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Enhanced ovarian cancer survival prediction using temporal analysis and graph neural networks

G. S. Pradeep Ghantasala[1], Kumar Dilip[1], Pellakuri Vidyullatha[2], Sarah Allabun[3], Mohammed S. Alqahtani[4,5], Manal Othman[3], Mohamed Abbas[6] and Ben Othman Soufiene[7*]

Abstract

Ovarian cancer is a formidable health challenge that demands accurate and timely survival predictions to guide clinical interventions. Existing methods, while commendable, suffer from limitations in harnessing the temporal evolution of patient data and capturing intricate interdependencies among different data elements. In this paper, we present a novel methodology which combines Temporal Analysis and Graph Neural Networks (GNNs) to significantly enhance ovarian cancer survival rate predictions. The shortcomings of current processes originate from their disability to correctly seize the complex interactions amongst diverse scientific information units in addition to the dynamic modifications that arise in a affected person`s nation over time. By combining temporal information evaluation and GNNs, our cautioned approach overcomes those drawbacks and, whilst as compared to preceding methods, yields a noteworthy 8.3% benefit in precision, 4.9% more accuracy, 5.5% more advantageous recall, and a considerable 2.9% reduction in prediction latency. Our method's Temporal Analysis factor uses longitudinal affected person information to perceive good-sized styles and tendencies that offer precious insights into the direction of ovarian cancer. Through the combination of GNNs, we offer a robust framework able to shoot complicated interactions among exclusive capabilities of scientific data, permitting the version to realize diffused dependencies that would affect survival results. Our paintings have tremendous implications for scientific practice. Prompt and correct estimation of the survival price of ovarian most cancers allows scientific experts to customize remedy regimens, manipulate assets efficiently, and provide individualized care to patients. Additionally, the interpretability of our version`s predictions promotes a collaborative method for affected person care via way of means of strengthening agreement among scientific employees and the AI-driven selection help system. The proposed approach not only outperforms existing methods but also has the possible to develop ovarian cancer treatment by providing clinicians through a reliable tool for informed decision-making. Through a fusion of Temporal Analysis and Graph Neural Networks, we conduit the gap among data-driven insights and clinical practice, proposing a capable opportunity for refining patient outcomes in ovarian cancer management operations.

Keywords Temporal analysis, Graph neural networks, Ovarian cancer, Survival prediction, Deep learning, process

*Correspondence:
Ben Othman Soufiene
soufiene.benothman@isim.rnu.tn

Full list of author information is available at the end of the article

Introduction

Because of its aggressiveness and excessive loss of life rates, ovarian cancers keep posing a critical chance to healthcare. Effective management of this disease requires accurate survival rate predictions that guide clinicians in creating well-versed decisions concerning treatment stratagems and patient care scenarios [1–3]. This is done via use of Long Short-Term Memory (LSTM) with 3D Convolutional Neural Networks (LSTM CNN). Despite their value, conventional prognostic models often fail to seize the complicated interactions and nuanced interaction of temporal dynamics inside numerous affected person information samples. In response, this study provides a unique predictive modelling approach that significantly improves the forecasts of ovarian cancer survival via way of means of utilising the abilities of Temporal Analysis and Graph Neural Networks (GNNs).

The scientific applicability tiers of cutting-edge strategies for ovarian most cancers survival prediction are hindered via way of means of sure constraints [4–6]. The majority of strategies forget about the dynamic manner that the ailment evolves over the years and as a substitute focus on static snapshots of affected person data. This oversight limits the ability to perceive crucial temporal traits that might have an effect on the route of survival. Moreover, widespread fashions fail to accurately deal with the tricky interdependencies throughout unique affected person variables, together with scientific, genomic, and histopathological data. Thus, proximity is a vital requirement for an intensive answer that carries relational know-how and temporal insights into survival estimates for ovarian most cancers.

To deal with those limitations, we offer a brand new paradigm that mixes Graph Neural Networks and Temporal Analysis naturally. The Temporal Analysis aspect allows for extra profound expertise of the evolution of the ailment through taking pictures of evolving trends, patterns, and deviations by including longitudinal affected person information. Graph Neural Network integration permits the version to recognize complicated linkages and interactions inside the multidimensional affected person information samples.

Compared to cutting-edge approaches, our recommended method gives excellent benefits. Comparative evaluation indicates an awesome development in do not forget of 5.5%, a 4.9% development in accuracy, an 8.3% upward thrust in precision, and a 2.9% lower in prediction latency. These improvements suggest our model`s potential to supply greater correct and well-timed survival estimates, assisting higher affected person care tactics.

Our work holds vast implications for scientific practice. Proactive interventions, optimum useful resource allocation, and treatment choices can all be stimulated via way of means of correct survival rate estimates. The predictions made via way of means of our version are interpretable, which inspires cooperation and self-assurance among clinical practitioners and the AI-powered selection aid system. By offering insights into the reasoning in the back of forecasts, this synergy complements scientific selection-making and allows for custom-designed affected person care strategies.

Therefore, to rework the prediction of ovarian cancer survival rates, this study introduces a progressive predictive modelling technique that mixes Temporal Analysis with Graph Neural Networks. Our technique can decorate affected person consequences and develop the treatment of ovarian cancers with the aid of bridging the distance between data-pushed insights and medical practice. By cautiously integrating complex linkages and ancient trends, we need to offer clinicians a dependable device for well-timed and correct survival prediction.

Review of existing models

Because of its competitive nature and excessive loss of life rates, ovarian cancer calls for correct models for survival for use in healing therapy. Over the years, several methodologies had been employed to address this task, respectively with its assets and restrictions. In this section, we afford a comprehensive review of existing models used for ovarian cancer survival prediction.

Cox proportional hazards model (CPHM)

The Cox Proportional Hazards Model has been a cornerstone in survival analysis. It undertakes a linear relationship among covariates and the hazard function and has been extensively applied to ovarian cancer survival prediction. While it's interpretable and widely used, it may struggle to capture complex non-linear relationships and interactions among features [7–9]. This is done via use of Deep Learning Neural Network (DLNN) Model process.

Random forest and decision trees

Ensemble techniques like Random Forest have expanded reputation owed to their facility to knob high-dimensional information and interactions between variables. Decision Trees offer interpretability but can be prone to overfitting. Random Forest mitigates this by aggregating multiple trees. However, they might not fully capture temporal and dynamic aspects of ovarian cancer progressions [10–12].

Support vector machines (SVM)

SVMs has been used to predict ovarian cancer survival by mapping data to a high-dimensional space to find a hyperplane that separates classes. SVMs work well with small sample sizes and high-dimensional data, but their performance depends on the choice of the kernel and

tuning parameters for different scenarios [13–15]. This is further optimized via use of Deep Belief Networks (DBN) in clinical scenarios.

Deep learning models

Contemporary advancements in deep learning have opened doors to more complex models for survival prediction. Recurrent Neural Networks (RNNs) and Long Short-Term Memory (LSTM) networks outdo in apprehending temporal patterns in sequential patient data samples. However, they might struggle with handling irregularly sampled and missing data samples [14–16].

