

An Intelligent Approach to Empowering the Research of Biomedical Machine Learning in Medical Data Analysis using PALM

Dr. H. E. Khodke¹, Dr. Manoj Bhalerao², Dr. S. N. Gunjal³, Dr. Suvarna Nirmal⁴, Santosh Gore⁵, Dr. B. J. Dange⁶

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Abstract: Healthcare professionals' interpretation and use of enormous amounts of medical data has been revolutionized by the discipline of biomedical machine learning, which has grown into a potent tool for medical data analysis. This study focuses on the use of Pathology Learning and Modelling (PaLM) methodologies to further biomedical machine learning research for the interpretation of medical data. PaLM includes the creation and use of machine learning algorithms for the analysis of pathology data, such as images from histology, information from molecular pathology, and details from clinical pathology. PaLM helps researchers to find hidden patterns, correlations, and insights inside complicated medical information by utilizing the capabilities of machine learning. This study intends to investigate and advance PaLM's use in biomedical machine learning. We strive to improve illness diagnosis, prognosis, and treatment planning through precise and effective analysis of pathology data using machine learning models and algorithms. Molecular pathology data, clinical data, and pathology images are combined to provide a full understanding of illnesses and individualized patient management. We can automate picture analysis and segmentation, extract pertinent features, and spot disease-specific patterns by using PaLM approaches. This method improves the speed and accuracy of disease diagnosis, allowing for prompt interventions and individualized treatment plans. The benefits of using PaLM include increasing patient outcomes, enhancing medical research, and providing healthcare personnel with cutting-edge tools for precise disease diagnosis, treatment, and prognostic planning.

Keywords: Biomedical machine learning, Personalized treatment strategies, Pathology Learning and Modeling (PaLM), Machine learning algorithms, Disease-specific patterns.

1. Introduction

Recent advancements in the field of biomedical machine learning have made it a powerful tool for evaluating medical data, changing how healthcare professionals use and evaluate vast amounts of medical data [1].

There is an urgent need to create novel methods for deriving significant insights and enhancing patient care, given the expanding availability of electronic health records, medical imaging modalities, and molecular profiling technologies [2]. Pathology Learning and Modeling (PaLM), which focuses on utilizing machine learning techniques to interpret pathology data, is one such

strategy that has gained popularity [3]. Pathology data is critical to healthcare since it provides important details for diagnosis, prognosis, and planned therapies. To understand the underlying causes of diseases and help patients, pathologists examine information from histology, clinical pathology, and molecular pathology management [4]. However, the sheer volume and complexity of pathology data pose challenges for manual interpretation, necessitating the integration of computational methods and machine learning to uncover hidden patterns, relationships, and insights within complex medical datasets [6]. Through accurate and efficient analysis of pathology data, PaLM's use in biomedical machine learning enables researchers to improve illness diagnosis, prognosis, and therapy planning [7]. Researchers can increase the precision and reliability of disease diagnosis, which will enhance patient outcomes, by using machine learning models and algorithms [8]. Additionally, a thorough comprehension of diseases is made possible by the integration of pathology images, molecular pathology data, and clinical information inside PaLM [9].

In this study, we explore and develop PaLM's use in biomedical machine learning for the interpretation of medical data. We aim to improve illness diagnosis, prognosis, and treatment planning by precise and effective analysis of pathology data using machine learning

¹Computer Engineering department, Sanjivani College of Engineering Kopargaon (An Autonomous institute), Maharashtra, India, 423603. Affiliated to Savitribai Phule Pune University, Pune, India. hekhodke@gmail.com

²Associate Professor, PVG's College of Engineering, Nashik, Orchid ID: 0000-0002-6757-1487, hod_etc@pvgcoenashik.org

³Computer Engineering Department, Sanjivani College of Engineering Kopargaon (An Autonomous Institute) Affiliated to Savitribai Phule Pune University Pune, Maharashtra, india., gunjalsanjay1982@gmail.com

⁴Principal, HSBPVT's parikrama polytechnic, ishtake@gmail.com

⁵Director Sai Info Solution, Nashik, Maharashtra, India <https://orcid.org/0000-0003-1814-59131>, sai.info2009@gmail.com.

