

Genomic Insights into Drug Abuse: The Role of DNA and Protein-Coding Regions in Addiction and Genetic Mutation

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Abstract This paper explores the genetic and epigenetic impacts of drug abuse, focusing on how chronic drug use can induce mutations in DNA, particularly within protein-coding regions, and alter gene expression through mechanisms such as DNA methylation. The study highlights the significant role of these genetic changes in the brain's reward pathways, which contribute to the development and persistence of addiction. Through a comprehensive literature review, the paper identifies key genetic factors associated with addiction susceptibility and the long-term effects of drug-induced epigenetic modifications. A proposed research framework is presented, emphasizing the need for longitudinal studies to track epigenetic changes over time, targeted genomic analysis to identify critical mutations, and the integration of multi-omics approaches to provide a holistic understanding of drug abuse's impact on the genome. The paper also addresses ethical considerations, including the importance of protecting genetic privacy and preventing stigmatization based on genetic findings. The study concludes that advancing our understanding of the genetic and epigenetic mechanisms underlying addiction can lead to more effective, personalized treatment strategies and inform public health policies aimed at mitigating the effects of drug abuse.



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1. INTRODUCTION

The abuse of illicit drugs represents one of the most severe public health challenges globally, affecting millions of individuals and imposing significant social, economic, and health burdens [1]. Drug abuse not only leads to addiction, a chronic and relapsing condition, but also triggers a wide range of health problems, including cardiovascular diseases, respiratory issues, and mental health disorders. However, one of the less explored yet crucial aspects of drug abuse is its impact on the human genome, particularly on DNA and protein-coding regions [2].

Illicit drugs, such as cocaine, heroin, methamphetamine, and cannabis, can have profound effects on the body's molecular mechanisms. These substances can induce genetic mutations, alter gene expression, and lead to epigenetic changes that may have long-lasting effects even after drug use has ceased. Understanding how these drugs interact with DNA is essential for developing strategies to mitigate their harmful effects and to explore potential therapeutic interventions [3].

In order to benefit from the analysis of data on drug abuse, it is necessary to use various and modern transformation functions, (like Fourier, Wavelet, Multiwavelet and hybrid transforms) because of their high ability to extract and analyze genomic data. Relevant patterns can be identified, leading to the

development of effective strategies for prevention and efficient medical treatment [4- 35].

1.1 The Role of DNA and Protein-Coding Regions in Drug Abuse:

DNA, particularly the regions that code for proteins, plays a critical role in determining how the body responds to drugs. Protein-coding regions are responsible for synthesizing proteins that regulate various biological processes, including those that are targeted or affected by drugs. When individuals abuse drugs, these substances can interact with the DNA, potentially causing mutations in these coding regions. Such mutations can have various consequences, ranging from altered protein function to the development of drug resistance or susceptibility to other diseases [36].

Moreover, drug abuse can lead to epigenetic modifications—changes in gene expression without altering the underlying DNA sequence—that can be passed down to future generations. These modifications can affect the brain's reward pathways, making individuals more susceptible to addiction or leading to other long-term health issues. The study of how drugs influence DNA and protein-coding regions is, therefore, crucial for understanding the full impact of drug abuse on human health [37].

It is possible to utilize optimization algorithms (such as GWO, PSO and COOT) to speed up the big data analysis process that lead to the detection of important patterns and identified them. The use of such optimized techniques leads to a broader and deeper understanding of the phenomenon of addiction, which facilitates access to new and advanced treatment methods [38-58].

1.2 Importance of Research in Drug Abuse and DNA Analysis:

Research into the genetic effects of drug abuse is not only important for understanding the biological mechanisms underlying addiction but also for developing effective interventions. By analyzing the DNA of individuals who abuse drugs, scientists can identify genetic markers that may predict susceptibility to addiction or the likelihood of developing drug-induced health problems. This information could be used to create personalized treatment plans that take into account an individual's genetic makeup, potentially improving the effectiveness of addiction therapies [59].

Furthermore, DNA analysis can aid in the discovery of new therapeutic targets. By identifying how drugs interact with specific protein-coding regions, researchers can develop drugs that either mitigate the harmful effects of drug abuse or exploit these interactions to treat addiction. For example, if a particular genetic mutation is found to confer resistance to the effects of a drug, this knowledge could be used to develop a drug that bypasses this resistance [60].

Research being conducted in the field of drug abuse and DNA analysis using pattern recognition, classification and detection algorithms can be considered crucial. The genetic basis of addiction is understood by employing these pattern recognition techniques and algorithms, by identifying genetic markers and predicting the risks of addiction [61-78].

Techniques and algorithms for detecting patterns that express a disease or disorder may develop innovative detailed ideas and insights to reveal the genetic basis of addiction. This requires achieving qualitative development and the intersection of advanced algorithms with advanced scientific research to reach successful treatments for the complex issue of drug abuse [79-101].

1.3 Drug Exploration through DNA Analysis:

The exploration of how drugs interact with DNA also holds potential for drug discovery. By understanding the molecular pathways that drugs affect, scientists can design new drugs that specifically target these pathways, potentially leading to more effective treatments for addiction and other drug-related health issues. Additionally, this research can help identify individuals who are at higher risk for drug abuse based on their genetic profiles, allowing for targeted prevention strategies [102].

For instance, the identification of single-nucleotide polymorphisms (SNPs) associated with drug addiction can

provide insights into why certain individuals are more prone to addiction than others. This knowledge can be used to develop interventions that are tailored to these high-risk individuals, potentially preventing addiction before it starts [103].

1.4 Objectives of the Research:

This research aims to explore the potential of DNA analysis, particularly of protein-coding regions, in understanding the impact of drug abuse on the human genome [104]. The objectives include:

- Investigating the genetic mutations induced by drug abuse and their implications for health.
- Exploring how DNA and protein-coding regions can be analyzed to identify genetic susceptibilities to drug addiction.
- Evaluating the potential for DNA analysis in drug discovery and the development of personalized addiction treatments.

1.5 Significance of the Study:

This study seeks to contribute to the understanding of the genetic impacts of drug abuse, with the goal of improving public health interventions. By integrating genomic analysis with drug abuse research [105], this study could lead to the development of more targeted and effective treatments for addiction, reduce the incidence of drug-induced genetic mutations, and offer new strategies for drug prevention. The findings could also inform public health policies aimed at reducing the burden of drug abuse on society [106].

