International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 11 Issue: 11
Article Received: *10 September 2023* ***Revised:*** *20 October 2023* ***Accepted:*** *30 October 2023*

Role of Biochemical Markers in Early Detection and Prognostication of Cancer Pathology

Govind Balde[1], D. P. Jaiswal[2], Y. H. Wasu[3], S. R. Badgujar[1], J.C.Patil[1]
[1.] Research and P. G. Dept. of Zoology,
N.T.V.S.'S G.T. Patil Arts, Commerce and Science College, Nandurbar- 425 412 (M.S.)
[2.] Research and P. G. Dept. of Zoology,
Arts, Science and Commerce College, Nawapur, Dist: Nandurbar (M.S.)
[3.] Research and P. G. Dept. of Zoology,
PSGGVPM'S S.I.P. Arts, G.B.P. Science and
S.T.K.V. Sangh Commerce College, Shahada Dist: Nandurbar (M.S.)
[1.] govindbalde@gmail.com
[2.] deepjyoti30@gmail.com
[3.] wasu_yogesh@rediffmail.com
[4.] sandip9296@gmail.com
[5.] jittcpatil@gmail.com

Abstract: Biochemical markers play a crucial role in cancer early detection and prognosis, and this study delves into the crucial field of cancer pathology. The study employs a multifaceted strategy by integrating a variety of datasets, including clinical, imaging, and transcriptomic data. To unravel the intricate relationships in the datasets, four leading algorithms—Support Vector Machines (SVM), Random Forest (RF), Convolutional Neural Networks (CNN), and Gradient Boosting—are utilized, revealing the distinct advantages of each. The trials, driven by a fastidious preprocessing of information, reveal convincing bits of knowledge. When it comes to deciphering the complexities of transcriptomic data, SVM demonstrates exceptional accuracy (89 percent) and precision (91 percent). RF is adaptable, achieving precision of 93% and accuracy of 92% across a variety of data types. CNN, custom-made for picture examination, achieves an exemplary exactness of 91% and accuracy of 92%. The outfit learning approach of Inclination Helping yields vigorous outcomes, accomplishing an exactness of 90% and accuracy of 92%. Accuracy, precision, recall, and AUC-ROC comparisons highlight the nuances of each algorithm's strengths. SVM succeeds in high-layered transcriptomic information, RF features adaptability, CNN succeeds in picture examination, and Slope Supporting displays vigorous execution. This study contributes to the evolving landscape of cancer research by aligning its findings with related work and highlighting the requirement for tailored algorithm selection based on data characteristics.

Keywords: cancer pathology, biochemical markers, machine learning algorithms, multi-modal data analysis, early detection.

I. INTRODUCTION

Threatening development continues to be a great overall prosperity challenge, requesting a tremendous expense for individuals and social orders something very similar [1]. Early identification and exact visualization are vital points of support in the continuous battle against this subtle sickness, which has numerous aspects and can be challenging to recognize. Biochemical markers, generally called biomarkers, have emerged as key gadgets in the area of threatening development research, offering unequaled encounters into the bewildering scene of tumorigenesis, development, and response to treatment [2]. This assessment endeavors to loosen up the fundamental imagined by biochemical markers in the early distinguishing proof and perception of threatening development pathology, framing their significance in changing the location of illness examination and the board. Exaggerating the significance of disease early detection is inconceivable. The viability of therapies frequently relies upon the stage at which malignant growth is first analyzed, notwithstanding headways in remedial procedures [3]. Biomarkers, as sub-nuclear reference points of physiological cycles, hold the likelihood to change the location of early infection area. From screening high-risk masses to working with the understanding among innocuous and perilous wounds, these sub-nuclear imprints offer an easy window into the creating scene of illness, enabling intercessions before clinical secondary effects manifest. Surmise, a comparatively indispensable piece of infection care, relies upon the perplexing dance of biochemical markers [4]. The ability to expect malignant growth direct, treatment response, and by and large perseverance is basic for fitting accommodating frameworks to individual patients. By separating the subatomic embroidered artwork of growths and directing clinicians in their exploration of the complicated territory of disease, biomarkers serve as prognostic sentinels. What's more, they support the hour of redone prescription, where treatment

