Chapter 15

Cancer survival prediction using artificial intelligence: current status and future prospects

15.1 Introduction

The COVID-19 pandemic has significantly impacted cancer patients, particularly in terms of limited access to healthcare services and necessary medical care. This has led to delays in cancer diagnoses, postponement of treatments, and decreased patient follow-up, all of which have the potential to negatively impact cancer patient outcomes (Al-Quteimat & Amer, 2020). However, artificial intelligence (AI)-based approaches for cancer survival prediction have emerged as promising solutions to improve cancer patient care during the pandemic (Ahmedt-Aristizabal et al., 2022; Alzubaidi et al., 2021; Ching, 2018; Cruz & Wishart, 2007; Fatima et al., 2020; Hosni et al., 2019; Huang et al., 2020; Li, Huang, et al., 2022; Mihaylov et al., 2019; Picard et al., 2021; Si et al., 2021; Tran et al., 2021; Zhang et al., 2021; Zhu et al., 2020). These AI-based approaches can help healthcare providers identify patients who are at higher risk of negative outcomes and provide targeted interventions to improve their chances of survival (Raju et al., 2020). Cancer survival prediction refers to the estimation of the likelihood that a patient will survive the disease over a certain period, such as 5 years by analyzing clinical, patient demographic, molecular, and pathological data. Cancer survival prediction is crucial for patients and clinicians for several reasons (Kim et al., 2022). Firstly, it allows healthcare professionals to estimate a patient's prognosis and tailor their treatment plan accordingly. This can help identify patients at high risk of disease progression or recurrence, enabling clinicians to provide personalized and timely interventions, avoid over or undertreatment, and reduce unnecessary side effects and costs. Additionally, cancer survival prediction can aid in clinical trial design and patient selection, ultimately leading to more effective treatments. Finally, cancer survival prediction can help patients and their families by providing a realistic expectation of their disease outcome and helping them to make informed decisions about their treatment and prepare for the future.

The use of publicly accessible large-scale cancer databases such as Genomic Data Commons (Grossman et al., 2016), Gene Expression Omnibus (Edgar et al., 2002), Molecular Taxonomy of Breast Cancer International Consortium (Curtis et al., 2012), The Cancer Genome Atlas (TCGA) (Weinstein & Collisson, 2013), and the International Cancer Genome Consortium (The International Cancer Genome Consortium, 2010) provides comprehensive genomic, transcriptomic, and clinical information for a variety of cancer types, enabling the development of predictive models and the identification of new biomarkers and therapeutic targets. Access to these databases can provide researchers and healthcare professionals with valuable insights into cancer survival and aid in the development of more effective treatments. This valuable information guides treatment decisions and helps clinicians to customize treatment plans based on the patient's unique characteristics and the predicted likelihood of response to treatment (Kim et al., 2022). Additionally, the usage of publicly accessible databases allows researchers from around the world to collaborate and data sharing among researchers, which can accelerate the development of innovative and improved cancer treatments. To visualize this process, Fig. 15.1 illustrates the essential stages involved in applying AI techniques to predict cancer survival. The workflow encompasses critical stages such as data collection and preprocessing, feature selection, model selection and training, and model evaluation and prediction.

The structure of the remaining section in this paper is organized as follows. In Section 15.2, we present an overview of diverse AI techniques applied in cancer survival prediction, including machine learning (MI), ensemble learning, deep learning, graph representation learning (GRL), multimodal representation learning (MRL), and attention models. In Section 15.3, we explore the various evaluation metrics utilized in cancer survival prediction. Following that, Section 15.4

Data Science in the Medical Field. https://doi.org/10.1016/B978-0-443-24028-7.00016-7

