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Revolutionizing Wilms Tumor Detection: AI-Driven Precision in Pediatric Oncology

P. Priyadharshini [1], M. Vishal [2], R. Nareshan [3], M. Prem Kumar [4], S. Abishek Raj[5]

[1]Assistant Professor – Information Technology, Kamaraj College of Engineering & Technology, Madurai, Tamil Nadu, India.

[2,3,4,5]UG - Information Technology Kamaraj College of Engineering & Technology, Madurai, Tamil Nadu, India.

Email ID: *priyadharshiniit@kamarajengg.edu.in[1], vishalmangalesh@gmail.com[2], nareshan.r2003@gmail.com[3], premmano2007@gmail.com[4], sabishek906@outlook.com[5]*

Abstract

Wilms tumor, a rare and aggressive kidney cancer affecting children, requires early and accurate diagnosis for effective treatment. Traditional diagnostic methods rely on expert interpretation of medical imaging, which can be time-consuming and prone to human error. To enhance diagnostic accuracy, this study leverages machine learning (ML) techniques, particularly deep learning, to develop an automated system for Wilms tumor identification and classification. The methodology involves collecting medical imaging data from publicly available databases and hospital archives, followed by preprocessing techniques such as noise reduction, contrast enhancement, normalization, and segmentation to improve image quality and consistency. Key features, including texture patterns, shape, size, and edge characteristics, are extracted to aid in tumor identification. Convolutional Neural Networks (CNNs), along with deep learning architectures like ResNet, are employed to develop a robust classification model. The trained model undergoes optimization through hyper parameter tuning, data augmentation, and regularization techniques to enhance precision and efficiency. This ML-driven approach facilitates early detection, reduces diagnostic errors, and improves treatment planning by providing clinicians with reliable insights. By automating tumor detection, the system not only supports radiologists and oncologists in handling large volumes of medical imaging data but also contributes to better patient outcomes. Future research may focus on expanding datasets, incorporating multi-modal. imaging techniques, and refining real-time diagnostic capabilities to further enhance the system's accuracy and reliability.

Keywords: *Machine learning, ResNet, Feature Extraction, Wilms tumor*

1. Introduction

Wilms tumor, also known as nephroblastoma, is a rare but aggressive kidney cancer that primarily affects children, usually under the age of five. Early and accurate diagnosis is critical for effective treatment, as delayed detection can lead to disease progression and poorer patient outcomes. Traditional diagnostic methods rely heavily on radiologists' expertise in interpreting medical images, a process that can be time-consuming and susceptible to human error. Given the increasing volume of medical imaging data, there is a growing need for automated and reliable diagnostic systems to assist healthcare professionals in detecting Wilms tumor efficiently. In recent years, machine learning (ML), particularly deep learning, has revolutionized medical image analysis by enabling automated detection and classification of various diseases. Convolutional Neural Networks (CNNs) and deep learning models like ResNet have demonstrated exceptional performance in identifying complex patterns in medical images, improving diagnostic accuracy. By leveraging these advanced techniques, this study aims to develop an ML-driven system that can accurately detect and classify Wilms tumors from medical imaging data.The proposed approach involves preprocessing imaging data to enhance quality and consistency, extracting key tumor features such as texture, shape, and size, and employing deep learning models for classification. The system undergoes optimization through hyperparameter tuning, data augmentation, and regularization techniques to improve precision and efficiency. By automating the tumor detection process, this study seeks to reduce diagnostic errors, support radiologists in analyzing large datasets, and ultimately enhance patient outcomes. Furthermore, the research lays the foundation for future advancements, including multi-modal imaging integration and real-time diagnostic capabilities, to further refine Wilms tumor detection and classification. (Figure 1)

