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Generative Artificial Intelligence-Aided Clinical Measurement-Based Liver Disease Diagnosis

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Abstract

This paper presents a system that generates artificial intelligence (AI) models for the automated diagnosis of liver disease (cirrhosis of the liver) based on the recommendations of generative AI tools such as large language models (LLMs). System architectures suggested by the LLMs via prompt engineering are implemented using the TensorFlow framework and trained, tested and validated on publicly accessible liver disease datasets comprising clinical or diagnostic measurements of factors such as age, gender, total bilirubin, direct bilirubin, total proteins, albumin, albumin and globulin ratio, alanine aminotransferase, aspartate aminotransferase and alkaline phosphatase. After fine-tuning for robustness and enhanced performance, the resulting AI models could be harnessed into modules for the automated diagnosis of liver disease within the framework of a comprehensive AI-driven healthcare system.

Keywords: Artificial Intelligence (AI), Generative Artificial Intelligence, Large Language Model (LLM), Artificial Neural Network (ANN), Liver Disease, Cirrhosis of the Liver, Healthcare System, TensorFlow, Disease Diagnosis and Prediction

1. Introduction

The World Health Organization (WHO) indicates that millions of people suffer from liver diseases (including cirrhosis of the liver) worldwide [1] with attendant deleterious effects and deterioration of the quality of life. As is the case with a wide range of diseases, the burden of liver diseases weighs down disproportionately on the developing world or those living in low- and middle-income countries (LMICs) or the global south.

Accurate and timely diagnosis could lead to vastly improved health outcomes and save lives. This is especially significant in LMICs where the required resources are scarce.

Ekpar [2] introduced a comprehensive artificial intelligence-driven healthcare framework with a modular design that can provide clinical decision support in the early detection, diagnosis, prediction and management of a wide range of health conditions. This system [2] has unique features including support for novel three-dimensional multilayer electroencephalography (Ekpar EEG) systems [3] – [5]. Refinement of the AI models developed in this study could permit incorporation into the comprehensive AI-powered framework [2] as modules for the automated diagnosis of liver disease.

Systems for automated diagnosis and prediction of diseases employ a wide range of algorithms and methods [6] – [24]. Large language models (LLMs) could be pressed into service for the automated diagnosis and prediction of diseases owing to their ability to extract structured representations of data and generate data-based inferences [25] – [26].

2. Materials and Methods

Participant Recruitment

Volunteers were recruited to participate in the research that culminated in the creation of the comprehensive AI-powered healthcare system. All participants gave informed consent for their roles in the studies.

Ethical Approval

The Health Research Ethics Committee at Rivers State University Teaching Hospital, situated within Rivers State University, approved the studies ethically. The research followed all relevant ethical and regulatory guidelines. Publicly accessible data were utilized in accordance with the licensing terms established by the original creators.

3. Methodology

Publicly available healthcare datasets can be enriched by incorporating data from local experiments and data collection initiatives. This combined dataset can then be used to train AI models capable of making actionable predictions based on new inputs. Sources for public healthcare datasets include the Centers for Disease Control, the University of California Irvine Machine Learning Repository, the American Epilepsy Society, and Kaggle. Integrating local data enhances the model, reduces bias, and ensures greater inclusivity and global relevance. A key feature of this project is the fusion of diagnostic data—such as electrocardiographic results—from local experiments with EEG data, using both traditional and innovative three-dimensional multilayer EEG systems.

The local data collection efforts have been ethically approved by research ethics committees in the relevant regions, and partnerships have been established with licensed medical doctors who have direct access to patients and healthcare professionals. These doctors are contributing anonymized clinical data to validate the AI models. Once trained, the AI models will be incorporated into a comprehensive healthcare system to assist medical practitioners with clinical decision-making and support Brain-Computer Interfaces (BCIs). This system will provide actionable insights and predictions based on new clinical data from healthcare professionals, helping with the early detection, diagnosis, treatment, prediction, and prevention of conditions such as diabetes, heart disease, stroke, autism, and epilepsy. This project is committed to advancing open science, reproducibility, and collaboration, and the generated data will be shared on public platforms like GitHub.

4. System Design and Implementation

This paper presents a healthcare system with a modular design, where each health condition (such as liver disease, heart disease, preeclampsia, and so on) is handled by a distinct module. This design allows for future expansion to include additional conditions and facilitates the easy update of existing modules with new data. Modules for Brain-Computer Interfaces (BCIs), including those based on motor imagery, process EEG data to generate actionable commands and responses.