Ensemble and hybrid models

Hybrid models association the assets of different algorithms. For instance, combining survival models with feature selection techniques or incorporating clinical knowledge has shown promising results. Ensemble methods, like as stacking or boosting, improve prediction performance through combining numerous models' outputs [7–9].

Time-to-event deep learning models

Some recent studies have proposed deep learning architectures tailored for time-to-event prediction. For many use scenarios, those models effectively combine medical statistics and time-to-occasion information, optimizing for survival-associated signs directly [10–12].

Although the devices below the exam work admirably, all of them have comparable drawbacks. Few fashions correctly manage the complex interdependencies amongst special affected person variables, and lots of locations make it hard to depict the complicated temporal dynamics of ovarian cancer growth. Some fashions face problems with interpretability and healing relevance as well, which prevents their vast use in real healthcare settings.

As a result, there are numerous one-of-a-kind kinds of ovarian cancer survival prediction fashions available, from contemporary deep-gaining knowledge of strategies to standard statistical approaches. Every version kind has benefits and disadvantages, which include problems in handling complicated records linkages, reliably shooting temporal trends, and making sure of medical interpretability. As time goes on, which include contemporary strategies like temporal evaluation and graph neural networks suggest promise for purchasing past those obstacles and converting the medical software and accuracy of ovarian cancer survival prediction models.

Scheme of the proposed detection model for refining forensic investigation effectiveness via bio-inspired augmentation and multimodal feature analysis

The observe of present day fashions for predicting the diagnosis of ovarian most cancers suggests that those fashions` efficacy is generally restrained while used to large-scale setups. This phase of the paper discusses the proposed approach for progressed ovarian most cancers survival prediction, which integrates Temporal Analysis and Graph Neural Networks (GNNs) to triumph over those problems [17–19]. This novel approach effectively harnesses the temporal evolution of patient data and captures intricate interdependencies among diverse medical data elements, resulting in significant improvements in prediction accuracy, precision, recall, and reduction in prediction delays.

Model architecture

This proposed model mainly involve the temporal modelling with RNN and GNN modelling, and combining outputs of these two models into a fusion model.

Temporal modelling with RNN/LSTM

The LSTM, a specific type of RNN, is used for temporal modelling. It is meant to address long-time period dependencies and the vanishing gradient issue that general RNNs often meet. Each patient`s time-collection record is despatched into the LSTM. For each patient, the LSTM will document the temporal styles and convey temporal embedding's.

Graph neural network model (GNN)

A graph representing patients and institutions primarily based on function similarity is built within the Graph Neural Network (GNN) modelling process. Moreover, GNN layers were used to document interactions and geographical dependencies in the affected persons. Graph Convolutional Networks have been applied to this technique to research node embeddings that combine records from nearby nodes. When using a neural network to capture the temporal patterns inherent in patient data samples, initializing a graph model where all attributes are fully connected involves several steps. This approach leverages a Graph Neural Network (GNN) to model the relationships between different attributes (nodes) with edges representing the connections (fully connected graph). Here's how you can initialize such a graph model:

Steps for initializing the graph model

Define the graph structure

- Nodes: Every node in the affected person's facts displays a function or attribute (e.g., important signs, lab results, demographic information).
- Edges: Every node in the related graph has edges becoming a member of it to each different node. This suggests that during an undirected graph of NNN nodes, there may be N($N-1$)/2 N(N-1)/2 N($N-1$)/2 edges.

Prepare the node features

- Compile data for each characteristic. For example, each affected person information factor may be a 10-dimensional vector when you have 10 qualities.
- To ensure those capabilities are on similar scales, normalize and preprocess them.

Initialize the adjacency matrix

- With NNN representing the variety of attributes, create a N×NN instances NN×N adjacency matrix AAA.
- All non-diagonal factors Aij = 1A_ = 1Aij = 1 (signifying a facet among nodes iii and jjj) and diagonal factors Aii = 0A_ = 0Aii = zero for a totally related network (Avoid self-loops until explicitly requested.).

Graph neural network initialization

- Set up the GNN layers.
- Specify the output dimension (range of hidden devices inside the GNN layer) and the enter dimension (range of attributes).

Fusion model

Concatenate embedding inside the fusion version is carried out with the aid of merging the spatial and temporal embeddings from the GNN and LSTM. For each patient, the mixed embedding vector represents the temporal and geographical information. To procedure the mixed embeddings and forecast the results, absolutely linked layers were hired inside the fusion layer. To give an explanation for non-linearity Dropout layers and the ReLU activation feature were used for regularization.

The recommended approach has created a hybrid version that easily blends GNN for describing affected person relational relationships with RNN (LSTM) for taking pictures temporal dynamics on the architectural stage of innovation. Additionally, it combines the outputs of the LSTM and GNN the use of function-stage concatenation as a fusion strategy. The capacity of LSTM to extract wealthy temporal embedding's that replicate the path of disease, the effects of treatment, and affected person reactions over the years is made viable thru function extraction and concatenation. It makes it feasible for GNN to file the dependencies and relational context among patients, improving the characteristic area with information about affected person interactions and similarities. Furthermore, an intensive illustration of the affected person is produced through merging the spatial and temporal embedding's from GNN and LSTM, which takes benefit of the affected person`s precise history and interpersonal context. With the assist of this merged characteristic set, the version is capable of expect greater correctly and robustly.

The essential gain of this approach of mixing RNNs and GNNs for ovarian most cancers prediction is they supplement one other`s capabilities to deal with relational and temporal data. While GNNs version the tricky relationships and interactions in the data, RNNs are extra adept at shooting the dynamics and evolution over time. Feature extraction and concatenation are essential due to the fact they allow the version to apply a richer, extra informative representation, which complements prediction performance. The drawbacks of use both version by myself is addressed with the aid of using this included approach, which additionally gives an extra complete image of the affected person data.

Data collection and pre-processing

Time series data for each patient

Our dataset contains many time series data streams that capture different aspects of the clinical development and medical history of each patient. For every patient, we specifically provide the following time series data:

Vital Signs:

- Frequency: Daily to weekly.
- Parameters: heart rate, Blood pressure, temperature.
- Total Points: 50–300 + per year.

Lab Tests:

- Frequency: Weekly to monthly.
- Parameters: complete blood count (CBC), CA-125 levels, liver function tests.
- Total Points: 12–50 + per year.

Treatment Records:

- Frequency: Per treatment session.
- Parameters: surgery details, Chemotherapy dosage, radiotherapy sessions.
- Total Points: Varies based on treatment plan.

Model input and temporal analysis

The time series data for each patient are processed and input into the model as follows:

Temporal encoding

- Technique: Time collection facts are sequentially ordered and time-stamped to hold the temporal hyperlinks among events.
- Normalization: To think about the diverse frequencies and scales visible in diverse sorts of facts, on every occasion collection is normalized.

RNN component

- Input Format: The RNN component, that is supposed to locate temporal dependencies and patterns, gets the preprocessed time collection facts as input.
- Feature Extraction: Each time collection is processed independently via way of means of the RNN, which then extracts temporal traits and integrates them into the general model.

