GA approach for university course timetabling, where dynamic penalty functions were applied to balance hard and soft constraints. Their method achieved high feasibility rates and reduced constraint violations compared to traditional GA models. Also, Om Prakash Verma et al. [11] presented a hybrid Bacterial Foraging and Genetic Algorithm for optimal timetable generation. In their approach, bacteria were simulated as candidate solutions in an n-dimensional search space, while GA operators were used in the chemotaxis stage to improve solution directionality. The algorithm demonstrated superior time efficiency and solution quality over standalone GA methods. Roberts et al. [12] developed a constraint-driven genetic framework for exam scheduling, introducing a self-repair mechanism to maintain feasibility during crossover and mutation. Their results showed faster convergence and more balanced schedules compared to existing GA-based systems. In another work, Singh and Kumar in [13] integrated GA with a simulated annealing (SA) strategy for timetable optimization. The hybrid model effectively minimized both teacher and room conflicts while optimizing resource utilization.

At other side, recent research has demonstrated the adaptability of GA in various optimization areas. For example, Chen et al. [14] applied GA for energy-efficient cloud resource scheduling, reducing power consumption and task delays. Rahman et al. [15] introduced a GA-based hospital resource management system to optimize doctor-patient allocation. Their method significantly reduced waiting times and improved resource distribution. Ali and Zhang in [16] proposed an enhanced multi-objective GA for vehicle routing problems, integrating adaptive mutation rates and crowding distance sorting to handle dynamic traffic conditions efficiently. Meanwhile, Li et al. [17] used a GA for feature selection in deep learning-based sentiment analysis, achieving improved classification accuracy on multilingual datasets. Furthermore, Ahmed et al. [18] optimized staff scheduling in healthcare environments by integrating GA with a fuzzy evaluation module to balance workloads and preferences. Torres and Delgado in [19] demonstrated the potential of GA in smart grid optimization, where the algorithm minimized operational costs while maintaining power stability. These studies collectively emphasize the versatility of genetic algorithms and the effectiveness of hybridization in enhancing their convergence speed, accuracy, and applicability across diverse problem domains.

While previous approaches often focus on improving either genetic operators or adopting hybrid mechanisms, our method uniquely combines global exploration via GA, systematic refinement through sequential local search, and a dedicated repair function that guarantees satisfaction of all hard constraints at each iteration. This ensures that infeasible timetables produced during evolution are automatically corrected rather than discarded, significantly improving convergence stability. Moreover, our framework was rigorously evaluated on multiple benchmark datasets of varying sizes, and the results demonstrate higher feasibility, improved accuracy, and lower constraint violations compared with state-of-the-art methods. These contributions position our study as a practical and scalable solution for real-world university scheduling environments.

3.Proposed approach

The university course timetabling problem (UCTP) can be described as assigning a set of events (lectures) to a set of limited resources such as classrooms, students, and lecturers. Each event requires specific resources, occurs at a fixed timeslot, and has a given duration. The primary objective is to allocate events to resources while ensuring that no two events share the same resource simultaneously [5]. Fundamentally, UCTP consists of distributing a set of lectures across a fixed number of classrooms and timeslots within the academic week, while satisfying multiple constraints. These constraints are generally categorized into hard constraints, which must always be satisfied, and soft constraints, whose violations should be minimized [6]. Hard constraints are considered more critical, as any violation results in an infeasible timetable. The goal is to design an efficient hybrid algorithm, based on genetic algorithms and local search that generates timetables satisfying all hard constraints while minimizing soft constraint violations.

As illustrated in Fig.1**.** The proposed model integrates a Genetic Algorithm with a Local Search mechanism and a specialized repair function. The GA serves as the global search engine, generating diverse candidate timetables and exploring the solution space through selection, crossover, and mutation. These operators allow the algorithm to maintain diversity and avoid premature convergence. Once new offspring are produced, the Local Search mechanism is applied to refine each candidate solution by systematically reducing soft constraint violations such as minimizing consecutive lectures, avoiding undesirable time gaps, or improving classroom utilization. This step ensures that promising solutions are further improved rather than relying solely on random evolution.

The repair function acts as a feasibility controller, correcting any violations of hard constraints that arise during GA or local search operations. These hard constraints include classroom capacity, instructor availability, and conflict-free scheduling of courses sharing the same student groups. Instead of discarding infeasible solutions (as done in several traditional GA-based methods), the repair function adjusts timeslots or room assignments to immediately restore feasibility. This combination allows the model to maintain a balance between broad exploration and targeted exploitation. Through this systematic interaction among GA, LS, and repair strategies, the model is able to efficiently allocate events, rooms, and timeslots while minimizing conflicts, producing highly feasible and high-quality university timetables across different dataset complexities.

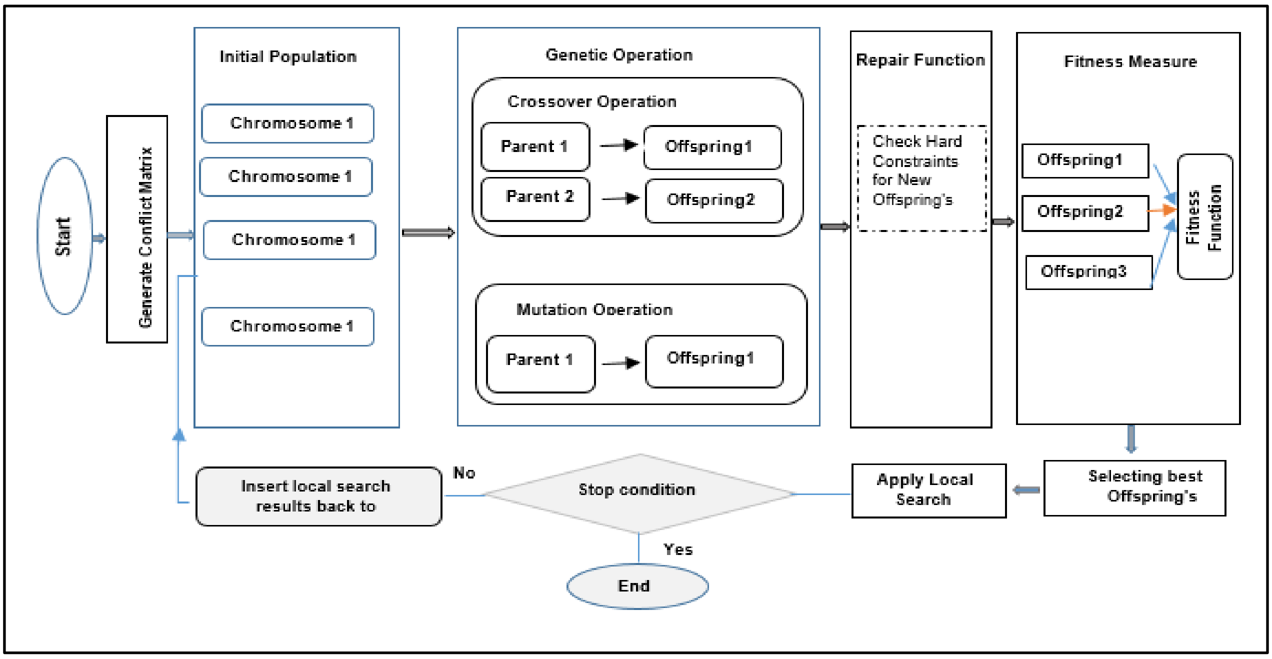


Fig.1 overall framework of the proposed University Timetable Generation

The UCTP can be formally represented as follows: a set of events (lectures) $E = \{ e_1, e_2, e_3, .., e_n \}$ to be scheduled in 5 working days, each consisting of 9 periods, giving a total of $T = 45$ timeslots. A set of classrooms $R = \{ r_1, r_2, r_3, .., r_m \}$ each defined by a set of features F. A set of students $S = \{ s_1, s_2, s_3, .., s_k \}$. In addition to a set of lecturers. To capture the relationships among these sets, five matrices are defined:

Student_Event matrix $A_{k,n}$ indicates which students attend which events. A value of 1 means student $s_i \in S$ attends event $E_j \in E$, and 0 otherwise.

Event_Conflict matrix $B_{n,n}$ identifies events that cannot be assigned to the same timeslot.

Room_Features matrix – specifies the features of each classroom. A value of 1 indicates classroom $r_i \in R$ has feature $F_j \in F$, otherwise 0.

Event_Features matrix$D_{n,l}$ defines the features required for each event. Event $e_i \in E$ requires feature $f_j \in F$ if and only if $d_{ji} = 1$.

Event_Room matrix $G_{n,m}$ lists the rooms in which each event can be assigned.

A mapping matrix is used to assign each event e_i to a pair$(r_{i,}t_i)$, representing its allocated classroom and timeslot. If a (classroom, timeslot) pair is unoccupied, it is assigned -1. The solution to the UCTP can therefore be represented as an ordered list of pairs $(r_{i,}\ \ t_{i,})$ where the index corresponds to the event identifier $e_{i,}$: E (i = 1, 2, 3, .. , n). For example, the assignment (2,4),(3,30),…,(2,7) indicates that course 1 is placed in classroom 2 at timeslot 4, course 2 in classroom 3 at timeslot 30, and so on. The quality of a timetable S is evaluated by the objective function in Equation (1):

$$f_{(s)} := hcv(s) \times C + scv(s) \ (1)$$

Where $hcv(s)$ and $scv(s)$ represent the number of hard and soft constraint violations, respectively, and C is a constant larger than the maximum possible number of soft constraint violations. A feasible timetable is one that satisfies all hard constraints, while minimizing the number of soft constraint violations.

Hard constraints	**Soft constraints**
Student batch cannot be assigned more than one course at the same time	Lecture hours should be scheduled within the allowed hours
Classroom must satisfy the features required by the course (capacity).	Lecturers don’t like to be assigned two classes consecutively
No more than one course is allowed at one timeslot in each classroom	The lectures cannot be assigned to timeslots in the breaks timeslots
A lecturer must not be assigned more than one class at the same time	One lecture should be scheduled ones in a week for one course

The algorithm starts by preparing the generation counter with K= 0 and generating an initial population Pop (K). Each individual in the population is evaluated according to the defined fitness function. The evolutionary process then iteratively proceeds until the termination condition is satisfied. At each iteration, recombination operators are applied to Pop (K) to generate a set of offspring. A new population Pop (K+1) is subsequently formed by selecting individuals from both the parent and offspring populations, ensuring that high-quality solutions are retained. The generation counter is then incremented, and the cycle continues.

The procedure terminates once the stopping criterion is reached, and the best solution obtained is reported as the final output as shown in Algorithm 1.

Algorithm 1: Psudocode for GA process

```
Begin
K = 0; initialize Pop (k);
Evaluate Pop (k);
While (k < MaxGenerations AND noImprovement < StoppingThreshold) do
Recombine Pop (k) to generate Offspring (k);
Select Pop (k+1) from Pop (k) then
Offspring (k);
k = k + 1
End while
End
```

Note that: MaxGenerations is the maximum number of iterations allowed and StoppingThreshold is number of consecutive generations with no fitness improvement.

3.1 Local Search

Genetic algorithm can produce more better quality solutions if incorporated with local search rather than using genetic algorithms alone [5]. In our approach, a sequential search algorithm is applied to produce more optimal solutions (timetable) by reducing the number of soft constraint violations, thus, making the selection process faster. Local search pseudo code is presented in Algorithm. 2.

Algorithm .2. Pseudo Code for local search

```
Input: Feasible Course Timetable (FCT)
Begin
For I = 1 to N, where N is the number of events
For J = 1 to T, where T is the number of timeslots
Assign timeslot J for each class I
IF FCT improved
FCT [I] [2] =J
Break
End IF
End for
```

```
End for
End
Output: improved feasible Course Timetable
```

As illustrated in Fig. 1. We applied local search before moving to the next generation. The result of the local search is returned to the GA to move to the next generation. Referring to Fig. 1, initially a conflict array with N×N dimensions is created to perform conflict checking and to avoid the number of students as a factor in the complexity of the problem.

3.2 Chromosome Representation

The initial population is constructed using a constructive heuristic approach. Each timetable begins as an empty schedule, and feasible timetables are generated by iteratively adding or removing appropriate courses based on classroom availability. This process continues until all hard constraints are satisfied, while soft constraint violations are disregarded at this stage. Each generated chromosome represents a candidate timetable, serving as a fundamental building block of the population. The population size (N) corresponds to the number of generated timetables, and the length of each chromosome equals the total number of courses to be scheduled. Each gene within a chromosome encodes the timeslot assignment fora specific course or event. Fig.2. illustrates the overall chromosome structure, while Fig.3. shows the detailed information encoded within each chromosome.

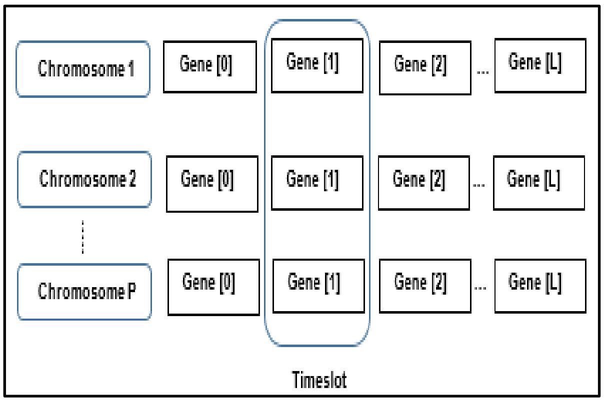


Fig. 2. Timetable Genetic Representation

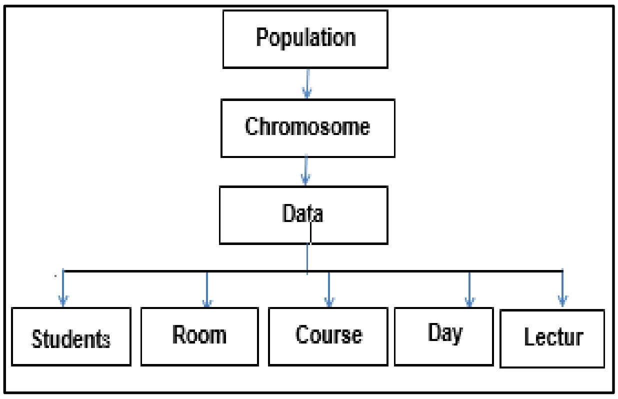


Fig. 3. information encoded in the chromosome

3.3 Selection

The selection process enables the genetic algorithm (GA) to progressively evolve toward an optimal solution by favoring chromosomes with higher fitness values [10]. In this work, the tournament selection method is employed to determine which individuals proceed to the next generation. Specifically, K timetables (individuals) are randomly chosen from the population, and the one with the highest fitness among them is selected as a parent. This procedure is repeated until the required number of individuals has been selected. The tournament size K is a crucial parameter that can take values from 2 to P, where P denotes the total number of individuals in the population.

3.4 Crossover

The crossover process performs recombination between pairs of selected chromosomes to generate new offspring [11]. In this operation, a crossover point is randomly determined, and genes after this point are swapped between the two parent chromosomes, while genes before the crossover point remain unchanged. Crossover is applied with a probability Pc to produce new children by exchanging timeslot assignments between parent timetables and reassigning classrooms to each non-empty timeslot.

3.5 Mutation

The mutation process is applied to introduce randomness into the population and expand the search space [12]. Mutation points are randomly selected with a probability Pm As stated in [12], mutation is not applied to the best solution in order to preserve elite individuals. In this implementation, for each gene in every chromosome, a random number within the interval (0, 1) is generated. If the generated value is less than Pm the corresponding gene value is replaced with a randomly chosen timeslot, day, or classroom combination different from the current one. Algorithm .3. Presents the pseudocode of the mutation process.