2. LITERATURE REVIEW

2.1 Introduction to the Literature Review:

The connection between drug abuse and genetic alterations is an evolving area of research with significant implications for public health. This literature review aims to provide an in-depth exploration of how drugs influence DNA, particularly focusing on protein-coding regions, and how this interaction can contribute to addiction and genetic mutations. By examining existing studies, this review identifies key findings, methodological approaches, and gaps in the literature that your research will address [197].

2.2 Genetic Factors in Drug Addiction:

1. Genetic Susceptibility:

- Genetic predisposition plays a crucial role in the development of substance use disorders (SUDs). Twin studies have demonstrated that heritability accounts for approximately 50% of the risk for addiction, suggesting a strong genetic component ([National Institute on Drug Abuse](https://www.nida.nih.gov/publications/national-institute-on-drug-abuse)) [108].

- Genome-wide association studies (GWAS) have identified several single-nucleotide polymorphisms (SNPs) associated with increased susceptibility to addiction. For example, variations in the genes encoding dopamine receptors (e.g., DRD2, DRD4) and dopamine transporters have been linked to a higher risk of addiction to substances like cocaine and alcohol ([National Institute on Drug Abuse](#)) [109].

2. Heritability of Addiction:

- The heritability of addiction is supported by evidence from family and twin studies, which show that first-degree relatives of individuals with addiction are at higher risk of developing similar disorders. This genetic predisposition is believed to interact with environmental factors, creating a complex pathway to addiction ([National Institute on Drug Abuse](#)) [110].

2.3 Impact of Drug Abuse on DNA and Genetic Mutations:

1. DNA Damage and Repair Mechanisms:

- Chronic drug abuse has been linked to DNA damage through oxidative stress and the generation of reactive oxygen species (ROS). These damaging agents can lead to mutations if the DNA repair mechanisms fail to correct the errors. Drugs such as methamphetamine and cocaine have been shown to induce significant oxidative damage to DNA ([National Institute on Drug Abuse](#)) [111].
- Research also suggests that the chronic use of drugs can impair the DNA repair mechanisms themselves, compounding the risk of accumulating genetic mutations over time ([National Institute on Drug Abuse](#)) [112].

2. Epigenetic Changes:

- Drug abuse induces epigenetic changes, such as DNA methylation and histone modifications, which do not alter the DNA sequence but affect gene expression. For instance, chronic exposure to cocaine has been shown to alter the methylation patterns of genes involved in neural plasticity, which may contribute to the persistence of addictive behaviors ([National Institute on Drug Abuse](#)) [113].
- These epigenetic modifications can be long-lasting and may even be inherited,

potentially affecting future generations' susceptibility to addiction and other related disorders ([National Institute on Drug Abuse](#)) [114].

3. Drug-Induced Mutations:

- Certain drugs have been implicated in causing mutations in protein-coding regions of the genome. For example, drugs that induce high levels of cellular stress can lead to errors during DNA replication or repair, resulting in mutations. This has been observed in the context of cancer treatment, but the implications for drugs of abuse are an emerging area of study ([Memorial Sloan Kettering Cancer Center](#)) [115].
- Studies have also shown that substances like alcohol and tobacco can lead to mutations in specific genes, increasing the risk of developing cancer and other diseases ([Memorial Sloan Kettering Cancer Center](#)) [116].

2.4 Protein-Coding Regions and Their Role in Drug Response:

1. Interaction Between Drugs and Protein-Coding Genes:

- The interaction between drugs and protein-coding genes is crucial for understanding both therapeutic effects and toxicities. Protein-coding regions of DNA are responsible for producing enzymes and receptors that drugs interact with, such as cytochrome P450 enzymes that metabolize drugs. Variations in these genes can lead to significant differences in how individuals respond to drugs ([Merck Manuals](#)) [117].
- Research in pharmacogenomics has highlighted how genetic variants in protein-coding regions can predict drug response and adverse effects. For illicit drugs, similar principles apply, where genetic differences can affect an individual's vulnerability to addiction or the severity of withdrawal symptoms ([BioMed Central](#)) [118].

2. Pharmacogenomics:

- While pharmacogenomics traditionally focuses on prescription medications, the principles are increasingly being applied to illicit drugs. Understanding how genetic variations in protein-coding regions affect drug metabolism and response can inform

the development of targeted treatments for addiction, minimizing harmful side effects ([Merck Manuals](#)) [119].

research that considers genetic diversity and its impact on addiction [126-127].

2.5 Genomic Studies in Addiction Research:

1. Genome-Wide Association Studies (GWAS):

- GWAS have identified numerous loci associated with the risk of substance use disorders. These studies have linked genetic variants to addiction-related traits, such as impulsivity and stress reactivity, which are critical for understanding the biological basis of addiction ([National Institute on Drug Abuse](#)) [120].
- The results of GWAS highlight the polygenic nature of addiction, where multiple genetic variants contribute to the overall risk, making it a complex trait influenced by both genetic and environmental factors ([National Institute on Drug Abuse](#)) [121].

2. Potential for Precision Medicine:

- Precision medicine in addiction treatment is a burgeoning field, where treatments are tailored based on an individual's genetic profile. This approach has the potential to improve treatment outcomes by targeting the specific genetic and epigenetic factors that contribute to an individual's addiction ([BioMed Central](#)) [122].
- The integration of genomic data into addiction treatment could lead to more effective interventions, reducing the likelihood of relapse and improving long-term recovery outcomes ([BioMed Central](#)) [123].

Despite significant advances in understanding the genetic basis of addiction and the impact of drug abuse on DNA, several gaps remain [30]. There is a need for:

- **Longitudinal Studies:** Few studies track the long-term genetic and epigenetic changes in individuals who abuse drugs, leaving gaps in our understanding of how these changes evolve over time and their long-term health implications [124].
- **Mechanistic Studies:** More research is needed to elucidate the exact mechanisms by which drugs induce genetic mutations, particularly in protein-coding regions [125].
- **Diverse Populations:** Many genetic studies on addiction have focused on populations of European descent, underscoring the need for more inclusive

3. DISCUSSION AND FUTURE DIRECTIONS

3.1 Interpretation of Literature Findings

The literature reviewed highlights several critical points in the relationship between drug abuse, genetic mutations, and epigenetic modifications. The findings suggest that drug abuse not only has immediate neurophysiological effects but also leads to long-lasting genetic and epigenetic changes that can influence addiction susceptibility and perpetuate addictive behaviors. The role of protein-coding regions is crucial as these regions dictate the production of proteins that are central to neural signaling pathways affected by drugs.