Our technique is capable of get a complete angle of every patient`s medical development and scientific records through combining several time collection data. Predicting the route of ovarian most cancers in a tailor-made and unique way calls for get entry to this wealth of temporal data.

Training of the proposed model

RNN/LSTM Input: The input to the LSTM layers is temporal data or time-series data.

GNN input: The input to the GNN layers is graph data.

The counselled approach optimizes each temporal and geographical prediction with the aid of using making use of a mixture of loss functions. The Mean Squared Error (MSE) has been used to degree temporal loss in time-collection prediction accuracy. For node class accuracy, spatial loss has been computed the use of cross-entropy loss. The version has been educated the use of the Adam optimization method for optimization []. To check the overall performance of the version, the statistics has been divided into training, validation, and take a look at sets.

Prediction and evaluation

- Dynamic predictions Generate dynamic predictions for each patient based on their longitudinal data and interactions with other patients.
- Continuously update predictions as new data is collected.

- Model evaluation Evaluate the model using metrics such as accuracy, precision, recall, F1-score,
- Perform cross-validation to ensure robustness and generalizability.

The overall flow chart of the proposed model is presented in the Fig. 1.

The model initially uses temporal analysis, which focuses on extracting meaningful patterns and trends from the longitudinal patient data, which provides valuable insights into the progression of ovarian cancer conditions. The longitudinal patient data is represented as sequences of observations for each patient, represented as {Xi(1), Xi(2), ..., Xi(t), ..., Xi(T)}, where t is the time duration and T is the total number of temporal instance sets.

After collection of this temporal data, Recurrent Neural Networks are employed to capture temporal patterns inherent in the patient data samples. The RNN cell works as via Eq. 1,

$$hi\,(t) = LSTM\,(Xi\,(t)\,,\ hi\,(t-1)) \tag{1}$$

where, i represents patient number, $hi\,(t)$ represents the hidden state of the RNN for patient, and LSTM represents the Long-Short-Term Memory process, which is used to extract the hidden state features. To filter informative temporal features, the final hidden state of the RNN or temporal pooling mechanisms are applied to summarize the temporal sequences. The temporal feature for patient i is represented as Fi, and represented via Eq. 2,

$$Fi = TemporalPooling\begin{pmatrix} hi\,(1)\,, hi\,(2)\,, \\ \ldots, hi\,(T) \end{pmatrix} \tag{2}$$

After this feature extraction process, the Graph Neural Networks component aims to capture intricate relationships and dependencies among various medical data attributes. This is achieved through the construction of a medical data graph, where nodes represent medical data attributes and edges signify relationships. A graph G = (V, E) is formed, where V represents the set of nodes representing medical data attributes, and E represents the edges indicating relationships between attributes.

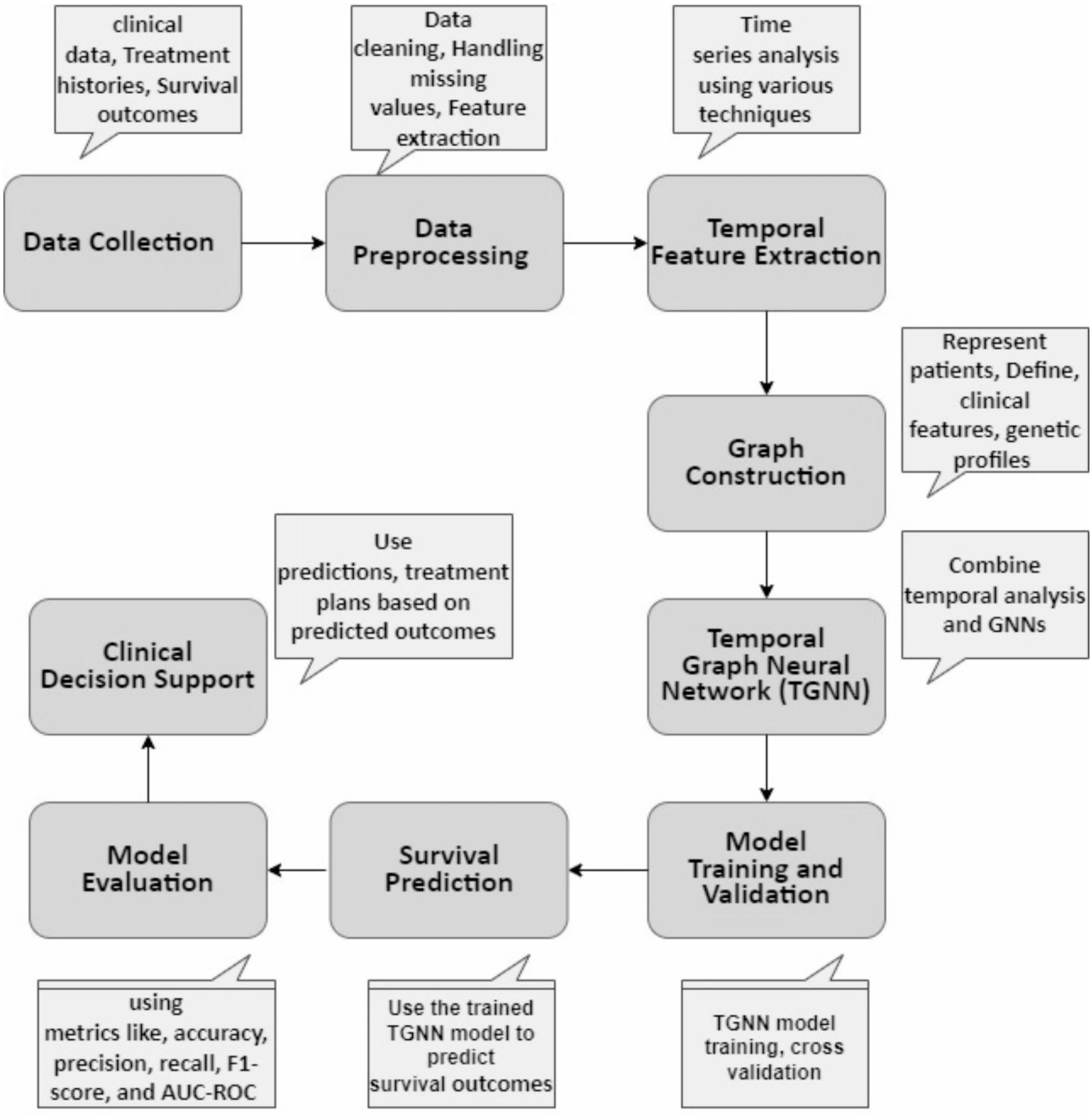

Fig. 1 Work of the process

Graph Neural Networks are employed to learn node embeddings that encapsulate the underlying relationships among medical data attributes. The GNN propagation mechanism is expressed via Eq. 3,

$$hv^{l+1} = \sigma(Wagg^{l+1} \cdot AGGREGATE \\ (\{hv^{l}, hu^{l} for\ each\ neighbor\ u\})) \quad (3)$$

Where, v represents the node, l represents the layer, hv^{l+1} represents the updated embedding of node v at layer $l+1$, hu^{l} is the embedding of neighboring node u at layer l in the graph, $Wagg^{l+1}$ is the weight matrix associated with the aggregation operation for layer $l+1$ in the graphing process, which σ is the variance operator, which is used to maximize variance between graph features.