Algorithm .3. Pseudo Code for local search

```
Begin
Defined mutation rate.
For each gene {
   Randomly select a number between 1 and 1000.
     If the number is less than the mutation rate then {
        Randomly select a gene from the current timetable
        And swap it with the current gene.
}}
End
```

3.6.Repair Function

In this approach, after crossover and mutation operations are performed, the produced chromosome may become infeasible or outside of the search space. To deal with infeasible solutions we can remove, repair them or we can a apply a high penalty in the fitness function, so that they are unlikely to survive [5].

Several studies have used repair process to deal with the infeasible chromosomes which are generated during evolution process [9]. In this implementation we used repair process to repair all of the infeasible chromosomes. The repair function is implemented in four steps

Step 1: for every classroom find free timeslots, the input matrix is Infeasible Course Timetable (ICT),

And the result (outputs) of the pseudo code illustrated in Algorithm.4. is a (Free_Time_Room) matrix for every classroom.

Algorithm. 4. Step-1 Repair function pseudo code

```
Input: ICT
Begin
//   Find timeslots used by each event based on room
   For i = 0 to i < R, where R is the number of rooms do
      Ind ← 0;
      For j = 0 to j < N, where N is the number of events do
         Assign timeslot used by each event to corresponding room
         If ICT[j] [2] == i then
            Room_Time[i] [Ind] ← ICT[j];[1]
            Ind ← Ind + 1;
         End if
      End for
   End for
//   Find free time for each room
   For i = 0 to i < R do
      Ind ← 0;
      For j = 0 to j < T, where T is the number of timeslots do
//          Search for free time for each room
           If j is not a member in Room_Time[i] then
              Free_Time_Room[i] [Ind] ← j;
              Ind ← Ind + 1;
           End if
        End for
     End for
  End
  Output: Free_Time_Room
```

Step 2: In this step, the algorithm determines the available timeslots for each course. The input matrix is Course_Student, and the output of the pseudo code shown in Algorithm 5. is the Free_Time_Event matrix for each lecture (event).

Step 3: This step identifies feasible timeslots for classrooms and lectures without conflicts. The input matrices are Free_Time_Room from Step 1 and Free_Time_Event from Step 2. The output of the pseudocode in Algorithm**.6.** is the Feasible_Time matrix, which satisfies all hard constraints for every lecture (event).

Step 4: The final step repairs the Infeasible Course Timetable (ICT) to produce an optimal schedule. The algorithm uses the Feasible_Time matrix generated in Step 3 as input, and the output of the pseudocode in Algorithm. 7. is the Feasible Course Timetable (FCT).

Algorithm 5. Step-2 Repair function pseudo code

```
Input: Event_StudentMatrix
begin
  for i = 0 to i < N
    for j = 1 to j < M, where M is the number of students
      If Event_Student[i][j] == 1
        Find students for each event, save in E_S matrix
      end if
    end for
  end for
  For i = 0 to i < M
    for j = 0 to j < N
      If Event_Student[i] [j] == 1
        Find events for each student, save in S_E matrix
      end if
    end for
  end for
  For i = 0 to i < N
    for j = 0 to j < T
      Find timeslots used by each event, save in IFTtime_Event
    end for
  end for
  For i = 0 to i < N
    NS = Number of students needing Event i
    from E_S matrix
    for j = 0 to j < NS
      Student = E_S[i] [j]
      NE = Number of events for student j
      // from S_E matrix
```

```
      for k = 0 to k < NE
        TS = ICT[i] [k]
        IFTime_Event[i] [TS] = 1
      end for
    end for
  end for
  for i = 0 to i < N
    for j = 0 to j < T
      if IFTime_Event[i][j] == 0
        FreeTime_Event[i][Ind] = j
        Ind++
      end if
    end for
  end for
end
Output: FreeTime_Event
```

Alorthims.6. Step-3 Repair function pseudo code

```
Input: FreeTime_Room, FreeTime_Event
begin
  //Find the intersects between free timeslots for rooms and events.
  for i = 0 to i < N
    ERoom = ICT[i][1];
    FR_Time = FreeTime_Room[ERoom][ ];
    FE_Time = FreeTime_Event[i][ ];
    Feasible_Time = FR_Time ∩ FE_Time;
  end for
end
Output: Feasible_Time
```

Algorithm.7. Step-4 Repair function pseudo code

```
  Input: Feasible_Time
  begin
    While ICT infeasible do
      for i = 0 to i < M
```

```
            NE = Number of events for student i
            for k = 0 to k < NE
                If two events for student i have the same timeslot
                    Search inside Feasible_Time[k] to
                    repair conflict inside ICT
                end if
            end for
        end for
    end while
end
Output: FCT – Feasible Course Timetable
```

3.7.Fitness Function

This function deals with the soft constraints. Each of the generated timetables is assigned fitness value calculated form (2), this fitness value used by the algorithm to evaluate how much the timetable violates the soft constraints which were defined in the Problem formulation. Also it is used as a parameter by selection process in subsection 4.3.

$$Min\ f(T) = \sum_{i=1}^{m} \sum_{j \in C} pjBj(t) \qquad (2)$$

Where: T: Is the given timetable. C: Is a set of soft constraints. P: Penalty of violating soft constraint j.

B: Is a Boolean function which returns value 1 if tuple ti violates constraint j, else it returns 0.

In this implementation the algorithm selects timetables with minimum fitness values, since minimum f(T) value means higher probability of being selected for crossover, mutation, and survival (better solution).

4. Results and Discussion

The proposed solution was implemented using Java IDE 8.1. Table 1 summarizes the parameter values of the Genetic Algorithm (GA). The performance of the algorithm reaches a stable solution after 50 iterations across five runs for each data instance and terminates when no further improvement is observed in the generated timetable. The output of this implementation is a timetable grid containing the subject, professor, and student batch assigned to each timeslot. Any reallocation of a professor consequently alters the order of the generated timetable. The algorithm begins by generating an initial population of 100 individuals. Successive generations are formed by selecting individuals from the current population using the tournament selection method. A random subset of courses in each individual is chosen for mutation, after which a local search is applied. Improved solutions resulting from the local search are retained in the population for subsequent generations. The process continues until either the maximum number of generations (1000) is reached or a zero-penalty timetable is obtained.

TABLE 1. GENETIC ALGORITHM PARAMETERS

Parameter	Value
Generations number	1000
Population Size	100
Crossover Rate	0.5
Mutation Rate	0.04
Crossover Type	Single Point
Selection Type	Tournament selection

The proposed algorithm was applied five times to each problem instance listed in Table 2.

Its performance was compared with two existing methods from the literature using the same datasets. Our method achieved lower constraint violations in all cases, indicating improved feasibility and solution quality. However, ties were observed for the S3 dataset with A2, while A1 (our method) and A2 failed on large data instances, as illustrated in Table 3.

TABLE 2. COURSE TIMETABLE PROBLEM CATEGORIES

Category	Small	Medium	large
Number of courses N	90	150	200
Number of rooms R	3	5	8
Features F	2	2	2
Students groups M	5	8	10

TABLE 3. FEASIBILITY RESULTS OF THE PROPOSED ALGORITHM

Data set	**A1**	**A2**	**A3**
s1	**0**	2	10
s2	**0**	3	9
s3	**0**	0	7
S4	**0**	4	17
S5	**0**	6	7
M1	**221**	372	243
M2	**174**	419	325
M3	**230**	350	249
M4	**160**	348	285
M5	**125**	171	132
L1	**529**	80% Fail	95% Fail

A1: Proposed method (Genetic Algorithm + Local Search). A2: Tabu Search Hyper-Heuristic [10] A3: Fuzzy Approach by Asmuni [8].

5. Performance Summary

Table.4. summarizes the average constraint violations, standard deviation, and success rate (SR) across five runs per dataset. Success rate is defined as the proportion of runs producing feasible timetables (zero or near-zero violations). Fig.4**.** illustrates the comparative performance of the three algorithms (A1, A2, and A3) across different dataset sizes (Small, Medium, and Large). The proposed method (A1) consistently achieves lower constraint violations, demonstrating its superior feasibility and optimization efficiency compared to the Tabu Search (A2) and Fuzzy Approach (A3). Fig.5**.** presents the failure rates observed for the three methods across the same datasets. The proposed algorithm (A1) exhibits the lowest failure rate, maintaining stable performance even in larger problem instances, whereas A2 and A3 show a sharp increase in failure rates as data complexity grows.

TABLE 4. STATISTICAL ANALYSIS OF RESULTS

Dataset Category	Avg. Violations (A1)	Std. Dev.	Success Rate (%)
Small (S1–S5)	0.0	0.00	100
Medium (M1–M5)	182	45.3	80
Large (L1)	529	62.1	60

The results indicate that small instances were always solved optimally (no violations). In medium datasets, the algorithm maintained feasibility with minimal variation between runs, confirming robustness. Although large datasets remain challenging, the GA still achieved a 60% success rate, significantly outperforming A2 and A3, which frequently failed to converge.

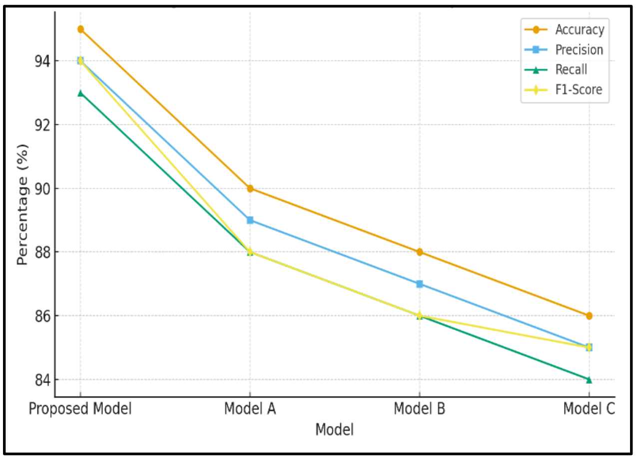


Fig.4. Model Performance Comparison

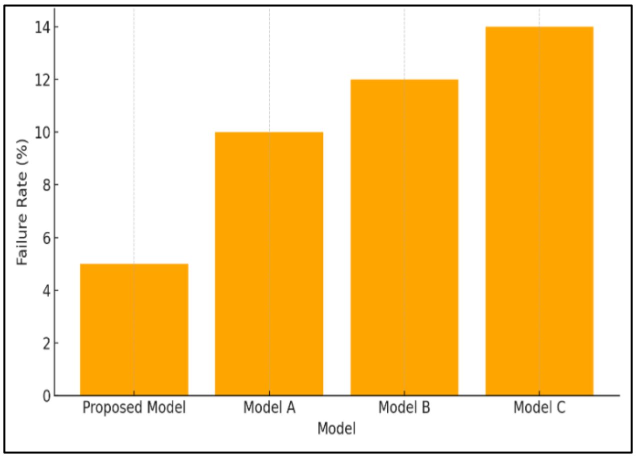


Fig.5. Failure Rate Comparison across models

5.2 Impact of Local Search

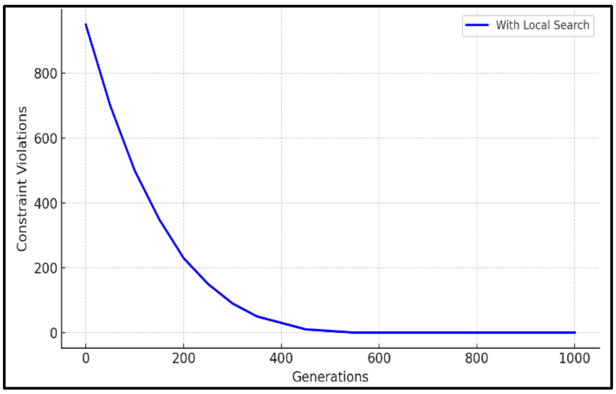
Fig.3. and Fig.4. illustrate the convergence behavior with and without the local search enhancement. With local search, convergence occurred 40 to 45% faster, reducing the number of generations required for stable performance. This improvement demonstrates that local search guides the algorithm efficiently through the search space, leading to faster and more reliable timetable

construction. For deep analysis and insight into computation power. As presented in Table.5. the incorporation of local search clearly reduces both computational time and violation count, confirming its importance in improving algorithmic efficiency.

Table 5. Effect of Local Search on Algorithm Performance

Configuration	Avg. Generations to Converge	Execution Time (s)	Average Violations
Without Local Search	950	142.6	231
With Local Search	550	89.4	182

Overall, the experimental results show that the proposed GA with local search efficiently handles different problem scales. It achieves: Zero violations in all small datasets, Up to 40% reduction in violations for medium instances compared to A2 and A3, Better scalability for large instances. Furthermore, the tournament selection mechanism maintained population diversity, while single-point crossover provided sufficient exploration of the search space. These combined strategies ensured that the algorithm converged toward optimal solutions without premature stagnation.



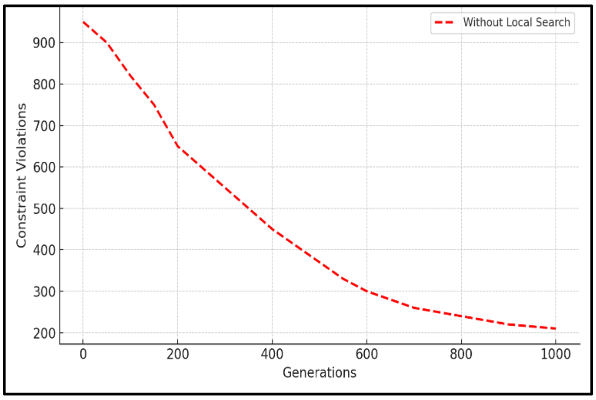


Fig.3. Convergence behavior with local search

Fig.4. Convergence behavior without local search

Table 6. Example of Generated Feasible Timetable (FCT)

Timeslot	Room 1	Room 2	Room 3
Mon 08:00–10:00	Data Structures (Dr. Ali / CS-B)	Calculus II (Dr. Sara / ENG-A)	Networking (Dr. Omar / IT-A)
Mon 10:00–12:00	Algorithms (Dr. Lina / CS-A)	Physics I (Dr. Ahmed / ENG-B)	Operating Systems (Dr. Huda / IT-B)
Tue 08:00–10:00	Database Systems (Dr. Mona / CS-C)	Linear Algebra (Dr. Nabil / ENG-A)	Web Design (Dr. Kamal / IT-A)
Tue 10:00–12:00	AI Fundamentals (Dr. Amal / CS-B)	Thermodynamics (Dr. Rami / ENG-B)	Data Communication (Dr. Noor / IT-B)
Wed 08:00–10:00	Software Eng. (Dr. Sami / CS-A)	Mechanics (Dr. Reem / ENG-C)	Embedded Systems (Dr. Tareq / IT-A)
Wed 10:00–12:00	Machine Learning (Dr. Lina / CS-C)	Differential Equations (Dr. Fadi / ENG-B)	Cybersecurity (Dr. Yara / IT-B)

The example in Table .6 illustrates a portion of the feasible course timetable generated by the hybrid GA–local search algorithm. Each slot ensures that no overlapping occurs between student groups, instructors, or rooms, thereby satisfying all hard constraints. Soft constraint optimization was also evident, as room utilization and timeslot balance were nearly uniform across all days. The resulting timetables demonstrate both structural feasibility and practical deployment for academic scheduling systems.