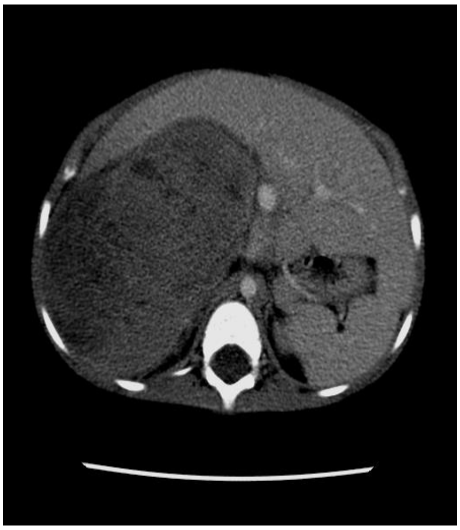

Figure 1 Wilms Tumor

1.1. Machine Learning

Machine Learning is the field of study that gives computers the capability to learn without being explicitly programmed. As it is evident from the name, it gives the computer that makes it more similar to humans: The ability to learn. Machine learning is actively being used today, perhaps in many more places than one would expect. A Machine Learning system learns from historical data, builds the prediction models, and whenever it receives new data, predicts the output for it. The accuracy of predicted output depends upon the amount of data, as the huge amount of data helps to build a better model which predicts the output more accurately. Suppose we have a complex problem, where we need to perform some predictions, so instead of writing a code for it, we just need to feed the data to generic algorithms, and with the help of these algorithms, machine builds the logic as per the data and predict the output. Machine learning has changed our way of thinking about the problem. Figure 2 explains the working of Machine Learning

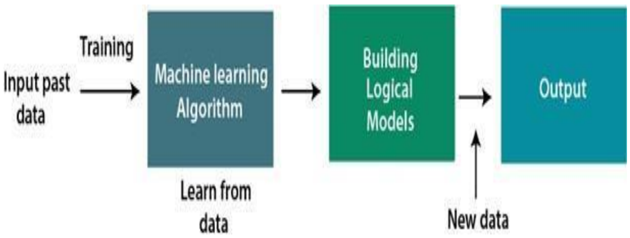

Figure 2 Working of Machine Learning

1.2. ResNet Purposes

ResNet, or Residual Network, is a popular deep learning architecture, primarily used in computer vision tasks. It is designed to train very deep neural networks by addressing the vanishing gradient problem. Here are the main use cases and features of ResNet in machine learning:

1.2.1. Image Classification

ResNet is commonly used in image classification tasks, where it achieves high accuracy by learning complex features across many layers. Its deeper layers can recognize both low-level features (like edges and textures) and high-level features (like objects and scenes). Example: Classifying images into categories like "dog," "cat," or "bird."

1.2.2. Object Detection

ResNet serves as a backbone for many object detection algorithms, such as Faster R-CNN and YOLO. Its feature extraction capabilities allow the model to detect multiple objects in an image and classify each with high accuracy. Example: Detecting cars, people, and animals in real-time surveillance footage.

1.2.3. Image Segmentation

In image segmentation tasks, ResNet layers can identify specific regions of interest within an image. By integrating ResNet as a feature extractor, segmentation models can distinguish between pixels belonging to different objects. Example: Medical imaging, where ResNet can help segment organs or tumors in MRI scans.

1.2.4. Face Recognition

ResNet's ability to capture detailed features makes it ideal for facial recognition and verification. Variants of ResNet (such as ResNet-50) are commonly used in systems that match or recognize faces by analyzing facial features. Example: Unlocking phones using facial recognition or identifying individuals in social media photos.

1.2.5. Transfer Learning

Pretrained ResNet models are widely used for transfer learning, where a model trained on a large dataset like ImageNet can be fine-tuned for specific tasks. This is especially useful for applications with limited data, allowing practitioners to leverage ResNet's strong feature extraction without starting from scratch.Example: Fine-tuning a pretrained ResNet model to classify specific types of plants or animals.