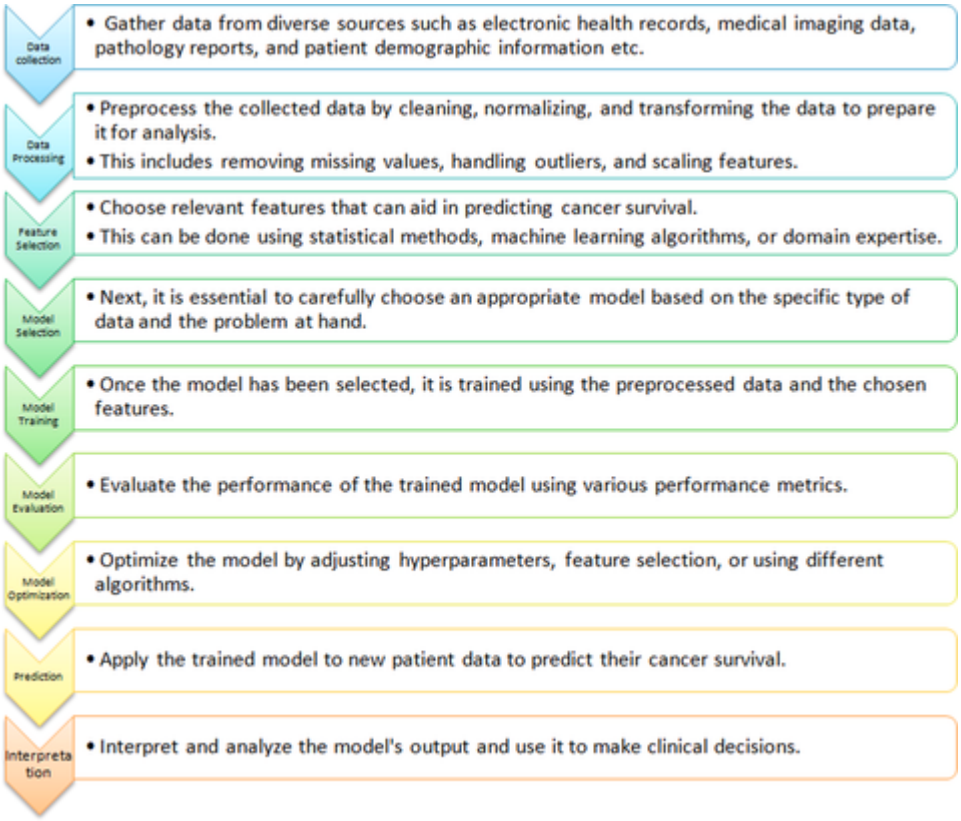

FIGURE 15.1 High-level workflow of artificial intelligence techniques for cancer survival prediction.

addresses the challenges and limitations associated with the implementation of AI techniques for predicting cancer survival prediction. Finally, in Section 15.5, we will wrap up by discussing potential research directions in this critical field.

15.2 Literature review

In recent years, AI techniques have gained significant attention for their potential to improve cancer survival prediction accuracy and enable personalized treatment, as well as their ability to process large and complex datasets and identify patterns and relationships that may be challenging for human analysts to identify. Fig. 15.2 illustrates various AI techniques, such as MI (Cruz & Wishart, 2007; Fatima et al., 2020; Mihaylov et al., 2019; Picard et al., 2021), ensemble learning (Hosni et al., 2019), deep learning (Alzubaidi et al., 2021; Ching, 2018; Huang et al., 2020; Si et al., 2021; Tran et al., 2021; Zhu et al., 2020), GRL (Ahmedt-Aristizabal et al., 2022; Li, Huang, et al., 2022; Zhang et al., 2021), MRL, and attention models. By integrating various data sources, such as clinical, genomic, and imaging data, these techniques aim to enhance survival prediction accuracy and offer deeper in Fig. 15.2 sights into the factors influencing cancer survival (Chen et al., 2019; Gao, 2022; Li, Huang, et al., 2022; Vale-Silva & Rohr, 2021; Wu et al., 2023; Yan & Feng, 2022).

15.2.1 Classical machine learning techniques for cancer survival prediction

In this section, we will explore classical machine-learning techniques that have been applied to cancer survival prediction. These include logistic regression, K-nearest neighbors, decision trees, naive Bayes (NB), and support vector machines. We will discuss their principles, strengths, and weaknesses in the context of cancer prognosis.

