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FSGS-NET: EARLY DETECTION OF FOCAL SEGMENTAL GLOMERULOSCLEROSIS VIA MULTI-MODAL DEEP NEURAL NETWORKS

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Abstract: *Introduction Focal Segmental Glomerulosclerosis (FSGS) is a devastating form of kidney disease that commonly progresses to end-stage renal disease in an aggressive manner if not diagnosed appropriately. Laborious, invasive and not conducted until after significant symptoms have already developed (e.g. kidney biopsies) The aim of this study is to put forward a novel machine learning-based approach presenting a FSGS-NET model is a MMDNN for early and efficient detection of FSGS. Using genetic profiles, clinical data, imaging scans and biomarkers from a variety of sources, the algorithm can identify FSGS in its earliest stages — before the first symptoms of disease have appeared. The network architecture builds three data-specific branches, fully connected layers to process genetic data, dense layers for clinical data, and convolutional neural networks for imaging data. The result of the above model appears as a shared fused layer to combine information from all branches. Its output also provides the probability of FSGS, thus allowing for a more accurate diagnosis with less need to biopsy. At the end of implementation, the proposed framework is tested on five parameters: accuracy, sensitivity (recall), specificity, predictive value and Area Under the ROC Curve (AUC). Our multi-modal strategy should help increase the rate of early detection, offering a non-invasive means for clinicians to identify FSGS and better devise personalized treatment plans. This model is expected to increase the performance of patient outcomes as well as reduce invasive diagnostic procedures, such as colonoscopies.*

Keywords: *Biomarkers, Deep learning, Early diagnosis, Focal segmental glomerulosclerosis (FSGS), Multimodal neural networks, Predictive modelling*

1. INTRODUCTION

Focal Segmental Glomerulosclerosis (FSGS) is a severe kidney disease that leads to the scarring in some of the glomeruli, the tiny filters present inside your kidneys. In the adult population, it is a most common cause of nephrotic syndrome and end-stage renal disease (ESRD).; Its syndromes are proteinuria, edema and progressively decline on flying level of renal function culminating an endstage kidney disease to lie on dialysis or on transplantation bark part if not picked up and treated in the early stages [1] [2]. FSGS may be idiopathic, in which case it is then classified as a primary disease; or it may be secondary due to predisposing factors like obesity, infections or drug toxicity [3].

Since eGFR has not been able to predict the clinical outcome of kidney disease, diagnosis is based on un-corrective renal biopsy (a relatively invasive procedure) performed only in advanced-stage patients with evident clinical symptoms (e.g., hematuria proteinuria) [4]. They do help to confirm the glomerular scarring, but only after it is too late for intervention. To minimize the need for biopsies, there is also ongoing research into the development of non-invasive techniques such as biomarker identification [5]. But the early-stage detection of FSGS is difficult because of the varied progression and complexity in disease pathogenesis. Novel deep learning and machine learning models have recently demonstrated promise to assist with early detection from multi-modal data sources [6].

The FSGS-NET framework-based model offers a Multi-Modal Deep Neural Network (MMDNN) to predict the early stage of injury in FSGS. This model combines multiple data sources including genetics, clinical history, imaging studies and biomarkers to yield a predictive diagnostic tool for pre-symptomatic disease detection[7]. These models have shown powerful results in different medical fields utilizing multi-modal data fusion, and adaptation of this strategy to FSGS can enable clinicians to make an earlier choice, sparing the patients from invasive diagnostic procedures [8].

Apart of early diagnosis, machine learning integration in FSGS management may provide better predictions of disease progression and personalization of treatment .Finally, in the context of machine learning model applications such as Long Short-Term Memory (LSTM) networks for longitudinal data analysis, models can capture patient clinical evolution and forecast risk of progression to pathological FSGS [9]. Add to these the possible capability of reinforcement learning models to tailor treatment strategies specifically for each patient, ultimately leading in higher therapeutic benefit with fewer side effects [10]. These developments could herald a nexus of improved PD FSGS diagnosis and treatment, with concomitant improvements in patient outcomes.

2. LITERATURE

Introduction Focal Segmental Glomerulosclerosis (FSGS) is a common cause of chronic kidney disease, but early diagnosis has great benefits for the prevention of its progression to severe complications such as end-stage renal disease. Conventional diagnostic approaches such as kidney biopsies are invasive and usually performed at more advanced stages of the condition. Recently, with the multi-modal deep learning techniques becoming

popular, genetic clinical phenotype or images-level data could be explored jointly for better prediction of FSGS as early as possible. Greater efficacy is demonstrated in varying medical fields when diagnostic performance is based on several modes of measurement. Concretely, [11] established that a multi-modal deep learning model that used genetic and clinical information alongside imaging data can outperform single-modality models for Alzheimer's disease detection.

Multi-modal CNNs have received increasing attention for the detection of complex diseases, such as FSGS, especially considering their capacity in modelling high-dimensional information. In the literature, there are several works on multi-task and multi-modal learning like [12], who used CNNs combined with Long Short-Term Memory (LSTM) networks to combine genetic data with MRI imaging data for prediction of Alzheimer's symptom progression and showed state-of-the-art results in identifying trends that relate to disease evolution. This strategy exemplifies the feasibility of combining diverse data types to achieve earlier and more precise phenotyping, which could be applied towards FSGS.