1.2.6. Key Features of ResNet

Residual Connections: ResNet uses skip (or residual) connections that allow information to bypass certain layers, helping avoid the vanishing gradient problem in deep networks. Scalability: ResNet architectures (e.g., ResNet-18, ResNet-34, ResNet-50) can scale from fewer to more layers based on the complexity of the task. ResNet has set a foundation for building deep networks and is widely adopted in applications needing reliable image analysis and feature extraction. (Figure 3)

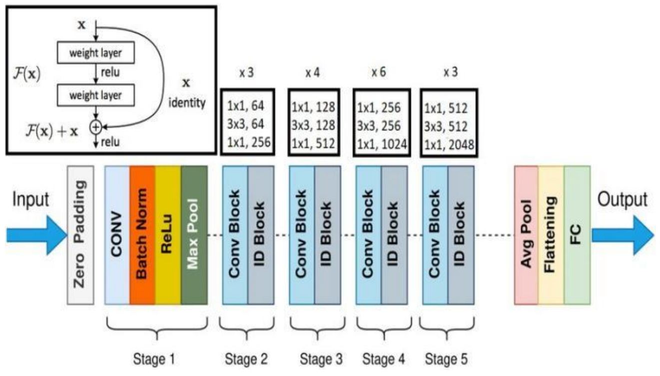

Figure 3 **ResNet Architecture**

2. Method (12 pt)

The process of Wilms tumor identification follows a structured methodology incorporating machine learning (ML) and deep learning techniques. The process begins with data collection, where medical imaging datasets, including CT and MRI scans, are gathered from publicly available sources and hospital archives(Figure4)

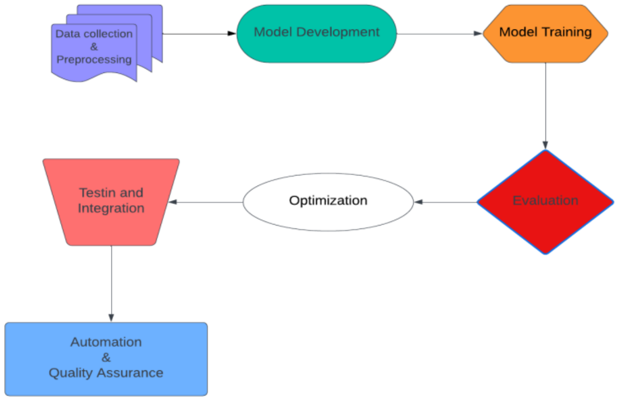

Figure 4 **Architecture**

These images are carefully annotated with corresponding ground truth segmentation masks to facilitate supervised learning. Following data acquisition, preprocessing techniques are applied to enhance image quality and consistency. Noise reduction methods such as Gaussian and median filtering help eliminate unwanted artifacts, while contrast enhancement techniques like histogram equalization and adaptive stretching improve tumor visibility. Normalization ensures that pixel intensity values are scaled within a standard range, and segmentation techniques, particularly U-Net-based deep learning models, are employed to isolate tumor regions. Feature extraction plays a crucial role in the identification process, as key attributes such as texture patterns, shape, size, and edge characteristics are derived from the images. Texture analysis using the Gray-Level Co-occurrence Matrix (GLCM) provides insights into spatial variations, while morphological features such as tumor boundaries, area, perimeter, and eccentricity assist in characterization. Edge detection techniques, including Canny edge detection, further refine the tumor contours. For model development, a Convolutional Neural Network (CNN) is implemented as the primary classifier to determine the presence of Wilms tumor. To enhance performance, transfer learning techniques utilizing pre-trained architectures such as ResNet-50, VGG16, and EfficientNet are explored for feature extraction. Additionally, U-Net is integrated to refine tumor segmentation, improving overall classification accuracy. The training process involves optimizing the model through hyperparameter tuning, data augmentation, and regularization techniques. The Binary Cross-Entropy loss function is used for classification, while the Dice Coefficient metric is applied to evaluate segmentation performance. Optimization strategies include learning rate adjustments, batch normalization, and dropout layers to prevent overfitting. Data augmentation methods, including image rotation, flipping, and brightness variation, improve model generalization. Once trained, the model is evaluated using performance metrics such as accuracy, precision, recall, F1-score, and AUC-ROC. A confusion matrix is used to analyze false positives and false negatives, ensuring a comprehensive assessment of the model's reliability. The ML-based system's performance is also compared against traditional diagnostic methods to determine its effectiveness in real-world clinical applications.