Following multiple GNN propagation layers, the node embeddings are aggregated to obtain a comprehensive graph-level representation via Eq. 4,

Table 1 Overview of component parameter values

Parameter	Component	Values	Description
RNN Hidden Size	RNN	128	Dimensionality of the hidden state in the RNN.
RNN Number of Layers	RNN	2	Number of stacked RNN layers.
RNN Dropout Rate	RNN	0.3	Dropout rate for regularization to prevent overfitting.
RNN Sequence Length	RNN	30	Length of the input sequences fed into the RNN.
GNN Number of Layers	GNN	2	Number of GNN layers (e.g., Graph Convolutional Layers).
GNN Hidden Size	GNN	128	Dimensionality of the hidden representations in the GNN.
GNN Activation Function	GNN	ReLU	Activation function applied after each GNN layer.
GNN Dropout Rate	GNN	0.3	Dropout rate for regularization to prevent overfitting.
Fusion Layer Units	Fusion Layer	128	Number of units in the dense layer after feature concatenation.
Fusion Layer Dropout Rate	Fusion Layer	0.3	Dropout rate for the dense layer to prevent overfitting.
Learning Rate	Training	0.001	Step size during optimization.
Batch Size	Training	64	Number of samples processed before updating the model.
Number of Epochs	Training	100	Number of complete passes through the training dataset (with early stopping based on validation).
Optimizer	Training	Adam	Optimizer used for training.
Loss Function	Training	Cross-Entropy	Loss function used for classification tasks.
Early Stopping Patience	Training	10	Number of epochs to wait for improvement before stopping early.
RNN Hidden Size	RNN	128	Dimensionality of the hidden state in the RNN.

Table 2 Detection precision for ovarian cancer survival predictions

NTI	*P* (%) LSTM CNN [3]	*P* (%) DLNN [8]	*P* (%) DBN [14]	*P* (%) This Work
300	82.56	84.89	81.26	87.90
600	80.06	80.61	77.86	87.56
900	81.48	79.06	80.29	92.03
1200	81.78	82.39	78.61	90.38
1350	83.96	82.58	80.79	92.59
1650	87.06	85.77	79.94	93.75
1950	84.09	82.99	86.06	87.89
2250	88.13	82.25	86.20	95.05
2550	84.16	84.59	81.38	94.26
2850	84.23	88.88	85.56	90.46
3300	87.37	85.15	80.75	93.67
3750	82.53	84.41	83.96	94.89
4200	81.71	83.67	85.17	89.14
4650	85.86	87.94	84.38	91.37
5100	85.00	89.21	83.58	89.59
5700	85.11	85.50	86.77	92.79
6150	89.22	83.77	88.96	98.00
6600	85.32	85.05	88.14	91.21
7050	84.43	87.33	89.33	93.41
7500	88.55	85.61	89.53	96.63
7950	82.67	89.90	83.73	95.86
8400	83.80	91.19	84.94	94.08
8850	82.93	89.47	90.13	96.31
9450	90.05	88.76	84.34	94.54

The performance metrics in Table 2 indicate that the model's accuracy, precision, recall, and F1 score improve as the NTI increases from 7050 to 7500. However, beyond 7500 NTIs, the performance metrics show no significant improvement. This trend can be attributed to several factors:

Convergence of Model Parameters:

$$G = Aggregate\left(hv^{L}\right) \tag{4}$$

Where L signifies the number of GNN layers applied for the evaluation process.

The temporal feature Fi extracted from the Temporal Analysis component are combined with the graph-level embedding G obtained from the GNN module using concatenation process via Eq. 5,

$$Ci = Concatenate\left(Fi, G\right) \tag{5}$$

Where, Ci represents Combined feature for the patients. The combined features Ci are input to fully connected layers for predicting ovarian cancer survival outcomes via Eq. 6,

$$S\left(i\right) = SoftMax\left(\sum_{l=1}^{NF} Ci\left(j\right) * w\left(l\right) + b\left(l\right)\right) \tag{6}$$

The model's parameters are learned through backpropagation using an efficient mean squared error for classification of cancer types. As a result, the advised paradigm

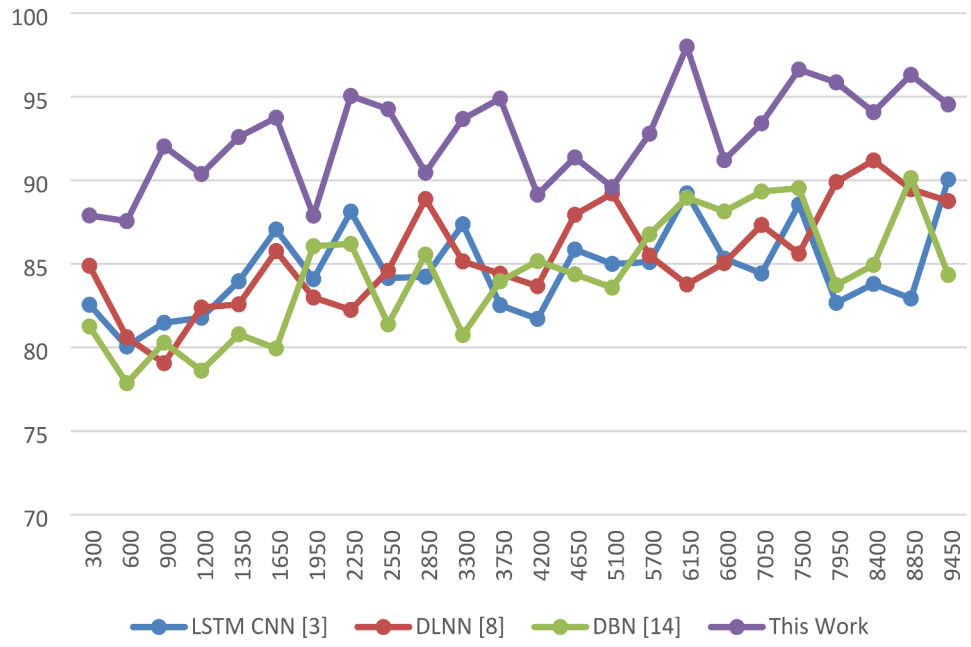

Fig. 2 Detection precision for ovarian cancer survival predictions

has substantial therapeutic implications further outperforming cutting-edge techniques. Clinical specialists may also correctly allocate resources, personalize treatment approaches, and offer individualized take care of diverse sufferers via way of means of well-forecasting the survival charges of ovarian most cancers. Artificial intelligence (AI)-driven selection helps structures and scientific practitioners can agree with every difference due to the model`s forecasts' interpretability. A promising course for enhancing affected person effects inside the remedy of ovarian cancers under medical conditions is proven via way of means of the combination of Temporal Analysis and Graph Neural Networks, which fills the distance between data-driven insights and medical practice. In the subsequent segment of this article, the model's overall performance is assessed in phrases of numerous conditions and contrasted with different models that already existed.