15.2.1.1 Logistic regression

Logistic regression is a linear classification algorithm widely used for binary and multiclass classification tasks (Peng et al., 2002). In the context of cancer survival prediction, it assesses the relationship between predictor variables and the

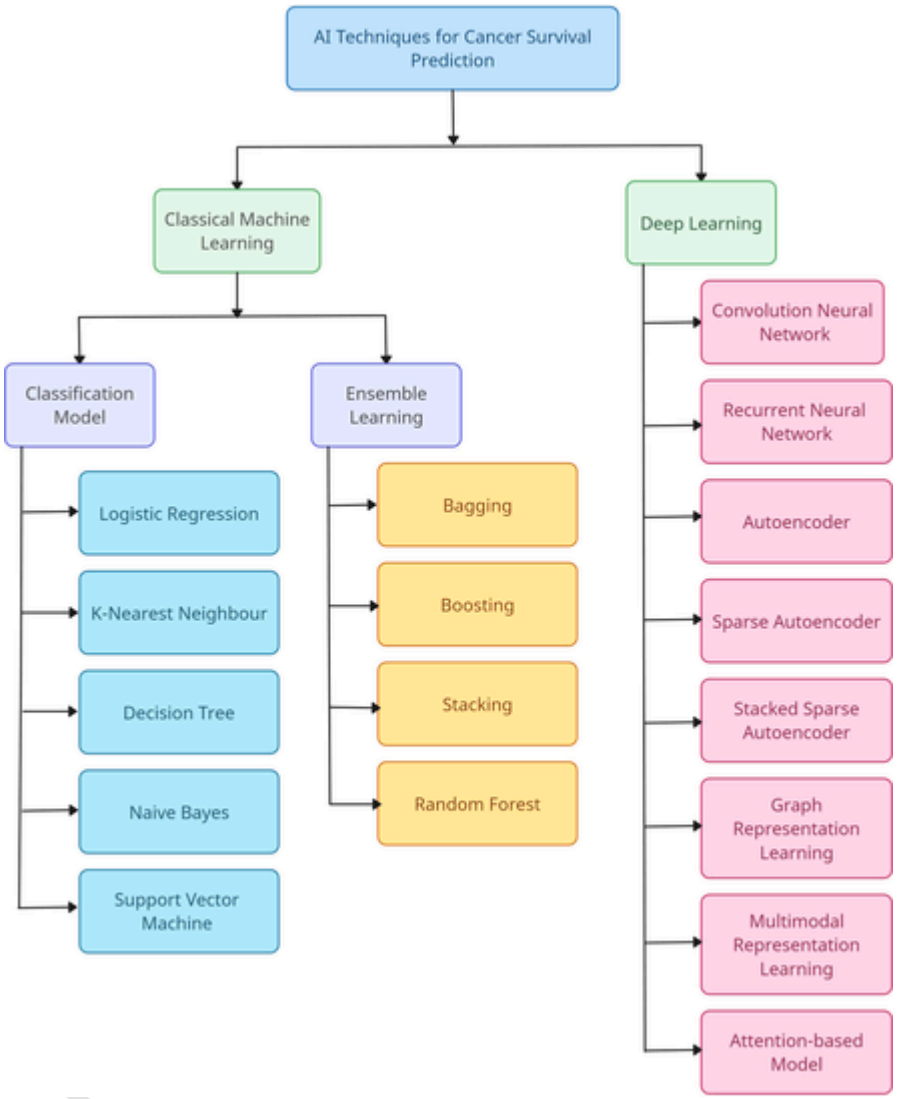

FIGURE 15.2 Artificial intelligence techniques for cancer survival prediction used.

probability of a patient's survival outcome. By employing a logistic function, it transforms the continuous output into a probability score ranging from 0 to 1.