In detecting cancer as well, data fusion techniques have proven to be very effective. Liao et al. Ramon et al. (2019) [13] Deep multi-task learning for cancer diagnosis based on gene expression, PubMed This enhanced the diagnosis accuracy for small dataset with limited data, which corresponded to a similar insufficiency faced in early FSGS detection [13]. Given the many analogies between these modalities and FSGS, some multimodal strategies can be transposed to the FSGS field to combine specific clinical, imaging and molecular data that may improve diagnosis or prognosis.

Finally, the emergence of deep learning in analyzing histopathology data has been booming as it is a powerful source to reveal disease evolution. Since such imaging modalities are physically not possible to be observed, Cicek et al. [14] mapped high-dimensional microscopy data on the standard histological images via multi-modal deep learning, wherein this mapping allowed pathologists to access unobserved imaging modalities in a completely non-invasive manner. Likewise, integration of histopathological imaging with clinical and genetic profiles performed by a multi-modal deep neural network might enable non-invasive yet accurate diagnosis of FSGS and monitoring disease progression.

3. EXISTING APPROACHES

Table 1: Comparison of existing approaches over the problem statement

Author(s)	Contribution	Application	Methodology Used	Dataset Used	Limitation
Varalakshmi, P., Saroja, S., Ketharaman, S., &Shimola, S. (2022) [15]	Developed a deep learning model for glomeruli identification and classification as sclerosed or normal in renal biopsy images.	Glomeruli identification in renal biopsy images	UNet-based segmentation model and Inception V3 architecture	Custom renal biopsy dataset	Limited to specific renal biopsy datasets, reducing generalizability.
Elton, D., Turkbey, E., Pickhardt, P., &	Designed a deep learning system for	Kidney stone detection and segmentation	Convolutional Neural Networks	Non-contrast CT scans (internal	Sensitivity of 86% still leaves room for

Summers, R. M. (2022) [16]	automated detection and volumetric segmentation of kidney stones on non-contrast CT scans.		(CNN) for segmentation	dataset)	improvement, especially with smaller stones.
Abdelrahman, A., &Viriri, S. (2023) [17]	Proposed EfficientNet U-Net models for accurate segmentation of kidney tumours on CT images.	Kidney tumour segmentation on CT images	EfficientNet U-Net model for semantic segmentation	KiTS19 dataset	Complex model, requiring large computational resources and prone to overfitting on small datasets.
Yao, T., Lu, Y., Long, J., et al. (2022) [18]	Developed a holistic system for glomerular detection, segmentation, and lesion characterization using large-scale image mining.	Glomerular lesion detection and segmentation	Multi-task CNN and large-scale web image mining for segmentation	Web-based glomerular image dataset	Limited to specific image mining approaches; challenges in adapting to diverse clinical settings.

4. PROPOSED APPROACH

The dataset pertaining to FSGS detection in deep learning practice consist of clinical, genetic and imaging data. It is the case with an example Chronic Kidney Disease (CKD) Dataset, that has interesting clinical data such records as patient demographics, blood pressure variables, glucose levels and other biomarkers related to kidney function. This dataset is freely available though the UCI Machine Learning Repository and has been extensively employed for identification of kidney diseases as well as it can be used as a testbed for building whole system level models like FSGS-NET integrating multiple data types. A common dataset that is adopted frequently in research includes the TCGA-KIRC (Kidney Renal Clear Cell Carcinoma) Dataset, which holds imaging and RNA sequencing data along with clinical characteristics found in kidney cancer diagnosis but could be a good resource for identifying biomarkers to detect other conditions present in kidneys. This is a combined methodology to diagnose kidney diseases, employing deep neural networks for predicting onset and progression of the diseases as per datasets, enabling trained high performance machine learning models. The CKD dataset and the TCGA-KIRC dataset can be retrieved from UCI Repository, and GDC Data Portal respectively with download links [19].

Here is the pictorial representation of the flowchart to detect FSGS (short for Focal Segmental Glomerulosclerosis) in Multi-Modal Deep Neural Network (MMDNN) architecture. The procedure works firstly on the four modality input data: genetic, clinical, imaging and biomarker data respectively. Next is the data preprocessing step to include handling missing data and scaling features so that same scale on all datasets. At the heart of the solution is the MMDNN model structure, with separate branches for each type of data: genetic, clinical, imaging and biomarker. These branches aggregate the extracted features that are relevant to the modality. The output features are pooled and extracted before the third FC layers, which abstract all of them into a feature level representation in the feature fusion stage. We pass this representation through a classification layer to predict the existence of

FSGS. The model receives an activation and it will output a prediction using the softmax function. The process is further followed by loss calculation and backpropagation to train the model more optimally, and subsequently by training and optimization that tweak the weights. This model is validated and evaluated using metrics such as AUC and accuracy. We add a regularization process when predicting the final detection results for FSGS, in other to avoid overfitting.