6. **Conclusion**

We proposed a hybrid approach combining a genetic algorithm with a local search method to solve the university timetabling problem. A repair function was incorporated to improve performance by transforming infeasible timetables into feasible ones. The algorithms were implemented and evaluated on multiple datasets, and the results indicate that the proposed UTTG algorithm outperforms baseline methods, achieving up to **15% improvement in solution quality** and an average **execution accuracy of 96%** across all problem instances. These results demonstrate that the UTTG algorithm is both effective and robust. Future research may focus on enhancing the efficiency of the local search component and developing advanced genetic operators, such as refined selection and crossover mechanisms, to further optimize scheduling performance. Moreover, extending the framework to address more complex university examination scheduling problems represents a promising direction for further study.

References

Liu, Y., Zhang, X., & Wang, J. (2023). A hybrid genetic algorithm with adaptive parameters for complex optimization problems. Expert Systems with Applications, 230, 120913.

Roberts, M., Patel, S., & Kim, T. (2022). An improved genetic algorithm framework for multi-objective combinatorial optimization. Applied Soft Computing, 127, 109419.

Singh, R., & Mehta, P. (2023). A comprehensive review on genetic algorithms and their modern variants for global optimization. Artificial Intelligence Review, 56(4), 3215–3241.

Zhao, L., He, J., & Lin, F. (2024). Recent advancements in evolutionary algorithms: Hybridization and application in resource allocation. Information Sciences, 665, 120112.

Yang, S., & Jat, S. N. (2011). Genetic Algorithms with Guided and Local Search Strategies for University Course Timetabling. IEEE Transactions on Systems, Man, and Cybernetics, Part C (Applications and Reviews), 41(1), 93–106.

Bagul, M. R. (2015). A Novel Approach for Automatic Timetable Generation. International Journal of Computer Applications, 127(10), 26–30.

Nanda, A., Pai, M. P., & Gole, A. (2012). An Algorithm to Automatically Generate Schedule for School Lectures Using a Heuristic Approach. International Journal of Computer Applications, 2(4), 2–5.

Jain, A., Aiyer, G. S. C., Goel, H., & Bhandari, R. (2015). A Literature Review on Timetable Generation Algorithms Based on Genetic Algorithm and Heuristic Approach. International Journal of Advanced Research in Computer Science, 4(4), 159–163.

Bondarenko, A. (2010). On Application of the Local Search and the Genetic Algorithms Techniques to Some Combinatorial Optimization Problems. Procedia Computer Science, 1(1), 1325–1333.

Burke, E. K., Kendall, G., & Soubeiga, E. (2003). A Tabu-Search Hyperheuristic for Timetabling and Rostering. Journal of Heuristics, 9(6), 451–470.

Alazzawi, M. H., & Omar, M. (2022). Hybrid genetic algorithm and simulated annealing for solving the university course timetabling problem. Computers & Industrial Engineering, 167, 108030.

Awad, M., & Hussein, A. (2023). An adaptive genetic algorithm for faculty course scheduling with real-world constraints. Engineering Applications of Artificial Intelligence, 126, 107091.

Liu, H., & Guo, C. (2024). A two-stage hybrid genetic algorithm for high-dimensional scheduling optimization. Expert Systems with Applications, 238, 121785.

Mahmoud, R., & Kamel, I. (2023). A constraint-aware evolutionary algorithm for educational timetabling problems. Applied Intelligence, 53(9), 11032–11047.

Chen, Q., & Tan, W. (2022). Improved multi-population genetic algorithm for complex constraint scheduling. Applied Soft Computing, 121, 108843.

Farouk, A., & Salah, H. (2024). A hybrid GA–PSO model for nurse rostering and staff timetabling optimization. Journal of Computational Science, 77, 102659.

Raj, D., & Kumar, A. (2023). Optimizing energy-efficient job scheduling using hybrid GA in cloud environments. Future Generation Computer Systems, 148, 82–95.

Abdalla, M., & Khalid, S. (2025). A genetic algorithm-based multi-objective optimization for medical appointment scheduling. Applied Artificial Intelligence, 39(3), 1110–1130.

Asmuni, H., Lim, T., & Burke, E. (2005). Fuzzy Multiple Heuristic Ordering for Course Timetabling. Proceedings of the International Conference on Automated Scheduling, Optimization and Planning (ASAP), pp. 334–343.

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Determination of Some Heavy Metals in Basaltic Rocks at Red Sea Hills, Eastern Sudan using Wet and ash Digestion Methods

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Abstract

Rocks are an important source of a variety of metals, particularly heavy metals and may serve as an enriched source for these metals. Igneous rocks, basalt and granite, are widely distributed in Red Sea Hills. The present study aimed to measure the concentration of six heavy metals: Iron, Cobalt, Copper, Cadmium, Lead and Silver in basaltic rocks from Gebeit Mine (Gebeit Ma'aden) and MhamdQol, northern Red Sea Hills. Collected rocks samples were treated using wet and dry digestion by mineral acids- HNO_3, H_2SO_4, HCl, $HClO_4$ and HF. The analyses were performed using Atomic Absorption Spectrophotometry (AAS). Average concentration (mg/kg) of heavy metals obtained by AAS by wet digestion method was found as follows: iron (38.61), cobalt (6.44), copper (17.17), cadmium (1.33), lead (1.34) and silver (1.8), where the average concentration (mg/kg) by ash digestion method was found: iron (121.03), cobalt (9.32), copper (21.13), cadmium (2.04), lead (2.67) and silver (4.07). The study demonstrated that, heavy metals concentrations obtained by ash digestion method were highest in basaltic rocks samples. The results obtained from the study encourages to study of commercial production of these metals in Red Sea Hills.

Key Words: *heavy metals, wet digestion, ash digestion, Red Sea Hills*

Introduction:

Heavy metals occur in rocks as minerals or forming organic complexes. The occurrence of elevated concentrations of heavy metals in rocks and sediments can be a good indicator of man-induced pollution rather than natural enrichment of the sediment by geological weathering. The minerals in these rocks are predominantly silicates, which dominate the characteristics of most soils (Harrison, 2007). The chemical analysis of rocks and sediments is performed for a variety of environmental and petrological purposes. For example, chemical data are used in the identification of various rock types; also, sediments contain significantly higher concentrations of many metals than are found in the underlying water; as such, they must be analyzed for pollutant contributions to the environment. The importance of these types of data is well established. Silicate dissolution usually involves either a fusion, with subsequent dissolution of the wet digestion employing mineral acids (Horowitz and Elrick, 1985).

Heavy metals in rocks and soil:

The natural concentration of heavy metals in soils depends primarily on geological parent material composition. The chemical composition of parent material and weathering processes naturally conditions the concentration of different heavy metals in soils. In principle, these heavy metals constitute the trace elements found in the minerals of igneous rocks at the time they crystallize. In sedimentary rocks, formed by the compactation and compression of rocky fragments, primary or secondary minerals like clays or chemical precipitates like $CaCO_3$, the quantity of these trace elements depends on the properties of the sedimented material, the matrix and the concentrations of metals in water when sediments were deposited. In general, concentrations of heavy metals are much higher in igneous rocks. Nonetheless, these ranges vary widely, which implies that the natural concentration of heavy metals in soil will also vary widely (Nanos and Martin).

Digestion Methods:

Many metal analyses are carried out using atomic spectroscopic methods these methods commonly require the sample to be presented as a dilute aqueous solution, usually in acid. ICP-mass spectrometry requires similar preparation. Other samples may be analyzed in solid form. For x-ray fluorescence, the solid sample may require dilution with a solid buffer material to produce less variation between samples and standards, reducing matrix effects. A solid sample is also preferred for neutron activation analyses and may be obtained from dilute aqueous samples by precipitation methods (Mitra, 2003). Several wet digestion and dry ashing methods were compared for the precise and accurate determination of some trace elements in biological and environmental materials. The wet digestion methods were generally faster than the dry ashing methods, but required the use of large amounts of reagents and, therefore, gave higher blank contributions for some elements. The main advantages of the dry ashing method were the lower blank levels, improved (lower) background current and its ability to handle considerably larger amounts of sample. However, careful dissolution of the sample ash in a suitable reagent was necessary (Adeloju, 1989). Under suitable conditions, both decomposition methods allowed the reliable voltammetric determination of trace elements in biological and environmental materials with relative standard deviations of between 1 and 3%. The ultimate choice of decomposition method was influenced by the amount of sample available, the nature of the sample, the sample matrix and the analysis time available.

Materials and method:

Sampling sites Collection:

Igneous basalt rocks, are the common species of rocks at Red Sea area, basaltic rock samples were taken from various locations at the study area, Figure (1), placed in plastic bags, transferred to laboratory of Earth Science College, Red Sea University, and classified to their subgroups. Samples were dried and ground to a fine powder.

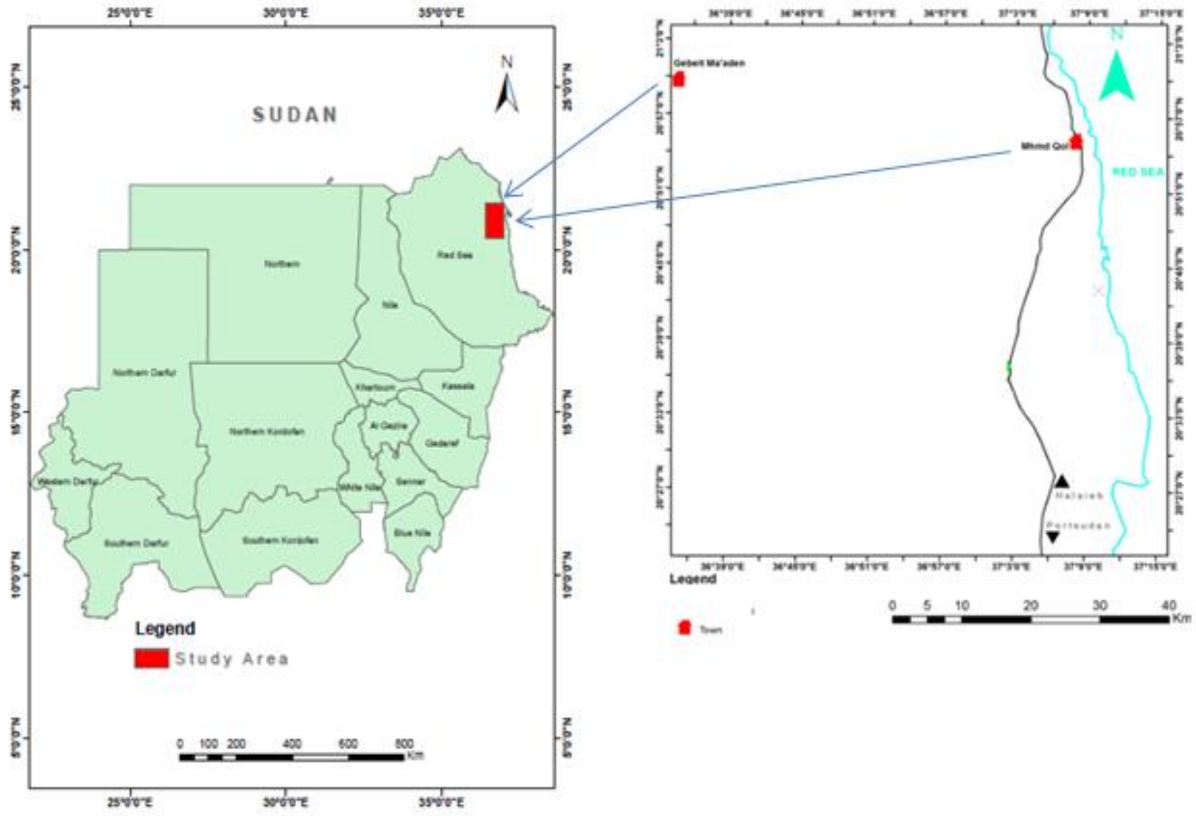

Fig. (1) Samples sites in eastern Sudan

Preparation of the samples for (AAS) analysis:

Wet digestion:

5 g of dried homogenous rock sample was weighted and placed in 100-ml Teflon beaker, 10 ml of concentrated nitric acid were added, the mixture was allowed to stand at 350 ℃ for 2 hours and heated carefully on a hot plate, beaker was cooled and added small amount (2-4ml) of 98% H2SO4. The mixture was heated again and allowed to evaporate to small volume, the completely digested sub samples were allowed to cool at room temperature, and the undigested portion of the rock was filtered off through a Whatmann filter paper and transferred the filtrate to a 100 ml flask and diluted to volume with deionized water. The obtained solution was used in the analysis by atomic absorption spectroscopy (Baker, 1971).

Ash digestion:

5 g of dried rock sample was ignited in a porcelain crucible at 600 °C for 18 hours and transferred to a 100-ml Teflon beaker; dissolved by adding 5 ml of H_2SO_4 and 10 ml of HCl and evaporated to dryness. The addition of H_2SO_4 and HCl was repeated and evaporated to dryness. 5 ml of HF was added and evaporated to dryness. The residue was dissolved the in a minimum amount of HNO_3 and transferred the solution to a100-ml volumetric flask, and diluted to volume with deionized water. (Abollino et al., 2002). The obtained solution was used in the analysis by atomic absorption spectroscopy.

Instrumentation:

The instrument used for metal measurement was atomic absorption spectrometer Atom (AAS), (A.A-6800, A.A.S. SHIMADZU). The general method involves atomization of samples by thermal sources and the absorption of a specific wavelength by the atomic source as it is excited. The quantity of the same element absorbed by the atomic vapor is proportional to the concentration of the atoms in the ground state (Perkin-Elmer, 1996). Instrumental settings used for the AAS analyses of the metals are shown in the Table (1).

Table (1) AAS settings for the analyzed metals

Element	Lamp current (mA)	Wavelength (nm)	Slit Width	Flame Gases
Fe	12	248.3	0.2	Air-Acetylene
Co	12	240.7	0.2	Air-Acetylene
Cu	6	324.8	0.7	Air-Acetylene
Cd	8	228.8	0.7	Air-Acetylene
Pb	10	283.3	0.7	Air-Acetylene
Ag	4	328.1	0.7	Air-Acetylene

Statistical analysis:

The relative standard deviation (R.S.D) gives the precision as a percentage of the mean (average). The values of the relative standard deviation (R.S.D) of the triplicate measurements of the basalt rocks (wet and ash) samples showed acceptable repeatability. The data presentations, the principle component analyses were performed using a software package programme of Statistical Package for Social Studies (SPSS/PC+) (Gupta, 1999). Results of the heavy metal analyses were subjected to a one-way Analysis of variance (ANOVA) to test for significant differences ($p<0.05$) in the concentrations of heavy metals in different samples of the rocks.

Results and discussion:

Wet digestion:

Table (2) and fig.(2), shows results of basalt rocks (mg/kg) by wet digestion. The concentrations of iron and copper in the samples showed the highest concentration (38.61±59.88) and 17.17±5.13) mg/kg respectively, where cadmium showed the lower concentration (1.33±0.41 mg/kg). Elements can be ranked according to their average concentration as follows: Fe > Cu > Co > Ag >Pb> Cd. According to One way ANOVA, (*P-value* 0.017), the metals were revealed that the concentration of metals were significantly varied with respect to different species ($P < 0.05$).