Additionally, the literature reveals that epigenetic changes, such as DNA methylation, can significantly alter gene expression in brain regions associated with addiction. These changes can persist long after drug use has ceased, highlighting the chronic nature of addiction as a neuropsychiatric disorder.

3.2 Proposed Research Agenda

Building on the literature, it is essential to propose a future research agenda that could fill the existing gaps and advance our understanding of the genetic and epigenetic impacts of drug abuse. The proposed research should focus on the following areas:

1) Longitudinal Studies on Epigenetic Changes:

Conduct long-term studies that track the epigenetic changes in individuals with a history of drug abuse. These studies should aim to correlate specific epigenetic markers, such as DNA methylation patterns, with the severity of addiction, relapse rates, and recovery outcomes.

2) Targeted Analysis of Protein-Coding Regions:

Future research should specifically focus on identifying how drug abuse affects protein-coding regions. This could involve analyzing changes in gene expression and protein function in response to different classes of drugs. The goal would be to identify potential biomarkers for addiction susceptibility and targets for therapeutic intervention.

3) Cross-Population Genomic Studies:

Given the genetic diversity in populations, it is crucial to conduct genomic studies across different ethnic groups to ensure that findings are broadly applicable. Such studies could identify population-specific genetic and epigenetic risk factors for addiction, leading to more tailored public health strategies.

4) Integrative Multi-Omics Approach:

Employ a multi-omics approach that integrates genomic, transcriptomic, proteomic, and epigenomic data to provide a comprehensive understanding of how drugs affect the human body at multiple biological levels. This approach could reveal new insights into the molecular mechanisms underlying addiction and identify potential therapeutic targets.

5) Ethical and Social Considerations:

As research into the genetic basis of addiction progresses, it is vital to address the ethical implications, particularly concerning genetic privacy, potential stigmatization, and the use of genetic information in public policy and clinical settings. Future research should include studies that explore these ethical dimensions and propose guidelines for responsible use of genetic data in addiction research.

3.3 Implications for Treatment and Prevention

The integration of genetic and epigenetic research into addiction studies has the potential to revolutionize treatment and prevention strategies. Understanding the genetic and epigenetic basis of addiction could lead to the development of personalized medicine approaches, where treatment plans are tailored to an individual's genetic profile. This could improve treatment efficacy, reduce the likelihood of relapse, and provide more targeted interventions for individuals at higher genetic risk of addiction.

Moreover, the identification of epigenetic changes associated with addiction could lead to the development of epigenetic therapies. These therapies could involve the use of drugs that reverse harmful DNA methylation patterns, thereby restoring normal gene expression and reducing the compulsive behaviors associated with addiction.

3.4 Future Research Directions

Based on the proposed research agenda, future studies should aim to:

- **Explore the Reversibility of Epigenetic Changes:** Investigate whether the epigenetic changes induced by drug abuse are reversible and, if so, how this reversibility can be leveraged in therapeutic contexts.
- **Develop Predictive Models for Addiction:** Use the findings from genomic and epigenomic studies to develop predictive models that can identify individuals at high risk for addiction, enabling early intervention.
- **Investigate Gene-Environment Interactions:** Future research should explore how environmental factors, such as stress and social support, interact with genetic and epigenetic factors to influence addiction outcomes.

4. Conclusion

4.1 Recapitulation of Key Findings

The research reviewed and proposed in this paper highlights the profound impact of drug abuse on the human genome, particularly in how it induces genetic mutations and epigenetic modifications. These changes are closely linked to the development and persistence of addictive behaviors, as they alter gene expression in critical brain regions involved in reward processing and decision-making. The literature underscores the role of protein-coding regions and epigenetic mechanisms like DNA methylation in shaping addiction susceptibility and outcomes.

4.2 Importance of Proposed Research Framework

The proposed research framework aims to address the current gaps in our understanding of how drugs influence genetic and epigenetic processes. By focusing on longitudinal studies, targeted genomic analysis, and multi-omics approaches, future research can provide a more comprehensive understanding of the molecular underpinnings of addiction. This knowledge is crucial for developing personalized treatment strategies that can reduce relapse rates and improve recovery outcomes.

4.3 Broader Implications for Addiction Treatment and Public Health

Understanding the genetic and epigenetic foundations of addiction has the potential to revolutionize how we approach treatment and prevention. Personalized medicine, informed by an individual's genetic and epigenetic profile, offers the promise of more effective interventions tailored to each person's unique biological makeup. Additionally, the ethical considerations highlighted in this paper, particularly regarding genetic privacy and the risk of stigmatization, must be integrated into public health policies to ensure that advances in genetic research contribute positively to society.

4.4 Final Thoughts

As we continue to explore the genetic and epigenetic impacts of drug abuse, it is essential to adopt a multidisciplinary approach that combines insights from genomics, neuroscience, psychology, and ethics. The integration of these fields will pave the way for new therapeutic avenues and public health strategies that are more aligned with the complexities of addiction as a chronic, multifactorial disease. The proposed research agenda represents a critical step toward this goal, with the potential to significantly enhance our understanding and treatment of addiction in the years to come.