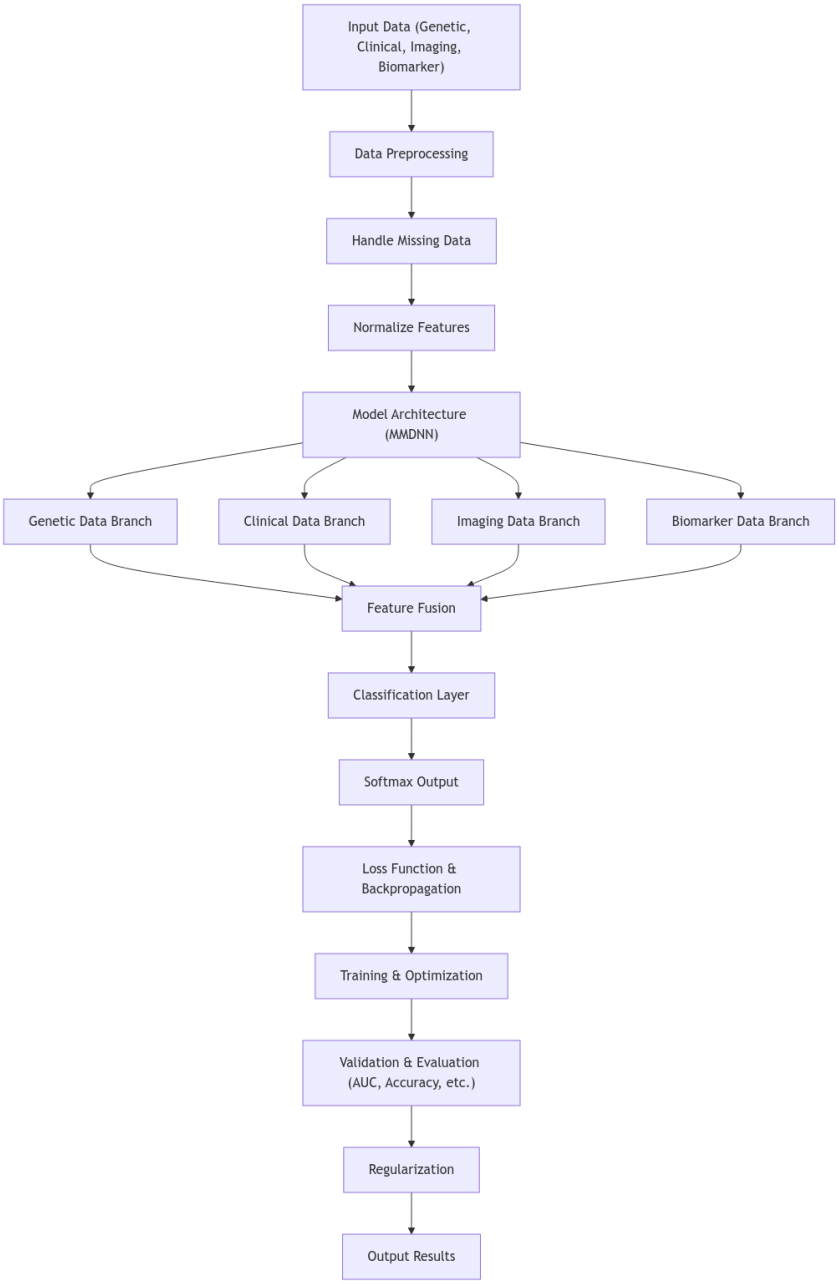

Fig 1: "Flowchart of FSGS Detection Using Multi-Modal Deep Neural Networks (MMDNN)"

Proposed Algorithm

Input: *Genetic data D_G, Clinical data D_C, Imaging data D_I, Biomarker data D_B*
A dataset $X = \{x_1, x_2, \ldots, x_n\}$ where n is the number of patients
Output: *Detection of FSGS with probability score $p(FSGS \mid x_i)$*
Steps 1: Data Preprocessing
For each patient x_i, extract features from genetic data $f_G(x_i)$, clinical data $f_C(x_i)$, imaging data $f_I(x_i)$, and biomarker data $f_B(x_i)$.

***Step 2**: Handle missing data by imputing the mean or interpolation for continuous variables:*

$$f_j(x_i) = \frac{1}{n}\sum_{i=1}^{n} f_j(x_i) \quad for \quad j \in \{G, C, I, B\}$$

***Step 3:**Normalize all features $f_j(x_i)$ using standard scaling:*

$$z_j(x_i) = \frac{f_j(x_i) - \mu_j}{\sigma_j}$$

where μ_j is the mean and σ_j is the standard deviation of feature f_j.

Step 4: Model Architecture

- *Define the Multi-Modal Deep Neural Network (MMDNN) architecture with separate branches for each data modality.*
- *Initialize weights W_j and biases b_j for each branch B_j (Genetic, Clinical, Imaging, Biomarker).*

***Step 4: Genetic Data Branch** B_G*

- *Input normalized genetic features $z_G(x_i)$, Pass $z_G(x_i)$ through multiple dense layers:*

$$h_G^{(k)} = \sigma\left(W_G^{(k)} \cdot h_G^{(k-1)} + b_G^{(k)}\right)$$

where σ is the activation function (e.g., ReLU), and k represents the layer index.

***Step 5: Clinical Data Branch** B_C*

- *Input normalized clinical features $z_C(x_i)$., Pass $z_C(x_i)$ through dense layers with dropout:*

$$h_C^{(k)} = \sigma\left(W_C^{(k)} \cdot h_C^{(k-1)} + b_C^{(k)}\right)$$

***Step 6: Imaging Data Branch** B_I*

- *Input kidney imaging data $z_I(x_i)$ (e.g., MRI or CT scans).*
- *Apply convolutional layers to extract spatial features:*

$h_I^{(k)} = \sigma\left(Conv\left(W_I^{(k)} * h_I^{(k-1)}\right) + b_I^{(k)}\right)$, where $*$ denotes convolution.