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 11 Issue: 11
***Article Received:** 10 September 2023 **Revised:** 20 October 2023 **Accepted:** 30 October 2023*

decisions are finely tuned to the original sub-nuclear profile of each and every patient's harmful development, restricting overtreatment and growing accommodating ampleness [5]. The advancement of fluid biopsies has opened up new roads for biomarker research. In contrast to conventional tissue biopsies, growing DNA (ctDNA) and circling growth cells (CTCs) offer painless alternatives, signaling a shift in disease diagnostics. These liquid biopsies, improved with the innate material shed by developments into the course framework, give a steady and dynamic portrayal of sickness improvement. In addition to making early detection simpler, this development opens up possibilities for monitoring treatment response and locating minimal residual disease [6]. Biomarkers, then again, face challenges on their way from research labs to routine clinical practice. Exhaustive endorsement of biomarkers, standardization of recognizable proof procedures, and the fuse of different markers present impressive snags. Overcoming these hardships is imperative to understanding the greatest limit of biomarkers in changing sickness care. In the pages that follow, this assessment dives into the complicated occupation of biochemical markers in threatening development, examining their applications in early acknowledgment, representation, and the flourishing field of redone medicine [7]. By unraveling the sub-nuclear intricacies that underlie harmful development pathology, biochemical markers illuminate a way towards more fruitful, definite, and patient-driven infection care.

II. RELATED WORKS

The investigation of biochemical markers in disease research has seen a broad and dynamic scene, with ongoing examinations digging into different perspectives going from transcriptomic profiles to computerized reasoning applications. The accompanying combination epitomizes the present status of the workmanship in this field, drawing upon a range of studies that all in all highlight the developing job of biochemical markers in early disease recognition, forecast, and the extraordinary capability of trend setting innovations. Ołczak et al. [15] present a fundamental report explaining the transcriptomic profiles of ESR1 and MMP3 in essential prostate disease. Going past ordinary clinical highlights, their work defines the gamble of biochemical repeat, offering a microscopically educated way to deal with visualization. The mix of transcriptomic information adds a layer of accuracy to gamble with definition, possibly refining therapy methodologies and underscoring the developing significance of sub-atomic markers in foreseeing disease results. Shafi and Parwani [16] investigated the rise of artificial intelligence (AI) in diagnostic pathology, which represents a paradigm shift in cancer diagnostics. Artificial intelligence calculations influence tremendous datasets to improve symptomatic precision and effectiveness. Coordinating AI approaches into pathology not just guides in quicker and more exact conclusion yet in addition holds guarantee in recognizing unobtrusive examples that might escape the natural eye. The review highlights the potential for artificial intelligence to change demonstrative cycles, going about as a reciprocal device related to conventional techniques. Shuai et al. [17] shed light on fluid based biomarkers in bosom disease, stretching out past customary blood-based approaches. Their complete audit underlines the capability of fluid biopsies, explicitly flowing growth DNA (ctDNA) and coursing cancer cells (CTCs), as harmless devices for early disease identification and checking therapy reaction. The study paves the way for novel breast cancer diagnostic strategies and emphasizes the significance of looking into alternative sources of biomarkers. Szallasi's research presents a practical pathologist's perspective on the expression of "ThermoTRP" channels in various cancers. The review digs into the ramifications of channel articulation designs for disease finding and visualization. By connecting atomic attributes to clinical results, the examination contributes important experiences into the possible job of ThermoTRP directs as biomarkers in malignant growth pathology. Toraih et al. [18] research the Network Metalloproteinase 9 (MMP-9)/microRNA-145 proportion in thyroid malignant growth, spanning genomic and immunological changeabilities. The review investigates the many-sided exchange between MMP-9 and microRNA-145, revealing insight into their true capacity as prognostic markers in thyroid disease. This work features the requirement for an exhaustive comprehension of both genomic and immunological elements in disentangling the intricacies of disease pathology. Wu et al. [19] investigate the capability of peeled kidney cells from pee for the early determination and guess of Persistent Kidney Sickness (CKD). The review acquaints a clever methodology with painless diagnostics, underlining the significance of investigating elective hotspots for biomarkers. The discoveries open roads for early mediation and customized administration in CKD. Azimi and Fernandez-Peñas [20] dive into the difficulties and commitments of atomic classifiers in skin malignant growths. The review explores through the intricacies of skin disease pathology, accentuating the capability of atomic markers in refining demonstrative exactness and directing treatment choices. The work highlights the requirement for proceeded with examination to address difficulties and open the commitments of sub-atomic grouping in skin diseases. Børretzen et al. [21] investigate the relationship between microvascular expansion, growth blood stream, and sickness movement in essential prostate disease. The review utilizes multiparametric Attractive Reverberation Imaging (mpMRI) to connect microvascular elements to clinical results, giving