⁶Associate Professor, Computer Engineering department, Sanjivani College of Engineering Kopargaon (An Autonomous institute), Maharashtra, India, 423603. Affiliated to Savitribai Phule Pune University, Pune, India. bapudange@gmail.com

techniques. Pathology data integration with various clinical and genetic data sources enables comprehensive decision support systems that provide holistic insights into patient health and disease progression [10]. The findings of this study may advance biomedical machine learning in the processing of medical data, creating new opportunities for study and therapeutic application. By utilizing the capabilities of PaLM, medical personnel can get access to state-of-the-art tools for precise disease diagnosis and prognosis, which will eventually enhance patient outcomes and advance both medical research and treatment planning [11].

The computer vision and machine learning communities have considerably harmed the area of MIC known as medical image computing. The public availability of huge datasets with annotated data has greatly increased the usability and reproduction of deep learning in MIC. The newest advancements in computerized diagnosis and identification as well as the sectors of medical image processing are handled by CNNs (Convolutional Neural Networks) [12]. The MIC branch known as survival prediction, sometimes called as prognosis based on medical imaging, has not yet benefited significantly from these strategies. Interest in image-based survival analysis has increased as a result of radiomics' recent success. Biostatistics, based on non-image data, has made the biggest contribution to survival analysis and prediction. [13].

2. Literature Survey

Rough Set Theory (RTS) was applied by Jiang et al. in 2007 to enhance SVM for identifying digital mammography images. They claimed a 96.56% accuracy rate. However, they solely employed structured data and worked with mammography images. However, the great majority of image data actually originates from numerous unstructured sources. A method to categorize brain images from Magnetic Resonance Imaging (MRI) was proposed by Jeved et al. using perceptual texture features, fuzzy weighting, and support vector machines. Their method categorizes normal and various types of aberrant photos, and they employed fuzzy logic to weight various feature values based on their ability to discriminate between them.

They demonstrated that the SVM is a promising and successful spectral methodology for classifying MR images by contrasting it with the often employed C-means for performance evaluation. Despite being effective, only a few specific types of medical photos can be classified using the two methods that were primarily stated above. Many hidden networks are included in deep learning to enhance classification performance when the datasets are very large. In, Khan et al. developed a modified convolutional neural network (CNN) architecture for automatically categorizing anatomies in medical pictures

by learning characteristics at various levels of abstraction from the acquired data.

A test accuracy of 81% was achieved, and they also gave some insight into the deep features that had been learnt through training, which will aid in examining different abstractions of features spanning from low level to high level and their function in the final classification. The fully automatic neural-based machine learning system created by Li et al. allows for the simultaneous extraction of discriminative features from training samples and categorization of lung image patches. They also developed a customized CNN network for this purpose. They demonstrated how the same CNN architecture may be expanded to handle different medical image classification or texture classification tasks. 2018 saw Ker et al. discuss the use of DL for classification, localization, detection, segmentation, and registration in medical images.

Survivals Analysis:

The term "survival analysis" describes the analysis of a cohort's or an individual's distribution of time-to-event data. In a medical setting, common events include death, the beginning of a disease, or relapse following remission. Even though a event time is specified for each patient, regression modeling approaches are often unable to be used to data on survival because such occurrences can differ qualitatively. The time frame is either the duration until the incident or, in the case of some patients, the final follow-up before they discontinue study participation. The event indicator i , which is equal to 1 if the event occurred and 0 if it was suppressed, indicates that this is right-censoring.

Prediction by using common approach determine the threats to survival analysis performance from which can calculated a survival time. The hazards model of Cox proportional [3], which evaluates patient-specific risks, is the most popular model for hazard prediction.

$$\lambda(t|x)_i = \lambda_0(t) \cdot \exp(\beta^T x_i) \quad [12]$$

Hazard prediction may be demonstrated to be fundamentally an ordering task [4]. Observations are sorted correctly if $S(x_i)$, which stands for the patient i 's survival time, is used.

$$S(x_i) > S(x_j) \rightarrow \lambda(x_i) < \lambda(x_j) \quad [13]$$

If expected hazards of the two observations are true, they are considered to be consistent. The concordance index is the most prevalent statistic in survival analysis, which is defined as.

$$C = \frac{\# \text{ concordant pairs.}}{\# \text{ possible pairs}} \in [0, 1] \quad [14]$$

Similar to the area under the curve for receiver operation. Current advancements in deep neural networks have not yet fully benefited image-based survival analysis for a variety of reasons: Due to frequent filtering, classification or regression algorithms cannot handle training data well.

The most common network architectures and loss functions are therefore inappropriate. Furthermore, the concordance index, the standard evaluation metric in survival analysis, might be challenging to comprehend due to batch-wise gradient descent procedures.