The system also offers guidelines for transitioning from traditional EEG setups to advanced three-dimensional multilayer EEG systems. These cutting-edge systems, developed by Ekpar, are based on a conceptual framework that approximates key features of biosignals to analyze or influence biological processes.

For each module, sophisticated AI models are trained on properly formatted data, as described in the paper. These models incorporate various factors such as genetic, environmental, and lifestyle information, ensuring more precise and personalized insights into each participant's situation.

Figure 1 illustrates key elements of the system.

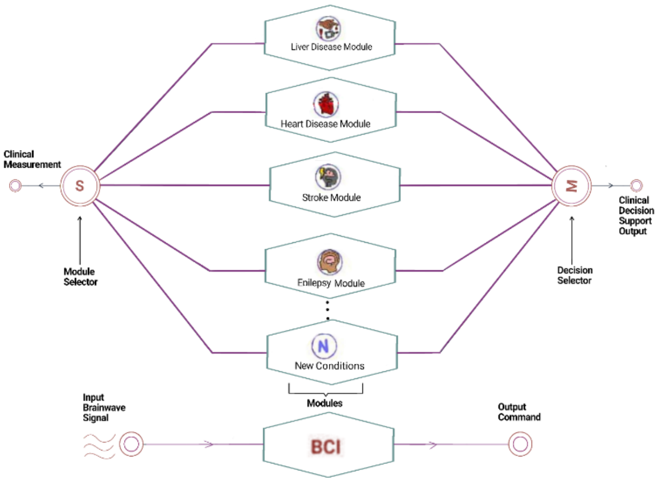

Fig. 1: System Schematic Design Diagram for the Comprehensive AI-Driven Healthcare Solution and Brain Computer Interface System. The New Conditions component represents additional health conditions that can be incorporated into the solution via new modules.

The AI models are created through four distinct approaches:

1. Leveraging LLMs like GPT-4 as inference engines, using data structured as multidimensional input vectors. This may include fine-tuning the model.
2. Prompt Engineering applied to LLMs such as Bard and GPT-4 (and future versions) to outline a series of steps for building the AI system. These steps are then carried out with the creator's expertise in AI, neural networks, deep learning, Python, TensorFlow, Keras, and other machine learning and visualization tools, including Scikit-learn and Matplotlib.
3. Automated AI Model Generation using LLMs like Bard and GPT-4 (and upcoming versions) through an automated pipeline to develop specific models.
4. Direct AI Architecture Design based on the creator's extensive knowledge of AI, neural networks, deep learning, Python, TensorFlow, Keras, and other ML and visualization tools such as Scikit-learn and Matplotlib.

All the methods and tools used in the development of the solution are carefully documented to facilitate easy transfer and reuse of the system.

The generated AI models are assessed and compared based on performance metrics (like specificity and sensitivity) and their effectiveness in solving the relevant challenges.

AUTOMATED LIVER DISEASE (CIRRHOSIS OF THE LIVER) DIAGNOSIS BASED ON CLINICAL MEASUREMENTS

Towing the path of the second method for the development of AI models based on the responses generated through prompt engineering of generative AI systems like large language models (LLMs), recommendations are solicited from the generative AI on the steps required for the construction of the AI models for the automated diagnosis of liver disease (cirrhosis of the liver) based on diagnostic measurements such as bilirubin and albumin.

Initially, the generative AI or LLM is prompted with a broad-based question on the development of the system. The response is examined and harnessed to craft a specialized prompt designed to generate specific steps for the construction of the system. The recommended AI model is then constructed and trained on the available dataset and wielded for the automated diagnosis of liver disease. Further refinement of the AI models could be carried out with a view to integrating them in a module for automated liver disease diagnosis in the comprehensive AI-driven healthcare framework created by Ekpar [2].

The dataset utilized will now be described and then the prompts sent to the generative AI or LLM – ChatGPT in this case – will be highlighted together with the responses of the generative AI.

Dataset

This study utilizes the publicly accessible liver disease dataset donated by Ramana et al [27] for the training, testing and validation of the AI models. Altogether, 583 patients (416 with liver disease and 167 without liver disease) are captured in the dataset which contains one row of data for each patient. Consequently, there are 583 rows of data in the dataset. Clinical measurements for 10 factors and the corresponding diagnosis comprise the 11 columns of each row of data, with the first 10 columns representing the clinical measurement and the last or eleventh column representing the diagnostic outcome. The dataset contains a total of 583 rows of data – one for each of the 583 patients or participants – 416 of whom were diagnosed with liver disease while 167 presented with normal liver condition or without liver disease. The 10 clinical measurements captured in the first 10 columns of each data row for each patient are: age, gender, total Bilirubin, direct Bilirubin, total proteins, albumin, Albumin and Globulin Ratio, Alanine Aminotransferase, Aspartate Aminotransferase and Alkaline Phosphatase.