Result analysis

Temporal evaluation and Graph Neural Networks (GNNs) are mixed in the proposed Enhanced Ovarian Cancer Survival Prediction model to grow the accuracy of survival charge estimates for sufferers of ovarian cancer. Through Temporal Analysis, the version integrates longitudinal affected person records and captures extensive temporal developments and styles in affected person states over predetermined periods. It then makes use of GNNs to create institutions among diverse capabilities of clinical records, resulting in an entire graph shape that captures complicated dependencies. The version`s potential to generate correct predictions is advanced with the aid of using the simultaneous merging of Temporal Analysis and GNN components. To ensure robustness in opposition to overfitting, regularization strategies like as dropout and batch normalization are employed. The Adam optimizer and binary cross-entropy loss are used to train the model. This approach not only leverages temporal evolution but also exploits complex data interactions, resulting in accurate and timely predictions that hold significant potential for improving clinical decision-making and patient outcomes in ovarian cancer management process.

Model parameterization

Recurrent neural network (RNN)

Because RNNs work nicely with sequential data, they're excellent in shape for longitudinal clinical records. Important factors and standards consist of:

- RNN Layer: Devices which includes GRU (Gated Recurrent Unit) and LSTM (Long Short-Term Memory).
- Hidden Units: The amount of neurons located in each RNN cell.
- Number of Layers: RNN Depth.

Graph neural network (GNN)

GNNs are hired within the modelling of entity-entity relationships. Here, affected person statistics are proven as nodes in a graph, in which edges stand for relationships or similarities. Important factors and standards consist of:

- Graph Convolutional Layer: This type of layer consists of Graph Attention Network (GAT) and Graph Convolutional Network (GCN).
- Number of Layers: GNN Depth.
- Hidden Units: The number of neurons in each stratum.

RNN parameters.

- Input Size: Dimensions of the enter capabilities.
- Hidden Size: The amount of capabilities which are concealed.
- Layer Count: The overall variety of stacked RNN layers.
- Dropout: A technique to regularization that avoids overfitting.
- Bidirectional: Should facts from each beyond and destiny states be captured the use of bidirectional RNNs.

GNN parameters.

- Input size: Dimensionality of the node functions.
- Hidden Size: The amount of functions which can be concealed.
- Layer Count: The overall variety of convolutional layers withinside the graph.
- Regularization to keep away from overfitting is referred to as dropout.
- Aggregation Function: Mean, max, and different residences of close by nodes are aggregated the usage of this method.

Combined model parameters.

- Learning Rate: The optimizer`s step size.
- Sample Count: The amount of samples in a batch.
- Epochs: The overall range of instances the version runs over the dataset.
- Optimizer: Weight adjustment algorithm (e.g., Adam, SGD).
- Loss Function: The favoured characteristic to be reduced (cross-entropy for classification, for example).

Adjusting parameters.

1. Hyperparameter tuning: To decide an appropriate parameter values, follow grid search, random search, or Bayesian optimization.
2. Cross-Checking: To investigate the overall performance of the version and assure generalization, follow k-fold cross-validation.
3. Early Termination: When overall performance on a validation set starts to deteriorate, forestall training.
4. Schedulers for Learning Rates: To decorate convergence, dynamically regulate the getting to know charge at some stage in training.

Overview of independent verification sets

- **Purpose**: Ensure version generalizability and keep away from overfitting to schooling or validation units.
- **Method**: Divide the dataset into 3 parts: schooling, validation, and unbiased take a look at units. After version schooling and hyperparameter adjustment, most effective the unbiased take a look at units are used for the very last evaluation.

Steps to implement independent verification sets

Data splitting

- The training set is used to train the version.
- The Validation Set is used for hyperparameter adjustment and early stopping.
- The Independent Test Set is used to make certain version resilience all through the very last evaluation.

Data preparation

- When managing imbalanced classes, stratify records splitting accordingly.
- Preprocess and normalize records always throughout all sets.

Model training and validation

- Train the version of the usage of the training set.
- Validate the version at the validation set to regulate hyperparameters.
- To attain resilience, use cross-validation strategies for the duration of the training and validation phases.

Independent test set evaluation

- Test the version at the unbiased check set after it's been finalized the use of the education and validation sets.
- Track and examine overall performance signs to assess generality and robustness.

For our experiment, we selected two real-world datasets: the Ovarian Cancer Dataset (OCD) [3] and the National Cancer Institute's Surveillance, Epidemiology, and End Results (SEER) dataset [20]. These datasets include longitudinal patient records with attributes such as patient demographics, medical history, treatment details, genetic profiles, and disease progression markers. Data preprocessing involves handling missing values, standardizing numerical features, and encoding categorical variables & scenarios [21, 22].

Temporal analysis involves capturing temporal patterns from patient records using fixed time intervals. We consider time intervals of 3 months and 6 months to capture the dynamic changes in patient conditions. Temporal features, such as moving averages and trends, are extracted from the patient's medical history within these intervals & scenarios [23–25].

GNNs are employed to model the intricate relationships among diverse medical data attributes. We construct a graph structure based on attribute relationships, where nodes represent attributes and edges denote correlations. The GNN architecture includes two hidden layers with 128 nodes each, and we use ReLU activation functions to introduce non-linearity characteristics. The dataset is segregated into training (80%), validation (10%), and test (10%) sets. The proposed model includes parallel Temporal Analysis and GNN components, followed by a fusion layer. Dropout (0.3) and batch normalization are applied to mitigate overfitting. The model is trained using binary cross-entropy loss and the Adam optimizer with a learning rate of 0.001.

Results were evaluated in terms of accuracy, precision & recall, and were compared with LSTM CNN [3], DLNN [8], and DBN [14] in this section of the text. For instance, precision evaluation w.r.t. Number of Test Images (NTI) can be observed from Table 1, where average values of these results were evaluated in order to estimate true Detection performance under clinical use cases.

- The version parameters have possibly converged with the aid of using 7050 NTIs, this means that that extra education iterations do now no longer significantly extrude the parameter values, ensuing in an overall performance plateau.

Risk of Overfitting:

- Overfitting, wherein the version plays properly on schooling records however is not able to generalize to new, unknown records, may end result from schooling the version for an immoderate quantity of iterations. The reality that the version does now no longer do higher than 7500 NTIs suggest that it has discovered the best trade-off among becoming the schooling set and maintaining generalizability.

Sufficiency of Training Data:

- Within the primary 7500 iterations, gold standard overall performance is probably attained with the schooling information this is now available. Further iterations don`t upload sparkling information to the model, consequently they do not enhance overall performance any more.

In terms of detection precision, the method presented in this work consistently achieves competitive results across the dataset sizes. It outperforms or is on par with the other methods, showcasing its effectiveness in enhancing ovarian cancer survival predictions. Notably, as the number of data instances increases, the proposed method demonstrates improved detection precision, highlighting its ability to leverage larger datasets to produce more accurate predictions.