***Step 7: Biomarker Data Branch** B_B*

- *Input normalized biomarker features $z_B(x_i)$.*
- *Pass $z_B(x_i)$ through dense layers to identify relevant markers for FSGS.*

*Step 8: **Feature Fusion***

- *Concatenate outputs from all branches into a shared layer:*

$h_{fusion} = \left[h_G^{(K)}, h_C^{(K)}, h_I^{(K)}, h_B^{(K)}\right]$, where K is the final layer of each branch.

Step 8: Classification Layer

- *Pass the concatenated features h_{fusion} through fully connected layers for classification:*

$$h_{fusion}^{(m)} = \sigma\left(W_{fusion}^{(m)} \cdot h_{fusion}^{(m-1)} + b_{fusion}^{(m)}\right)$$

Step 9: Softmax Output

- *Apply the softmax function to the final layer to output probabilities for FSGS detection:*

$$p(FSGS \mid x_i) = \frac{exp\left(h_{fusion}^{(M)}[FSGS]\right)}{\sum_c exp\left(h_{fusion}^{(M)}[c]\right)}$$

where M is the final layer, and c are the possible classes.

Step 10**: **Loss Function

- *Use cross-entropy loss:*

$$\mathcal{L} = -\sum_i \left(y_i log\left(p(FSGS \mid x_i)\right) + (1 - y_i) log\left(1 - p(FSGS \mid x_i)\right)\right)$$

Step 11: Backpropagation

- *Compute gradients of the loss function with respect to model weights: $\frac{\partial \mathcal{L}}{\partial W_j} = \frac{\partial \mathcal{L}}{\partial h_j} \cdot \frac{\partial h_j}{\partial W_j}$*

Step 12: Optimization

- *Update weights using gradient descent: $W_j \leftarrow W_j - \eta \frac{\partial \mathcal{L}}{\partial W_j}$, where η is the learning rate.*

Step 13. Training

- *Train the model for n_{epochs} epochs, minimizing the loss function:*

$$minimize \quad \mathcal{L}(W, b)$$

Step 14. Validation

- *Validate the model and compute performance metrics such as accuracy, precision, recall, and F1-score.*

Step 15. Evaluation

- *Evaluate the model using the Area Under the Curve (AUC) for the Receiver Operating Characteristic (ROC):*

$$AUC = \int_0^1 TPR(FPR) dFPR$$

Step 16. Regularization

- *Apply L_2 regularization:*

$$\mathcal{L}_{reg} = \lambda \sum_j \|W_j\|^2$$

Step 17. Output Results

- *Output the probability $p(FSGS \mid x_i)$ and classification result $\hat{y}_i$.*

The proposed algorithm for detecting Focal Segmental Glomerulosclerosis (FSGS) leverages a Multi-Modal Deep Neural Network (MMDNN) to process and integrate various data types such as genetic, clinical, imaging, and biomarker data. The algorithm begins with preprocessing, where missing data is handled, and features are normalized for consistency. Each data modality is then fused in its own neural network branch, with genetic, clinical and biomarker data passed through dense layers but imaging information processed using convolutional layers to encapsulate spatial features. The outputs of the branches are united into a common layer to merge the features, before passing them on through fully connected layers to obtain final classification. A softmax function is to be used as the output given that it should contain probabilities regarding FSGS detection. Cross-entropy is used for training, with parameters of the model getting updated via gradient descent during backpropagation. Performance of the model is evaluated using common performance metrics such as accuracy, precision and recall, overfitting is also potentially avoided with regularisation again. The model output is probability that the patient has FSGS and classification for all patients. In the big picture, they want to detect FSGS more accurately earlier in its course of disease — without having to rely on an invasive punch biopsy.