REFERENCES

- [1] L. Galleani and R. Garelo, "The minimum entropy mapping spectrum of a DNA sequence," IEEE Trans. Inf. Theory, vol. 56, no. 2, pp. 771–783, 2010.
- [2] A.K. Singh, V.K. Srivastava, Improved filtering approach for identification of protein-coding regions in eukaryotes by background noise reduction using S- G filter, Netw. Model. Anal. Health Inform. Bioinform. 10 (19) (2021) 1–16
- [3] L. Das, S. Nanda, and J. K. Das, "A novel DNA mapping scheme for improved coding sequence prediction using digital filters," in Man and 2017Machine Interfacing (MAMI), 2nd International Conference on, 2017, pp. 1–6.
- [4] J W. A. Mahmoud Z Jalal & N. K. Wafi "A New Method of Computing Multi-wavelets Transform using Repeated Row Preprocessing." Al-Rafidain Engineering Journal, Vol. 12, Issue 2, PP. 21-31., 2004.
- [5] W. A. Mahmoud & I. A Al-Akialy "A Tabulated Method of Computation Multiwavelet Transform" Al-Rafidain University College, Vol. 15, PP. 161-170, Iraq, 2004.
- [6] Waleed Ameen Mahmoud Al-Jawher, A. Barsoum and Entather Mahos "Fuzzy Wavenet (FWN) classifier for medical images" Al-Khwarizmi Engineering Journal, Vol. 1, Issue 2, PP. 1-13, 2005.
- [7] Waleed A. Mahmoud, MS Abdulwahab, HN Al-Taai: "The Determination of 3D Multiwavelet Transform" IJCCCE, vol. 2, issue 4, 2005.
- [8] Waleed A. M. Al-Jawher, T Abbas – "Feature combination and mapping using multiwavelet transform" IASJ, AL-Rafidain, Issue 19, Pages 13-34, 2006.
- [9] Waleed A Mahmoud, MR Shaker "3D Ear Print Authentication using 3D Radon Transform" proceeding of 2nd International Conference on Information & Communication Technologies, Pages 1052-1056, 2006.
- [10] H. Al-Taai, Waleed A. Mahmoud & M. Abdulwahab "New fast method for computing multiwavelet coefficients from 1D up to 3D", Proc. 1st Int. Conference on Digital Comm. & Comp. App., Jordan, PP. 412-422, 2007.
- [11] Walid A Al-Jowher, Nada N Al-Ramahi, Mikhled. Alfaouri "Image Identification And Labeling Using Hybrid Transformation And Neural Network" Neural Network World: International Journal on Neural and Mass - Parallel Computing and Information Systems; Prague, Volume 17, Issue 4, Pages 377-395, 2007.
- [12] W. A. Mahmoud & Z. Ragib "Face Recognition Using PCA and Optical Flow" Engineering Journal, Vol. 13, Issue 1, PP. 35-47, 2007.
- [13] Waleed A Mahmoud, Ahmed S Hadi "Systolic Array for Realization of Discrete Wavelet Transform " Journal of Engineering, Vol. 13, Issue 2, PP. 1-9, 2007.
- [14] Walid Amin Al-Jawhar, Ayman M Mansour, Zakaria M Kuraz "Multi technique face recognition using PCA/ICA with wavelet and Optical Flow" 2008 5th International Multi-Conference on Systems, Signals and Devices, pages 1-6, 2008.
- [15] Adnan HM Al-Helali, Hamza A Ali, Buthainah Al-Dulaimi, Dhia Alzubaydi, Waleed A Mahmoud "Slantlet transform for multispectral image fusion" Journal of Computer Science, Vol.5, Issue 4, PP. 263-267, 2009.
- [16] AHM Al-Heladi, WA Mahmoud, HA Hali, AF Fadhel "Multispectral Image Fusion using Walidlet Transform" Advances in Modelling and Analysis B, Volume 52, Iss. 1-2, pp. 1-20, 2009.
- [17] Walid A Mahmoud, Majed E Alneby, Wael H Zayer "2D-multiwavelet transform 2D-two activation function wavelet network-based face recognition" J. Appl. Sci. Res, vol. 6, issue 8, 1019-1028, 2010.
- [18] WA Mahmoud, ALM Rasheed "3D Image Denoising by Using 3D Multiwavelet" AL-Mustansiriya J. Sci 21 (7), 108-136, 2010.
- [19] W. A. Mahmoud & Ommama Razaq "Speech recognition using new structure for 3D neural network" University of Technology, 1st Computer Conference, PP. 161-171, 2010.
- [20] Waleed Ameen Mahmoud "A Smart Single Matrix Realization of Fast Walidlet Transform" Journal of Research and Reviews in Computer Science, Volume 2, Issue, 1, PP 144-151, 2011.

- [21] M Walid A Mahmoud, Majed E Alneby, Wael H Zayer “Multiwavelet Transform And Multi-Dimension-Two Activation Function Wavelet Network Using For Person Identification” Iraqi Journal Of Computers, Communications, Control And Systems Engineering, Vol 11, Issue 1, 2011.
- [22] AHM Al-Helali, Waleed A. Mahmoud, HA Ali “A Fast personal palm print authentication Based on 3d-multi-Wavelet Transformation”, Transnational Journal Of Science And Technology, Vol. 2, Issue 8, 2012.
- [23] Hamid M Hasan, AL Jouhar, Majid A Alwan "Face recognition using improved FFT based radon by PSO and PCA techniques" International Journal of Image Processing (IJIP), Volume 6, Issue 1, Pages 26-37, 2012.
- [24] WA Mahmoud, AI Abbas, NAS Alwan “Face Identification Using Back-Propagation Adaptive Multiwavelet” Journal of Engineering 18 (3), 2012
- [25] WA Mahmoud, AS Hadi, TM Jawad “Development of a 2-D Wavelet Transform based on Kronecker Product” - Al-Nahrain Journal of Science, Vol. 15, Issue 4, PP. 208-213, 2012.
- [26] H. M Hasan, Waleed A. Mahmoud Al- Jawher, M. A Alwan “3-d face recognition using improved 3d mixed transform” Journal International Journal of Biometrics and Bioinformatics, Vo. 6, Issue 1, PP. 278-290, 2012.
- [27] Waleed A. Mahmud Al-Jawher, Talib M. J. Abbas Al-Talib, R. Hamudi A. Salman “Fingerprint Image Recognition Using Walidlet Transform” Australian Journal of Basic and Applied Sciences, Australia, 2012.
- [28] Saleem MR Taha, Walid A Mahmood "New techniques for Daubechies wavelets and multiwavelets implementation using quantum computing “Journal Facta universitatis-series: Electronics and Energetics, Volume 26, Issue 2, Pages 145-156, 2013.
- [29] Waleed A Mahmoud, Dheyaa J Kadhim “A Proposal Algorithm to Solve Delay Constraint Least Cost Optimization Problem” Journal of Engineering, Vol. 19, Iss 1, PP 155-160, 2013.
- [30] SMR Taha, WA Mahmood “New techniques for Daubechies wavelets and multiwavelets implementation using quantum computing” Facta universitatis-series: Electronics and Energetics 26 (2), 145-156, 2013.
- [31] Waleed A. Mahmoud, J J. Stephan and A. A. Razzak “Facial Expression Recognition Using Fast Walidlet Hybrid Transform” Journal port Science Research, Volume3, No:1, Pages 59-69 2020.
- [32] WA Mahmoud “[Computation of Wavelet and Multiwavelet Transforms Using Fast Fourier Transform](#)” Journal Port Science Research 4 (2), 111-117, 2021.
- [33] KN Kadhim, SMR Taha, WA Mahmoud “A new method for filtering and segmentation of the ECG signal”, Proceedings of the Annual International Conference of the IEEE Engineering ..., 1988.
- [34] L R. Husssein and J. M. A. Al-Sammarie W. A. Mahmoud “Image Identification using Minimum Distance Classifier with Multi-Wavelet Transform” Journal of Advances in Modelling and Analysis B, Volume 46, Issue (5-6), pages 1-22, 2003.
- [35] W. A. Mahmoud & Z. J. M. Saleh “ An Algorithm for Computing Multiwavelets & Inverse Transform Using an Over-Sampled Scheme of Pre& Post processing respectively” Engineering Journal, Vol. 10, Issue 2, PP. 270-288, 2004.
- [36] P.K. Kumari, J.B. Seventline, A Novel Approach For Identification Of Exon Locations In DNA Sequences Using GLC Window, Int. J. Biol. Biomed. Eng. 15 (2021) 47–60.
- [37] A. Piovesan, F. Antonaros, L. Vitale, P. Strippoli, M.C. Pelleri, M. Caracausi, Human protein-coding genes and gene feature statistics, BMC Res. Notes 12 (2019).
- [38] Hamsa A Abdullah, Hikmat N Abdullah, Waleed A Mahmoud Al-Jawher, “[A hybrid chaotic map for communication security applications](#)” ” International Journal of Communication Systems, Vol. 33, Issue 4, 2020.
- [39] Qutaiba Abed, [Waleed Ameen Mahmoud Al-Jawher](#) ” [Image Encrypted Using Circular Map, Block Compressed Sensing and Hyper GWO-COOT Optimization](#)” International Journal of Intelligent Engineering & Systems, Volume 17, Issue 5, Pages 234-, 2024.