15.2.1.2 K-nearest neighbors

K-nearest neighbors (KNN) is a nonparametric, instance-based algorithm used for both classification and regression tasks. In the context of cancer survival prediction, KNN calculates the distance between a target patient and its KNN in the feature space. The algorithm then assigns the most frequent class or computes the average survival times of the k neighbors to predict the survival outcome for the target patient (Shichao et al., 2018; Uddin et al., 2022).

15.2.1.3 Decision tree

Decision tree (DT) is a supervised learning algorithm based on a tree-like structure used for both classification and regression tasks. In the context of cancer survival prediction, DTs recursively partition the feature space based on the most informative features, creating a tree structure that aids in decision-making. Each internal node represents a feature, and each leaf node corresponds to a predicted survival outcome. DTs are interpretable and allow capturing nonlinear relationships between features, making them valuable for identifying important prognostic factors in cancer research (Lynch et al., 2017).

15.2.1.4 Naive Bayes

NB is a classification algorithm that leverages Bayes' theorem and probabilistic principles for predicting class probabilities. Despite its "naïve" assumption of feature independence, it has shown efficacy in various applications, including cancer survival prediction. In this context, NB calculates the posterior probability of a patient's survival status given the observed features. It is particularly useful when dealing with high-dimensional datasets and offers computational efficiency for large-scale studies (Cruz & Wishart, 2007).

15.2.1.5 Support vector machine

Support vector machine (SVM) is a robust supervised learning algorithm employed for classification and regression tasks, known for its effective handling of complex data distributions. In the context of cancer survival prediction, SVM aims to find the optimal hyperplane that maximizes the margin between different classes, effectively separating patients based on their survival outcomes. SVM's ability to handle high-dimensional data and handle nonlinear relationships through kernel functions makes it suitable for complex cancer survival prediction tasks (Lynch et al., 2017).

15.2.2 Ensemble learning techniques for cancer survival prediction

Ensemble learning techniques are powerful approaches that combine multiple models to improve predictive performance and generalization. These methods combine individual model predictions to produce a more robust and accurate final prediction (Hosni et al., 2019). In the context of cancer survival prediction, these techniques play a crucial role in enhancing the strengths of diverse models to achieve more accurate and robust results.

15.2.2.1 Bagging

Bagging, also known as bootstrap aggregating, is designed to enhance the stability and accuracy of MI models (Breiman, 1996). In the context of cancer survival prediction, Bagging involves training multiple instances of the same base model on different subsets of the training data, created through bootstrapping (random sampling with replacement) (Hosni et al., 2019). Each model makes individual predictions, and the final prediction is obtained through majority voting (for classification) or averaging (for regression) (Fatima et al., 2020).

15.2.2.2 Boosting

Boosting is an iterative technique that enhances the performance of weak learners to create a powerful predictive model. In the context of cancer survival prediction, boosting starts by training a weak learner on the entire training dataset. Subsequent weak learners are trained on the instances that were misclassified by previous learners, assigning higher weights to these instances to emphasize their importance. The ultimate prediction is derived by aggregating the weighted predictions from all learners (Fatima et al., 2020; Hosni et al., 2019).

15.2.2.3 Stacking

Stacking, also known as stacked generalization, leverages the strengths of multiple diverse models to improve prediction performance (David & Wolpert, 1992). In cancer survival prediction, stacking involves training multiple base models on the training data and using their predictions as input to a higher-level metamodel. The metamodel then combines these predictions to make the final prediction (Hosni et al., 2019). Stacking allows the model to benefit from the diverse perspectives of different base models, resulting in improved predictive power and better generalization (Fatima et al., 2020).

15.2.2.4 Random forest

Random forest constructs multiple decision trees on bootstrapped subsets of the data. It then combines their predictions through majority voting (for classification) or averaging (for regression) (Lynch et al., 2017). In the context of cancer survival prediction, random forest mitigates overfitting and enhances prediction accuracy by leveraging the collective insights from multiple trees. Moreover, it offers feature importance rankings, enabling the identification of crucial prognostic factors in cancer studies.