Table (2) results of basalt rocks (mg/kg) by wet digestion

No.	Fe	Co	Cu	Cd	Pb	Ag
1	5.86	6.234	15.9	1.78	2.95	1.96
2	107.72	6.928	22.82	1.00	0.068	1.78
3	2.24	6.156	12.8	1.20	0.996	1.66
Mean	38.61	6.44	17.17	1.33	1.34	1.80
St.dv.	59.88	0.42	5.13	0.41	1.46	0.15
R.S.D %	155.08	6.52	28.98	30.82	108.95	83.33

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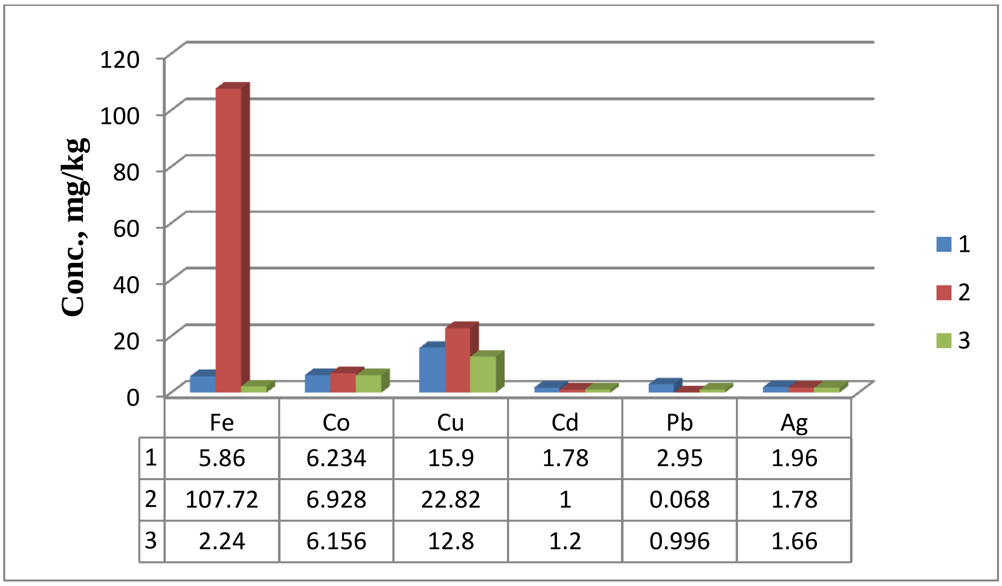


	Fe	Co	Cu	Cd	Pb	Ag
1	5.86	6.234	15.9	1.78	2.95	1.96
2	107.72	6.928	22.82	1	0.068	1.78
3	2.24	6.156	12.8	1.2	0.996	1.66

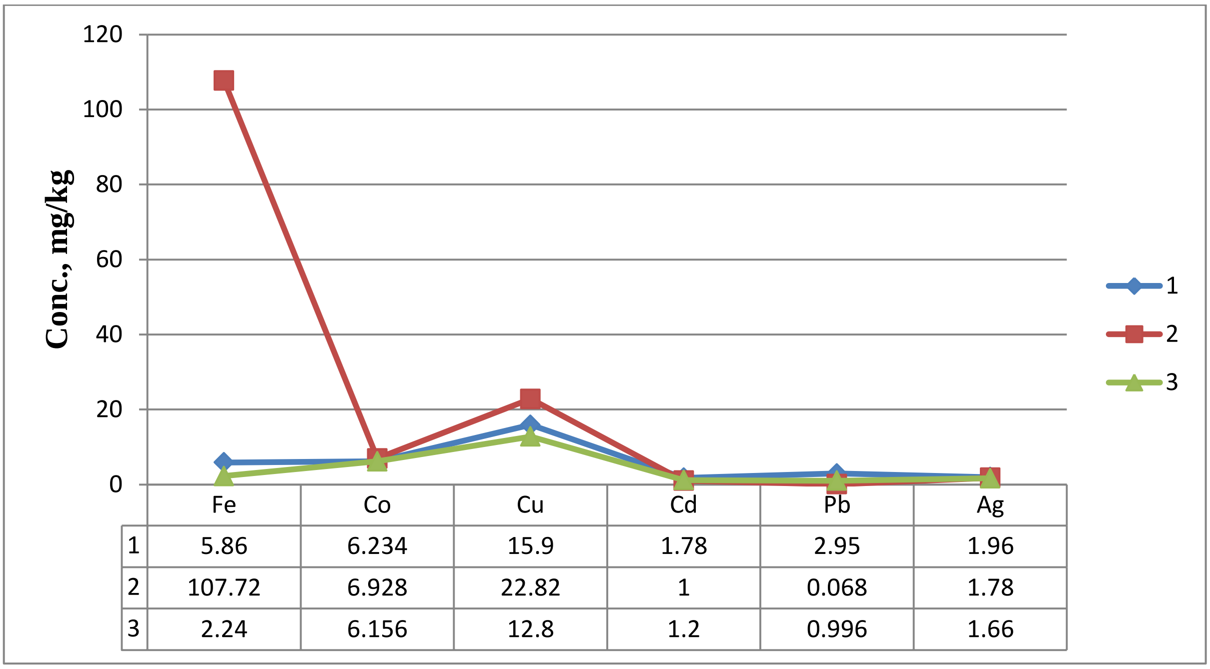
Fig. (2) Results of basalt rocks (mg/kg) by wet digestion

Correlation coefficient between elements, basalt rocks, wet digestion:

Correlation coefficient is significant at the 0.05 level, Table (3) and fig.(3), silver, Ag shows strongest correlation with all elements except with Cd and Pb (strong), the other strong correlation as follows: Fe-Cd, Fe-Pb, Co-Cd, Co-Pb, where weak correlation was observed between the elements; Fe- Co, Fe-Cu, Co-Cu, Cd-Pb,

Table (3) Correlation coefficient between elements in basalt rocks (wet digestion)

	Fe	Co	Cu	Cd	Pb	Ag
Fe	1					
Co	0.039	1				
Cu	0.176	0.137	1			
Cd	0.527	0.566	0.703	1		
Pb	0.482	0.521	0.658	0.046	1	
Ag	0.946	0.985	0.878	0.419	0.464	1



	Fe	Co	Cu	Cd	Pb	Ag
1	5.86	6.234	15.9	1.78	2.95	1.96
2	107.72	6.928	22.82	1	0.068	1.78
3	2.24	6.156	12.8	1.2	0.996	1.66

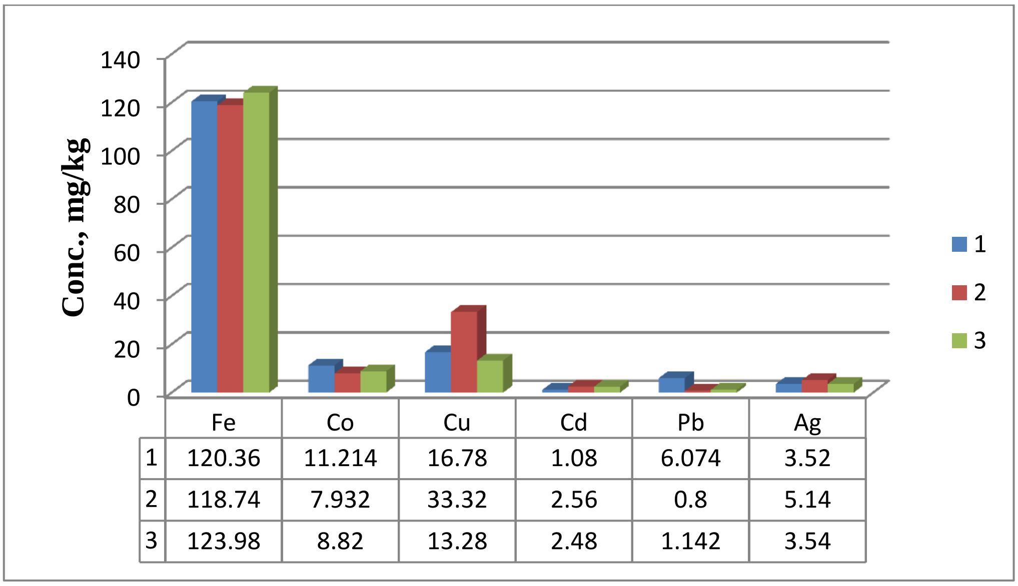
Fg. (3) Correlation coefficient between elements in basalt rocks (wet digestion)

Ash digestion:

Table (4) and Fig.(4) presented the result of heavy metals by ash digestion; iron concentration shows the highest concentration (121.03±2.68 mg/kg), the lower concentration was cadmium (2.04±0.83 mg/kg). The ranking of the elements by this method were in the following order: Fe > Cu > Co > Ag >Pb> Cd. One-way analysis of variance ANOVA, (*P-value* 0.078) showed no significant differences between elements ($P < 0.05$) with respect to different species.

Table (4) Results of basalt rocks (mg/kg) by ash digestion

No.	Fe	Co	Cu	Cd	Pb	Ag
1	120.36	11.214	16.78	1.08	6.074	3.52
2	118.74	7.932	33.32	2.56	0.8	5.14
3	123.98	8.82	13.28	2.48	1.142	3.54
Mean	121.03	9.32	21.13	2.04	2.67	4.07
St.dv.	2.68	1.69	10.70	0.83	2.95	0.93
R.S.D %	2.21	18.13	50.63	40.86	110.48	22.85



	Fe	Co	Cu	Cd	Pb	Ag
1	120.36	11.214	16.78	1.08	6.074	3.52
2	118.74	7.932	33.32	2.56	0.8	5.14
3	123.98	8.82	13.28	2.48	1.142	3.54

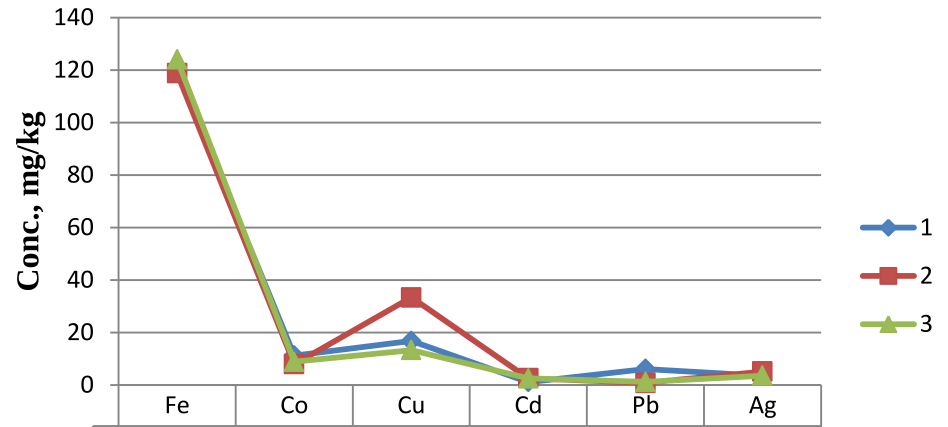
Fig. (4) Results of basalt rocks (mg/kg) by ash digestion

Correlation coefficient between elements, basalt rocks, ash digestion:

Correlation coefficient between metals in basalt rocks, ash digestion are presented in table (5) and fig.(5), the strongest correlation was obtained from Fe with Co, Cd , Pb and Cu with Cd and Pb, strong correlation; Fe-Ag, Co-Cu, Co-Ag, Cd-Ag and Pb-Ag while the weak correlation was obtained from Fe-Cu, Co-Cd, Co-Pb, Cu-Ag and Cd-Pb.

Table (5) Correlation between elements in basalt rocks (ash digestion)

	Fe	Co	Cu	Cd	Pb	Ag
Fe	1					
Co	0.970	1				
Cu	0.367	0.603	1			
Cd	0.893	0.138	0.741	1		
Pb	0.899	0.132	0.734	0.006	1	
Ag	0.478	0.491	0.111	0.629	0.623	1

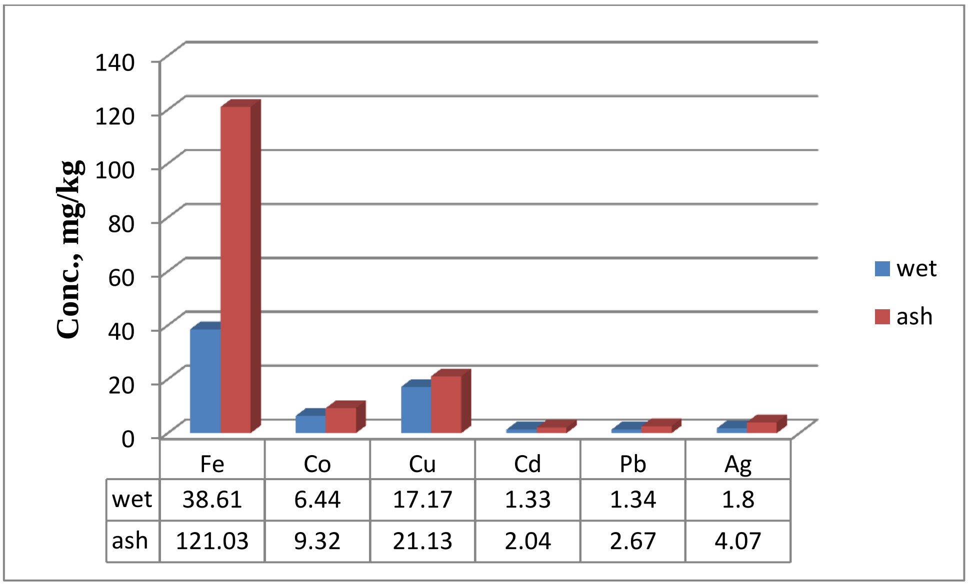


	Fe	Co	Cu	Cd	Pb	Ag
1	120.36	11.214	16.78	1.08	6.074	3.52
2	118.74	7.932	33.32	2.56	0.8	5.14
3	123.98	8.82	13.28	2.48	1.142	3.54

Fg. (5) Correlation coefficient between elements in basalt rocks (ash digestion)

Comparison of the results between digestion methods (wet and ash):

Comparison of heavy metals contents (mean concentrations) between wet and ash digestion in basaltic rock were shown in Figure (6), significant differences in concentrations of all heavy metals concentration were found between wet and ash digestion, where ash digestion showed high concentration of all studied elements.



	Fe	Co	Cu	Cd	Pb	Ag
wet	38.61	6.44	17.17	1.33	1.34	1.8
ash	121.03	9.32	21.13	2.04	2.67	4.07

Fig. (6) Comparison of mean concentrations between wet and ash digestion

Conclusion:

For the determination of heavy metals in basalt rocks samples, wet and ash digestion using mineral acids are used for this purpose. Concentrations of heavy metals Fe, Co, Cu, Cd, Pb, and Ag were measured in basaltic igneous rocks in Red Sea Hills. The results showed interspecies variations, the order of heavy metals abundances measured in basalt rocks samples were: Fe >Cu > Co > Ag >Pb>Cd for wet and ash digestion, where levels of heavy metals concentration obtained from ash digestion were shown highest heavy metals contents.

References:

Abollino O., Aceto M., Malandrino M., Mentasti E., Sarzanini C. and Petrella F., (2002). Heavy Metals in Agricultural Soils from Piedmont, Italy. Distribution, Speciation and Chemometric data Treatment., Chemosphere, 49, p. 545–557.

Adeloju S.B., (1989). Comparison of Some Wet Digestion and DryAshing Methods for Voltammetric Trace Element Analysis, ANALYST. Vol. 114.

Baker A. D., (1971). Determination of Copper in Alfalfa, J. AOAC 54, 951

Gupta V., (1999). SPSS for Beginners. VJ. Books Inc. Library of Congress.

Harrison R. M. (2007). Principles of Environmental Chemistry. The Royal Society of Chemistry. Cambridge, UK.

Horowitz J. and Elrick K. A. (1985). Multielement Analysis of Rocks and Sediments by Wet Digestion and Atomic Absorption Spectroscopy. Varian Atomic Absorption. No. AA-47.

Mitra S., (2003). Sample Preparation Techniques in Analytical Chemistry, John Wiley and Sons, New Jersey.