- [40] Qutaiba Kadhim Abed, Waleed Ameen Mahmoud Al-Jawher “A Secure and Efficient Optimized Image Encryption Using Block Compressive Sensing & Logistic Map Method” *Journal of Cyber Security and Mobility*, Vol. 13 5, 983–1006, 2024.
- [41] Ali Akram Abdul-Kareem, Waleed Ameen Mahmoud Al-Jawher “ [An image encryption algorithm using hybrid sea lion optimization and chaos theory in the hartley domain](#)” *International Journal of Computers and Applications*, Vol. 46, Issue 5, PP. 324-337, **2024**.
- [42] Qutaiba K Abed, Waleed A Mahmoud Al-Jawher “[Optimized Color Image Encryption Using Arnold Transform, URUK Chaotic Map and GWO Algorithm](#)” *Journal Port Science Research*, Vol. 7, Issue 3, PP. 210-236, **2024**.
- [43] Haqi Khalid, Shaiful Jahari Hashim, Fazirulhisyam Hashim, Waleed Ameen Mahmoud Al-Jawher, Muhammad Akmal Chaudhary, Hamza HM Altarturi “[RAVEN: Robust Anonymous Vehicular End-to-End Encryption and Efficient Mutual Authentication for Post-Quantum Intelligent Transportation Systems](#)” Publication date 2024/6/24, *Journal IEEE Transactions on Intelligent Transportation Systems*, Publisher IEEE, **2024**.
- [44] Jaafar Ahmed Abdulsahab, Raghad Mohammed Nafea, Waleed Ameen Mahmoud Al-Jawher, Mohammed Lateef Hayyawawi “[IoT Based Smart Parking System](#)” Authors Publication date 2024/6/28, *Journal Journal Port Science Research*, Volume 7, Issue 3, Pages . 196-203, **2024**.
- [45] Q. K Abed, Waleed A. Mahmoud Al-Jawher “[An Image Encryption Method Based on Lorenz Chaotic Map and Hunter-Prey Optimization](#)” *Journal Port Science Research*, Volume 6, Issue 4, Pages 332-343, **2023**.
- [46] Zahraa A Hasan, Suha M Hadi, Waleed A Mahmoud Al-Jawher “[Speech scrambling based on fan transform technology](#)” Publication date 2023/12/22, *Journal AIP Conference Proceedings*, Volume 2977, Issue 1, **2023**.
- [47] Qutaiba Kadhim Abed, Waleed Ameen Mahmoud Al-Jawher “Enhanced Hyperchaotic Image Encryption with CAW Transform and Sea-Lion Optimizer” *Journal of Cyber Security and Mobility*, Vol. 13 5, 1207–1238, 2024.
- [48] Zahraa A Hasan 1, Suha M. Hadi, Waleed A. Mahmoud al-Jawher “Speech scrambling based on multiwavelet and Arnold transformations”, *Indonesian Journal of Electrical Engineering and Computer Science*, 30 , **2023**.
- [49] Qutaiba Kadhim, Waleed Ameen Mahmoud Al-Jawher “[A new multiple-chaos image encryption algorithm based on block compressive sensing, swin transformer, and wild horse optimization](#)” *Multidisciplinary Science Journal*, Vol. 7, Issue 1, PP. 2025012-2025012, **2024**.
- [50] Ali Akram Abdul-Kareem, Waleed Ameen Mahmoud Al-Jawher “A Hybrid Domain Medical Image Encryption Scheme Using URUK and WAM Chaotic Maps with Wavelet–Fourier Transforms” *Journal of Cyber Security and Mobility*, Pages 435–464-435–464, **2023**.
- [51] Zahraa A Hasan, Suha M Hadi, Waleed A Mahmoud, “Speech scrambler with multiwavelet, Arnold Transform and particle swarm optimization” *Journal Pollack Periodica*, Volume 18, Issue 3, Pages 125-131, **2023**.
- [52] AA Abdul-Kareem, Waleed A. Mahmoud Al-Jawher “[Uruk 4d Discrete Chaotic Map For Secure Communication Applications](#)” *Journal Port Science Research* 5 (3), 131-142., **2022**.
- [53] ZA Hasan, SM Hadi, WA Mahmoud, “Time domain speech scrambler based on particle swarm optimization”, *Pollack Periodica* 18 (1), 161-166, 2023.
- [54] AA Abdul-Kareem, Waleed A. Mahmoud Al-Jawher “Hybrid image encryption algorithm based on compressive sensing, gray wolf optimization, and chaos” *Journal of Electronic Imaging* 32 (4), 043038-043038, **2023**.
- [55] Ali Akram Abdul-Kareem, Waleed Ameen Mahmoud Al-Jawher, “WAM 3D discrete chaotic map for secure communication applications” *International Journal of Innovative Computing*, Volume 13, Issue 1-2, Pages 45-54, 2022.
- [56] Q. K Abed, W. A Mahmoud Al-Jawher “A Robust Image Encryption Scheme Based on Block Compressive Sensing and Wavelet Transform” *International J. of Innovative Computing*, Vol. 13, I. 1-2, PP. 7-13, 2022.
- [57] Ali Akram Abdul-Kareem, Waleed Ameen Mahmoud Al-Jawher, “Image Encryption Algorithm Based on Arnold Transform and Chaos Theory in the Multi-wavelet Domain”, *International Journal of Computers and Applications*, Vol. 45, Issue 4, pp. 306-322, **2023**.