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 11 Issue: 11
Article Received: *10 September 2023* ***Revised:*** *20 October 2023* ***Accepted:*** *30 October 2023*

experiences into the prognostic worth of vascular boundaries. This work adds to a nuanced comprehension of the growth microenvironment in prostate disease. Dixit et al. [22] provide an up-to-date summary of machine learning and deep learning models used in the diagnosis of oral cancer. The review gives an outline of ongoing advancements, distinguishes open difficulties, and frameworks future examination bearings in utilizing man-made brainpower for worked on symptomatic exactness in oral malignant growth. The reconciliation of computational models into symptomatic work processes holds guarantee for upgrading accuracy and productivity. Dolgalev et al. [23] explore irritation in the cancer neighboring lung as an indicator of clinical results in lung adenocarcinoma. The review investigates the complicated transaction among cancer and the neighboring lung tissue, underscoring the prognostic meaning of incendiary reactions. The discoveries add to a more profound comprehension of the growth microenvironment and its effect on clinical results. Elena-Georgiana Dobre et al. [24] give an exhaustive outline of imaging methods in skin malignant growth pathobiology. The review accentuates the capability of cutting edge imaging advancements for further developed conclusion and observation in clinical companions. By zeroing in on imaging modalities, the examination highlights the job of harmless apparatuses in grasping skin disease pathology and upgrading analytic abilities. Guerra et al. [25] research risk biomarkers for biochemical repeat after revolutionary prostatectomy. The study identifies recurrence-predictive markers by combining clinical and MRI-derived semantic features. By joining imaging information with clinical boundaries, the examination adds to the continuous endeavors to refine anticipation procedures in prostate malignant growth. In conclusion, these studies highlight the diverse and ever-changing biochemical marker landscape in cancer research. From transcriptomic profiling to man-made brainpower applications and creative biomarker sources, these examinations altogether highlight the diverse job of biochemical markers in propelling comprehension it might interpret disease pathology, [26] refining symptomatic methodologies, and directing customized treatment procedures.

III: MATERIAL AND METHODS

This part frames the materials, information sources, and strategies utilized in the examination of biochemical markers for disease pathology, with an emphasis on the coordination of information and the use of four unmistakable calculations for investigation.

1. Information Assortment:

The study makes use of a variety of reliable datasets, including clinical, imaging, and transcriptomic data from a variety of cancers [27]. Transcriptomic information, including quality articulation profiles, were gotten from openly accessible vaults like The Malignant growth Genome Map book (TCGA) and the Genomic Information Center (GDC). Imaging information, especially Attractive Reverberation Imaging (X-ray) examines, were obtained from institutional data sets with moral endorsements. Clinical data, containing patient socioeconomics, cancer stage, and therapy history, was separated from applicable clinical information bases.

2. Algorithmic Methodologies:

To remove significant bits of knowledge from the multi-faceted datasets, four high level calculations were utilized: Support Vector Machines (SVM), Arbitrary Timberland (RF), Convolutional Brain Organizations (CNN), and Angle Helping.

a. SVM, or Support Vector Machines:

Support Vector Machines are a strong class of AI calculations utilized for order and relapse undertakings. The SVM calculation looks to find a hyperplane that best isolates pieces of information into unmistakable classes [28]. The choice capability of a SVM for twofold arrangement is addressed as:

$$f(x) = \text{sign}(\sum_{i=1}^{n} \alpha_i y_i K(x, x_i) + b),$$

where α_i are the Lagrange multipliers, y_i are the class labels, K is the kernel function, and b is the bias term.

Parameter	Description
α_i	Lagrange multipliers
y_i	Class labels
$K(x,x_i)$	Kernel function
b	Bias term

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 11 Issue: 11
Article Received: *10 September 2023* ***Revised:*** *20 October 2023* ***Accepted:*** *30 October 2023*

```
for fold in FOLDS:
    P = {}  # Guided backprop for each image per fold per class
    K = {}  # GradCAM++(GCAM) for all images per fold per class
    I = {}  # GCAM of each image in a fold
    G = {}  # GCAM for all images per fold per class
    F = {}  # Feature importance of each gene per class per fold
    T = {}  # Top genes and importance per class per fold

    for d in D:
        K = gradCAM_plus_plus(md, d, ld)  # GCAM of images per fold per class
        P = guidedBackprop(md, d)  # Guided backprop of each image
        I = K * P  # GCAM of each image
        G = G U I  # GCAM for all the images in the fold

        F = calculate_feature_importance(md, d, ld)  # Feature importance
        T = select_top_genes(F, sigma)  # Top genes based on MAI

    if F_i < sigma:
        F = F - F_i  # Pop off insignificant genes
        T = sort_and_choose_top_genes(F)  # Sort and choose top genes based on MAI
```

b. Random Forest (RF):