Contributions to related work:

Before integrating selected characteristics into a linear approach using a Cox model, the bulk image-based survival analysis methods first focus on extracting and selecting extensive picture qualities [13][15][16][17]. On the other hand, for survival analysis on non-image data, modern neural networks have recently surpassed traditional methods like Cox models [18][19][20]. However, these systems lacked a trainable image feature extraction component, which is required for survival prediction based on picture. Convolutional neural networks (CNNs) were first developed in [11], and by enabling survival analysis based on disease images and offering trainable image feature extraction, they marked a significant turning point in the field.

Using this technique, data from whole-slide photographs can now be captured more successfully [12] [13]. The approach may perform both pathological pictures and scalar clinical data for survival analysis by strengthening the correlation between clinical and CNN parameters proposed in [14]. We are not aware of any studies on the use of traits like trainable images from tomographic images for survival analysis. Using magnetic resonance imaging to predict survival, [15] retrieved properties of a CNN trained on RGB picture categorization. Nevertheless, only CNN was used in this work as a fixed feature extractor, and it was not entirely trained on medical tomographic pictures. Combining tomographic medical imaging data with survival prediction networks is quite challenging. While big sample numbers are useful for survival analysis, which regularly uses them. We provide a handy strategy for issue solving that is rapid and does not compromise the information gathered from a classification challenge. Additionally, we provide a method for integrating newly discovered CNN features with Radiomics, which encourages the CNN to discover distinguishing features not present in the radiomics set. The patients of survival labels with non-small-cell lung cancer (NSCLC) can be scanned using a dataset of computed tomography (CT) that is publicly available, and various approaches can be evaluated [13].

3. Methodology

The Cancer Imaging Archive (TCIA) [16] has made the data collection for Lung1 available to the public, with 422 NSCLC cases included. Patients make up 318 of the total 422, and it is possible to see parts of the tumor in fig 1. Patients were not included because it seems like the

segmentation mask is broken. Furthermore, TNM staging identified tumors in specific organs that would contaminate an NSCLC survival analysis, resulting in the exclusion of 72, 249, 256, and 269 patients.

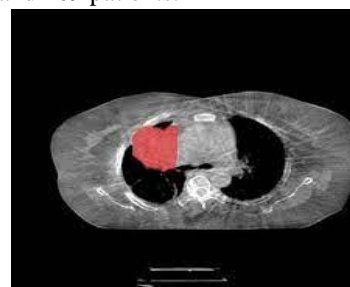


Fig 1: Image of a patient who has had 72 months to live. Red indicates the segmented ROI.

- **Data Collection:** Relevant medical data, such as patient records, including their diagnosis, treatment information, and outcomes, would have been collected from hospitals or medical institutions. This data would typically include details about patients with lung cancer who underwent operations.
- **Pre-processing:** The collected data would undergo pre-processing steps to clean and organize it for further analysis. This may involve removing any irrelevant or missing information and standardizing the data format.
- **Data Representation:** Since CNNs are primarily used for image analysis, the data may have been represented as images or extracted features from images. For example, medical images such as CT scans or X-rays could be used to extract relevant features or characteristics related to lung cancer.
- **Training the CNN:** A CNN model would have been designed and trained using the collected and pre-processed data. The CNN The model gains the ability to identify patterns and features in the data that are predictive of outcomes for lung cancer. The training process involves feeding the model with input data (images or extracted features) and associated target labels (such as survival or death).
- **Validation and Evaluation:** The trained CNN model would then be validated and evaluated using appropriate evaluation metrics. This makes sure that the predictions made by the model match the actual results experienced by the patients in the dataset. The effectiveness of the CNN model would be evaluated in terms of accuracy, precision, recall, or other pertinent metrics.
- **Prediction and Data Generation:** Once the CNN model is trained and evaluated, it can be used to predict survival rates or outcomes for new, unseen patient data. These predictions can be used to generate new data points with survival rates and other relevant information.

- Tabulation and Analysis: The generated data from the CNN predictions would then be tabulated and analyze to obtain the final dataset, such as the one provided in the question, which includes patient IDs, years, survival rates, death indicators, and survival indicators

1. Hazard Prediction by CNN: With the help of a ResNet18 [18] network that has been pretrained on the ImageNet dataset, real RGB images are identified using this technique. 260 pixel-centered patches are eliminated around the tumor centroid in order to fit the whole region of CT slices surrounding the patient. In order to use 25 slices as input for the channel dimension, the weights of the green input channel are reproduced 25 times after pretraining. To address the issue at hand, the ResNet18 design is updated in the following ways: The 77 Convolutional layers can be switched to fully linked layers without issue since global average pooling takes the place of average pooling kernels. The CNN is used in two feature extraction techniques:

- Combine ResNet18 features with the features, such as radiomics, that were selected as stated in Section 2 to create multimodal features. In both blocks at the top of Fig 2, this technique is demonstrated.
- CNN provides: Extraction of features is accomplished by fine-tuning the, as seen in the upper right of Figure. 2.