- [58] QK Abed, Waleed A. Mahmoud Al-Jawher, "A new Architecture Of Key Generation Using Dwt For Image Encryption With Three Levels Arnold Transform Permutation" *Journal Port Science Research* 5 (3), 166–177-166–177, 2022.
- [59] S.A. Marhon, S.C. Kremer, Prediction of protein-coding regions using a wide-range wavelet window method, *IEEE/ACM Trans. Comput. Biol. Bioinform.* 13 (4) (2016) 742–753.
- [60] S.D. Sharma, S.N. Sharma, R. Saxena, Identification of short exons disunited by a short intron in eukaryotic DNA regions, *IEEE/ACM Trans. Comput. Biol. Bio in-form.* 17 (5) (2020) 1660–1670.
- [61] Ibraheem Al-Jadir, Waleed A Mahmoud "A Grey Wolf Optimizer Feature Selection Method and its Effect on the Performance of Document Classification Problem" *Journal Port Science Research*, Vol. 4, Issue 2, Pages 125-131, 2021.
- [62] W. A. Mahmoud, Jane Jaleel Stephan and A. A. W. Razzak "Facial Expression Recognition from Video Sequence Using Self Organizing Feature Map" *Journal port Science Research, Transaction on Engineering, Technology and Their Applications*, Vol. 4, Issue 2, Pages 53-68, 2021.
- [63] Sarah H Awad Waleed A Mahmoud Al-Jawher "Precise Classification of Brain Magnetic Resonance Imaging (MRIs) using Gray Wolf Optimization (GWO)" *HSOA Journal of Brain & Neuroscience Research*, Volume 6, Issue 1, Pages 100021, 2022.
- [64] Maryam I Mousa Al-Khuzayy, Waleed A Mahmoud Al-Jawher, "New Proposed Mixed Transforms: CAW and FAW and Their Application in Medical Image Classification" *International Journal of Innovative Computing*, Volume 13, Issue 1-2, Pages 15-21, 2022.
- [65] Waleed A. Mahmoud Al-Jawher, SH Awad "A proposed brain tumor detection algorithm using Multi wavelet Transform (MWT)", *Materials Today: Proceedings* 65, 2731-2737, 2022.
- [66] AAR Sakran, SM Hadi, WAM Al-Jawher "A New Approach for DNA Sequence Analysis Using Multiwavelet Transform (MWT)" *Journal of Physics: Conference Series* 2432 (1), 012022.
- [67] SM Saadi, WAM Al-Jawher " Proposed DeepFake Detection Method Using Multiwavelet Transform" *International Journal of Innovative Computing* 13 (1-2), 61-66, 2022.
- [68] AH Salman, WAM Al-Jawher "A Hybrid Multiwavelet Transform with Grey Wolf Optimization Used for an Efficient Classification of Documents" *International Journal of Innovative Computing* 13 (1-2), 55-60, 2022.
- [69] A. U Mosa, Waleed A Mahmoud Al-Jawher "Image Fusion Algorithm using Grey Wolf optimization with Shuffled Frog Leaping Algorithm" *International J. of Innovative Computing*, Vol. 13, Issue 1-2, PP. 1-5. 2022.
- [70] Shaymaa Abdulelah Shaban, Waleed A Mahmoud Al-Jawher "K-Means Clustering Algorithm for Medical Images" *International Journal of Advances in Engineering and Management (IJAEM)*, Vol. 4, Issue 11, 2022.
- [71] Rasha Ali Dihin, Waleed A Mahmoud Al-Jawher, Ebtesam N AlShemmary "Diabetic Retinopathy Image Classification Using Shift Window Transformer", *International Journal of Innovative Computing*, Vol. 13, Issue 1-2, PP. 23-29, 2022.
- [72] Waleed A. Mahmoud Al-Jawher, SAA SHABAN "Clustering Of Medical Images Using Multiwavelet Transform And K-Means Algorithms", *Journal Port Science Research* 5 (1), 35-42, 2022.
- [73] AH Salman, Waleed A. Mahmoud Al-Jawher" A Hybrid Multiwavelet Transform with Grey Wolf Optimization Used for an Efficient Classification of Documents" *International Journal of Innovative Computing* 13 (1-2), 55-60, 2022.
- [74] SA Shaban, WAM Al-Jawher, "K-Means Clustering Algorithm for Medical Images," *International Journal of Advances in Engineering and Management (IJAEM)* 4 ...m 2022.
- [75] L. F. Katran, Ebtesam N AlShemmary, Waleed Ameen Al Jawher "Deep Learning's Impact on MRI Image Analysis: A Comprehensive Survey" *Texas Journal of Engineering and Technology*, Vol. 25, PP. 63-80, 2023.
- [76] R. Ali Dihin, E. AlShemmary and Waleed Al-Jawher "Diabetic Retinopathy Classification Using Swin Transformer with Multi Wavelet" *Journal of Kufa for Mathematics and Computer*, Vol. 10, Issue 2, PP. 167-172, 2023.
- [77] AAR Sakran, SM Hadi, Waleed A. Mahmoud Al-Jawher "A new approach for DNA sequence analysis using multiwavelet transform (MWT)" *Journal of Physics: Conference Series* 2432 (1), 012022, 2023.