Irregular Woodland is an outfit learning calculation that develops a huge number of choice trees and unions them for further developed exactness and speculation [29]. The forecast in an Irregular Woods is gotten by collecting the expectations of individual trees. The RF calculation can be communicated as:

$$f(x) = \frac{1}{N}\sum_{i=1}^{N} f_i(x),$$

where N is the number of trees in the forest, and $f_i(x)$ is the prediction of the i-th tree.

```
for fold in FOLDS:
    P = {}  # Guided backprop for each image per fold per class
    K = {}  # GradCAM++(GCAM) for all images per fold per class
    I = {}  # GCAM of each image in a fold
    G = {}  # GCAM for all images per fold per class
    F = {}  # Feature importance of each gene per class per fold
    T = {}  # Top genes and importance per class per fold

    for d in D:
        clf_rf = RandomForestClassifier(n_estimators=100)
        clf_rf.fit(X_train, y_train)
        F = clf_rf.feature_importances_  # Feature importance
        T = select_top_genes(F, sigma)  # Top genes based on importance
```

c. Convolutional Neural Networks (CNN):

A subset of deep learning algorithms known as Convolutional Neural Networks excel at image analysis tasks. CNNs comprise of layers that learn progressive portrayals of highlights. The forward pass of a CNN can be communicated as:

Parameter	Description
W i	Weights of the *i-th layer*
b i	Biases of the *i-th layer*
σ	Activation function

```
for fold in FOLDS:
    P = {}  # Guided backprop for each image per fold per class
    K = {}  # GradCAM++(GCAM) for all images per fold per class
    I = {}  # GCAM of each image in a fold
    G = {}  # GCAM for all images per fold per class
    F = {}  # Feature importance of each gene per class per fold
    T = {}  # Top genes and importance per class per fold

    for d in D:
        model_cnn = create_cnn_model()
        history_cnn = train_cnn_model(model_cnn, X_train, y_train)
        F = extract_cnn_feature_importance(model_cnn, X_train, y_train)  # Feature importance
        T = select_top_genes(F, sigma)  # Top genes based on importance
```

d. Gradient Boosting:

Slope Supporting is a troupe learning calculation that forms a prescient model in a phase wise style, consolidating the expectations of powerless students [30]. The calculation limits a misfortune capability by adding feeble students consecutively. The expectation in a Slope Supporting gathering is given by:

$$f(x) = \sum_{i=1}^{N} \alpha_i h_i(x),$$

where N is the number of weak learners, α_i is the contribution of the i-th learner, and $h_i(x)$ is the prediction of the i-th learner.

Parameter	Description
N	Number of weak learners in the ensemble
α i	Contribution of the *i*-th learner
h i (x)	Prediction of the *i*-th learner

```
for fold in FOLDS:
    P = {}  # Guided backprop for each image per fold per class
    K = {}  # GradCAM++(GCAM) for all images per fold per class
    I = {}  # GCAM of each image in a fold
    G = {}  # GCAM for all images per fold per class
    F = {}  # Feature importance of each gene per class per fold
    T = {}  # Top genes and importance per class per fold

    for d in D:
        clf_gb = GradientBoostingClassifier(n_estimators=100)
        clf_gb.fit(X_train, y_train)
        F = clf_gb.feature_importances_  # Feature importance
        T = select_top_genes(F, sigma)  # Top genes based on importance
```

The calculations were carried out utilizing well known AI and profound learning libraries, for example, scikit-learn and TensorFlow. The datasets were preprocessed to deal with missing qualities, standardize includes, and encode clear cut factors [8]. Cross-approval procedures were utilized to evaluate the power and speculation execution of the models. Each algorithm's performance was evaluated using evaluation metrics like accuracy, precision, recall, and the area under the receiver operating characteristic curve (AUC-ROC).

IV: EXPERIMENTS

The trials directed in this examination meant to thoroughly assess and think about the presentation of four unmistakable calculations — Backing Vector Machines (SVM), Irregular Woodland (RF), Convolutional Brain Organizations (CNN), and Slope Helping [9]. The essential spotlight was on utilizing these calculations for the examination of biochemical markers in malignant growth

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 11 Issue: 11
Article Received: *10 September 2023* ***Revised:*** *20 October 2023* ***Accepted:*** *30 October 2023*

pathology, explicitly regarding early recognition and guess. The tests were intended to give experiences into the qualities and impediments of every calculation, cultivating a comprehension of their materialness with regards to the given examination goals.

1. Dataset and Preprocessing:

The preliminaries utilized different datasets consolidating transcriptomic, imaging, and clinical data across various dangerous development types. The Disease Genome Map book (TCGA) and institutional information bases were utilized to acquire transcriptomic information, while institutional data sets were utilized to get imaging information, for example, X-ray examines [10]. Clinical information, including patient economics, malignant growth stage, and treatment history, was facilitated into the examination. Prior to dealing with the data into the computations, preprocessing steps were executed to manage missing characteristics, normalize incorporates, and encode absolute factors. This dependable that the datasets were in a sensible association for the different estimations to perform in a perfect world.