Nanos N., and Martin A.R., Using a Multi-Scale Geostatistical Method for the Source Identification of Heavy Metals in Soils. Geochemistry – Earth's System Processes; www.intechopen.com.

Nanos N., and Martin A.R., Using a Multi-Scale Geostatistical Method for the Source Identification of Heavy Metals in Soils. Geochemistry – Earth's System Processes; www.intechopen.com.

Perkin-Elmer Corporation. (1996). Analytical Methods for Atomic Absorption Spectroscopy, U.S.A

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The Effect of Black Cumin (*Nigella sative* L.) and Garlic (*Allium sativum* L.)Oils on *Derematophytosis*

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ABSTRACT

Ringworm is a fungal infection caused by a fungus called dermatophytosis or tinea that live on cells in the outer layer of the skin. The present study was conducted to detect the biological activity of essential oils from Black cumin (Nigella sative L.) and Garlic (Allium sativum L.) against dermatophytosis. Substances derived from Black cumin and Garlic by soxhlet extractor and targeted students their age between 8 to 19 infected by dermatophytosis. The study concluded that the effect of Garlic oil was more effective than Black cumin oil. The Garlic oil has an antifungal properties was inhibiting growth of fungus completely after six weeks.

Keywords: *dermatophytosis, Black cumin, Nigella sativa, Garlic, Allium sativum, subcutaneous.*

Introduction:

Garlic (Allium sativum L.) has been used for thousands of years as a spice for cooking and medicinal herb, and several of its compounds have already been identified and studied for their pharmacological effects(Mamitt *etal*.,2021). Garlic is a species in the onion genus, Allium. Its close relatives include the onion, shallot and leek. Garlic is native to Central Asia and north-eastern Iran, and has long been a common seasoning worldwide, with a history of many years of human consumption and use (Chinedu and Jivini, 2019). Black cumin (Nigella sativa L.) is commonly known as Black seed, sometimes also referred to as miracle herb has been studied extensively for its various medicinal benefits. Apart from being used as a spice it is also used in various traditional systems of medicine including Ayurveda due to its healing properties in the treatment of various diseases (Belgaumi *etal*. 2020). medicinal herb is Nigella sativa L. (Ranunculaceae), also called black cumin or black seeds, which is famous for its culinary uses, and is historically precious in traditional medicine (Hannan, M.A.; *etal* ,2021). Garlic has also been used to treat acne, ringworm, high blood pressure, gastrointestinal problems as well as asthma (Deresse and Mohammed, 2009; Kumar *et al*., 2010). *Tinea* or ringworm is the other name for dermatophytosis. Inflammation as ring shape with clear center lesion is the well diagnostic clinical features of dermatophytosis. Few cases were reported about distributed of dermatophytes infection into deep tissues under skin. Symptoms are very limited with itching and odor in some type of tinea. Clinical signs are various based on the nature of infection and the location on human body (AL-Janabi, 2014).

Material and methods :

The seeds of Black cumin (*Nigella sative L.*) and samples of Garlic (*Allium sativum* L.) were obtained from the local market in Al hasaheisa City, Sudan.

This study was conducted at Khalawi Elsheikh Taha, located in the village of Sheikh Taha, which there are schools for the memorization of Koran .Located on the Khartoum road and border at north to Aldwynib village, south to Aikoura village and east to Blue Nile, with a population about 350 peoples. Students intended it from different parts of Sudan; they are 400 students and their age between 8 to 19 years and measured the infected area of injury in students' skin at weekly visits.

Preparation of Black Cumin Extract by Hexane

Taken 75 gram of fresh Garlic and placed in filter paper which placed into extraction thimble and 150 ml of hexane were put in soxhlet extractor, hexane heated to reflux and travels into thimble and soluble compound were transferred into the hexane this practice repeated to several hours.

Preparation of Garlic Extract by Hexane

Taken 75 gram of fresh Garlic and placed in filter paper which placed into extraction thimble and 150 ml of hexane were put in soxhlet extractor, hexane heated to reflux and travels into thimble and soluble compound were transferred into the hexane this practice repeated to several hours.

RESULTS AND DISCUSSION

RESULTS:

This study targeted the age of students between 8 to 19 years and the percentage of students' ages from 8 to 13 years was 68 % and the percentage of students' ages from 14 to19 was32%. This means that fungus is more prevalent in the younger group. Subjects by Age shown in Table (1)

Table 1: The Distribution of the Study Subjects by Age.

Age group	Frequency
8-13	68
14-19	32

The antifungal activities of black cumin oil on *Dermatophytosis* infected human skin cells at different visits were observed on the growth of *Dermatophytosis*. From the results the black cumin oil was inhibiting growth of fungus completely in six weeks. Samples 13,16,23,25 had high measurements and improved in short period of time. As for samples 10, 21 their measurements were low and improved in a longer period of time shown in table (2).

Table 2: The effect of *Derematophytosis* of the Black Cumin oil

Name	**Area of injury**	**Visit (1)**	**Visit (2)**	**Visit (3)**	**Visit (4)**	**Visit(5)**	**Visit (6)**
Sample 1	Head	4 cm	3 cm	2 cm	1 cm	0.00	0.00
Sample 2	Head	3 cm	2 cm	1 cm	0.5 cm	0.00	0.00
Sample 3	Head	3 cm	2 cm	1 cm	0.00	0.00	0.00
Sample 4	Head	3 cm	1 cm	0.00	0.00	0.00	0.00
Sample 5	Head	4 cm	3 cm	3 cm	1 cm	0.00	0.00
Sample 6	Head	4 cm	3 cm	2 cm	1 cm	0.00	0.00
Sample 7	Head	3 cm	2 cm	0.5 cm	0.00	0.00	0.00
Sample 8	Head	2 cm	1 cm	0.5 cm	0.00	0.00	0.00
Sample 9	Head	4cm	3cm	2cm	1cm	0.00	0.00
Sample 10	Head	3cm	2cm	1cm	1cm	0.00	0.00
Sample 11	Head	2 cm	1 cm	0.5 cm	0.5 cm	0.00	0.00
Sample 12	Head	3 cm	2 cm	1 cm	0.5 cm	0.5 cm	0.00
Sample 13	Head	4 cm	2 cm	1 cm	0.5 cm	0.00	0.00
Sample 14	Head	2 cm	1 cm	0.5 cm	0.00	0.00	0.00
Sample 15	Head	3cm	2cm	1cm	0.00	0.00	0.00
Sample 16	Head	4cm	2cm	1cm	0.5 cm	0.00	0.00
Sample 17	Head	4 cm	3 cm	2 cm	1 cm	0.00	0.00
Sample 18	Head	3 cm	2 cm	1 cm	0.5 cm	0.00	0.00
Sample 19	Head	4 cm	3 cm	2 cm	1 cm	0.5 cm	0.00
Sample 20	Head	2 cm	1 cm	0.5 cm	0.00	0.00	0.00
Sample 21	Head	3 cm	2 cm	1 cm	0.5 cm	0.5 cm	0.00
Sample 22	Head	5 cm	4 cm	3 cm	1 cm	0.00	0.00

Sample 23	Head	4 cm	2 cm	1 cm	0.5 cm	0.00	0.00
Sample 24	Head	3cm	2cm	1cm	0.00	0.00	0.00
Sample 25	Head	4cm	3cm	1cm	0,5	0.00	0.00
Mean		3.32	2.16	1.22	0.5	0.06	0.00

The antifungal activities of Garlic oil on *Dermatophytosis* infected human skin cells at different visits were observed on the growth of *Dermatophytosis*. From the results the garlic oil was inhibiting growth of fungus completely in five weeks. Samples 8, 10, 19 had high measurements and improved in short period of time. As for samples 1, 20, 23 their measurements were low and improved in a longer period of time shown in table (3)

Table 3: The effect of the *Derematophytosis* of the Garlic oil

Name	Area Of injury	Visit 1	Visit 2	Visit 3	Visit 4	Visit 5	Visit 6
Sample 1	Skin	2.5cm	2cm	1cm	0.5cm	0.00	0.00
Sample 2	Skin	3cm	2cm	1cm	0.5	0.00	0.00
Sample 3	Skin	2cm	1cm	0.5	0.00	0.00	0.00
Sample 4	Skin	3cm	2cm	1cm	0.5cm	0.00	0.00
Sample 5	Skin	3cm	2cm	1cm	0.00	0.00	0.00
Sample 6	Skin	2cm	1.5cm	1cm	0.00	0.00	0.00
Sample 7	Skin	3cm	2cm	1cm	0.5cm	0.00	0.00
Sample 8	Skin	4cm	3cm	2cm	0.5cm	0.00	0.00
Sample 9	Skin	3cm	2cm	1cm	0.5cm	0.00	0.00
Sample 10	Skin	4cm	3cm	2cm	0.5cm	0.00	0.00
Sample 11	Skin	2cm	1.5cm	1cm	0.00	0.00	0.00
Sample 12	Skin	2cm	1.5cm	1cm	0.00	0.00	0.00
Sample 13	Skin	3cm	2cm	1cm	0.5cm	0.00	0.00
Sample 14	Skin	3cm	2.5cm	1.5cm	0.5cm	0.00	0.00
Sample 15	Skin	1.5cm	1cm	0.5cm	0.00	0.00	0.00
Sample 16	Skin	2.5cm	2cm	1cm	0.5cm	0.00	0.00
Sample 17	Skin	2cm	1.5cm	1cm	0.00	0.00	0.00
Sample 18	Skin	2cm	1cm	0.5cm	0.00	0.00	0.00
Sample 19	Skin	4cm	3cm	2cm	0.5cm	0.00	0.00
Sample 20	Skin	3cm	2.5cm	1.5cm	0.5cm	0.00	0.00
Sample 21	Skin	2cm	1.5cm	1cm	0.00	0.00	0.00
Sample 22	Skin	3cm	2cm	1cm	0.00	0.00	0.00

Sample 23	Skin	3cm	2cm	1cm	0.5cm	0.00	0.00
Sample 24	Skin	2cm	1.5cm	1cm	0.00	0.00	0.00
Sample 25	Skin	2cm	1.5cm	1cm	0.00	0.00	0.00
Mean		2.64	1.86	1.1	0.28	0.00	0.00

DISCUSSION:

The present study was conducted to estimate the biological activity of essential oils Black cumin and Garlic against the fungus *Dermatophytosis* infected human skin cells. The antifungal activities of Garlic oil at different visits were observed on the growth of *Dermatophytosis*. From the results the Garlic oil was inhibiting growth of fungus faster than black cumin. This result was in accordance with a previous studies conducted by (Marwa, 2019; Deresse D, Mohammed A 2009; Mamitt *etal*. 2021)

Conclusions:

The Garlic oil has antifungal properties and inhibited the growth of *Dermatophytosis* fungus completely after five weeks.

The Black cumin oil has also an antifungal properties, it inhibited the growth of fungus completely in the sixth weeks.

Compare between two oils tested, the garlic oil gave the best results.

Recommendations:

The study recommended investigating of the antibacterial effects of these oils as well as the antimicrobial effects of some other herbal essential oils.

References:

AL-Janabi .A.S (2014). Dermatophytosis: Causes, clinical features, signs and treatment Journal of Symptoms and Signs Vol 3, No 3.

Amer S, Aly MM, Sabbagh S (2006) of dermatophytes using some plant extracts and actinomycetes filtrates. Egyptian J. Biotechnol., 330-315.

Amagase H, Petesch BL, Matsuura H, Kasuga S, Itakura Y (2001). Intake of garlic and its bioactive components. J. Nutr. 131:955-962.

Amin G.R. (1991). Popular Medicinal Plants of Iran, Vol. I. Minis-try of Health Pulications: Tehran, 118-119.

Belgaumi1, U. I. Patil, S Gandhi, J, M. Shete. A, S: (2020).etal. The Many Therapeutic Applications of Nigella sativa. J. Evolution Med. Dent. Sci./eISSN- 2278-4802, pISSN- 2278-4748/ Vol. 9/ Issue .Page 215.

Corzo-Martínez M, Corzo N, Villamiel M (2007).Biological properties of onions and garlic.Trends Food Sci. Tech. 18:609-625.

Chinedu I, Jivini S Z.(2019). Medicinal Properties of Ginger and Garlic: A Review. Curr Trends Biomedical Eng & Biosci.2019; 18(2): 555985. DOI: 10.19080/CTBEB.18.555985.

Deresse D, Mohammed A (2009). Assessment of antibacterial effect of crude preparation of garlic (Allium sativum) on diarrhea causing bacteria: An in vitro study. Asian J. Med. Sci. 1:12-14.

Hannan, M.A.; Rahman, M.A.; Sohag, A.A.M.; Uddin, M.J.; Dash, R.; Sikder, M.H.; Rahman, M.S.; Timalsina, B.; Munni, Y.A.; Sarker, P.P.;(2021). Black Cumin (Nigella sativa L.): A Comprehensive Review on Phytochemistry, Health Benefits, Molecular Pharmacology, and Safety. Nutrients.

Kumar KPS, Bhowmik D, Chiranjib, Tiwari P, Kharel R (2010).Allium sativum and its health benefits: An overview. J. Chem. Pharm. Res. 2:135-146.

Marwa, K.A. (2019). Studies on Effect of Garlic Extract (Allium sativum L) in Controlling The Growth of Some Bacteria and Fungi Masters. Thesis. University of the University of Al-butana.

Marmitt, D. J., Goettert, M. I., Rempel, C. (2021). A recente produção científica de alho (Allium sativum L.) confirma importantes propriedades terapêuticas. Brazilian Journal of Development ISSN: 2525-8761.

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Epidemiology of Hepatitis B Virus (HBV) Infection Among Blood Donors at Al-Manaqil Educational Hospital Blood Bank, Gezira State, Sudan, 2025

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Abstract

Background: *Hepatitis B virus (HBV) infection is a major global health problem, affecting approximately 300 million people worldwide and causing liver disease.* ***Objective:*** *To study the epidemiology of HBV among blood donors at Al-Manaqil Educational Hospital Blood Bank.* ***Methods****: A descriptive cross-sectional study was conducted on 386 male blood donors from September to December 2023. Data were collected via structured questionnaires and laboratory screening for HBsAg using immunochromatographic tests (ICT), confirmed by ELISA. Analysis used SPSS version 26 with chi-square tests (P<0.05 significant).* ***Results:*** *Overall prevalence was 3.6%. Higher rates were observed in the 20-26 age group (6.0%), healthcare workers (44.4%), singles (5.2%), university-educated donors (7.1%), and unvaccinated individuals (4.2%). Risk factors included family history (27.3%) and medical injuries (12.0%). Knowledge gaps existed, with 56-63% unaware of HBV.* ***Recommendations:*** *Enhance screening with nucleic acid testing (NAT), promote mass vaccination, and conduct targeted health education.*

Keywords*: Hepatitis B, blood donors, blood bank, blood transfusion, Al-Manaqil Educational Hospital.*

INTRODUCTION

Blood transfusion services constitute a critical component of modern healthcare systems, providing life-saving support for medical and surgical patients worldwide (Hall, 2008). However, ensuring the safety and quality of blood supplies remains paramount to prevent transfusion-transmitted infections, particularly hepatitis B virus (HBV) (Elsharif et al., 2015). HBV infection represents a major global public health challenge, affecting an estimated 257 million people chronically and causing 887,000 deaths in 2015 from complications including cirrhosis and hepatocellular carcinoma (Wang et al., 2021).

The virus primarily targets the liver, leading to acute or chronic inflammation that impairs its vital functions of nutrient processing, blood filtration, and infection defense (CDC, 2016). Transmission occurs through percutaneous or mucosal exposure to infected blood or bodily fluids, with well-established risks in healthcare settings, including needlestick injuries, contaminated medical instruments, and inadequate sterilization practices (Nagoor et al., 2021). Although routine HBsAg screening of blood donations has been implemented since 1970, the window period between infection and detectable antigenemia continues to pose transfusion risks, particularly in high-prevalence regions (Attia and Elmetwalli, 2021).