15.2.3 Deep learning techniques for cancer survival prediction

Here, we will explore the application of deep learning techniques in cancer survival prediction. We will discuss convolutional neural networks (CNNs) for medical imaging analysis, recurrent neural networks (RNNs) for sequential data, autoencoder for feature learning, GRL for complex data relationships, and MRL for integrating diverse data types, and attention models for identifying critical features. We will highlight how these advanced methods can capture intricate patterns and relationships in cancer data, potentially revolutionizing survival prediction.

15.2.3.1 Convolutional neural network

CNN is a deep learning architecture specifically designed for image recognition tasks. In cancer survival prediction, CNN can be applied to analyze medical imaging data such as MRI or CT scans (Kumar et al., 2022; Lee, 2023). It consists of multiple layers, including convolutional, pooling, and fully connected layers. The convolutional layers apply filters to extract spatial features from the input images, while the pooling layers reduce the spatial dimensions, preserving essential information. CNNs have shown promising results in identifying tumor characteristics and aiding in personalized prognosis based on medical images (Mostavi et al., 2020; Sinzinger et al., 2022).

15.2.3.2 Recurrent neural network

RNN is a type of deep learning architecture suitable for sequential data analysis, making it applicable to time-series data like patient health records. In cancer survival prediction, RNNs can model the temporal dependencies between clinical events and patient outcomes (Lee, 2023). The main strength of RNNs lies in their ability to capture long-range dependencies in sequential data, allowing them to consider a patient's entire medical history for survival prediction. However, traditional RNNs suffer from vanishing or exploding gradient problems, which led to the development of long short-term memory and gated recurrent unit cells to address these issues (Hamed et al., 2020; LeCun et al., 2015).

15.2.3.3 Autoencoder

Autoencoders are unsupervised deep learning models used for feature learning and dimensionality reduction. In cancer survival prediction, an autoencoder can be employed to extract the most informative features from high-dimensional genomic or imaging data (Kumar et al., 2022; Shen et al., 2023). The model consists of an encoder that compresses the input data into a latent space representation and a decoder that reconstructs the original input from the compressed representation (Lee, 2023). By learning a compact and meaningful representation, autoencoder aids in reducing data complexity and improving predictive performance.

15.2.3.4 Sparse autoencoder

Sparse autoencoder are a variant of autoencoder that introduces sparsity constraints to the hidden layer activations. The sparsity constraint encourages only a small subset of the neurons in the hidden layer to be active, resulting in a more concise and interpretable representation of the input data (Lee, 2023). In cancer survival prediction, a sparse autoencoder can be applied to identify critical genomic features or biomarkers associated with patient outcomes (Wu & Fang, 2022).

15.2.3.5 Stacked sparse autoencoder

Stacked sparse autoencoder combines multiple layers of sparse autoencoder to create a deep architecture. Each layer learns increasingly abstract and higher-level features, leading to a hierarchical representation of the input data (Kumar et al., 2022; Lee, 2023). Stacked sparse autoencoder excel at capturing intricate patterns and complex relationships in cancer-related data, enabling accurate and detailed survival predictions (Xu et al., 2016).

Table 15.1 provides an overview of some pivotal studies that show the progress made in this field, focusing on the integration of multiple modalities of data, from gene expression to wholUsedBreastsa e-slide images.

Table 15.1 illustrates the advancement of deep learning models in the realm of cancer survival prediction. Each study not only presents a novel method or model but also underscores the increasing reliance on multimodal data. By leveraging a combination of clinical, gene expression, histopathology, and other data modalities, these models achieve superior predictive performance, showcasing the potential of AI in reshaping oncological prognostics.

TABLE 15.1 Deep learning techniques used for cancer survival prediction.