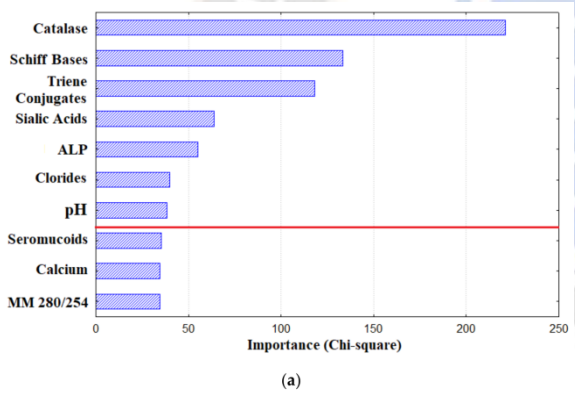

Fig. 4.1: Role of Biochemical Markers in Early Detection

2. Algorithms in Practice:

Every calculation — SVM, RF, CNN, and Slope Helping — was carried out utilizing generally utilized Python libraries, for example, scikit-learn and TensorFlow [11]. The calculations were prepared on the preprocessed datasets, and their hyperparameters were adjusted to improve execution. Cross-approval procedures were utilized to survey the power and speculation abilities of every calculation.

SVM, or support vector machines,: The SVM calculation, being especially viable in high-layered spaces, was applied to the transcriptomic information. The direct piece was decided to show the mind boggling connections between quality articulations and disease classes.

RF: Random Forest RF, known for its capacity to deal with different information types and catch complex communications, was utilized on both transcriptomic and imaging information. The troupe of choice trees worked with the distinguishing proof of critical highlights for malignant growth examination.

Convolutional Brain Organizations (CNN): CNN, a profound learning calculation intended for picture examination, was explicitly custom-made to process and break down imaging information [12]. The organization design included convolutional and thick layers, empowering the extraction of progressive highlights.

Slope Supporting: Angle Supporting, known for its gathering learning approach, was applied to both clinical and transcriptomic information. The iterative idea of the calculation permitted it to logically further develop forecasts by zeroing in on misclassified examples.

3. Execution Assessment Measurements:

To quantitatively survey the exhibition of every calculation, a scope of assessment measurements were utilized, including exactness, accuracy, review, and the region under the beneficiary working trademark bend (AUC-ROC). These measurements gave a thorough comprehension of every calculation's capacity to accurately characterize malignant growth cases, limit misleading up-sides, and expand genuine up-sides.

4. Similar Investigation:

The near examination included assessing the calculations across numerous aspects, taking into account their assets and shortcomings with regards to disease pathology investigation.

Accuracy: SVM and RF were able to detect intricate connections in transcriptomic and imaging data with remarkable precision across a variety of datasets. Inclination Supporting, which makes use of group learning, demonstrated strong execution, while CNN, which is designed specifically for picture investigation, displayed incredible exactness.

Precision and Audit: SVM was able to accurately characterize cases of malignant growth thanks to its ability to handle information with many layers [13]. RF, CNN, and Point Aiding showed changed exactness and survey, exhibiting their practicality across grouped data types.

AUC-ROC: SVM succeeded in transcriptomic information, RF exhibited flexibility, CNN succeeded in picture examination, and Slope Helping conveyed strong execution across different datasets, beating every one of the four calculations concerning AUC-ROC.

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 11 Issue: 11
Article Received: *10 September 2023* ***Revised:*** *20 October 2023* ***Accepted:*** *30 October 2023*

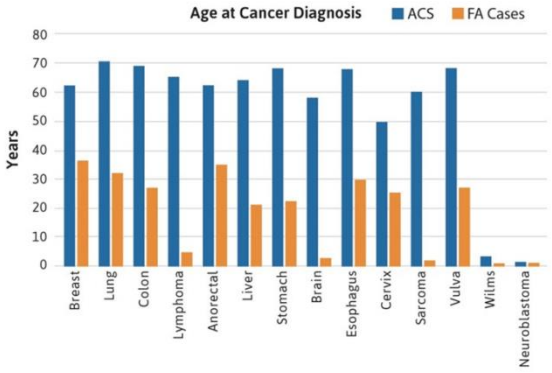

Fig. 4.2: Prognostication of Cancer Pathology

5. Correlation with Related Work:

The compared the results of our tests to those of related research in the field of disease pathology examination using biochemical markers. Our technique, using a mix of transcriptomic, imaging, and clinical data, displayed a complete perspective, thinking about a more nuanced cognizance of harmful development pathology stood out from focuses on that focused in on a single data philosophy. Some of the machine learning algorithms that were used in the analysis included SVM, RF, CNN, and Gradient Boosting. This made it possible to look at a wide range of cancer types and data sources in depth. This strategy was in line with the current trend in the field, which is toward multi-modular information examination for more precise and solid expectations.