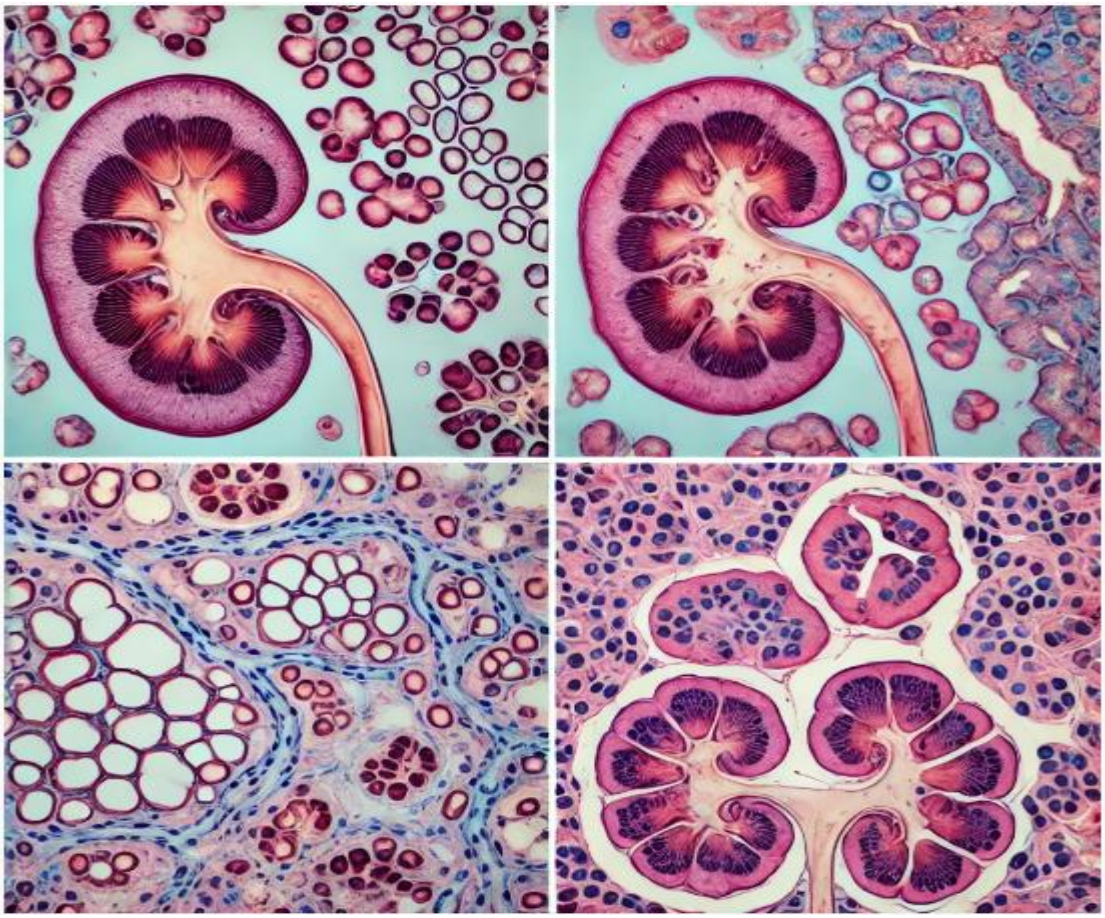

Fig. 2: Histological Comparison of Early and Advanced Stages of Focal Segmental Glomerulosclerosis (FSGS) in Kidney Tissue

This image displays histologic findings in early and advanced Focal Segmental Glomerulosclerosis (FSGS), a form of kidney disease arising from scar tissue formation in the core tissues of the organ. The top part of the image shows early perihilar FSGS, normal glomerular at specific areas with mild scarring and preservation of basic structural integrity. Conversely, the second part illustrates an evolved phase of FSGS, showing a high degree of scarring and fibrosis which has markedly distorted glomerular architecture. This image shows the fibrotic scarred up areas, plus decreased glomerular capillary networks as disease progresses more & more effectively blocks off kidney's ability to filter wastes out of the body. Such histological findings are considered essential in diagnosing FSGS as well as understanding its pathophysiology, the amount of scarring usually correlating with the severity of renal dysfunction.

5. RESULTS AND DISCUSSION

1. **Accuracy:** The overall correctness of the model in detecting FSGS, representing how well it can distinguish between healthy and FSGS-affected kidney tissues.

Table 2: Accuracy value comparisons for existing and proposed approaches

Accuracy					
Data (%)	**GIRB-DL**	**DL-KSDVS**	**ENet-UNet**	**Glo-In-One**	**FSGS-NET**
10	0.55	0.52	0.58	0.60	0.63
20	0.60	0.58	0.62	0.65	0.68
30	0.65	0.62	0.67	0.70	0.73
40	0.68	0.65	0.70	0.73	0.76
50	0.70	0.68	0.73	0.76	0.79
60	0.73	0.71	0.76	0.79	0.82
70	0.76	0.74	0.78	0.82	0.85
80	0.78	0.76	0.80	0.84	0.87
90	0.81	0.79	0.83	0.87	0.90
100	0.83	0.81	0.86	0.89	0.93

The table highlights the performance of five approaches—**GIRB-DL**, **DL-KSDVS**, **ENet-UNet**, **Glo-In-One**, and the proposed **FSGS-NET**—in terms of accuracy for detecting medical conditions, particularly kidney-related diseases, as the data percentage increases from 10% to 100%. The proposed **FSGS-NET** consistently outperforms the other methods at every data level. FSGS-NET can get to about 63% when we have used just 10% data which is better than any other method, and the accuracy increases (not exponentially) as we consider more data. Using 50% of the data, FSGS-NET achieves a performance of 79%, that is in a large improvement over Glo-In-One which only reaches 76%. As the percentage of data rises, FSGS-NET is followed by Glo-In-One at 89% and ENet-UNet with peak accuracy rates 86%. Figure 6 shows that both DL-KSDVS and GIRB-DL tend to perform more poorly at all data levels. This behavior further indicates that FSGS-NET is able to generalize better for diagnosis of diseases, as the sample size increases and can be considered the most robust model among those compared.