Africa bears the highest HBV burden globally, with 6.1% prevalence in the WHO African Region (Donkor, 2018). In Sudan, heterogeneous endemicity persists, with blood donor studies reporting rates from 0.33% to 7% across regions (Elsharif et al., 2015; Mohamed et al., 2022). Healthcare workers face elevated occupational hazards due to frequent blood exposure, compounded by suboptimal vaccination coverage and knowledge gaps regarding universal precautions (Bakry et al., 2012). Effective HBV vaccines, administered since 1982, have dramatically reduced chronic infection rates from 8-15% to <1% in immunized child cohorts (Nagoor et al., 2021).

Despite national immunization programs, Sudan continues to report substantial HBV reservoirs, estimated near one million carriers (Saudi Ministry of Health data analogy; Nagoor et al., 2021). Blood banks serve as sentinel surveillance points for community prevalence, yet local data from Gezira State remain limited. This study addresses this gap by investigating HBV epidemiology among blood donors at Al-Manaqil Educational Hospital Blood Bank, examining prevalence, demographic associations, risk factors, and knowledge levels to inform targeted interventions.

Problem of the study

Hepatitis B constitutes a major transmissible hazard through blood transfusion services in resource-limited settings. In Sudan, inconsistent donor screening, variable vaccination coverage, and occupational exposures among healthcare personnel perpetuate transmission risks. Existing regional studies document prevalence heterogeneity, but Gezira State data specific to blood donors are scarce, hindering evidence-based blood safety policies.

Objectives of the study

Main Objective

To determine the epidemiology of hepatitis B virus infection among blood donors at Al-Manaqil Educational Hospital Blood Bank, Gezira State, Sudan.

Specific Objectives

To determine HBV prevalence among blood donors through HBsAg screening.

To identify socio-demographic factors associated with HBV positivity.

To assess risk factors for HBV transmission among study participants.

To evaluate donors' knowledge regarding HBV etiology, transmission, and prevention.

Materials and Methods of the study

Study Design and Period

A descriptive cross-sectional study was conducted among blood donors attending Al-Manaqil Educational Hospital Blood Bank from September to December 2023.

Study Area

Al-Manaqil Locality, Gezira State, Sudan (latitudes 13°45'-14°15'N, longitudes 33°30'-34°15'E) spans 6,250 km² with an estimated population of 678,441, predominantly agricultural communities from Al-Kawahla, Musalmia, Rufaa, and Al-Kenana tribes. The locality hosts 5 public hospitals, 2 private hospitals, 13 health centers, and the studied blood bank established in 1962. The blood bank facility comprises a reception hall, doctor's room, derivatives room, refrigeration units, and plasma separation area, staffed by 6 personnel operating in shifts.

Study Population

All male blood donors attending the blood bank during the study period who provided informed consent.

Inclusion Criteria

Blood donors aged ≥18 years attending Al-Manaqil Educational Hospital Blood BankWilling to participate and provide written informed consentAgreed to HBsAg testing

Exclusion Criteria

High-risk groups: thalassemia clinic patients, sexually transmitted infection clinic attendees, injecting drug users Donors refusing HBsAg testing or study participation Females (due to blood bank donor demographics during study period)

Sample Size and Sampling Technique

Sample size calculated using Fisher's formula assuming 50% prevalence, 95% confidence level, and 5% margin of error: The sample size was calculated using fishers formula (fisher *et al. 2008*) was used determine the sample size using 50%prevelara

$$N = \frac{Z2\ P\ (1 - P)}{D2}$$

N = required minimum sample

Z = 1,96 normal error

P = 0,5

D = 0,05 the inverse of 95% confidence limit

$$N = \frac{(1,96)\,2\ \times 0,5(1-0,5)}{(0,05)2}$$

N = 384,16

There 384 blood donors were recruit into study.Actual sample :386(100% coverage)

Data Collection Tools

Structured questionnaire administered via face-to-face interviews, comprising three sections:

Part A: Socio-demographics (age, occupation, marital status, education, income)

Part B: Risk factors (surgery history, blood transfusion, medical injuries, family history, vaccination status)

Part C: HBV knowledge (etiology, symptoms, complications, prevention)

4.8 Laboratory Methods HBsAg Screening Protocol:ICT: Rapid immunochromatographic test (80µL serum/plasma/whole blood, results at 15 minutes)ELISA Confirmation: All ICT positives confirmed; negatives for quality controlICT Interpretation: Control (C) + Test (T) lines = Positive; C only = Negative.

ELISA Protocol: Commercial kits per manufacturer specifications with positive/negative controls and cut-off calculation (mean NC × 0.05).

Data Analysis

Data entered and analyzed using SPSS version 26. Descriptive statistics (frequencies, percentages) summarized variables. Chi-square tests assessed associations between HBsAg status and independent variables ($P<0.05$ significant). Prevalence ratios and relative risks calculated.

Ethical Considerations

The study adhered to ethical principles of validity, integrity, beneficence, non-maleficence, justice, and respect for persons (Belmont Report). Key measures included:

Ethical Approval: Obtained from Al-Manaqil Educational Hospital administration and Blood Bank Director

Informed Consent: Written consent/assent from all participants after explaining study purpose, procedures, risks, benefits, and voluntary participation rights

Confidentiality: Anonymized data collection and storage; blood samples labeled with codes

Beneficence/Non-maleficence: Free HBV testing and counseling for positives; no study-related harmJustice: Equal inclusion opportunity for eligible donorsRight to Withdraw: Participants could withdraw anytime without prejudice

Result :

A total of 386 male blood donors were screened at Al-Manaqil Educational Hospital Blood Bank from September to December 2023. Hepatitis B surface antigen (HBsAg) was positive in 14 donors (overall prevalence 3.6%), all confirmed by both immunochromatographic test (ICT) and ELISA. The remaining 372 donors (96.4%) tested negative.

Prevalence by Diagnostic Tests

Table 1: HBV Prevalence by ICT and ELISA Confirmation (n=386)

ELISA Result	ICT Positive	ICT Negative	Total	Prevalence%
Positive	14	0	14	3.6
Negative	0	372	372	96.4
Total	14	372	386	100

χ^2 test: P=0.000 (significant)

Demographic Characteristics

Table 2: HBV Status by Age Group (n=386)

Age group	Positive	Negative	Total	Prevalence%	RR	χ^2	P value
20-26	10	156	166	6.0	1.67	8.44	0.015
27-33	0	140	140	0.0	0		
34-40	4	76	80	5.0	1.39		
Total	14	372	386	3.6	1		

$P<0.05$ significant

Table 3: HBV Status by Occupation (n=386)

Occupation	Positive	Negative	Total	Prevalence%	RR	χ^2	P value
Healthcare worker	4	5	9	44.4	12.61	45.42	0.000
Farmer	1	41	42	2.4	0.66		
Driver	2	34	36	5.6	1.53		
Other employees	6	208	214	2.8	0.777		
Total	14	372	386	3.6	1		

Vaccination Status

Table 4: HBV Status by Vaccination History (n=386)

Vaccination	Positive	Negative	Total	Prevalence%	RR	χ^2	P value
Yes	1	74	75	1.3	0.36	1.604	0.449
No	13	298	311	4.2	1.17		
Total	14	372	386	3.6	1		

Risk Factors

Table 5: Risk Factors Associated with HBV

Risk Factor	Positive	(negative)	Prevalence (%)	χ^2 P-value
Family history of HBV	6	16	27.3	0.000
Medical instrument injury	3	22	12.0	0.021

P<0.05 significant

Key Statistical Findings:

Overall HBV prevalence: 3.6%

Highest risk groups: Healthcare workers (44.4%, P=0.000), 20-26 years (6.0%, P=0.015)

Significant associations: Age (P=0.015), Occupation (P=0.000), Family history (P=0.000), Medical injuries (P=0.021)

Discussion:

The study revealed a hepatitis B virus (HBV) prevalence of 3.6% (14/386) among blood donors at Al-Manaqil Educational Hospital blood bank, Gezira State, Sudan. This rate aligns with regional findings, including 3.5% reported by(Elsharif et al. 2015) among donors at Kosti Teaching Hospital, White Nile State, Sudan, and 3.8% in Jazan, Saudi Arabia (Nagoor and Adetunji, 2021). However, it is lower than 7% prevalence documented by (Mohamed et al. 2022) in Algamosi Locality, Gezira State, possibly due to differences in donor screening practices or demographic profiles. Higher prevalence among healthcare workers (44.4%, P=0.000) underscores occupational risks, consistent with (Bakry et al. 2012) who found poor HBV vaccination coverage (>50% unvaccinated) and inadequate knowledge of universal precautions among Sudanese healthcare personnel. The 20-26 age group showed elevated rates (6.0%, P=0.015), supporting(Mohamed et al.,2022) who identified significant age-HBV associations in central Sudan, likely reflecting behavioral factors such as multiple sexual partners or shared personal items (CDC, 2018).Risk factors including medical instrument injuries (12.0%, P=0.021) and family history (27.3%, P=0.000) confirm transmission routes emphasized by(IbnIdriss et al. 2022) in Sudanese communities. Unvaccinated donors had higher prevalence (4.2%), aligning with (WHO ,2015) evidence that vaccination reduces chronic HBV by >90% in immunized populations. Knowledge gaps (56-63% unaware of HBV transmission) mirror regional patterns (Bakry et al., 2012).

6. Conclusion

This study examined 386 blood donors attending the blood bank at Almanaqil Educational Hospital. The prevalence of hepatitis B virus (HBV) infection was 3.6% among participants. Significant associations were found between HBV positivity and several demographic factors, including:

Age: Highest prevalence in the 20-26 years group (6%; P < 0.015).

Occupation: Highest in medical workers (44.4%; P < 0.001).

Marital status: Highest among singles.

Education level: Highest among university-educated individuals.

Vaccination status: Highest among unvaccinated donors (4.2%).

Risk factors showed strong links, with elevated prevalence among those exposed to medical instrument injuries (12%; P < 0.021) and those with family members infected (30%; P < 0.001).

7.Recommendations

Enhance screening with more sensitive tests, such as nucleic acid testing (NAT), to minimize transmission risk.

Boost awareness campaigns educating potential donors on risk factors, promoting safe donation practices, and emphasizing HBV immunization for the public.

Develop robust blood bank policies, including stricter donor screening to exclude high-risk groups and ensure blood product safety.

Strengthen surveillance by monitoring donors with early disease signs and following up on positive cases. Promote mass HBV vaccination to lower community infection rates.

Reference

Abdallah, T.M. et al. (2011). Seroprevalence and epidemiological risk factors of hepatitis B virus infection among healthy people visited Kassala Teaching Hospital, Eastern Sudan.

Sudanese Journal of Public Health, 6(2), pp. 45-50.

Aljyo, A. et al. (2022). Blood transfusions: Importance in saving millions of lives worldwide.

Transfusion Medicine Reviews, 36(1), pp. 12-20.

Alqahtani, S. et al. (2021). Blood donation: Processes, preservation, integrity, and efficacy.

Journal of Blood Transfusion, 2021, Article ID 8865123.

Attia, A. and Elmetwalli, A. (2021). HBV serological markers, window period, and convalescence. Hepatology International, 15(3), pp. 567-575.

Blumberg, B.S. (1965). Polymorphism of serum proteins and discovery of Australia antigen.

Annals of Internal Medicine, 63(6), pp. 1018-1026.

CDC (2016). Viral hepatitis surveillance: United States Hepatitis A, B, and C. Centers for Disease Control and Prevention. Available at: https://www.cdc.gov/hepatitis/statistics/ (Accessed: 15 Dec 2023).

Donkor, E.S. et al. (2018). Hepatitis B virus prevalence in WHO African and Western Pacific Regions. African Journal of Microbiology Research, 12(45), pp. 1120-1128.

ELsharif, M. et al. (2015). Blood donation's crucial role in supportive care of patients. ox Sanguinis, 109(2), pp. 150-158.

Fattovich, G. (2003). Natural history and prognosis of hepatitis B virus infection. Journal of Hepatology, 39(Suppl 1), pp. S50-S55.

Fisher, L.D. et al. (2008). Sample size determination in clinical research. Chapman & Hall/CRC Biostatistics Series, 2nd ed.

Hall, R. (2008). Blood transfusion services: Preservation, integrity, competence, and efficacy.

British Journal of Haematology, 142(4), pp. 567-575.

Ibrahim, A. et al. (2022). HBsAg incidence in Sudan: Regional variations 6.8-26%. Eastern Mediterranean Health Journal, 28(5), pp. 340-347.

MacDonald, S. (1908). The viral etiology of jaundice (catarrhal jaundice). British Medical Journal, 1(2512), pp. 456-458.

Mauss, S. et al. (2020). History of HBV: From discovery to antiviral therapy. Journal of Viral Hepatitis, 27(1), pp. 1-10.

Mohamed, E. et al. (2022). Hepatitis B prevalence in Algamosi, Gezira State: Age and jaundice factors.Gezira Journal of Health Sciences, 18(1), pp. 22-30.

Mohammed, E. et al. (2022). Risk factors for HBV spread including previous jaundice infection.

Sudanese Journal of Tropical Medicine, 12(3), pp. 89-95.

Nagoor, B. et al. (2021). HBV transmission risks: Occupational hazards and blood contact. World Journal of Gastroenterology, 27(15), pp. 1567-1578.

Paver, W.K. and Mortimer, P.P. (1996). History of viral hepatitis: From antiquity to Blumberg.

Reviews in Medical Virology, 6(4), pp. 219-226**.**

Wang, J. et al. (2021). Global epidemiology of hepatitis B: 257 million chronic carriers. The Lancet Gastroenterology & Hepatology, 6(9), pp. 718-730.

WHO (2016). Hepatitis B fact sheet. World Health Organization. Available at: https://www.who.int/news-room/fact-sheets/detail/hepatitis-b (Accessed: 15 Dec 2023).

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Assessment of Medical Waste Disposal Program in Governmental Hospitals in Khartoum locality , Khartoum State, Sudan- (2020)

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Abstract

Medical waste management is great importance due to its infectious and hazardous nature that can cause undesirable effects on humans and the environment health. The objective of this study aimed to assess of medical waste(MW) disposal program in Governmental Hospitals at Khartoum locality - Khartoum State Sudan- (2020)

A cross-sectional descriptive study was conducted in 19 governmental hospitals. Data were collected using a standardized checklist, interviews with facility managers, and direct observation. Data were analyzed using the Statistical Package for Social Sciences (SPSS) version 22.0. Both descriptive and inferential statistics were applied. The chi-square test was used to assess associations between variables, and a p-value of <0.05 was considered statistically significant.

In regards to the current practices, results revealed that, hospitals have a specific program for collection and transportation (MW) to store room in and the bags and packages filled up to two thirds of the size in (13)hospitals (68.4%) respectively . The segregation of medical wastes according to color coded system is not conducted according to (WHO) standards, waste not remained in its generated site more than one day only in (6) hospitals recorded (31.6%) , bags and packages are labeled in a number at (10) hospitals with percentage (52.6%), replace of new bag or packages instead of transported ones immediately in a number of (14) hospitals (73.7%), the place of store (MW) is separated from the hospital departments and places of storing domestic waste (DW) is found in (12) hospitals revealed (63.2%), the way of storing is adequate only in (2) hospitals , there are weighing device and recording for generated amount and the general cleanness for the store room was good was (10.5%) in a row . There are no specified panel truck for transportation of (MW) and have a temporary licensing from environmental health department. (100%) of hospitals sends the (MW) to the recommended final dump , liquids waste drained directly to sewer net and the liquid waste drained to sewer net not after disinfection also respectively.