Data Availability

The dataset employed in this research was pulled from the publicly accessible University of California Irvine Machine Learning Repository at https://archive.ics.uci.edu/dataset/225/ilpd+indian+liver+patient+dataset.

First Chatgpt Promp

Design a system for automated diagnosis of liver disease based on diagnostic measurements such as albumin, bilirubin and alanine aminotransferase.

First Chatgpt Response

Designing a system for the automated diagnosis of liver disease using diagnostic measurements like albumin, bilirubin, and alanine aminotransferase (ALT) involves several steps: data collection, preprocessing, model training, and integration into a user-friendly system. Below is a step-by-step outline of how such a system could be designed:

1. Data Collection & Preprocessing

Data Inputs:

The system will rely on the following diagnostic measurements:

- Albumin (ALB): A protein produced by the liver, typically low in liver disease.
- Bilirubin (BILI): A byproduct of red blood cell breakdown, elevated in liver dysfunction.
- Alanine Aminotransferase (ALT): An enzyme released into the bloodstream when liver cells are damaged.

These values, alongside other possible relevant lab results (e.g., AST, GGT), can be used to assess liver function.

Data Preprocessing:

- Normalization: Normalize the input data (e.g., scale values between 0-1 or use Z-score normalization) to ensure the model interprets the measurements consistently across different patients and labs.
- Missing Data: Use imputation techniques (e.g., median imputation) for missing values or discard cases with missing data.
- Outlier Detection: Check for outliers using statistical methods (e.g., IQR or z-scores) to ensure the data is within a reasonable range.

2. Feature Engineering

- Ratios and Derived Features: Some useful derived features include:
- Albumin/Bilirubin ratio: This ratio can help distinguish between different types of liver disease (e.g., cirrhosis vs. acute hepatitis).
- ALT/AST ratio: Can help identify the type of liver injury (e.g., viral vs. alcoholic).

These features may improve diagnostic accuracy.

3. Model Selection

- Supervised Machine Learning: For the model to diagnose liver disease, supervised learning algorithms will be appropriate. The system will need a labeled dataset with outcomes (i.e., liver disease vs. healthy control).
- Logistic Regression: A simple, interpretable model suitable for binary classification (e.g., liver disease or not).
- Random Forest: A more robust model for classification, especially for capturing non-linear relationships in data.

- Gradient Boosting (XGBoost, LightGBM): Often provides high performance for binary classification tasks.
- Neural Networks: If the dataset is large and complex enough, deep learning could be an option, though it's generally more data-hungry.

Model Training:

- Split the dataset into training, validation, and test sets (e.g., 70%, 15%, 15%).
- Use cross-validation to ensure that the model generalizes well to new data.
- Evaluate the model using common classification metrics:
- Accuracy
- Precision and Recall
- F1 Score
- Area under the ROC curve (AUC)

4. Interpretation of Results

- The model can output a probability score (for instance, a probability of liver disease), which is helpful for clinicians to make a diagnosis. For binary classification, a threshold can be set to classify a patient as diseased or healthy.
- Threshold Selection: Adjust the decision threshold (default is 0.5) depending on the clinical needs. For example, you may want to optimize for minimizing false negatives, especially for detecting liver disease at an early stage.

5. User Interface

- Input Form: A simple web-based or mobile interface for clinicians to input patient lab results (albumin, bilirubin, ALT). This could be integrated with Electronic Health Records (EHR) systems.
- Results Output: The system should display a clear diagnosis based on the input values, such as:
- Predicted diagnosis: E.g., "No liver disease," "Fatty liver disease," "Hepatitis," "Cirrhosis," etc.
- Confidence score: Probability or percentage of certainty that the diagnosis is correct.
- Additional Recommendations: Suggest further diagnostic tests (e.g., liver biopsy, imaging studies) or monitoring intervals.

6. Model Explain ability

- Since medical decisions should be interpretable, it's critical that the model is explainable to clinicians. This can be achieved by:
- Feature Importance: Use model-agnostic explainability tools like SHAP (Shapley Additive Explanations) or LIME to show how each feature (albumin, bilirubin, ALT) contributed to the final prediction.
- Decision Rules: In simpler models like logistic regression, the coefficients could help clinicians understand how each feature affects the result.