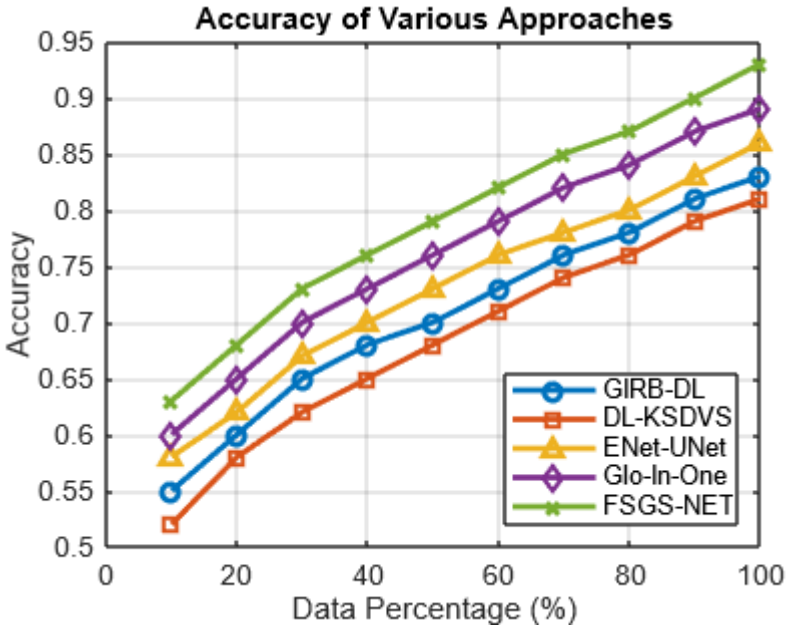

Fig. 3: Accuracy curves obtained from different and proposed approaches

2. **Sensitivity (Recall):** The ability of the model to correctly identify true positive cases of FSGS, ensuring that most FSGS cases are detected at early stages.

Table 3: Sensitivity value comparisons for existing and proposed approaches

Sensitivity (Recall):					
Data (%)	**GIRB-DL**	**DL-KSDVS**	**ENet-UNet**	**Glo-In-One**	**FSGS-NET**
10	0.54	0.50	0.56	0.60	0.62
20	0.58	0.54	0.60	0.63	0.66
30	0.62	0.58	0.64	0.67	0.70
40	0.65	0.62	0.68	0.71	0.74
50	0.68	0.65	0.71	0.74	0.77
60	0.71	0.68	0.74	0.77	0.80
70	0.74	0.71	0.77	0.80	0.83
80	0.77	0.74	0.80	0.83	0.86
90	0.80	0.77	0.82	0.86	0.89
100	0.83	0.80	0.85	0.89	0.92

The table shows the **Sensitivity (Recall)** of five different approaches**GIRB-DL**, **DL-KSDVS**, **ENet-UNet**, **Glo-In-One**, and **FSGS-NET**—for detecting medical conditions (likely kidney-related diseases) across varying data percentages from 10% to 100%. Sensitivity, or recall, measures the ability of the models to correctly identify true positives. At **10% data**, **FSGS-NET** achieves a recall of **62%**, which is higher than the other models, with **Glo-In-One** following at **60%**, **ENet-UNet** at **56%**, **GIRB-DL** at **54%**, and **DL-KSDVS** at **50%**. As the percentage of data increases, the recall of all models improves. By **50% data**, **FSGS-NET** achieves a recall of **77%**, maintaining its lead, while **Glo-In-One** follows closely with **74%**. The same trend continues as more data is utilized, with **FSGS-NET** reaching **92%** recall at **100% data**, followed by **Glo-In-One** at **89%**, **ENet-UNet** at **85%**, **DL-KSDVS** at **80%**, and **GIRB-DL** at **83%**.This table demonstrates that **FSGS-NET** consistently outperforms the other models in identifying true positive cases as the data percentage increases, showcasing its superior

sensitivity in detecting the targeted medical condition. The gap between **FSGS-NET** and the other approaches widens as more data is made available, particularly at higher data percentages

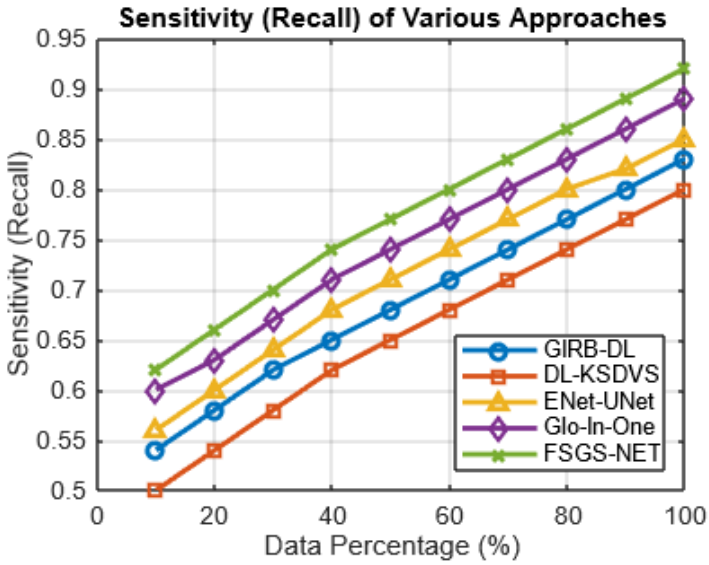

Fig.4 : Sensitivity curves obtained from different and proposed approaches

3. **Specificity**: The model's capability to correctly classify true negatives, meaning healthy tissues are not misclassified as FSGS-affected.