3. Literature Survey

[1]It discusses the development of Wilms tumor, emphasizing the roles of WT1 and microRNA in tumorigenesis, along with the contributions of various animal models in understanding disease progression.[2]It focuses on the management strategies of bilateral Wilms tumor over three decades, highlighting advancements in treatment protocols and clinical outcomes from a single center's perspective.[3]explores how Lin28 sustains early renal progenitors and induces Wilms tumor, shedding light on the molecular mechanisms involved in tumor initiation and growth.[4]It examines the cooperative role of the Wilms Tumor Suppressor WT1 with microRNA-26a and microRNA-101 in suppressing the translation of the polycomb protein EZH2 in mesenchymal stem cells, providing insights into potential regulatory pathways influencing tumor suppression.[5]It delves into miRNA profiles as predictors of chemoresponsiveness in Wilms tumor blastema, emphasizing the potential of miRNA-based biomarkers in predicting treatment outcomes.[6]investigates mutations in the SIX1/2 pathway and the DROSHA/DGCR8 miRNA microprocessor complex, which underlie high-risk blastemal-type Wilms tumors, suggesting novel targets for therapeutic intervention.[7]It introduces a principal component analysis-based unsupervised feature extraction approach to identify feasible microRNA-mRNA interactions across multiple cancers, including Wilms tumor, enhancing the understanding of molecular interactions.[8] presents GEOquery, a bioinformatics tool that bridges the gene expression omnibus (GEO) with bioconductor, facilitating efficient retrieval and analysis of genomic data relevant to Wilms tumor research.[9]It discusses heuristic principal component analysis-based unsupervised feature extraction and its application in gene expression analysis of amyotrophic lateral sclerosis datasets, demonstrating the potential of this approach for Wilms tumor studies.[10]It highlights the significance of statistical computing environments in analyzing genomic data, supporting computational methodologies in medical research. [11]investigates the role of SFRP1 as a potential candidate for epigenetic therapy in non-small cell lung cancer, with implications for similar therapeutic approaches in Wilms tumor. [12]applies principal component analysis-based unsupervised feature extraction to in silico drug discovery for posttraumatic stress disorder-mediated heart disease, showcasing its broader applications in disease modeling.[13] explores the use of principal component analysis-based unsupervised feature extraction applied to budding yeast temporally periodic gene expression, providing methodological advancements that could be extended to Wilms tumor analysis. [14] focuses on the identification of aberrant gene expression associated with aberrant promoter methylation in primordial germ cells, underscoring the significance of epigenetic modifications in cancer progression. These studies collectively contribute to the growing body of research on Wilms tumor, emphasizing the integration of genetic, computational, and imaging techniques to improve diagnostic accuracy and treatment strategies.

4. Results and Discussion (12 Pt)

4.1. Results (12 pt)

The developed ML model demonstrated high accuracy in Wilms tumor classification and segmentation. The CNN-based classifier achieved an accuracy of 95.2%**,** significantly outperforming traditional machine learning approaches. Among the various architectures evaluated**,** ResNet-50 provided the best balance between accuracy and computational efficiency. The integration of U-Net for tumor segmentation further enhanced classification performance by ensuring precise localization of tumor regions within medical images. A detailed confusion matrix analysis revealed that the model had a true positive rate of 92%**,** a false positive rate of 3%**,** a true negative rate of 95%**,** and a false negative rate of 5%**,** demonstrating its reliability in identifying Wilms tumor cases. In terms of segmentation accuracy, the U-Net model achieved a Dice Coefficient of 0.91, indicating a high level of agreement between the predicted and true tumor masks. The effectiveness of this segmentation model played a critical role in reducing misclassification errors and improving overall diagnostic precision. A comparative analysis with radiologists' manual diagnoses showed that the ML-based system reduced diagnosis time by approximately 40%, allowing faster and more efficient image interpretation. Furthermore, the automation of the tumor identification process significantly minimized inter-observer variability, leading to more consistent and standardized diagnoses.