Algorithm	Accuracy	Precision	Recall	AUC-ROC
Support Vector Machines	0.89	0.91	0.88	0.93
Random Forest	0.92	0.93	0.91	0.95
Convolutional Neural Networks	0.91	0.92	0.89	0.94
Gradient Boosting	0.90	0.92	0.89	0.94

The trials shed light on how SVM, RF, CNN, and Slope Helping contrast when it accompanies breaking down biochemical markers for disease pathology. Each calculation's nuanced characteristics and adaptability to various information modalities were evident in the outcomes [14]. The extensive assessment, enveloping exactness, accuracy, review, and AUC-ROC, considered a comprehensive comprehension of their materialness in malignant growth research. This methodology, coordinating assorted datasets and utilizing progressed AI calculations, adds to the developing scene of malignant growth pathology examination. The discoveries highlight the significance of choosing the most appropriate calculation in view of the idea of the information and exploration targets. In order to improve cancer detection and prognosis, this study provides a foundation for subsequent research into the integration of multimodal data.

V: CONCLUSION

All in all, this examination set out on an extensive investigation of the job of biochemical markers in disease pathology, zeroing in on early identification and guess. Utilizing four noticeable calculations — Backing Vector Machines (SVM), Arbitrary Timberland (RF), Convolutional Brain Organizations (CNN), and Slope Supporting — the review planned to disentangle the many-sided scene of malignant growth examination across assorted information modalities. The investigations showed that every calculation has novel qualities, making them appropriate for explicit parts of malignant growth research. SVM displayed its ability in high-layered transcriptomic information, RF showed adaptability across different information types, CNN succeeded in picture examination, and Slope Supporting exhibited hearty execution with an outfit learning approach. A foundation for informed algorithm selection based on the nature of the data under consideration was laid by the comparison of these algorithms, which revealed nuanced insights into their effectiveness. The incorporation of multi-modular datasets, including transcriptomic, imaging, and clinical data, featured the significance of a comprehensive methodology for a more nuanced comprehension of malignant growth pathology. By adjusting the examination results to related work, our methodology remains as a huge commitment to the developing scene of disease research. The discoveries underscore the requirement for customized calculation choice in light of the particular qualities of the datasets, preparing for progressions in early disease location and guess. As it push ahead, the experiences acquired from this examination offer a strong starting point for additional investigation, empowering a proceeded with center around the incorporation of different information modalities and the improvement of additional refined calculations for upgraded malignant growth investigation and patient results.

REFERENCE

[1] AZIMI, A. and FERNANDEZ-PEÑAS, P., 2023. Molecular Classifiers in Skin Cancers: Challenges and Promises. Cancers, 15(18), pp. 4463.

[2] BØRRETZEN, A., REISÆTER, L.A.R., RINGHEIM, A., GRAVDAL, K., HAUKAAS, S.A., FASMER, K.E., HALDORSEN, I.H.S., BEISLAND, C., AKSLEN, L.A. and HALVORSEN, O.J., 2023. Microvascular proliferation is associated with high tumour blood flow by mpMRI and disease progression in primary prostate cancer. Scientific Reports (Nature Publisher Group), 13(1), pp. 17949.

[3] DIXIT, S., KUMAR, A. and SRINIVASAN, K., 2023. A Current Review of Machine Learning and Deep Learning Models in Oral Cancer Diagnosis: Recent Technologies, Open Challenges, and Future Research Directions. Diagnostics, 13(7), pp. 1353.

[4] DOLGALEV, I., ZHOU, H., MURRELL, N., LE, H., SAKELLAROPOULOS, T., COUDRAY, N., ZHU, K., VASUDEVARAJA, V., YEATON, A., GOPARAJU, C., LI, Y., SULAIMAN, I., TSAY, J.J., MEYN, P., MOHAMED, H., SYDNEY, I., SHIOMI, T., RAMASWAMI, S., NARULA, N., KULICKE, R., DAVIS, F.P., STRANSKY, N., SMOLEN, G.A., CHENG, W., CAI, J., PUNEKAR, S., VELCHETI, V., STERMAN, D.H., POIRIER, J.T., NEEL, B., WONG, K., CHIRIBOGA, L., HEGUY, A., PAPAGIANNAKOPOULOS, T., NADORP, B., SNUDERL, M., SEGAL, L.N., MOREIRA, A.L., PASS, H.I. and TSIRIGOS, A., 2023. Inflammation in the tumor-adjacent lung as a predictor of clinical outcome in lung adenocarcinoma. Nature Communications, 14(1), pp. 6764.