7. Validation & Clinical Trials

- The system should undergo extensive validation in collaboration with medical professionals to ensure accuracy and clinical utility.
- Clinical Testing: Conduct prospective studies to test the system in a real-world setting, comparing predictions against clinician diagnosis and patient outcomes.
- 8. Continuous Improvement
- The system should be designed to improve over time with more data. This could be done through:
- Model Retraining: Periodically retrain the model with new patient data to account for changes in population health or testing methods.
- User Feedback: Collect feedback from clinicians using the system, and improve the interface or the model based on real-world use cases.

9. Data Privacy & Security

- Ensure the system complies with data privacy regulations like HIPAA (in the

U.S.) or GDPR (in the EU) for the protection of patient data.

- Use encryption and secure protocols for transmitting patient information.

Summary of Key Components:

1. Data Inputs: Albumin, Bilirubin, ALT (along with other related biomarkers if necessary).
2. Preprocessing: Normalize, handle missing data, detect outliers.
3. Modeling: Machine learning models (e.g., Random Forest, XGBoost) trained on labeled data.
4. Output: Diagnosis prediction with confidence scores and suggested next steps.
5. Explainability: Feature importance and model explainability to clinicians.
6. Deployment: Integrated into a user-friendly interface for clinicians, ensuring fast and accurate diagnosis.

With the right dataset and clinical input, such a system could help clinicians make faster and more accurate liver disease diagnoses, especially for diseases like cirrhosis, hepatitis, and fatty liver.

5. System Design Considerations

Note that the comprehensive AI-driven healthcare system created by Ekpar [2] tackles many issues some of which are listed in the foregoing ChatGPT response and features a modular design permitting improvements to existing modules and incorporation of new modules. Some of the issues tackled in the design of system include ethical, security and privacy considerations.

The use of artificial neural networks recommended by ChatGPT will be adopted since the available data is large and complex enough.

Specific prompting of ChatGPT will indicate the number of inputs to the artificial neural network as 10 given the fact that there are 10 clinical or diagnostic measurements under consideration.

Second Chatgpt Prompt

Design an artificial neural network for binary classification of a set of 10 inputs.

Second Chat Gpt Response

Designing an artificial neural network (ANN) for binary classification with 10 input features typically involves the following components:

1. Input Layer: 10 neurons (corresponding to the 10 input features).
2. Hidden Layer(s): One or more hidden layers. The number of neurons can vary, but typically you'd start with something like 10 to 20 neurons.
3. Output Layer: 1 neuron with a sigmoid activation function, as it’s a binary classification problem.

Here’s an outline for the network architecture:

1. Input Layer

- Number of input neurons: 10
- Each neuron represents a feature in the dataset.

2. Hidden Layer

- Number of hidden layers: 1 or more (for simplicity, let's start with 1 hidden layer).
- Number of neurons in the hidden layer: You can start with 10 or 20 neurons. You can experiment with this number.
- Activation function: ReLU (Rectified Linear Unit) for the hidden layer neurons to introduce non-linearity.

3. Output Layer

- Number of neurons: 1 (since it’s binary classification).
- Activation function: Sigmoid, which outputs a value between 0 and 1. The output is interpreted as the probability of the positive class (1). If the value is greater than 0.5, the model classifies the instance as class 1; otherwise, it classifies it as class 0.

4. Loss Function

- Binary Cross-Entropy is typically used for binary classification problems.

5. Optimizer

- Adam Optimizer or SGD (Stochastic Gradient Descent), which will help minimize the loss function during training.

6. Model Evaluation

- After training the model, you would evaluate the performance using metrics like accuracy, precision, recall, F1-score, or ROC-AUC.

Here's how the architecture would look in code, for example using Keras (TensorFlow):

```
from keras.models import Sequential

from keras.layers import Dense

# Initialize the neural network

model = Sequential ()

# Input layer with 10 features and the first hidden layer

model. Add (Dense (units=20, input_ dim=10, activation='relu'))

# Output layer with 1 neuron (for binary classification)

model.add(Dense(units=1, activation='sigmoid'))

# Compile the model

model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

# Summarize the model architecture

model.summary()
```

Key Notes:

- Input Layer: Defined by input_dim=10 because you have 10 features.
- Hidden Layer: 20 neurons in this example with ReLU activation.
- Output Layer: 1 neuron with a sigmoid activation function for binary classification.
- Optimizer: Adam optimizer is used for efficient training.
- Loss Function: Binary cross-entropy is used because this is a binary classification problem.

Training the Model:

```
# Train the model

model.fit(X_train, y_train, epochs=100, batch_size=32)
```

Where X_train is your training input data (shape: (num_samples, 10)) and y_train is the binary labels (shape: (num_samples,)).