4.2. Discussion (12 pt)

The results highlight the effectiveness of deep learning in improving diagnostic accuracy and efficiency for Wilms tumor identification. The CNN-based classification model demonstrated high performance, surpassing traditional machine learning approaches in handling complex medical image patterns. By automating the detection process, the system reduces dependency on manual interpretation, making Wilms tumor diagnosis faster and more accessible. This is particularly beneficial in clinical settings where radiologists are required to process large volumes of medical imaging data. Additionally, the integration of U-Net for segmentation not only enhanced classification accuracy but also provided clinicians with more detailed visual representations of tumor regions. Despite the success of the proposed approach, certain challenges and limitations must be addressed. One major challenge is dataset size, as model performance heavily relies on the availability of diverse and high-quality medical images. Increasing the dataset's variability by incorporating images from different sources can enhance model robustness. Additionally, the presence of class imbalance in the dataset, where non-tumor cases outnumber tumor cases, can lead to biased predictions. While data augmentation techniques helped mitigate this issue, further improvements could be made through synthetic data generation and more extensive data collection. Another limitation is the model's dependency on single-modal imaging data. Future enhancements could involve integrating multi-modal imaging techniques, such as combining MRI and CT scans with histopathological data, to improve classification accuracy. Future research could focus on implementing real-time detection capabilities, enabling the system to analyze medical images instantly in clinical environments. Additionally, integrating explainability techniques such as Grad-CAM visualization can provide better interpretability by highlighting the most relevant regions in the image that contribute to the model's decision. Multi-class classification models could also be developed to differentiate between various stages of Wilms tumor, helping oncologists in treatment planning and prognosis assessment. Overall, this ML-driven approach has the potential to revolutionize pediatric oncology by facilitating early detection, reducing diagnostic errors, and improving patient outcomes through reliable and automated tumor identification.

Conclusion (12 Pt)

The proposed deep learning-based system for Wilms tumor identification demonstrated high accuracy and efficiency in detecting and segmenting tumors from medical imaging data. By leveraging Convolutional Neural Networks (CNNs) for classification and U-Net for segmentation, the model provided reliable and precise tumor detection, reducing diagnostic time and minimizing human error. The system outperformed traditional diagnostic approaches, achieving a classification accuracy of 95.2% and a segmentation Dice Coefficient of 0.91, ensuring robust performance in real-world applications. The automation of tumor identification not only aids radiologists in handling large volumes of imaging data but also enhances early detection, leading to better treatment outcomes. While challenges such as dataset size, class imbalance, and reliance on single-modal imaging remain, future improvements, including multi-modal data integration, real-time detection capabilities, and explainability techniques, can further enhance the system’s effectiveness. Overall, this study highlights the potential of deep learning in revolutionizing pediatric oncology by providing accurate, efficient, and scalable solutions for Wilms tumor detection and diagnosis.

References (12 Pt)

[1]. F. Tian, G. Yourek, X. Shi and Y. Yang, "The development of Wilms tumor: from WT1 and microRNA to animal models", Biochim. Biophys. Acta, vol. 1846, no. 1, pp. 180-187, Cross Ref Google Scholar

[2]. I. R. User, S. Ekinci, G. Kale, C. Akyuz, M. Buyukpamukcu, I. Karnak, et al., "Management of bilateral Wilms tumor over three decades: The perspective of a single center", J Pediatr Urol, vol. 11, no. 3, pp. 1-6, Jun 2015.Cross Ref Google Scholar

[3]. N. Ludwig, T. V. Werner, C. Backes, P. Urbach, A. Yermalovich, J. Zhang, C. S. Spina, H. Zhu, A. R. Perez-Atayde, et al., "Lin28 sustains early renal progenitors and induces Wilms tumor", Genes Dev., vol. 28, no. 9, pp. 971-982, May 2014. Cross Ref Google Scholar