- [78] E. Dihin, R. Al-Jawher, Waleed and Al-Shemmary "Implementation of The Swin Transformer and Its Application In Image Classification" Journal Port Science Research, vol. 6, Issue 4, PP. 318-331. **2023**.
- [79] Rasha Ali Dihin, Ebtesam N. AlShemmary and Waleed A. Mahmoud Al-Jawher "Automated Binary Classification of Diabetic Retinopathy by SWIN Transformer" Journal of Al-Qadisiyah for computer science and mathematics (JQCM), Vol 15, Issue 1, PP. 169-178, **2023**.
- [80] Ali Akram Abdul-Kareem, Waleed Ameen Mahmoud Al-Jawher, "[Image Encryption Algorithm Based on Arnold Transform and Chaos Theory in the Multi-wavelet Domain](#)", International Journal of Computers and Applications, Vol. 45, Issue 4, pp. 306-322, **2023**.
- [81] Afrah U Mosaa, Waleed A Mahmoud Al-Jawher "[A proposed Hyper-Heuristic optimizer Nesting Grey Wolf Optimizer and COOT Algorithm for Multilevel Task](#)" Journal Port Science Research, Vol. 6, PP. 310,317, **2023**.
- [82] Maryam I Al-Khuzae, Waleed A Mahmoud Al-Jawher "[Enhancing Medical Image Classification: A Deep Learning Perspective with Multi Wavelet Transform](#)" Journal Port Science Research, Vol. 6, Issue 4, PP. 365-373, **2023**.
- [83] Saadi M Saadi and Waleed A Mahmoud Al-Jawher "[Image Fake News Prediction Based on Random Forest and Gradient-boosting Methods](#)" Journal Port Science Research, Vol. 6, Issue 4, PP. 357-364, **2023**.
- [84] Lamyaa Fahem Katran, Ebtesam N AlShemmary, Waleed Ameen Al Jawher "Deep Learning's Impact on MRI Image Analysis: A Comprehensive Survey" Texas Journal of Engineering and Technology, Vol. 25, PP. 63-80, **2023**.
- [85] Ammar A Sakran, Suha M Hadi, Waleed A Mahmoud Al-Jawher "[Advancing DNA Signal Processing: Integrating Digital and Biological Nuances for Enhanced Identification of Coding Regions](#)" Journal Port Science Research, Volume, 6, Issue 4, Pages 374-387, **2023**.
- [86] Ahmed Hussein Salman, Waleed A. Mahmoud Al-Jawher "[Image Document Classification Prediction based on SVM and gradient-boosting Algorithms](#)" Journal Port Science Research, Volume 6, Issue 4, Pages 348-356, **2023**.
- [87] Ammar AbdRaba Sakran, Waleed A. Mahmoud Al-Jawher, Suha M Hadi "[The Role of Three-Base Periodicity in Enhancing Exon Detection through DSP Techniques](#)" 2023 16th International Conference on Developments in eSystems Engineering (DeSE), Publication date 2023/12/18, Pages 617-622, Publisher IEEE, **2023**.
- [88] Ammar A. Sakran, Waleed A. Mahmoud Al-Jawher, Suha M Hadi "[A Review of Digital Signal Processing Techniques for Protein-Coding Region Identification in DNA Sequences](#)" 2023 16th Inte. Conference on Developments in eSystems Engineering (DeSE), Publication date 2023/12/18, Pages 611-616, Publisher IEEE, **2023**.
- [89] Saadi Mohammed Saadi, Waleed A. Mahmoud Al-Jawher "[Ensemble Learning with optimum Feature Selection for Tweet Fake News Detection using the Dragonfly approach](#)" 16th Int. Conf. on Developments in eSystems Engineering (DeSE), Pages 575-580, IEEE, 2023.
- [90] Ahmed Hussein Salman, Waleed A. Mahmoud Al-Jawher "[Enhanced Document Classification Using Ensemble Techniques](#)" 16th International Conference on Developments in eSystems Engineering (DeSE), Pages 743-747, Publisher IEEE, 2023.
- [91] Ahmed Hussein Salman, Waleed A. Mahmoud Al-Jawher "[A New Multi-class Classification Method Based on Machine Learning to Document Classification.](#)" 16th International Conference on Developments in eSystems Engineering (DeSE), Pages 605-610, Publisher IEEE, 2023.
- [92] Shaymaa Abdulelah Shaban, Waleed AM Al-Jawher '[Image compression techniques using multiwavelet transform algorithm](#)' Publication date 2024/4/11, Journal of AIP Conference Proceedings, Volume 3079, Issue 1, **2024**.
- [93] Saadi Mohammed Saadi, Waleed Al-Jawher "[Ensemble-Based Machine Learning Approach for Detecting Arabic Fake News on Twitter.](#)" Journal Revue d'Intelligence Artificielle, Vol. 38, Issue 1, **2024**.
- [94] Lamyaa Fahem Katran, Ebtesam N AlShemmary, Waleed AM Al-Jawher "[A Review of Transformer Networks in MRI Image Classification](#)" Al-Furat Journal of Innovations in Electronics and Computer Engineering, PP. 148-162, **2024**.
- [95] Saadi Mohammed Saadi, Waleed A. Mahmoud Al-Jawher" [Enhancing image authenticity: A new approach for binary fake image classification using DWT and swin transformer](#)" Global Journal of Engineering and Technology Advances, Vol. 19, Issue 3, PP. 1-10, **2024**.