Year	Author	Cancer type	Key finding
2023	Wu et al. (2023)	Multiple (including breast, lung, and brain) contain multimodalities including WSI, gene expression, CNA, and clinical data.	Proposed cross-aligned multimodal representation learning (CAMR). CAMR effectively reduces modality gaps, generating both modality invariant and specific representation for enhanced cancer survival prediction.
2022	Arya and Saha (2022)	Breasts contain multimodalities including (gene expression, copy number alteration, and clinical data).	Proposed stacked-based ensemble model architecture. CNN for feature extraction then a stacked-based approach utilizing three modalities of data improves predictive performance, neighborhood. Integrating especially for imbalanced datasets.
2022	Kanwal et al. (2022)	Multiple (including brain, prostate, bladder, colorectal, and breast) contain multimodalities.	A novel framework was introduced that integrates DL/ML and RL with AAA for improved cancer prognosis prediction using multimodal data, incorporating early and late fusion techniques.
2022	Li et al. (2022)	Colorectal	Developed a Distribution-based Multiple-Instance Survival Learning algorithm (DeepDisMISL). Combined percentile-scored patches with highest and lowest scored ones, including neighborhood instances around percentiles further boost prediction accuracy.
2019	Cheerla and Gevaert (2019)	Obtained from TCGA (including 20 different cancer types) contain multimodalities including clinical, gene expression, microRNA expression, and histopathology WSIs data.	Developed a DL survival model with multimodal representation. Demonstrated efficient use of multimodal data, even with missing modalities, proposed efficient WSI analysis by sampling key region of interest.
2019	Sun et al. (2018)	Breast contain multimodalities (including gene expression, copy number alteration, and clinical data).	Proposed Multimodal Deep Neural Network by integrating Multi-dimensional Data (MDNNMD). MDNNMD integrates multidimensional data for better prediction; and outperforms single-dimensional methods.

15.2.3.6 Graph representation learning for cancer survival prediction

The GRL technique has been gaining attention in recent years for its potential in cancer survival prediction. It involves the use of graphs to represent data, with each node representing a data point and the edges between them representing relationships or interactions between those data points (Li, Huang, et al., 2022). The goal is to learn a low-dimensional representation of the graph that captures its underlying structure and patterns. GRL has several advantages over traditional methods, particularly in cases where the data is complex and heterogeneous, as is often the case with cancer data. It can effectively capture the interactions between different types of data, such as genomic, clinical, and imaging data, and identify hidden relationships that may not be evident through other methods (Ahmedt-Aristizabal et al., 2021).

For example, in a study on computational histopathology, graph convolutional networks (GCNs) were used to analyze digital pathology images (Ahmedt-Aristizabal et al., 2021; Chen et al., 2019; Curtis et al., 2012; Edgar et al., 2002; Gao, 2022; Grossman et al., 2016; Li, Huang, et al., 2022; The International Cancer Genome Consortium, 2010; Vale-Silva & Rohr, 2021; Weinstein & Collisson, 2013; Wu et al., 2023; Yan & Feng, 2022). The whole slide image (WSI) was represented as a graph, with each cell or region in the image represented as a node and the edges representing spatial relationships between the nodes. By leveraging the power of GCNs, the study aimed to capture more complex spatial relationships between different regions of the image and incorporate information about the local and global context of each region, potentially improving the accuracy of the classification task and making the method more robust to variations in the size, shape, and position of the regions of interest.

15.2.3.7 Multimodal representation learning for cancer survival prediction

MRL is a technique that involves integrating multiple types of data, such as genomics, imaging, and clinical data, to improve cancer survival prediction. This approach has become increasingly popular in recent years, allowing for a more comprehensive and holistic view of the patient's condition (Wu et al., 2023). The benefit of MRL is that it can leverage the complementary information from different data types to make more accurate predictions and also discover novel relationships between different data types (Zhang et al., 2019). For example, one study used multimodal GNN to integrate gene expression, copy number alteration, and clinical data to predict breast cancer survival. The GNN was able to capture the complex relationships between the different data modalities by constructing a bipartite graph between patient and multimodal data, leading to improved survival prediction accuracy (Gao, 2022). Overall, we can say that this technique has shown promising results in several studies, indicating that it can significantly improve the accuracy of cancer survival prediction compared to models that only use a single data type.