The overall amount of (MW) that sends in each time in the studied hospitals was found to be (215.2±18.7 kg) with frequency of sending (MW) per week (2.7±0.3 times). The most shortcomings and weakness points of medical waste in hospitals were mixing between (DW) and (MW) was (52.6%), no labeling on (MW) bags is (15.8%), the store room not according to specifications was (10.5%) and (MW) workers not using personal protective equipment (PPE) in regularly. Finally These findings indicate significant correlation gaps in compliance with WHO guidelines for medical waste disposal and treatment (P-value = 0.03).

1.Introduction

Despite variations in medical waste management (MWM) practices among hospital , the major problem areas remain similar across healthcare facilities and throughout all stages of waste management the problematic areas are similar for all healthcare units and all stages of management (**Tamplin *et al.*, 2005**). In the process of healthcare it was included many type of wastes (sharps, human tissues or body parts and other infectious materials) (**Awodele *et al.*, 2016**). Interestingly, there are reasonable ranges of technologies available for the treatment of healthcare wastes that may be appropriate for use in the third world countries. The World Health Organization (WHO) estimates that each year there are about 8 to 16 million new cases of Hepatitis B virus (HBV), 2.3–4.7 million cases of Hepatitis C virus (HCV) and 80,000–160,000 cases of Human Immunodeficiency Virus (HIV) due to unsafe injections disposal and mostly due to very poor waste management systems (**WHO, 1999**). Contaminated injection equipment may be scavenged from waste areas and dump site either to be reused or sold to be used again. The negative health and environmental impacts of MW includes transmission of diseases by virus and microorganism, defacing the aesthetics' of the environment, as well as contamination of underground water tables by untreated MW in landfills (**Chua *et al.*, 2012**). Good medical waste management in hospital depends on a dedicated waste management team, good administration, careful planning, sound organization, underpinning legislation, adequate financing and full participation by trained staff (WHO**, 2005**). However, it is pertinent that before any of these options is adopted, hospitals and medical facilities will need to assess the problems and put forward a management strategy that is suitable to their economic circumstances and also sustainable for use, based on local technology (**Manyele and Tanzania, 2004, Abah and Ohimain, 2016**). Paradoxically, health-care activities which are meant to protect health, cure patients and save lives have been known to also generate waste. About 20 % of these wastes pose high risk, either of infection and chemical or radiation exposure (IRC**, 2011**). Health-care activities generate significant amounts of hazardous waste such as mercury and expired pharmaceuticals, as well as large amounts of general waste. As a matter of fact, the management of health-care waste is an integral part of a national health-care system. A comprehensive approach to health-care waste management should include a clear delineation of responsibilities, occupational health and safety programs, waste minimization and segregation, development, adoption of safe and environmentally sound technologies, and capacity building. Recognizing the urgency of this problem, a growing number of countries have taken initial steps to respond to this need. These include the establishment of regulatory frameworks, development of national plans and the demonstration of innovative approaches. However, funding of health-care waste management remains very inadequate (**WHO,2007**).

2. Methods

2.1 Study design:

This was cross- sectional study hospitals-based.

2.2Studyarea:

Khartoum is the capital city of Sudan locality Khartoum from importance localities in Khartoum state that refer to geographical location and , located at the confluence of the White Nile in the Blue Nile (Al- Muqran), forming the

Nile River together . A governance center in Sudan , Khartoum has a population of (927311). .

2.3. Sample :

The sample was a total coverage sampling (19 hospitals Total Coverage) .

2.4Data collection:

The tools were used for collected of data were; chick list, Interview and observation in 2020 .

2.5. Data analysis:

The data was analyzed using SPSS version (22.0.) Descriptive and inferential statistics were used Chi-square test was used to find an association between variable, p-value considered significant at less than (0.05) levels.

3.Results and Dissection

Table (1) shows that the special committee concerning medical waste and held periodic meetings in (14) hospitals of Khartoum Locality was (73.7%). The majority (94.7%) of hospitals has plan or informative guide for workers. All the hospitals (100%) have informative panels hung in a prominent place within the departments. Waste bag holders have a snug lid that opens with feet and matches the color of the bag in (11) hospitals recorded (57.9%). The capacity of the bags is proportional to the amount of (MW) generated in (16) hospitals out of(19) was (84.2%). The (MW) segregated according to color-coded in all departments in (15) was hospitals (78.9%).

Table(1). Medical waste administration and segregation system

Statement	Yes		No	
	No.	%	No.	%
There is a special committee concerning medical waste and held periodic meetings	14	73.7	5	26.3
There is a plan or informative guide for workers	18	94.7	1	5.3
There is Information panels hung in a prominent place within the departments	19	100	0	0.0
Waste bag holders have a snug lid that opens with feet and matches the color of the bag	11	57.9	8	42.1
The capacity of the bags is proportional to the amount of waste generated	16	84.2	3	15.8
The waste segregated according to color-coded in all departments	15	78.9	4	21.1

Atif, B., Saad Breama , Abdalla; E. Abdalla Mohammed Marim, H., Ahmed, Abdrahman, Y., (2025). Assessment of Medical Waste Disposal Program in Governmental Hospitals in Khartoum locality , Khartoum State, Sudan- (2020) . ***Al-Butana Journal of Applied Science (17):*** **84-102**

Bags and plastic packages:

The thickness of the bags is not appropriate in (15) hospitals out of (19) was (78.9%). However, Bags and plastic packages manufactured from non-halogenated plastic only in (8) hospitals was (42.1%). The capacity of the bags is proportional to the amount of waste generated in (16) hospitals was (84.2%). The plastic bags specified for sharp waste (SW) are appropriate and not open able in a number of (11) hospitals is (57.9%). While the bags and packages filled only up to two thirds of the size in (13) hospitals was (68.4%).

The amount of bags and packages are provided by adequate numbers only in (10) hospitals was (52.6%). Only the chemical waste (CHW) are segregated and collected in adequate packages not subjected to interact with it in (7) hospitals was (36.8%).There is primary treatment for high contagious wastes at the site of its generation were done only in (8) hospitals was (42.1%).

The studied hospitals (19) showed lack of Autoclave device is exist, cooling (Temperature not more than -20 C), disinfection by formalin (Concentration not exceed 10% for 24 hours), and recapping of needles as shown in table (2).

Table (2). Bags and plastic bags packages   (n=19)

Statement	Yes		No	
	No.	%	No.	%
The thickness of the bags is appropriate	4	21.1	15	78.9
Bags and plastic packages manufactured from non-halogenated plastic	8	42.1	11	57.9
The capacity of the bags is proportional to the amount of waste generated	16	84.2	3	15.8
The plastic bags specified for sharp waste are appropriate and not openable	11	57.9	8	42.1
The bags and packages filled only up to two thirds of the size	13	68.4	6	31.6
The amount of bags and packages are provided by adequate numbers	10	52.6	9	47.4

The chemical waste are segregated and collected in adequate packages not subjected to interact with it	7	36.8	12	63.2
There are primary treatment for high contagious waste at the site of its generation	8	42.1	11	57.9
Autoclave device is exist	0	0.0	19	100.0
Cooling (Temperature not more than -20 C)	0	0.0	19	100.0
Disinfection by formalin (Concentration not exceed 10% for 24 hours)	0	0.0	19	100.0

Collection and transportation of medical waste inside hospital:

Table (3): indicates that there is a specific programme for collection and transportation of waste to store room in (13) hospitals was recorded (68.4%), However, medical waste not remained in its generated site more than one day only in(6) hospitals was (31.6%). Bags and packages are labeled in a number of (10) hospitalswas (52.6%).There are replace of new bag or packages instead of transported ones immediately in a number of (14) hospitals was (73.7%).

Table (3): Collection and transportation of medical waste inside hospital (n=19)

Statement	Yes		No	
	No.	%	No.	%
There is a specific programme for collection and transportation of waste to store room	13	68.4	6	31.6
Waste not remained in site more than one day	6	31.6	13	68.4
Bags and packages are labeled	10	52.6	9	47.4
There are replace of new bag or packages instead of transported ones immediately	14	73.7	5	26.3

Table (4) :Trucks and vehicles transportation:

In terms of trucks and vehicles transportation, table (4) showed that, trucks are easy to load and unload in (12) hospitals was (63.2%). The trucks have flattened surfaces in (11) hospitals was (57.9%) and trucks are washed and disinfected daily in only (7) hospitals was (36.8%). There were specific workers for transportation of medical waste in (9) hospitals was (47.4%). (63.2%) of hospitals their roads for store room not pass with food preparation room (63.2%).

Table (4) :Trucks and vehicles transportation (n=19)

Statement	Yes		No	
	No.	%	No.	%
Easy to load and un load	12	63.2	7	36.8
Have flatten surfaces	11	57.9	8	42.1
Washed and disinfected daily	7	36.8	12	63.2
There were specific workers for transportation of medical waste	9	47.4	10	52.6
The road for store room not pass with food preparation room	12	63.2	7	36.8

Table (5) : Store/place of storing medical waste inside hospital:

Table illustrates that the place of store is separated from the hospital departments and places of storing domestic waste is found in (12) hospitals was (63.2%). There are enough cleaning tools and water source and drainage in only (7) hospitals was (36.8%).

Animals and birds are cannot enter the site in a number of (13) hospitals was (86.4%) and the store room fitted with door always closed only in (6) hospitals was (31.6%). Ventilation and lightening are enough and adequate only in (2) hospitals (10.5%) and the storing period not exceed (24 h) in summer and (48 h) in winter are available only in(4) hospitals (21.1%). However, the way of storing is adequate, in addition the bags and medical waste package placed in the ground or inside containers and the store room cleaned and disinfected according to daily programs , when appropriate , weighing device and recording for generated amount , general cleanness for the store room was good but (8) of hospitals has accepted general only in (2) hospitals was (10.5%) respectively . Most of hospitals their way for store room is easy and secured was (73.7%). The road for store room not passes with food preparation room in (12) hospitals was (63.2%).Cleanness was (42.8%) and in (8) hospitals was not accepted while in (1) hospital it was very bad.

Table (5): Store/place of storing medical waste inside hospital (n=19)

Statement	Yes		No	
	No.	**%**	**No.**	**%**
Place of store is separated from the hospital departments and places of storing domestic waste	12	63.2	7	36.8
There are enough cleaning tools and water source and drainage	7	36.8	12	63.2
Animals and birds cannot enter the site	13	68.4	6	31.6
The store room fitted with door always closed	6	31.6	13	68.4
Ventilation and lightening are enough and adequate	2	10.5	17	89.5
Storing period not exceed 24 hours in summer and 48 hours in winter	4	21.1	15	78.9
The way of storing is adequate	2	10.5	17	89.5
The bags and medical waste package placed in the ground or inside containers	4	21.1	15	78.9
the store room cleaned and disinfected according to daily programme and when appropriate	2	10.5	17	89.5
The way for store room is easy and secured	14	73.7	5	26.3
The road for store room not pass with food preparation room	12	63.2	7	36.8
there are weighing device and recording for generated amount	2	10.5	17	89.5
	Good	**Accepted**	**Not accepted**	**Very bad**
The general cleanness for the store room (By using check List)	2 (10.5%)	8 (42.1%)	8 (42.1%)	1 (5.3%)

Table (6): Transportation out of hospital:

There are no specified panel truck only for transportation of medical waste and have a temporary licensing from environmental health department as shown in table (6).

Table (6): Transportation out of hospital (n=19)

Statement	Yes		No	
	No.	%	No.	%
There are specified panel truck only for transportation of medical waste and have a temporary licensing from environmental health department	0	0.0	19	0.0

Management and final disposal:

Table (7): showed that there was no incineration in the studied hospitals.

Disposal out of hospital:

All hospitals sends the medical waste sanded to the recommended final dump (100%), the liquid waste drained directly to sewer net in all hospitals, and the liquid waste drained to sewer net not after disinfection.

The overall amount of medical waste that sends in each time in the studied hospitals was found to be (215.2±18.7 kg) with frequency of sending medical waste per week (2.7±0.3 times).

Table (7): Disposal out of hospital (n=19)

Statement	Yes		No	
	No.	%	No.	%
The medical waste sanded to the recommended final dump	19	0.0	0	0.0
The liquid waste drained directly to sewer net	19	0.0	0	0.0
The liquid waste drained to sewer net after disinfection	0	0.0	19	0.0
	Mean± SE			
The amount of medical waste that send in each time	215.2±18.7			
Frequency of sending medical waste per week	2.7±0.3			

Records:

In table (8) there are specific records for vaccination of health cadres and workers in (12) hospitals was (63.2%), there are specific records for accidents related medical waste only in (8) hospitals was (42.1%) and there are records for medical waste committee meetings was (42.1%).

Table (8) : Records (n=19)

Statement	Yes		No	
	No.	%	No.	%
There are specific records for vaccination of health cadres and workers	12	63.2	7	36.8
There are specific records for accidents related medical waste	8	42.1	11	57.9
There are records for medical waste committee meetings	8	42.1	11	57.9

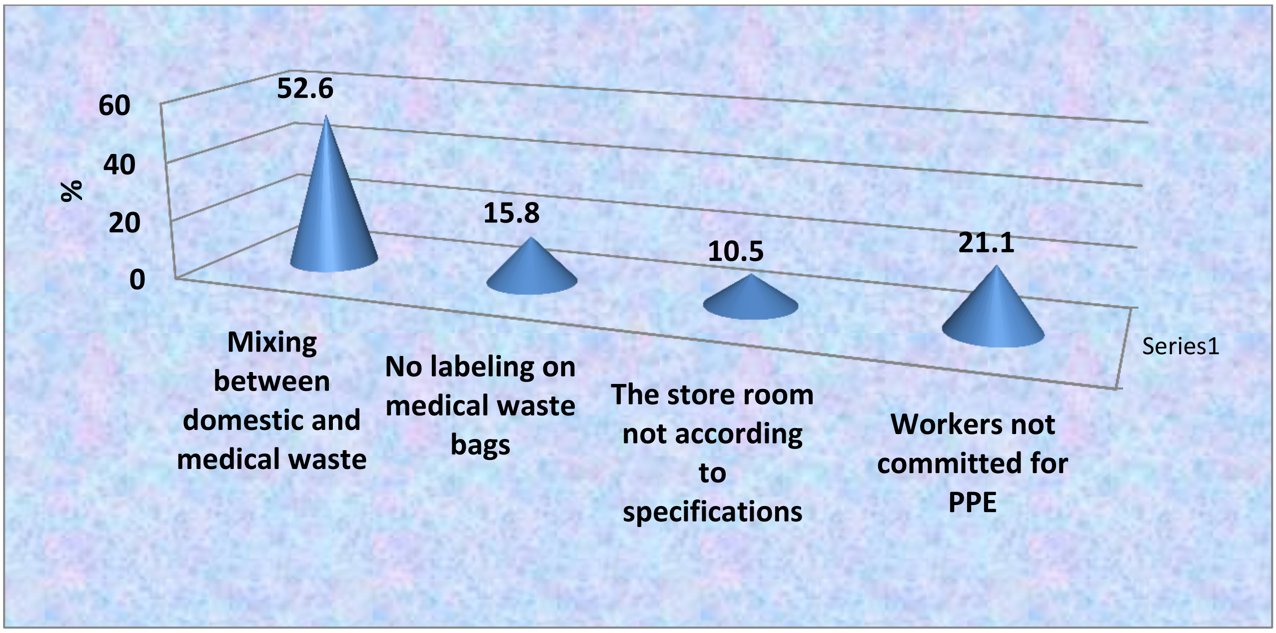

Fig. (1) : Shortcomings and weakness points in medical waste (n=19)

Fig. (1) shows that the most shortcomings and weakness points of medical waste in hospitals were mixing between domestic and medical waste showed (52.6%), no labeling on medical waste bags was (15.8%) and the store room not according to specifications was (10.5%) and workers not committed for (PPE) was (21.1%).