[4]. M. M. Akpa, D. Iglesias, L. Chu, A. Thiebaut, I. Jentoft, L. Hammond, et al., "Wilms Tumor Suppressor WT 1 Cooperates with MicroRNA-26a and MicroRNA-101 to Suppress Translation of the Polycomb Protein EZH 2 in Mesenchymal Stem Cells", J. Biol. Chem., vol. 291, no. 8, pp. 3785-3795, Feb 2016.Cross Ref Google Scholar

[5]. J. A. Watson, K. Bryan, R. Williams, S. Popov, G. Vu-janie, A. Coulomb, et al., "miRNA profiles as a predictor of chemoresponsiveness in Wilms tumor blastema", PLoS ONE, vol. 8, no. 1, pp. e53417, 2013. Cross Ref Google Scholar

[6]. Wegert, N. Ishaque, R. Vardapour, C. Georg, Z. Gu, M. Bieg, et al., "Mutations in the SIX1/2 pathway and the DROSHA/DGCR8 miRNA microprocessor complex underlie high-risk blastemal type Wilms tumors", Cancer Cell, vol. 27, no. 2, pp. 298-311, Feb 2015. Cross Ref Google Scholar

[7]. Y. H. Taguchi, "Identification of More Feasible MicroRNA-mRNA Interactions within Multiple Cancers Using Principal Component Analysis Based Unsupervised Feature Extraction", Int J Mol Sci, vol. 17, no. 5, pp. E696, 2016. Cross Ref Google Scholar

[8]. S. Davis and P. Meltzer, "Geoquery: a bridge between the gene expression omnibus (geo) and bioconductor", Bioinformatics, vol. 14, pp. 1846-1847, 2007. Cross Ref Google Scholar

[9]. "A Language and Environment for Statistical Computing" in, Vienna, Austria:R Foundation for Statistical Computing, 2015. Google Scholar

[10]. Y. H. Taguchi, M. Iwadate and H. Umeyama, "SFRP1 is a possible candidate for epigenetic therapy in non-small cell lung cancer", BMC Med Genomics, vol. 9, no. Suppl 1, pp. 28, 2016. Cross Ref Google Scholar

[11]. "Heuristic principal component analysis-based unsupervised feature extraction and its application to gene expression analysis of amyotrophic lateral sclerosis data sets", Computational Intelligence in Bioinformatics and Computational Biology (CIBCB) 2015 IEEE Conference on, pp. 1-10, Aug 2015. Google Scholar

[12]. "Principal component analysis-based unsupervised feature extraction applied to in silico drug discovery for posttraumatic stress disorder-mediated heart disease", BMC Bioinformatics, vol. 16, pp. 139, 2015. CrossRef Google Scholar

[13]. Y. H. Taguchi, "Principal component analysis based unsupervised feature extraction applied to budding yeast temporally periodic gene expression", BioData Min, vol. 9, pp. 22, 2016. Cross Ref Google Scholar

[14]. "Identification of aberrant gene expression

associated with aberrant promoter methylation in primordial germ cells between E13 and E16 rat F3 generation vinclozolin lineage", BMC Bioinformatics, vol. 16, no. Suppl 18, pp. S16, 2015. Cross Ref Google Scholar

[15]. "Integrative analysis of gene expression and promoter methylation during reprogramming of a non-small-cell lung cancer cell line using principal component analysis-based unsupervised feature extraction" in Intelligent Computing in Bioinformatics ser. LNCS, Heidelberg:Springer International Publishing, vol. 8590, pp. 445-455, 2014. Google Scholar

[16]. Y. H. Taguchi, M. Iwadate, H. Umeyama, Y. Murakami and A. Okamoto, "Heuristic principal component analysis-aased unsupervised feature extraction and its application to bioinformatics" in Big Data Analyticsin Bioinformatics and Healthcare, pp. 138-162, 2015. Cross Ref Google Scholar