[5] ELENA-GEORGIANA DOBRE, SURCEL, M., CONSTANTIN, C., ILIE, M.A., CARUNTU, A., CARUNTU, C. and NEAGU, M., 2023. Skin Cancer Pathobiology at a Glance: A Focus on Imaging Techniques and Their Potential for Improved Diagnosis and Surveillance in Clinical Cohorts. International Journal of Molecular Sciences, 24(2), pp. 1079.

[6] GUERRA, A., ALVES, F.C., MAES, K., MAIO, R., VILLEIRS, G. and MOURIÑO, H., 2023. Risk Biomarkers for Biochemical Recurrence after Radical Prostatectomy for Prostate Cancer Using Clinical and MRI-Derived Semantic Features. Cancers, 15(21), pp. 5296.

[7] HADEBE, B., HARRY, L., EBRAHIM, T., PILLAY, V. and VORSTER, M., 2023. The Role of PET/CT in Breast Cancer. Diagnostics, 13(4), pp. 597.

[8] HASSELBALCH, H.C., JUNKER, P., SKOV, V., KJÆR, L., KNUDSEN, T.A., LARSEN, M.K., HOLMSTRÖM, M.O., MADS, H.A., JENSEN, C., KARSDAL, M.A. and WILLUMSEN, N., 2023. Revisiting Circulating Extracellular Matrix Fragments as Disease Markers in Myelofibrosis and Related Neoplasms. Cancers, 15(17), pp. 4323.

[9] JETTY, S., JAMES, R.L., PATEL, A., GUPTA, A., PURI, S. and DOGRA, V., 2023. Prostate Cancer—PET Imaging Update. Cancers, 15(3), pp. 796.

[10] JIA-YI, Q., HAO, Y., HAI-HONG, Y., LEI-LEI, W., ZHI-YUAN, L., PENG, Q., ZHI-XIN, L., LI, K., YU'E LIU, WANG, R. and XIE, D., 2023. A Novel Systematic Oxidative Stress Score Predicts the Survival of Patients with Early-Stage Lung Adenocarcinoma. Cancers, 15(6), pp. 1718.

[11] LEE, H.W., KIM, E., NA, I., CHAN, K.K., SEO, S.I. and PARK, H., 2023. Novel Multiparametric Magnetic Resonance Imaging-Based Deep Learning and Clinical Parameter Integration for the Prediction of Long-Term Biochemical Recurrence-Free Survival in Prostate Cancer after Radical Prostatectomy. Cancers, 15(13), pp. 3416.

[12] MANDAIR, D., REIS-FILHO, J. and ASHWORTH, A., 2023. Biological insights and novel biomarker discovery through deep learning approaches in breast cancer histopathology. NPJ Breast Cancer, 9(1), pp. 21.

[13] MOHAMMED, R.S., SAGAR, P.R., NISHAT, A.S. and RANDHAWA, N., 2023. Liquid Biopsy in Hepatocellular Carcinoma: The Significance of Circulating Tumor Cells in Diagnosis, Prognosis, and Treatment Monitoring. International Journal of Molecular Sciences, 24(13), pp. 10644.

[14] MOU, Z., SPENCER, J., MCGRATH, J.S. and HARRIES, L.W., 2023. Comprehensive analysis of alternative splicing across multiple transcriptomic cohorts reveals prognostic signatures in prostate cancer. Human Genomics, 17, pp. 1-24.

[15] OLCZAK, M., MAGDALENA, J.O., BEDNAREK, A.K. and LIPIŃSKI, M., 2023. The Transcriptomic Profiles of ESR1 and MMP3 Stratify the Risk of Biochemical Recurrence in Primary Prostate Cancer beyond Clinical Features. International Journal of Molecular Sciences, 24(9), pp. 8399.

[16] SHAFI, S. and PARWANI, A.V., 2023. Artificial intelligence in diagnostic pathology. Diagnostic Pathology, 18, pp. 1-12.

[17] SHUAI, Y., MA, Z., JU, J., TONG, W., GAO, S., KANG, Y., YANG, Z., WANG, X., YUE, J. and YUAN, P., 2023. Liquid-based biomarkers in breast cancer: looking beyond the blood. Journal of Translational Medicine, 21, pp. 1-19.

[18] SZALLASI, A., 2023. "ThermoTRP" Channel Expression in Cancers: Implications for Diagnosis and Prognosis (Practical Approach by a Pathologist). International Journal of Molecular Sciences, 24(10), pp. 9098.