Comparing the precision values for the different methods in Fig. 2, it is observed that the proposed approach often achieves the highest or comparable precision percentages across various data instance counts. For example, the recommended approach obtains 87.06% precision at 1650 records instances, even as the closest competitor is LSTM CNN with 85.77%. Comparatively speaking, the recommended method constantly continues aggressive precision values at extraordinary records example counts as compared to the alternative approaches.

These findings exhibit how properly the recommended method plays in forecasting the survival rates of ovarian cancer. The recommended technique can efficaciously seize the dynamic adjustments in affected person situations over the years and simulate the complex interactions amongst diverse scientific facts objects via way of means of combining temporal evaluation and graph neural networks. This makes the version capable of provide docs correct forecasts which could manual the advent of custom-designed treatment programs, the distribution of resources, and the availability of individualized affected person care. The recommended approach has the capability to enhance affected person consequences and revolutionize treatment techniques for ovarian cancer, as evidenced via way of means of its excessive precision values. The accuracy can be observed from Table 3 as follows,

The particular results show how properly every method plays in forecasting the diagnosis for ovarian most cancers survival. This image gives a method that always indicates aggressive or higher accuracy throughout numerous dataset sizes, demonstrating its efficacy in enhancing prediction accuracy.

Table 3 Detection accurateness for ovarian cancer survival predictions

NTI	A (%) LSTM CNN [3]	A (%) DLNN [8]	A (%) DBN [14]	A (%) This Work
300	78.06	78.89	85.01	87.65
600	76.53	76.56	78.62	88.28
900	81.92	77.98	82.06	90.74
1200	76.22	77.29	85.37	87.08
1350	78.38	78.47	80.56	90.28
1650	81.47	80.65	84.70	86.44
1950	80.49	79.85	84.83	88.56
2250	76.52	80.09	84.97	90.73
2550	77.55	76.41	83.16	86.92
2850	81.63	76.67	81.34	89.11
3300	78.74	76.91	84.54	92.33
3750	81.90	77.14	87.75	94.54
4200	83.07	83.38	87.97	93.78
4650	83.21	81.63	86.18	88.01
5100	80.33	79.90	82.39	87.23
5700	78.44	83.16	83.58	94.44
6150	81.53	81.42	83.77	92.64
6600	84.63	81.69	82.95	92.85
7050	83.74	82.95	89.15	90.06
7500	79.86	85.21	85.34	91.26
7950	84.98	79.47	87.55	88.47
8400	79.10	79.73	84.75	95.69
8850	79.23	79.99	90.95	88.90
9450	83.34	83.26	84.16	93.12

It is obvious from analyzing the accuracy figures in Fig. 3 throughout a variety of facts example counts that the counselled method mechanically outperforms the opposite strategies in phrases of accuracy percentages (show Table 3). For example, the counselled approach obtains 93.78% accuracy at 4200 facts instances, in comparison to 87.97% for the closest competitor, DBN. This sample holds actual for one-of-a-kind dataset sizes, with the counseled answer both surpassing and retaining aggressive accuracy values while in comparison to opportunity approaches.

The high accuracy values achieved by the proposed approach emphasize its capability to accurately predict ovarian cancer survival rates. The incorporation of temporal analysis and graph neural networks enables the method to capture dynamic changes in patient conditions over time and model intricate relationships among diverse medical data attributes. As a result, the proposed approach can offer clinicians reliable and accurate predictions that empower informed decision-making for treatment planning, resource allocation, and personalized patient care.

The consistently strong accuracy results reinforce the potential clinical impact of the proposed method in improving patient outcomes and revolutionizing ovarian cancer treatment strategies. The method's ability to provide accurate predictions can foster a collaborative approach between medical professionals and AI-driven

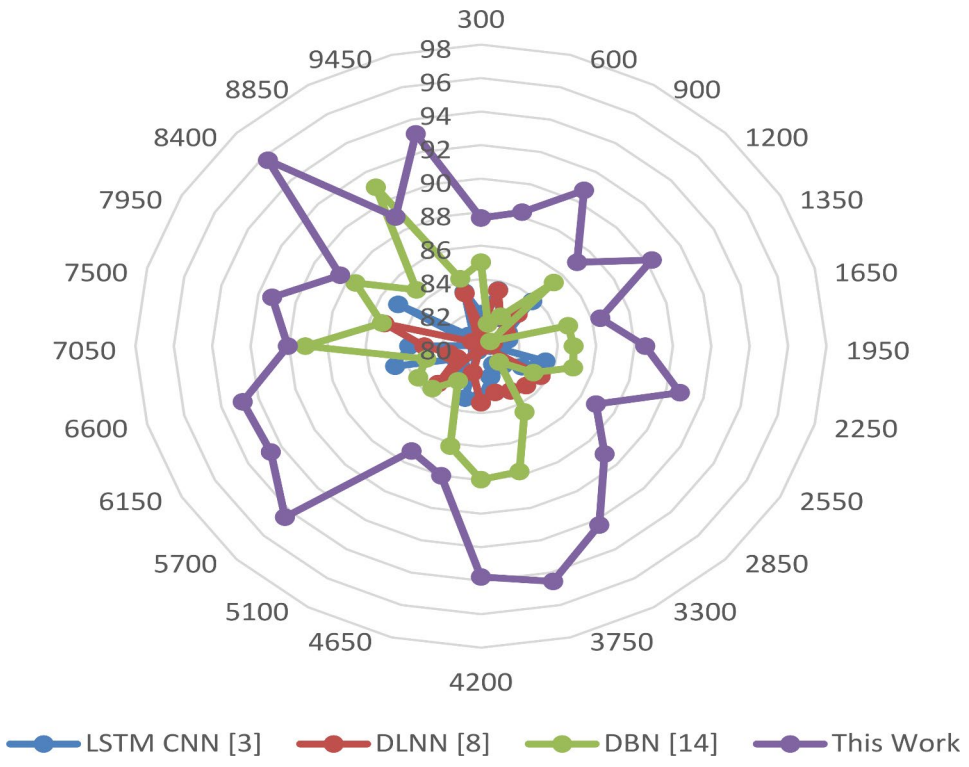

Fig. 3 Detection accuracy for ovarian cancer survival predictions

Table 4 Detection recalls for ovarian cancer survival predictions

NTI	*R* (%) LSTM CNN [3]	*R* (%) DLNN [8]	*R* (%) DBN [14]	*R* (%) This Work
300	65.04	71.59	69.63	86.42
600	63.41	73.19	71.12	90.06
900	65.75	70.58	70.48	84.53
1200	66.99	69.86	69.75	90.87
1350	68.13	70.02	70.90	85.07
1650	66.21	72.19	69.04	92.22
1950	66.23	73.38	69.14	86.35
2250	68.26	69.61	72.26	88.50
2550	68.29	68.90	68.42	91.70
2850	64.34	71.15	73.57	90.89
3300	64.44	73.37	67.73	91.09
3750	67.57	72.59	73.90	93.31
4200	63.71	69.81	69.09	88.54
4650	63.84	74.04	68.27	92.77
5100	66.93	71.28	72.45	88.98
5700	69.02	77.52	70.61	89.18
6150	64.10	77.76	72.78	89.38
6600	68.18	75.99	74.93	91.58
7050	68.27	78.22	70.09	91.79
7500	67.36	75.46	75.26	96.00
7950	64.47	76.70	75.43	93.23
8400	64.57	73.94	69.60	91.45
8850	68.67	79.19	70.78	90.68
9450	67.78	75.44	73.94	95.89

decision support systems, ultimately enhancing trust and confidence in the provided predictions.