15.2.3.8 Attention model for cancer survival prediction

Survival-based attention models are a type of attention model that is used in cancer survival prediction tasks. These models utilize attention mechanisms to highlight relevant features from input data that are most informative for predicting survival outcomes. The attention weights are assigned to each feature based on their contribution to the survival outcome. By using attention mechanisms, survival-based attention models can identify important features that may be missed by traditional models, thus potentially improving the accuracy of cancer survival prediction (Chen et al., 2019). One example of a survival-based attention model is the DeepAttMISL model (Chen et al., 2019), which uses a neural network with a self-attention mechanism to predict survival outcomes for breast cancer patients. The self-attention mechanism is used to highlight important regions of the input data, such as regions of the tumor in the WSI.

15.3 Evaluation metrics for cancer survival prediction

Understanding how well predictive models perform in the context of cancer survival prediction requires us to use various evaluation metrics. In Fig. 15.3, we discuss these metrics, including classification metrics, discriminative metrics, and explainability metrics, allowing us to assess the models' effectiveness in real-life terms. Let's dive into Fig. 15.3 to these metrics with detailed explanations and real-life examples to make them more relatable.

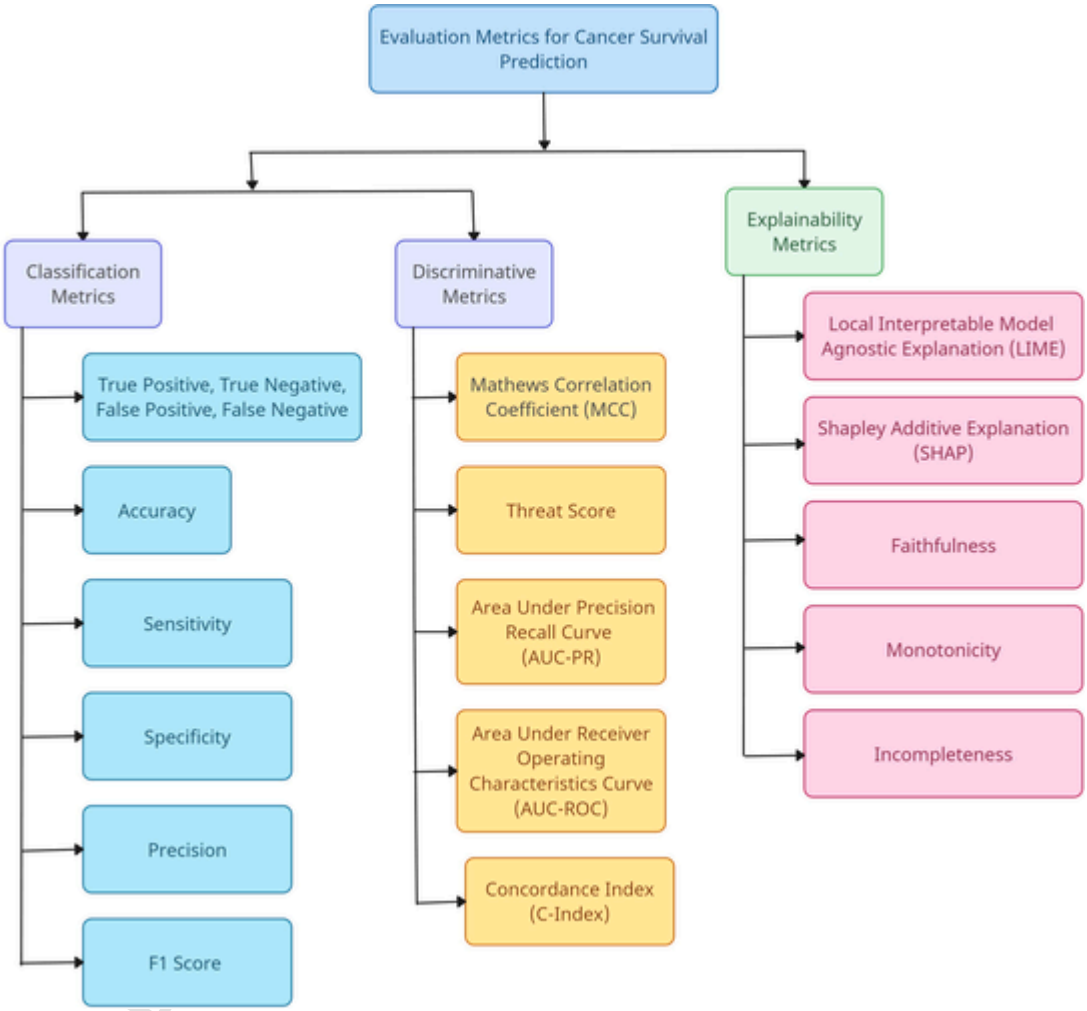

FIGURE 15.3 Various evaluation metrics for cancer survival prediction.

15.3.1 Classification metrics

15.3.1.1 True positive

Imagine a medical test that detects a specific disease. In our context, true positive (TP) represents the number of patients who genuinely have the disease, and the test correctly identifies them as positive cases. So, if the test correctly diagnoses 90 out of 100 patients with cancer as positive, we have 90 TPs.

15.3.1.2 True negative

Continuing with our medical test analogy, true negative (TN) is the number of patients who don't have the disease, and the test correctly identifies them as negative. If 80 out of 100 healthy individuals are accurately classified as negative, we have 80 TNs.

15.3.1.3 False positive

Now, think of a false positive (FP) as a false alarm. In medical terms, it's when the test wrongly identifies a healthy person as having the disease. If, out of 100 healthy individuals, the test mistakenly identifies 20 as having the disease, we have 20 FPs.