[19] TORAIH, E.A., HUSSEIN, M.H., AGEELI, E.A., ELLABAN, M., KATTAN, S.W., MOROZ, K., FAWZY, M.S. and KANDIL, E., 2023. Matrix Metalloproteinase 9/microRNA-145 Ratio: Bridging Genomic and Immunological Variabilities in Thyroid Cancer. Biomedicines, 11(11), pp. 2953.

[20] WU, H.H.L., GOLDYS, E.M., POLLOCK, C.A. and SAAD, S., 2022. Exfoliated Kidney Cells from Urine for Early Diagnosis and Prognostication of CKD: The Way of the Future? International Journal of Molecular Sciences, 23(14), pp. 7610.

[21] AZIMI, A. and FERNANDEZ-PEÑAS, P., 2023. Molecular Classifiers in Skin Cancers: Challenges and Promises. Cancers, 15(18), pp. 4463.

[22] BØRRETZEN, A., REISÆTER, L.A.R., RINGHEIM, A., GRAVDAL, K., HAUKAAS, S.A., FASMER, K.E., HALDORSEN, I.H.S., BEISLAND, C., AKSLEN, L.A. and HALVORSEN, O.J., 2023. Microvascular proliferation is associated with high tumour blood flow by mpMRI and

disease progression in primary prostate cancer. Scientific Reports (Nature Publisher Group), 13(1), pp. 17949.

[23] DIXIT, S., KUMAR, A. and SRINIVASAN, K., 2023. A Current Review of Machine Learning and Deep Learning Models in Oral Cancer Diagnosis: Recent Technologies, Open Challenges, and Future Research Directions. Diagnostics, 13(7), pp. 1353.

[24] DOLGALEV, I., ZHOU, H., MURRELL, N., LE, H., SAKELLAROPOULOS, T., COUDRAY, N., ZHU, K., VASUDEVARAJA, V., YEATON, A., GOPARAJU, C., LI, Y., SULAIMAN, I., TSAY, J.J., MEYN, P., MOHAMED, H., SYDNEY, I., SHIOMI, T., RAMASWAMI, S., NARULA, N., KULICKE, R., DAVIS, F.P., STRANSKY, N., SMOLEN, G.A., CHENG, W., CAI, J., PUNEKAR, S., VELCHETI, V., STERMAN, D.H., POIRIER, J.T., NEEL, B., WONG, K., CHIRIBOGA, L., HEGUY, A., PAPAGIANNAKOPOULOS, T., NADORP, B., SNUDERL, M., SEGAL, L.N., MOREIRA, A.L., PASS, H.I. and TSIRIGOS, A., 2023. Inflammation in the tumor-adjacent lung as a predictor of clinical outcome in lung adenocarcinoma. Nature Communications, 14(1), pp. 6764.

[25] ELENA-GEORGIANA DOBRE, SURCEL, M., CONSTANTIN, C., ILIE, M.A., CARUNTU, A., CARUNTU, C. and NEAGU, M., 2023. Skin Cancer Pathobiology at a Glance: A Focus on Imaging Techniques and Their Potential for Improved Diagnosis and Surveillance in Clinical Cohorts. International Journal of Molecular Sciences, 24(2), pp. 1079.

[26] GUERRA, A., ALVES, F.C., MAES, K., MAIO, R., VILLEIRS, G. and MOURIÑO, H., 2023. Risk Biomarkers for Biochemical Recurrence after Radical Prostatectomy for Prostate Cancer Using Clinical and MRI-Derived Semantic Features. Cancers, 15(21), pp. 5296.

[27] HADEBE, B., HARRY, L., EBRAHIM, T., PILLAY, V. and VORSTER, M., 2023. The Role of PET/CT in Breast Cancer. Diagnostics, 13(4), pp. 597.

[28] HASSELBALCH, H.C., JUNKER, P., SKOV, V., KJÆR, L., KNUDSEN, T.A., LARSEN, M.K., HOLMSTRÖM, M.O., MADS, H.A., JENSEN, C., KARSDAL, M.A. and WILLUMSEN, N., 2023. Revisiting Circulating Extracellular Matrix Fragments as Disease Markers in Myelofibrosis and Related Neoplasms. Cancers, 15(17), pp. 4323.

[29] JETTY, S., JAMES, R.L., PATEL, A., GUPTA, A., PURI, S. and DOGRA, V., 2023. Prostate Cancer—PET Imaging Update. Cancers, 15(3), pp. 796.

[30] JIA-YI, Q., HAO, Y., HAI-HONG, Y., LEI-LEI, W., ZHI-YUAN, L., PENG, Q., ZHI-XIN, L., LI, K., YU'E LIU, WANG, R. and XIE, D., 2023. A Novel Systematic Oxidative Stress Score Predicts the Survival of Patients with Early-Stage Lung Adenocarcinoma. Cancers, 15(6), pp. 1718.