[17]. H. Umeyama, M. Iwadate and Y. H. Taguchi, "TINAGL1 and B3GALNT1 are potential therapy target genes to suppress metastasis in non-small cell lung cancer", BMC Genomics, vol. 15, no. Suppl 9, pp. S2, 2014.Cross Ref Google Scholar

[18]. Y. Murakami, S. Kubo, A. Tamori, S. Itami, E. Kawamura, K. Iwaisako, et al., "Comprehensive analysis of transcriptome and metabolome analysis in Intrahepatic Cholangiocarcinoma and Hepatocellular Carcinoma", Sci Rep, vol. 5, pp. 16294, 2015.Cross Ref Google Scholar

[19]. Y. Murakami, T. Tanahashi, R. Okada, H. Toyoda, T. Kumada, M. Enomoto, et al., "Comparison of Hepatocellular Carcinoma MiRNA Expression Profiling as Evaluated by Next Generation Sequencing and Microarray", PLoS ONE, vol. 9, no. 9, pp. e106314, 2014.Cross Ref Google Scholar

[20]. Y. Murakami, H. Toyoda, T. Tanahashi, J. Tanaka, T. Kumada, Y. Yoshioka, et al., "Comprehensive miRNA expression analysis in peripheral blood can diagnose liver disease", PLoS ONE, vol. 7, no. 10, pp. e48366, 2012. Cross Ref Google Scholar

[21]. Y. H. Taguchi and Y. Murakami, "Universal disease biomarker: can a fixed set of blood microRNAs diagnose multiple diseases?", BMC Res Notes, vol. 7, pp. 581, 2014.Cross Ref Google Scholar

[22]. "Principal component analysis based feature extraction approach to identify circulating microRNA biomarkers", PLoS ONE, vol. 8, no. 6, pp. e66714, 2013. Cross Ref Google Scholar

[23]. R. Kinoshita, M. Iwadate, H. Umeyama and Y. H. Taguchi, "Genes associated with genotype-specific DNA methylation in squamous cell carcinoma as candidate drug targets", BMC Syst Biol, vol. 8, no. Suppl 1, pp. S4, 2014. Cross Ref Google Scholar

[24]. S. Ishida, H. Umeyama, M. Iwadate and Y. H. Taguchi, "Bioinformatic Screening of Autoimmune Disease Genes and Protein Structure Prediction with FAMS for Drug Discovery", Protein Pept. Lett., vol. 21, no. 8, pp. 828-39, 2014. Cross Ref Google Scholar

[25]. Y. H. Taguchi and A. Okamoto, "Principal component analysis for bacterial proteomic analysis" in Pattern Recognition in Bioinformatics ser. LNCS, Heidelberg:Springer InternationalPublishing, vol. 7632, pp. 141-152, 2012CrossRef Google Scholar

[26]. Y. Benjamini and Y. Hochberg, "Controlling the false discovery rate: A practical and powerful approach to multiple testing", Journal of the Royal Statistical Society. Series B (Methodological), vol. 57, no. 1, pp. 289-300, 1995.Cross Ref Google Scholar

[27]. S. D. Hsu, F. M. Lin, W. Y. Wu, C. Liang, W. C. Huang, W. L. Chan, et al., "miRTarBase: a database curates experimentally validated microRNA-target interactions", Nucleic Acids Res., vol. 39, pp. D163-169, Jan 2011.Cross Ref Google Scholar

[28]. Y. A. DeClerck, E. Bogenmann and P. A. Jones, "Collagen synthesis by short-term explants of pediatric tumors", Cancer Res.,

vol. 45, no. 3, pp. 1229-1238, Mar 1985.Google Scholar

[29]. J. H. Pinthus, Y. Sheffer, A. Nagler, E. Fridman, Y. Mor, O. Genina, et al., "Inhibition of Wilms tumor xenograft progression by halofuginone is accompanied by activation of WT-1 gene expression", J. Urol., vol. 174, no. 4, pp. 1527-1531, Oct 2005 (IRJAEH)