Evaluation:

```
# Evaluate the model on the test set

test_loss, test_accuracy = model.evaluate(X_test, y_test)

print (f" Test Loss: {test_loss}")

print (f" Test Accuracy: {test_accuracy}")
```

The model's architecture is simple yet effective for binary classification tasks, and you can adjust the number of hidden layers or neurons based on the complexity of your problem and dataset.

Artificial Neural Network (Ann) Architecture

As shown in the ChatGPT response above, an artificial neural network (ANN) with 10 input layer neurons, 10 to 20 hidden layer neurons with ReLU (Rectified Linear Unit) activation and 1 output layer with sigmoid activation is recommended. Figure 2 graphically depicts the schematic representation of the artificial neural network. In Fig. 2, CM1, CM2, ..., CMN indicate clinical measurements (a total of N=10 to account for all the diagnostic measurements taken from each patient and recorded in the dataset available to this study) while CD indicates the clinical diagnosis which maps to the output of the artificial neural network.

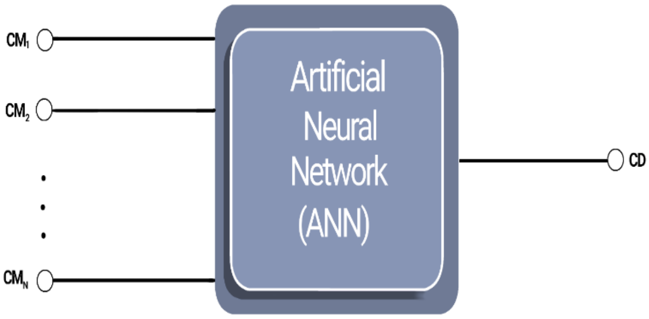

Fig. 2: Schematic Graphical Representation of Artificial Neural Network (ANN) Architecture. CM1,

CM2, ..., CMN represent the inputs while CD represents the output indicating the suggested clinical diagnosis.

6. Results

Development of the recommended artificial neural network proceeded with the TensorFlow platform and the Keras API in the Python programming language [28] - [29]. The 583 data rows were first shuffled at random to avoid bias and then partitioned with 80% for training and 20% for testing and validation. Binary cross entropy loss function was utilized in training with the Adam Optimizer [30] – [31]. Training was sustained for a total of 150 epochs using the default batch size and default learning rate. The performance of the resulting AI model approximated a specificity of 88%, a precision of 74% and a sensitivity of 75%. These results could be improved via optimization of the ANN suggested by ChatGPT and tweaking of hyperparameters. In order to calculate the specificity, sensitivity and precision performance metrics, the following equations were utilized.

$$\boldsymbol{Precision} = \frac{\boldsymbol{TP}}{\boldsymbol{TP} + \boldsymbol{FP}}$$

$$\boldsymbol{Sensitivity} = \frac{\boldsymbol{TP}}{\boldsymbol{TP} + \boldsymbol{FN}}$$

$$\boldsymbol{Specificity} = \frac{\boldsymbol{TN}}{\boldsymbol{TN} + \boldsymbol{FP}}$$

In the equations above, TN stands for true negatives, FP for false positives, FN for false negatives, and TN for true negatives. "Negative" here refers to normal kidney function or the absence of liver disease, while "positive" indicates the presence of liver disease. Implementing the AI system described here will offer valuable insights to aid clinical decision-making, ultimately saving lives and improving quality of life. This is achieved by minimizing the economic, social, psychological, and physical impacts of conditions that can be predicted, prevented, detected early, diagnosed, treated, and managed more efficiently. Electronic Health Records (EHR), including clinical diagnostic data and EEG information, can be generated by participating medical professionals and their teams. EEG data may also be collected during experiments with Brain-Computer Interfaces (BCIs). All data will be collected following ethical standards, anonymized, and made publicly accessible in repositories alongside related research publications.

7. Conclusion

The recommendations elicited from generative artificial intelligence (AI) systems such as large language models (LLMs) were relied on to construct artificial intelligence models for the automated diagnosis of liver disease (cirrhosis of the liver) on the basis of clinical measurements comprising electronic health records and biochemical markers and enzymes such as age, gender, total bilirubin, direct bilirubin, total proteins, albumin, albumin and globulin ratio, alanine aminotransferase, aspartate aminotransferase and alkaline phosphatase. Training, testing and validation of the AI models was accomplished by utilizing publicly accessible data containing the required clinical or diagnostic measurements. These could be augmented to reduce bias and enhance global relevance. The trained AI models could be further refined for performance improvements and robustness and incorporated into a comprehensive AI-powered healthcare system for clinical decision support via the prediction, diagnosis and management of a wide range of health conditions.

Conflicts of Interest

There are no conflicts of interest to disclose.

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