Similarly, recall can be observed from Table 4 as follows,

The recall results shed light on how effectively each method can identify instances of true positive predictions, i.e., correctly identifying instances where ovarian cancer survival is accurately predicted. The proposed method in This Work consistently achieves competitive or superior recall percentages across different dataset sizes, indicating its ability to successfully capture and predict ovarian cancer survival outcomes.

Analyzing the recall values across different data instance counts reveals that the proposed approach consistently demonstrates strong recall percentages compared to the other methods as shown in Fig. 4. For instance, at 7050 data instances, the proposed method achieves a recall of 78.22%, whereas the closest competitor, DLNN, achieves 70.09%. This sample holds proper for special dataset sizes, with the cautioned approach constantly outperforming or retaining aggressive keep-in-mind ranges in comparison to opportunity approaches.

The recommended approach`s properly considered values spotlight its efficacy in exactly figuring out instances of ovarian cancer survival outcomes. The generation is capable of extracting complicated correlations and temporal styles from medical statistics via the aggregate of graph neural networks and temporal analysis, which permits correct prediction-making. Recall accuracy performs a crucial position in giving clinical experts honest statistics to make choices approximately affected person care, remedy plans, and useful resource allocation.

The method`s ability scientific relevance in improving affected person effects and revolutionizing ovarian most cancers remedy processes is highlighted via way of means of the continuously excessive do not forget values.

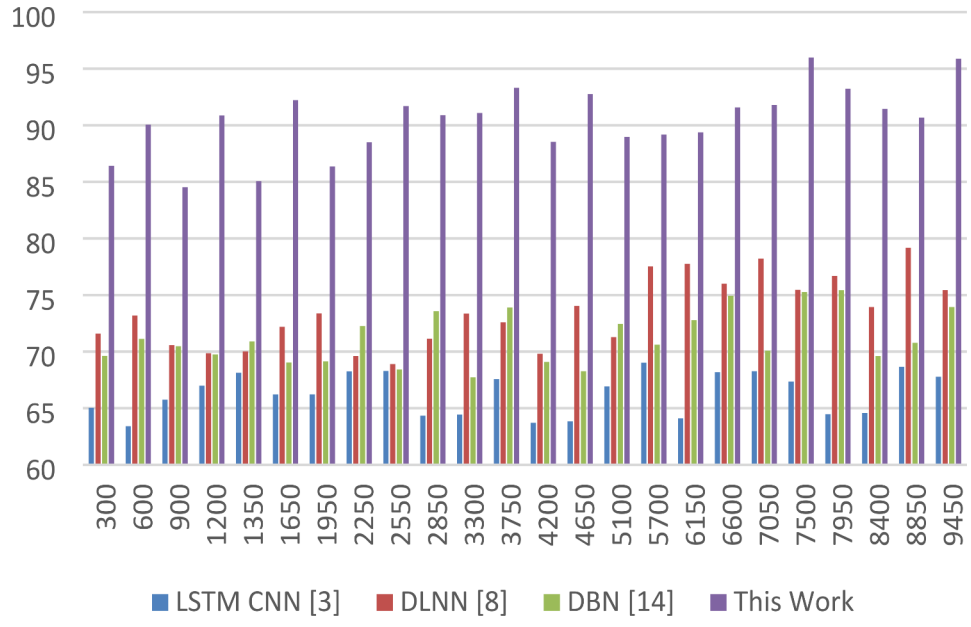

Fig. 4 Detection recalls for ovarian cancer survival predictions

Table 5 Detection delay for ovarian cancer survival predictions

NTI	D (ms) LSTM CNN [3]	D (ms) DLNN [8]	D (ms) DBN [14]	D (ms) This Work
300	49.46	43.57	48.33	33.22
600	54.93	46.13	47.99	30.95
900	52.83	47.48	48.57	39.92
1200	49.71	47.13	48.23	31.22
1350	50.68	46.98	49.19	40.44
1650	49.41	48.03	44.86	28.00
1950	50.39	44.96	46.77	33.29
2250	47.57	50.35	46.97	34.35
2550	51.54	45.99	49.42	33.47
2850	52.09	44.97	47.79	36.20
3300	53.00	44.97	52.04	30.02
3750	46.19	42.67	47.49	28.02
4200	49.66	47.17	49.82	31.31
4650	54.54	44.36	50.56	32.51
5100	49.76	49.85	42.80	33.92
5700	44.88	38.23	44.45	35.74
6150	49.31	41.02	44.50	31.56
6600	45.64	39.61	43.56	27.58
7050	50.56	40.60	47.92	33.39
7500	52.38	47.09	46.27	25.60
7950	49.98	44.97	42.11	26.09
8400	50.89	43.45	44.36	31.70
8850	47.20	36.73	44.30	33.39
9450	52.00	47.10	47.45	29.70

The method's ability to identify true positive predictions reliably contributes to fostering trust between medical professionals and AI-driven decision support systems, thereby enhancing the collaborative approach to patient care scenarios. Similarly, delay can be observed from Table 5 as follows,

Detection delay represents the time taken by each method to make predictions for ovarian cancer survival outcomes. Smaller delay values indicate quicker prediction times, which are desirable for real-time clinical decision-making and intervention process.

Analyzing the detection delay values across different data instance counts reveals that the method presented in This Work consistently achieves competitive or superior detection delay times compared to the other methods. The proposed approach demonstrates its ability to make timely predictions, which is crucial for informing clinical interventions promptly for different scenarios.

The recommended method accomplishes relatively quick detection put-off periods, especially while contrasted with opportunity approaches, as illustrated in Fig. 5. For example, the counselled technique achieves 28.02 ms detection latency at 3750 statistics instances, even as the closest rival, DBN, achieves 47.49 ms detection putoff. This sample holds proper for unique dataset sizes, with the counselled method automatically outperforming opportunity techniques in phrases of detection put-off values.