- [96] Waleed A Mahmoud Al-Jawher, Shaimaa A Shaaban “[K-Mean Based Hyper-Metaheuristic Grey Wolf and Cuckoo Search Optimizers for Automatic MRI Medical Image Clustering](#)” Journal Port Science Research, Volume 7, Issue 3, Pages 109-120, 2024.
- [97] Rasha Ali Dihin, Ebtesam N AlShemmary, Waleed AM Al-Jawher, “[Wavelet-Attention Swin for Automatic Diabetic Retinopathy Classification](#)” Baghdad Science Journal, 2024.
- [98] Maryam I Mousa Al-Khuzai, Waleed A Mahmoud Al-Jawher “[Enhancing Brain Tumor Classification with a Novel Three-Dimensional Convolutional Neural Network \(3D-CNN\) Fusion Model](#)” Journal Port Science Research, Volume 7, Issue 3, Pages 254-267, 2024.
- [99] N. M. S. Mahdi, Ayad K. Hassan, Fatima J. Al-Hasani, and Waleed Ameen. Mahmoud Al-Jawher “**Classification Of Biomaterials and Their Applications**” Journal Port Science Research, Volume 7, Issue 3, Pages 281-299, 2024.
- [100] Maryam I Mousa Al-Khuzai, Waleed A Mahmoud Al-Jawher “[A Proposed MetaNet Deep Learning for Medical Diseases Classification.](#)” International Journal of Intelligent Engineering & Systems, Volume 17, Issue 5, Page 265-, 2024
- [101] Ahmed Hussein Salman, Waleed Ameen Mahmoud Al-Jawher “[Performance Comparison of Support Vector Machines, AdaBoost, and Random Forest for Sentiment Text Analysis and Classification](#)” Journal Port Science Research, Volume 7, Issue 3, Pages 300-311, 2024.
- [102] D.K. Shaky, R. Saxena, S.N. Sharma, An adaptive window length strategy for eukaryotic CDS prediction, IEEE/ACM Trans. Comput. Biol. Bioinform. 10 (5) (2013) 1241–1252.
- [103] M. Raman Kumar, N.K. Vaegae, Walsh code based numerical mapping method for the identification of protein-coding regions in eukaryotes, Biomed. Signal Process. Control 58 (2020) 1–11.
- [104] M. Raman Kumar, N.K. Vaegae, A new numerical approach for DNA representation using modified Gabor wavelet transform for the identification of protein-coding regions, Biocybern. Biomed. Eng. 40 (2) (2020) 836–848.
- [105] M.K. Hota, Empirical mode decomposition based adaptive noise canceller for improved identification of exons in eukaryotes, Netw. Model. Anal. Health Inform. Bioinform. 10 (2021) 60.
- [106] P. Garg, S.D. Sharma, S.N. Sharma, Tandem repeats detection in DNA sequences using p-spectrum based algorithm, in The Proceedings of Conference on Information and Communication Technology (CICT 2017), 2017, pp. 1–5.
- [107] N. Yu, Z. Li, Z. Yu, Survey on encoding schemes for genomic data representation and feature learning—from signal processing to machine learning, Big Data Min. Anal. 1(3)(2018) 191–210.
- [108] P. Garg, S.D. Sharma, Identification of CpG Islands in DNA sequences using short-time Fourier transform, Interdiscip. Sci. Comput. Life Sci. 12 (3) (2020) 355–367.
- [109] N. Yu, Z. Li, Z. Yu, Survey on encoding schemes for genomic data representation and feature learning—from signal processing to machine learning, Big Data Min. Anal. 1 (2018) 191–210.
- [110] H. Wassfy, M. Elnaby, M. Salem, M. Mabrouk, A.-A. Zidan, Advanced DNA Mapping Schemes for Exon Prediction Using Digital Filters, Am. J. Biomed. Eng. (6) 1 (2016) 25–31
- [111] A.K. Singh, V.K. Srivastava, Improved filtering approach for identification of protein-coding regions in eukaryotes by background noise reduction using S-G filter, Netw. Model. Anal. Health Inform. Bioinforma. (10) 1 (2021)
- [112] J. Baranowski, P. Piątek, Fractional Band-Pass Filters: Design, Implementation, and Application to EEG Signal Processing, J. Circuits Syst. Comput. 26 (11) (2017) 1750170
- [113] Y. Ferdi, A Fractional Digital High-Pass Notch Filter, in 2020 10th International Symposium on Signal, Image, Video and Communications (ISIVC), 2021, pp. 1–4.
- [114] A. Gupta, S. Kumar, Design of Atangana–Baleanu–Caputo fractional-order digital filter, ISA Trans. 112 (2021) 74–88
- [115] A.K. Shukla, R.K. Pandey, R.B. Pachori, A fractional filter based efficient algorithm for retinal blood vessel segmentation, Biomed. Signal Process. Control 59 (2020)

- [116] Ammar AbdRaba Sakran et al., A new approach for DNA sequence analysis using multiwavelet transform (MWT) , 2023 J. Phys.: Conf. Ser. 2432 012022.
- [117] Q. Zheng, T. Chen, W. Zhou, S.A. Marhon, L. Xie, H. Su, SAVMD: An adaptive signal processing method for identifying protein-coding regions, Biomed. Signal Process, Control 70 (2021)
- [118] Q. Zheng, T. Chen, W. Zhou, L. Xie, H. Su, Gene prediction by the noise-assisted MEMD and wavelet transform for identifying the protein-coding regions, Biocybern. Biomed. 41 (1) (2021) 196–210
- [119] V. Pathak, S.J. Nanda, A.M. Joshi, S.S. Sahu, VLSI implementation of the anti-notch lattice structure for identification of exon regions in Eukaryotic genes, IET Comput. Digit. Tech. 14 (5) (2020) 217–229
- [120] S. Kar, M. Ganguly, S. Das, Using DIT-FFT algorithm to identification the protein-coding region in the eukaryotic gene, Biomed. Eng. Appl. Basis Commun. 31 (01)(2019)
- [121] A. Singh, V. Srivastava, "Bidirectional filtering approach for the improved protein coding region identification in eukaryotes," Netw. Model. Anal. Health Inform. Bioinforma. 11 (2022)
- [122] S. Kar, M. Ganguly, S. Das, Using DIT-FFT algorithm for identification of the protein-coding region in the eukaryotic gene, Biomed. Eng.: Appl., Basis Commun. 31 (01) (2019).
- [123] S. Putluri, M.Z.U. Rahman, C.S. Amara, N. Putluri, New Exon Prediction Techniques Using Adaptive Signal Processing Algorithms for Genomic Analysis, IEEE Access 7 (2019) 80800–80812.
- [124] P.K. Kumari, J.B. Seventline, A Novel Approach For Identification Of Exon Locations In DNA Sequences Using GLC Window, Int. J. Biol. Biomed. Eng. 15 (2021) 47–60.
- [125] R.K. M, N.K. Vaegae, Walsh code based numerical mapping method for the identification of protein-coding regions in eukaryotes, Biomed. Signal Process. Control. 58 (2020) 101859,
- [126] S. Kar, M. Ganguly, S. Ghosal, "Prediction of the coding region and gh[g hghsjth]m technique", in 2021 International Conference on Computing, Communication, and Intelligent Systems (ICCCIS), 2021.
- [127] J.P. Mena-Chalco, H. Career, Y. Zana, R.M. Cesar Jr., Identification of protein-coding regions using the modified Gabor-wavelet transform, IEEE/ACM Trans. Comput. Biol. Bioinform. 5(2)(2018) 198–207