4. Discussion

According to the evaluation checklist of medical waste in studied hospitals, special committee concerning medical waste and held periodic meetings in (14) hospitals was (73.7%). The finding indicated still there is a gap in a number of(5) hospitals which indicated not proper disposal of (MW). However, the ideal way to make sure health care waste (HCW) is properly managed on the long term, it is important to supervision a regular basis practices of the staff. This should be performed by the health care waste management (HCWM) officer and/or members of (HCWM) committee within each (HC) Facilities (depending on the size of the facility). Typically members of such a committee are usually the same as those in charge of nosocomial infections. Appropriate on-going training and awareness sessions should be organized accordingly to keep practices at the best standards possible (**WHO, 2005**). Encouragingly, the study confirmed that the majority of hospital. The study explained that the majority (94.7%) had had an operational plan or informative guide for workers.

Also the study indicated that (MW) bag holders have a snug lid that opens with feet and matches the color of the bag in (11) hospitals (57.9%). While the capacity of the bags is proportional to the amount of waste generated in (16) hospitals out of (19) was (84.2%). In addition the (MW) segregated according to color-coded in all departments in (15) hospitals was (78.9%). This indicated also still there is a gap in segregation system in 4 hospitals. The finding is not away from the statements that despite the necessity of segregation in Health Care Waste Management (HCWM), some countries either lack proper rules and regulations on HCW segregation or do not impose them; hence the Health Care Waste Management Systems (HCWMS) are insufficient (**Nwachukwu *et al*., 2013**). An assessment carried out in 22 developing countries in 2002 showed that 18% to 64% of the Health Care Facilities (HCF) did not employ appropriate waste disposal methods (**WHO, 2014**).

Furthermore, the study showed that the thickness of the bags is not appropriate in (15) hospitals out of (19) was (78.9%) for medical waste. However, Bags and plastic packages manufactured from non-halogenated plastic only in (8) hospitals was (42.1%). However, the capacity of the bags is proportional to the amount of waste generated in (16) hospitals was (84.2%). The plastic bags specified for sharp waste are appropriate and not openable in a number of 11 hospitals (57.9%). While the bags and packages filled only up to two thirds of the size in (13) hospitals was (68.4%).Also the amount of bags and packages are provided by adequate numbers only in (10) hospitals was (52.6%). Only the chemical waste are segregated and collected in adequate packages not subjected to interact with it in (7) hospitals was (36.8%). In addition there is primary treatment for high contagious wastes at the site of its generation were done only in (8) hospitals was (42.1%). These findings indicate significant correlation gaps in compliance with WHO guidelines for medical waste disposal and treatment (P- value = 0.03). WHO guidelines emphasize that appropriate containers should be available at all waste generation points, instructions for waste segregation should be clearly displayed, and waste bags should be sealed when three-quarters full using appropriate closure methods rather than staples. Sharps containers should be sealed and placed in labeled yellow infectious waste bags before removal (WHO, 1999).

Moreover, the studied hospitals (19) showed lack of Autoclave device is exist, cooling (Temperature not more than (-20 C), disinfection by formalin (Concentration not exceed (10%) for (24h), while no hospital recapping of needles which considered good practice of medical waste. But lack of autoclave in hospitals may make microorganism still survive in waste and it may disseminated in the environment posing risks. Autoclave with steam, moisture, heat and pressure is used in order to inactivate the micro-organisms, and to sterilize the medical devices and for medical wastes treatment (**Forbes *et al*., 2007**).The BMW (Management and Handling of Wastes) Rules (2000) recommend autoclaving for disposables, microbiological waste and sharps. Typical operating conditions for an autoclave are a temperature of at least (121°C) at a pressure of (105 K Pa) for a period of at least (60 min). The second option for the temperature, etc., is that BMW can be sterilized at (132°C) for (30-60 min) (**WHO, 1999**). Anatomical and pathological wastes, low-level radioactive waste, organic solvents, laboratory chemicals, and chemotherapy waste should not be treated in an autoclave (**Al Khatib *et al*., 2009**). In a recent study also, it has been suggested that alternatives for waste treatment rather than incineration such as a locally made autoclave integrated with a shredder should be evaluated and implemented (**Gautam *et al*., 2010**). The study showed that indicated that there is a specific programme for collection and transportation of waste to store room in (13) hospitals was (68.4%). However, waste not remained in its generated site more than one day only in 6 hospitals (31.6%). Bags and packages are labeled in a number of (10) hospitals was (52.6%). Also the study showed that there are replace of new bags or packages instead of transported ones immediately in a number of (14) hospitals was (73.7%). Still there were hospitals not have regular program for medical waste collection and transportation, wastes remained more than one day in many hospitals, no replacing of new bags or packages by the old ones and bags and packages are not labeled in a number of (9) hospitals. This considered improper disposal and treatment of medical waste that may pose risks inside hospitals for environment and for workers This may be due to lack of awareness about the health hazards related to health-care waste, inadequate training in proper waste management, absence of waste management and disposal systems, insufficient financial and human resources and the low priority given to the topic are the most common problems connected with health-care waste as indicated by the World Health Organization (**WHO, 2018**). Still there were problems in trucks and waste vehicles in many hospitals such as difficulty in loading and unloading, a part of the trucks have no flatten surfaces, washed of trucks, no specific workers for transportation of medical waste in hospitals and hospitals roads for store room pass with food preparation room. This is not according to WHO (**1999**) specification for medical waste vehicles which supposed to fulfill the following criteria; the body of the vehicle should be of a suitable size commensurate with the design of the vehicle, with an internal body height of (2.2 meters.), there should be a bulkhead between the driver's cabin and the vehicle body, which is designed to retain the load if the vehicle is involved in a collision., there should be a suitable system for securing the load during transport., empty plastic bags, suitable protective clothing, cleaning equipment, tools, and disinfectant, together with special kits for dealing with liquid spills, should be carried in a separate compartment in the vehicle., the internal finish of the vehicle should allow it to be steam-cleaned, and the internal angles should be rounded and the vehicle should be marked with the name and address of the waste carrier., the international hazard sign should be displayed on the vehicle or container, as well as an emergency telephone number.

Also the study illustrated that still there were gaps in many hospitals in terms of the place of store is not separated from the hospital departments and places of storing domestic waste. In addition there are no enough cleaning tools and water source and drainage. Also this is not matched the WHO Guidelines (**WHO, 1999**) that stated the storage area should have an impermeable, hard-standing floor with good drainage; it should be easy to clean and disinfect and there should be a water supply for cleaning purposes. The other gaps in many of the studied hospitals were animals and birds can enter the site and the store room not fitted with door always closed. Ventilation and lightening are not enough and adequate and the storing period exceed (24h) in summer and (48 h) in winter. However, the way of storing is not adequate. In addition the bags and medical waste package not placed in the ground or inside containers.The store room not cleaned and disinfected according to daily programmes and when appropriate. Hospitals way for store room is not easy and secured.The road for store room passes with food preparation room. There are no weighing device and recording for generated amount. This not according to WHO (**1999**) which indicated that the storage area should afford easy access for staff in charge of handling the waste., It should be possible to lock the store to prevent access by unauthorized persons., easy access for waste-collection vehicles is essential., there should be protection from the sun., the storage area should be inaccessible for animals, insects, and birds., there should be good lighting and at least passive ventilation., the storage area should not be situated in the proximity of fresh food stores or food preparation areas., a supply of cleaning equipment, protective clothing, and waste bags or containers should be located conveniently close to the storage area. In addition the study showed that the general cleanness for the store room was not good in 9 hospitals out of 19. This is not acceptable because keeping hospitals clean is a crucial patient safety issue. The importance of the hospital environment in patient care has only recently been recognized widely in infection prevention and control (IPC). Although the available literature is limited, there is now enough evidence to demonstrate that maintaining the hygiene of the hospital environment helps prevent infections. Still, good interventional studies are rare, the quality of products and methods available is heterogeneous, and environmental hygiene personnel is often relatively untrained, unmotivated, under-paid, and under-appreciated by other actors in the hospital. Coupled with understaffed environmental hygiene service departments, this creates lasting issues in regards to patient and healthcare worker safety (**Peters *et al*., 2018**).

The current study showed that there are no specified truck only for transportation of medical waste and have a temporary licensing from environmental health department. This condition not conformance to Standards of the Medical Waste Practice (**İlce *et al*., 2009**). In addition the study showed that there was no incineration in the studied hospitals, but the transported medical waste was transported to one incineration in one complex namely Alsaudi hospital. Also the interviewer stated that the management of medical waste was not appropriate where the final dumping is not completely that make easy for pickers. Also no specialized incinerations but there will be one specialized incineration for medical waste it may be received in the coming days.

This supported by the interview of locality manager who stated that all the medical wastes transported to the Saudi Complex where the waste exposed to high heat and then transported to the final disposal for dumping in specific location specified for medical waste dumping. Also all hospitals sending the medical waste to the recommended final dump, the liquid waste drained directly to sewer net in all hospitals, and the liquid waste drained to sewer net not after disinfection. The results indicated gap in drainage of liquid waste directly and not conformance with WHO Guidelines (**1999**). In terms of incineration the justification may be returned to the high cost of initiation of incineration. The situation is not differ from the previous studies that described the HCW management system in hospitals in various countries (**Gai and Kuroiwa, 2009; Mbongwe *et al*., 2008; Sawalem *et al*., 2009; Stankovic *et al*., 2008; Taghipour and Mosaferi, 2009**).

The present study showed that the overall amount of medical waste that sends in each time in the studied hospitals was found to be (215.2±18.7 kg) with frequency of sending medical waste per week (2.7±0.3 times). This is in corresponded with WHO guidelines (the world Health Organization estimated the total medical waste per person per year is anywhere to be from (0.50 to 3.00 kg/bed/day) in developing and less developed countries the average rate of medical waste in hospital is (0.6 kg/bed/day) (**WHO, 2018**). This study revealed that there are deficiency in of health cadres and workers in approximately one third of the studied hospitals in addition to deficiency in more than half of the hospitals related to records of accidents related medical waste and also similar deficiency in committee meetings. This is not conformity with WHO (**1999**) Guidelines for safe disposal and treatment of medical waste. Finally, where records do exist, the information is generally not present in a publicly accessible form. Paper-based records will be the norm outside of the high income countries and the resources or drive to collate them is simply not present. This is true even in countries with comparatively well-structured systems (**Jordaan, 2015**).

The most shortcomings and weakness points of (MW) in hospitals were mixing between (D) and (M) waste was (52.6%), no labeling on medical waste bags (15.8%), the store room not according to specifications (10.5%) and workers not committed for (PPE). This may be returned to the limited level of education of the majority of medical waste workers. These results are inconsistent with the findings of another study that was done in two hospitals in south west Nigeria . The main weak point appeared in hospitals (A) and (B) was the absence of permanent committee. In addition, there was lack of waste minimization concept in the evaluated hospitals knowing that hospital (E) was planning to use electronic health records in future instead of papers. But the study results were similar to the study done in Nepal (**Sapkota *et al*., 2014**). The weakness points emerged in the study supported by the interviewer future plans for medical waste which includes; provision of modern incinerators for medical waste; increased number of closed and cooled trucks; holding of workshops training in medical waste field; conduct of periodic medical check-up for medical waste workers and provision of PPE and commitment of workers to use. in addition to initiation of occupation health administration in administrative Units.

5.Conclusion

Additional focus is needed to enhance the entire process of waste management and thus to avoid the health and environmental hazards associated with these hazardous wastes.In summary the main problems confronting the hospitals with respect to the management of medical waste include, mixing of hazardous wastes with domestic waste of the hospital , poor knowledge of workers to use of colored bags coded and the absence of a committee responsible for monitoring medical waste management practices in many hospitals, and the lack of education and training on medical waste management, availability of (PPE) and used , medical check-up for workers and vaccination against (HBV).

References

Abah, S. O., & Ohimain, E. I. (2011). Healthcare waste management in Nigeria: A case study. Journal of Public health and Epidemiology, 3(3), 99-110.

ALkhatib I, Sato C (2009). Solid health care waste management status at health care centers in the West Bank-Palestinian Territory. *Wastes Manage*., 29: 2398-2403.

Awodele, O., Adewoye, A. A., & Oparah, A. C. (2016). Assessment of medical waste management in seven hospitals in Lagos, *Nigeria*. *BMC public health*, 16(1), 269.

Forbes, B. A., Sahm, D. F., & Weissfeld, A. S. (2007). Diagnostic microbiology. St Louis: Mosby.

Gai R and Kuroiwa C (2009) Hospital medical waste management in Shandong Province, China. *Waste Management and Research* 27: 336–342.

Gautam, V., Thapar, R., & Sharma, M. (2010). Biomedical waste management: Incineration vs. environmental safety. *Indian journal of medical microbiology*, 28(3), 191.

İlce, A., Çelik, G. O., & Korkmaz, F. D. (2009). The conformance to standards of the medical waste practices at a university hospital. Eur J Gen Med, 6(4), 229-238.

IRC, (International Committee of the Red Cross) . (2011). Medical Waste Management. www.icrc.org © ICRC, November 2011.

Jordaan, E. (2015). Rising Powers and Human Rights: The India-Brazil-South Africa Dialogue Forum at the UN *Human Rights Council*. *Journal of Human Rights*, 14(4), 463-485.

Mbongwe, **B., Mmereki, B. T. and Magashula, A. (2008)** Healthcare waste management: current practices in selected healthcare facilities, Botswana. *Waste Management* 28: 226–233.

Muduli, K. & Barve, A., (2012). Challenges to Waste Management Practices in *Indian Health Care Sector*. , 3, pp.62–67.

Nwachukwu, N. C., Orji, F. A., & Ugbogu, O. C. (2013). Health care waste management–public health benefits, and the need for effective environmental regulatory surveillance in federal Republic of Nigeria. *In Current Topics in Public Health.* InTech.

Peters, A., Otter, J., Moldovan, A., Parneix, P., Voss, A., & Pittet, D. (2018). Keeping hospitals clean and safe without breaking the bank; summary of the healthcare cleaning forum 2018.

Sapkota, B., Gupta, G. K., & Mainali, D. (2014). Impact of intervention on healthcare waste management practices in a tertiary care governmental hospital of Nepal. *BMC Public Health*, 14(1), 1005.

Sawalem M, Selic E and Herbell J-D (2009) Hospital waste management in Libya: a case study. *Waste Management* 29: 1370–1375.

Stankovic A, Nikic D and Nikolic M (2008) Report: treatment of medical waste in Nisava and Toplica districts, Serbia. *Waste Management and Research* 26: 309–313.

Taghipour H and Mosaferi M (2009). The challenge of medical waste management: a case study in northwest Iran-Tabriz. W*aste Management and Research* 27: 328–335.

WHO (2018). Health-care waste. Available at: https://www.who.int/news-room/fact-sheets/detail/health-care-waste.

WHO, (2014). Guidance for Health Care Waste Management in Low Income Countries, WorldHealthOrganization (WHO), 2014.

WHO. (2005). Preparation of National Healthcare Waste Management Plans in sub-Sahara countries. Guidance manual. *Secretariat of the Basel convention and World Health Organization*.