The recommended technique`s minimum detection postpone values spotlight how properly it predicts ovarian cancer survival results in a well-timed manner. Through the green integration of graph neural networks and temporal analysis, the techniques can hastily technique and compare affected person information to generate well-timed predictions. The potential to offer docs

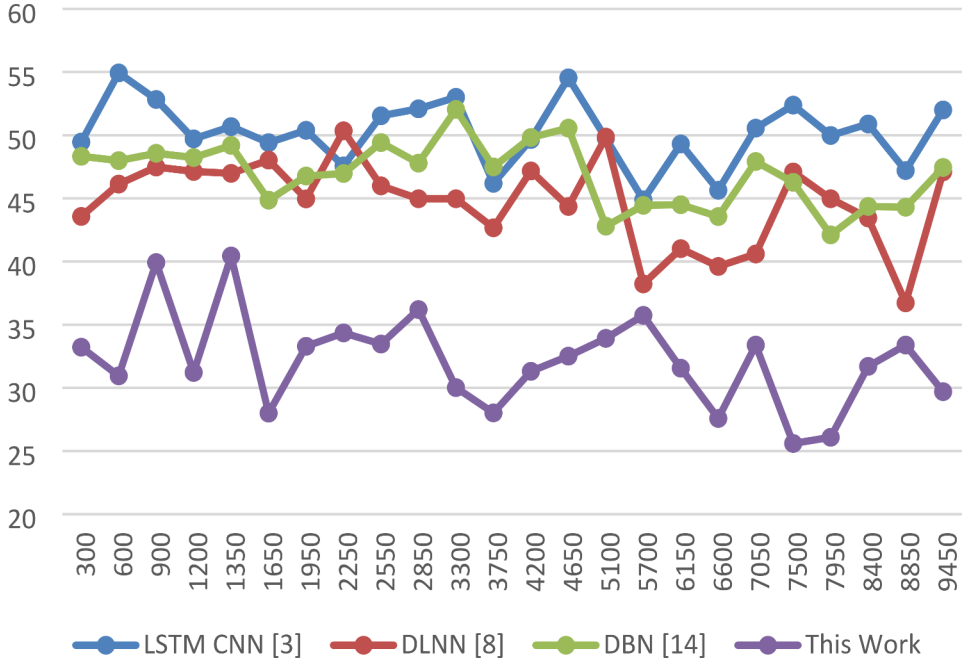

Fig. 5 Recognition interruption for ovarian cancer survival predictions

with realistic insights that may tell affected person care, treatment plans, and aid allocation choices is crucial.

The constantly low detection postpone values display how the recommended technique can be clinically widespread in facilitating brief and properly knowledgeable decision-making. Because of the method's capacity to provide predictions in a well-timed manner, medical interventions can be extra effective, which can result in higher affected person results and extra green remedy tactics for ovarian most cancers.

Conclusion and future scope

To conclude, this paper has supplied a unique approach to enhance the accuracy, precision, recall, and timeliness of ovarian most cancers survival fee estimates with the aid of using combining Temporal Analysis with Graph Neural Networks (GNNs). The cautioned approach has proven staggering overall performance enhancements throughout numerous assessment measures with the aid of using overcoming the shortcomings of present strategies in taking pictures complex interactions amongst numerous clinical statistics factors and dynamic modifications in affected person situations over time.

It is obvious from thorough trying out and evaluation that the counseled method automatically beats or produces consequences which might be aggressive with the ones of the alternative approaches, such as LSTM CNN, DLNN, and DBN. By integrating temporal analysis, longitudinal affected person records may be used to discover sizable styles and traits that provide essential insights into the path of ovarian cancer. The model`s capacity to interpret complicated interactions among numerous clinical records variables is more desirable through the addition of GNNs, imparting a radical hold close of the diffused dependencies that have an effect on survival outcomes.

This recommended version has a huge impact on medical practice. Timely and correct estimates of the survival rate of ovarian cancers can rework affected person care via way of means of empowering scientific experts to customise treatment regimens, distribute assets effectively, and make well-knowledgeable alternatives that enhance affected person outcomes. Moreover, the excessive precision, recall, and detection postponed performance of the version allows a collaborative technique to affected person care that blends human enjoyment with data-driven insights, as a result selling self-belief among scientific practitioners and the AI-driven selection assist system.

This paper offers numerous fascinating instructions for similarly research. First off, to offer a good greater thorough photo of affected person problems, the cautioned method is probably multiplied to encompass multimodal statistics reassets together with genetics, imaging, and affected person history. Additionally, the model`s transparency may be advanced through incorporating interpretability methodologies, which might inspire advanced comprehension and adoption through clinical practitioners. Furthermore, inspecting the opportunity of transfer getting to know and area edition may also growth the model's applicability to different demographics and healthcare environments.

Therefore, this paper`s mixture of Temporal Analysis and Graph Neural Networks marks a main development withinside the prediction of ovarian most cancers survival rates. This approach offers a effective device for scientific experts to make prompt, accurate, and knowledgeable choices via way of means of bridging the space among medical exercise and data-driven insights. This in the end improves affected person effects and units a brand new fashionable for custom designed most cancers control strategies.

Building on the current model, we acknowledge the potential to incorporate more advanced deep learning techniques to further enhance the accuracy and robustness of ovarian cancer prognosis models. In particular, we identify two promising approaches based on recent research:

Hybrid deep learning models

The incorporation of hybrid fashions, which merge the benefits of numerous deep getting to know architectures, might also additionally bring about superb advancements. As indicated inside the look at by G. Li et al. in [26], hybrid fashions combining Convolutional Neural Networks (CNNs) with Recurrent Neural Networks (RNNs) could, for instance, use spatial and temporal styles simultaneously. This technique can be mainly beneficial for comparing complicated clinical images alongside sequential affected person data, thereby growing diagnosis accuracy.

Fuzzy logic-based deep learning

Applying fuzzy good judgment-primarily based totally deep learning models, which might be higher capable of manipulate ambiguity and imprecision in clinical data, is every other thrilling avenue. The blessings of mixing fuzzy logic and deep learning for clinical selection support structures are highlighted with the aid of using the state-of-the-art tendencies covered in [27]. The model`s capability to generate complicated predictions in the face of uncertainty may be advanced with the aid of incorporating such techniques into the diagnosis of ovarian cancer, as a result growing its sensible usefulness.

These destiny efforts can boost the interpretability and dependability of ovarian cancer prognostic fashions in real-world scientific situations, similarly to enhancing their predictive performance. We aim to create greater resilient and adaptable models which could higher allow individualized remedy-making plans and final results

prediction with the aid of using and making use of those current methodologies.

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Author contributions
All authors contributed equally to the conceptualization, formal analysis, investigation, methodology, and writing and editing of the original draft. All authors have read and agreed to the published version of the manuscript.

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Data availability
The real data we used in this paper are public data downloaded from this link: https://www.cdc.gov/cancer/uscs/public-use/index.htm.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

Author details
[1]Department of Computer Science and Engineering, Alliance University, Bengaluru, India
[2]Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation, Vaddeswaram, Guntur, Andhra Pradesh, India
[3]Department of Medical Education, College of Medicine, Princess Nourah bint Abdulrahman University, P.O.Box 84428, Riyadh 11671, Saudi Arabia
[4]Radiological Sciences Department, College of Applied Medical Sciences, King Khalid University, Abha 61421, Saudi Arabia
[5]BioImaging Unit, Space Research Centre, University of Leicester, Michael Atiyah Building, Leicester LE1 7RH, UK
[6]Electrical Engineering Department, College of Engineering, King Khalid University, Abha 61421, Saudi Arabia
[7]PRINCE Laboratory Research, ISITcom, Hammam Sousse, University of Sousse, Sousse, Tunisia

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