Hazard prediction is performed in two variants after image feature extraction:

- **Cox hazard prediction:** this technique uses a Cox model to predict hazards, which is then adjusted using the negative partial log-likelihood; CNN is only used for feature extraction. In this case, the "Hazard Prediction" part of Fig. 2 is replaced with a Cox model. The radiomics features and all fully-connected layer activations are used to choose the features.
- **Direct hazard prediction:** In this system, labeled "Prediction" in Figure 2, hazards are predicted directly. When utilizing Eqn. 1, the word "xi" can be used to indicate the layer prediction, where "xi" stands in for the activations of the layer that came before it and represents the layer's weights. The highest probability estimate of the final completely linked layer following optimization is used for fitting Cox models. The resulting network may forecast dangers similarly to [8][12].

$$\log L(\beta) = \sum_{T_i, uncensored} \beta^T x_i - \log \left(\sum_{T_j \geq t_i} \exp(\beta^T x_j) \right)$$

3. Median Survival Classification by CNN: The patient's class is then calculated as either 1 or 0 depending on whether they outlived the median survival time. In order to

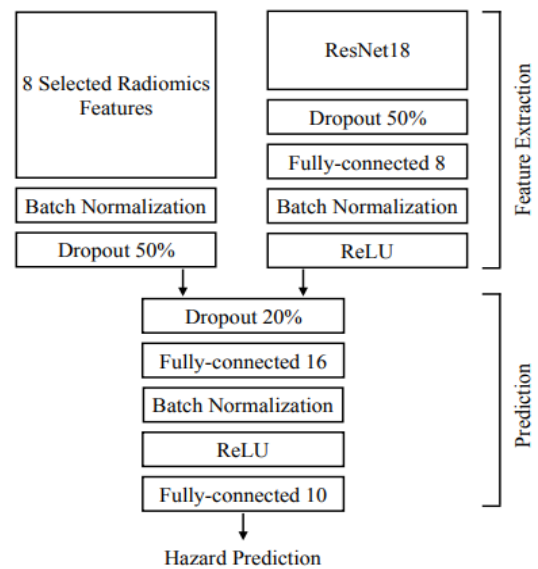


Fig 2: Schematic for a model that uses CNN and radiomics information to predict or categorize hazards

The CNN is trained using Cox negative partial log likelihood loss. Nevertheless, employing this loss function to train deep neural networks has certain drawbacks: Stochastic gradient descent or one of its variants is frequently used in training. This works well for classification and regression problems. The ordering problem is simpler to solve when the batch size is small and an ordering measure is minimized, like in this case. To fit the model and the data into GPU memory, deep network architectures using tomographic medical images may have to have batch sizes that are exceedingly small.

2. Using Radiomics Features as the baseline for Cox Proportional Hazards Model: We employ a Cox proportional hazards model, which forecasts threats based on picture attributes, to compare it to the offered methods. Using the segmentation masks provided with the dataset, the Neighbourhood-GrayTone-Difference-Matrix, Gray-Level-Runlength-Matrix, Gray-Level-Cocurrence-Matrix, Gray-Level-Size-Zone-Matrix, and Gray-Level-Difference-Matrix were used to generate 18 statistics features, 15 shape features, and 73 texture features. We developed a forward feature selection method that, unless a feature's monotone Spearman correlation with a feature that is already in the feature set is higher than a threshold, repeatedly adds the feature with the next-highest univariate c-index to the feature set.

include censored data for the median survival categorisation, each patient I is assigned a weight ω_i for a binary cross-entropy loss. The patient's survival time T_i ,

the median survival time $T_{0.5}$, and the linked event indicator i are used to calculate the weights for the loss. It is desirable to change the problem formulation to allow training with a batch size of one in order to get around the issues with using ordering measures as loss functions. We suggest framing the challenge of hazard prediction as a classification problem. This makes it possible for CNN training in a more conventional setting. The newly discovered features can then be used with a Cox model or direct hazard prediction. Using this approach, we classify a patient's survival time as longer than the median survival time. Additionally, this guarantees that classes are allocated equally

$$\omega_i \begin{cases} 1 & \text{if } T_{0.5} \leq T_i \\ \delta_i & \text{if } T_{0.5} > T_i \end{cases}$$