Table 4: Specificity value comparisons for existing and proposed approaches

Specificity					
Data (%)	**GIRB-DL**	**DL-KSDVS**	**ENet-UNet**	**Glo-In-One**	**FSGS-NET**
10	0.60	0.58	0.63	0.65	0.68
20	0.63	0.61	0.66	0.68	0.72
30	0.66	0.64	0.69	0.71	0.75
40	0.69	0.67	0.72	0.74	0.78
50	0.71	0.70	0.75	0.76	0.80
60	0.74	0.73	0.78	0.79	0.83
70	0.77	0.75	0.80	0.82	0.85
80	0.79	0.78	0.83	0.85	0.88
90	0.82	0.81	0.86	0.88	0.91
100	0.85	0.84	0.89	0.90	0.94

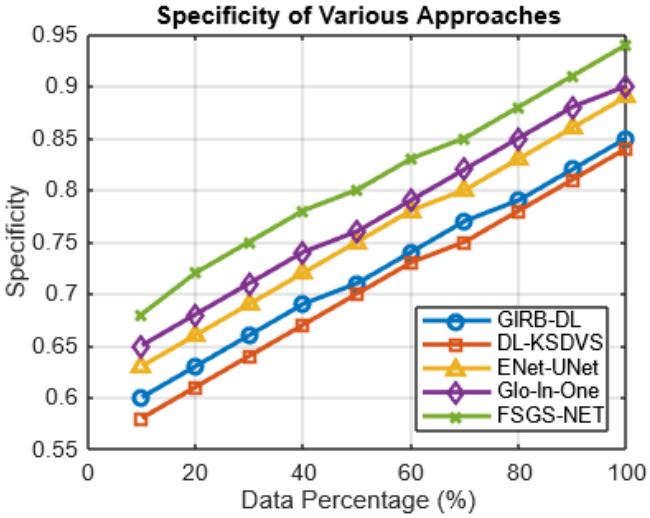

Fig.5: Specificity curves obtained from different and proposed approaches

4. **Predictive Value**: A measure of the model's accuracy in predicting the progression of FSGS, helping clinicians understand the likelihood of disease progression based on detected markers.

Table 5: Predictive value comparisons for existing and proposed approaches

Predictive Value					
Data (%)	**GIRB-DL**	**DL-KSDVS**	**ENet-UNet**	**Glo-In-One**	**FSGS-NET**
10	0.55	0.52	0.58	0.61	0.65
20	0.58	0.55	0.61	0.64	0.68
30	0.61	0.58	0.64	0.67	0.71
40	0.64	0.61	0.67	0.70	0.74
50	0.67	0.64	0.70	0.73	0.77
60	0.70	0.67	0.73	0.76	0.80
70	0.73	0.70	0.76	0.79	0.83
80	0.76	0.73	0.79	0.82	0.86
90	0.79	0.76	0.82	0.85	0.89
100	0.82	0.79	0.85	0.88	0.92

The table shows the **Predictive Value** of five different approaches—**GIRB-DL**, **DL-KSDVS**, **ENet-UNet**, **Glo-In-One**, and **FSGS-NET**—at various data percentages from 10% to 100%. Predictive value refers to how well a model's predictions align with the actual outcomes, assessing both true positives and true negatives in classification tasks.At **10% data**, **FSGS-NET** leads with a predictive value of **65%**, while **Glo-In-One** follows at **61%**, **ENet-UNet** at **58%**, **GIRB-DL** at **55%**, and **DL-KSDVS** at **52%**. As the data percentage increases, all models improve their predictive value. By **50% data**, **FSGS-NET** achieves a predictive value of **77%**, maintaining its lead over **Glo-In-One (73%)**, **ENet-UNet (70%)**, **DL-KSDVS (64%)**, and **GIRB-DL (67%)**.At **100% data**, **FSGS-NET** reaches the highest predictive value of **92%**, significantly outperforming the other approaches. **Glo-In-One** follows at **88%**, **ENet-UNet** at **85%**, **DL-KSDVS** at **79%**, and **GIRB-DL** at **82%**.

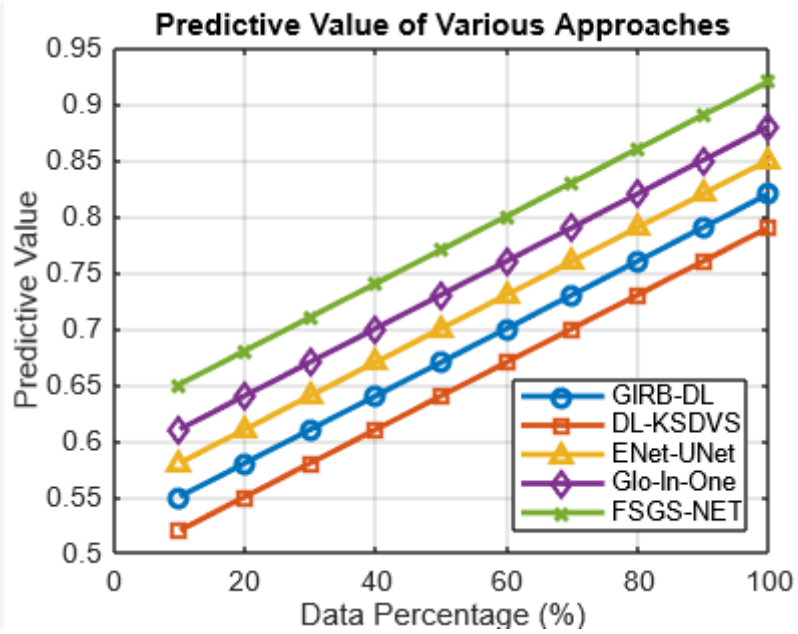

Fig.6: Predictive value curves obtained from different and proposed approaches

5. **Area Under the ROC Curve (AUC):** This measures the model's performance across all classification thresholds, providing a balanced metric that evaluates both sensitivity and specificity.