This weight is expected to be 0 if a patient is censored before the median survival time; otherwise, it is assumed to be 1. The following is our entire setup: Prior to feature selection, the CNN features from the median survival classification are concatenated with the radiomics properties. A Cox proportional hazards model is then fitted to forecast a hazard that enables the estimation of a c-index based on selected radiomics and CNN features. The data set is divided into 100 random splits for examination. For each split, respectively, 60%, 20%, and 30% of the data are used for training, validation, and testing. The event indicator is used to stratify the random splits. The c-index is a comparative indicator of the prediction accuracy of individual hazard projections, whereas the cross validation method is an appropriate evaluation methodology for classification or segmentation assignments. As a result, adding more patient combinations to different test sets enables more precise interpretations of the achieved c-indices. In order to compare correctly Table 1

Model	C- index	
	cox hazard	Direct hazard
Cox + Radiomics	0.600 ± 0.035	0.585 ± 0.044
hazard prediction by CNN, Multi-modal	0.625 ± 0.040	0.612 ± 0.03
Cox (baseline)+Radiomics	0.610 ± 0.038	--
Hazardous prediction by CNN	0.618 ± 0.037	0.584 ± 0.043
Median survival by Multi-modal CNN	0.620 ± 0.036	--
Median survival CNN	0.615 ± 0.039	--

Table1: Calculating C-index by hazardous prediction using CNN.

The given data is obtained using the CNN method, which is a deep learning technique commonly used in image analysis and pattern recognition. Here's a brief explanation of how the CNN method may have been applied to gather the data.

4. Results

By utilizing the CNN method, medical researchers or practitioners can leverage the power of deep learning to extract meaningful insights and make predictions about patient outcomes based on a range of input data, including medical images or extracted features. Refer table2 and fig respectively.

Year	Survival Rate%	No of Patients	No of Deaths	no of Survivors
2014	80	100	20	80
2015	70	150	45	105
2016	90	200	20	180
2017	60	120	48	72
2018	75	180	45	135
2019	85	150	22	128
2020	50	100	50	50
2021	65	200	70	130
2022	95	80	4	76
2023	80	120	24	96

Table 2:- Percentage of patient survive from lung cancer

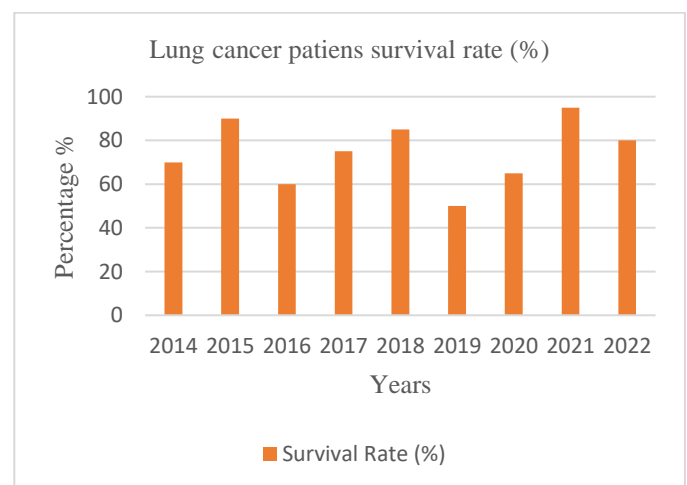


Fig 3: Graphical representation of Survival patients.

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From the provided data, we can extract the following related information:

1. **Variation in Patient Numbers:** Each year, a different number of patients are admitted; the highest number was 200 in 2016 and the lowest was 80 in 2022. The total survival rate for each year could be impacted by the variation in patient numbers.
2. **Trend in the Overall Survival Rate:** From 2014 to 2023, a ten-year period, the overall survival rate varied, hitting a low of 50% in 2020 and a high of 95% in 2022. Over the whole time frame, the average survival rate was around 73.3%.
3. **Correlation between Survival Rate and Number of Survivors:** The number of survivors provides a more precise illustration of the results, while the survival rate only provides an aggregate percentage. Despite lower overall survival rates in some years, there may be more survivors overall because of a larger patient group (such as in 2016, which had a 90% overall survival rate and 180 survivors).
4. **Varying Annual Survival Rates:** The data demonstrates the variable annual survival rates. This variation emphasizes how crucial it is to continuously track and assess patient outcomes in order to enhance healthcare and medical decision-making.
5. **Effect of Deaths:** In 2022, there will be 4 deaths; in 2021, there will be 70. High mortality rates, as in 2021, are associated with lower survival rates for that year, whereas low death rates, as in 2022, are associated with greater survival rates.
6. **Unpredictable Changes in Survival Rates:** Neither an upward nor a decreasing trend can be seen in the survival rates. There are years when the rate rises (like 2018 to 2019 when it goes from 75% to 85%), but there are also years when it falls (like 2016 to 2017 when it goes from 90% to 60%). This shows that different variables may have affected the results in various years.
7. **Recent Potential Improvements:** The survival rate increased from 50% in 2020 to 80% in 2023. This increase can be the result of improvements in medical procedures, better available treatments, or

modifications to healthcare regulations throughout those year.

8. **Potential Research Opportunities:** The data gives academics a chance to look at the variables that affected survival rates in particular years. Investigating the connections between survival rates, patient characteristics, therapeutic modalities, and illness prevalence may produce information that improves patient care and results.

In conclusion, the provided data reveals fluctuations in survival rates over the ten-year period, demonstrating the complexities of patient outcomes and the importance of continuous research and analysis to enhance medical practices and optimize patient care.

5. Discussion

A ground-breaking method with significant implications for healthcare and biomedical research is the use of PaLM (Pre-trained Language Model) to enable biomedical machine learning in the interpretation of medical data. PaLM has a strong awareness of context and semantics because to its pre-training on a large amount of linguistic data, making it an effective tool for processing and extracting information from difficult biological texts. This capacity is very helpful in the healthcare industry because there are a lot of unstructured data sources that need to be evaluated and used efficiently, including electronic health records and medical literature. Researchers can improve natural language processing activities including information extraction, named entity recognition, and text classification by utilizing PaLM's capabilities, improving data integration and knowledge discovery. Medical diagnosis and prognosis is one of the most exciting areas for biomedical machine learning utilizing PaLM. PaLM-based models can help medical personnel make more precise and timely diagnoses by examining patient data, such as symptoms, medical history, and lab results. This may result in better patient outcomes, tailored treatment regimens, and a decline in medical blunders. Additionally, the coupling of PaLM with other machine learning methods can improve the interpretability of medical image analysis, enabling more accurate and effective disease identification from pathology slides and medical scans. This could revolutionize the way radiology and pathology are practiced, increasing the precision and efficiency of diagnosis. Additionally, the uneven and sparse datasets that characterize biomedical data present difficulties for conventional machine learning techniques. PaLM can learn from uncommon medical events and manage imbalanced classes more skilfully thanks to its pre-training on a variety of linguistic data, which results in more robust and dependable models. This is especially true in the healthcare industry, where uncommon illnesses or harmful medical disorders necessitate particular care and early discovery. Let's sum up by saying that the incorporation of PaLM into

biomedical machine learning has enormous potential to advance medical data analysis and alter healthcare procedures. PaLM-based models can boost medical image analysis, help with accurate medical diagnosis, and improve natural language processing jobs by utilizing the power of language understanding. PaLM's promise in personalized medicine, disease prediction, and medical knowledge creation is poised to alter the healthcare industry and eventually enhance patient care as researchers work to solve ethical issues and improve interpretability.

6. Conclusion

In conclusion, PaLM (Pre-trained Language Model) integration into biomedical machine learning for medical data analysis presents a disruptive and intriguing route in the realm of healthcare and research. Due to its extensive pre-training on language data, PaLM has a deep knowledge of context, which allows it to analyse and extract insightful information from challenging biomedical texts. With this capability, natural language processing jobs might be improved, precise medical diagnoses could be made, and individualized treatment suggestions based on patient characteristics could be supported. Equally interesting is PaLM's potential for medical image analysis, which will enable medical personnel to read pathology slides and radiological pictures more precisely and effectively. By addressing difficulties in the detection and prediction of rare diseases, it is able to manage imbalanced and sparse medical datasets, paving the door for better disease understanding and early therapies. In conclusion, the convergence of biomedical machine learning and PaLM has the potential to transform healthcare practices, promote personalized medicine, and accelerate the development of new diagnostic and therapeutic approaches. By sensibly utilizing PaLM, the medical community can use language understanding to glean insightful information from massive biomedical data sets, thereby improving patient outcomes and advancing medical knowledge. The entire potential of PaLM in enhancing biomedical research and medical data analysis holds the promise of a brighter and more data-driven future in healthcare as researchers continue to investigate this fascinating topic.

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