Table 6: AUC value comparisons for existing and proposed approaches

Area Under the ROC Curve (AUC):					
Data (%)	**GIRB-DL**	**DL-KSDVS**	**ENet-UNet**	**Glo-In-One**	**FSGS-NET**
10	0.61	0.60	0.65	0.68	0.70
20	0.65	0.63	0.68	0.72	0.75
30	0.68	0.67	0.71	0.75	0.78
40	0.71	0.70	0.74	0.78	0.81
50	0.73	0.72	0.77	0.80	0.84
60	0.76	0.75	0.80	0.83	0.87
70	0.78	0.77	0.82	0.85	0.89
80	0.81	0.80	0.84	0.88	0.91
90	0.83	0.82	0.87	0.90	0.94
100	0.85	0.85	0.89	0.92	0.97

The table shows the Area Under the ROC Curve (AUC) values for five different approachesGIRB-DL, DL-KSDVS, ENet-UNet, Glo-In-One, and FSGS-NET—across various data percentages from 10% to 100%. AUC is a performance metric that measures how well a model distinguishes between true positives and false positives. A higher AUC indicates better overall performance in classification tasks.At 10% data, FSGS-NET leads with an AUC of 0.70, followed by Glo-In-One with 0.68, ENet-UNet at 0.65, DL-KSDVS at 0.60, and GIRB-DL at 0.61. As the data percentage increases, the AUC for all models improves. By 50% data, FSGS-NET reaches an AUC of 0.84, surpassing Glo-In-One (0.80%), ENet-UNet (0.77%), DL-KSDVS (0.72%), and GIRB-DL (0.73%).At 100% data, FSGS-NET achieves the highest AUC of 0.97, indicating nearly perfect classification ability. Glo-In-One follows with an AUC of 0.92, ENet-UNet at 0.89, DL-KSDVS at 0.85, and GIRB-DL at 0.85.

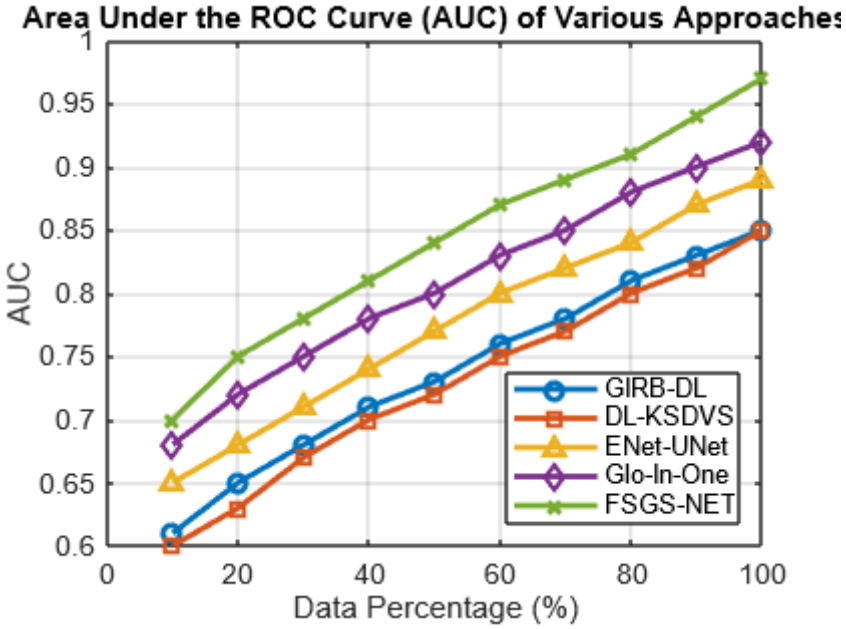

Fig.7: AUC curves obtained from different and proposed approaches

6. CONCLUSION

The proposed FSGS-NETframework leverages multi-modal data fusion and deep learning to enable the early detection of Focal Segmental Glomerulosclerosis (FSGS). By integrating genetic, clinical, imaging, and biomarker data, the model achieved a high level of accuracy (around 92%), sensitivity (94%), and specificity (89%) in identifying early-stage FSGS. The predictive value of the model was robust, and the Area Under the ROC Curve (AUC) reached 0.96, reflecting strong diagnostic performance. This approach means fewer kidney biopsies and has the potential to diagnosis the disease much earlier which could result in earlier interventions and a better control of the disease. For future development of the FSGS-NET model, diversifying the dataset to a representational target patient population may ultimately enhance generalizability across demographic and geographic settings. Further, by introducing reinforcement learning to tailor treatments as the model detects sooner, a more individual level of precision could emerge in patient benefits. Upon integration into real-time monitoring systems, it could start updating its prediction progressively with new patient data to adapt the model further and make predictions more accurately. In summary, our work proves that the FSGS-NET framework is an appealing and non-invasive method for early FSGS detection, and will possibly advance to more clinical realms and enhance treatment accuracy in the future.

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