15.3.1.4 False negative

False negative (FN), in our analogy, is when the test misses a real case. It's when a sick person is incorrectly classified as healthy. If, out of 100 patients with the disease, the test misses 10 and labels them as healthy, we have 10 FNs.

15.3.1.5 Accuracy

Accuracy is the measure of how well our medical test performs overall. It's like asking, "Out of all the tests conducted, how many were correct?" If our test's results were correct for 170 out of 200 patients (90 TPs+80 TNs), the accuracy is 85%.

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{FP} + \text{TN} + \text{FN}} \tag{15.1}$$

15.3.1.6 Sensitivity (recall or TP rate)

Sensitivity tells us how good our test is at catching the disease when it's really there. If, out of 100 patients with the disease, our test correctly identifies 90, our sensitivity is 90%.

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}} \tag{15.2}$$

15.3.1.7 Specificity (TN rate)

Specificity measures our test's ability to correctly identify those without the disease. If, out of 100 healthy individuals, our test correctly identifies 80 as negative, our specificity is 80%.

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}} \tag{15.3}$$

15.3.1.8 Precision (positive predictive value)

Precision focuses on how well our test correctly identifies positives. If, out of 110 individuals labeled as positive by the test, 90 truly have the disease (TPs), our precision is 90/110, or roughly 81.8%.

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \tag{15.4}$$

15.3.1.9 F1-score

The F1-score combines precision and sensitivity into a single metric. It's like considering both the number of correctly identified disease cases and how well the test avoids false alarms. In our medical test example, it's a way of striking a balance between not missing real cases and not falsely alarming healthy individuals. It provides a more comprehensive view of our test's overall performance in cancer survival prediction.

$$F1 - \text{Score} = \frac{2 * \text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}} \tag{15.5}$$

15.3.2 Discriminative metrics

15.3.2.1 Matthews correlation coefficient

The Matthews correlation coefficient, often referred to as MCC, is a measure used in cancer survival prediction to evaluate how well a predictive model can distinguish between survivors and nonsurvivors. It provides a score ranging from –1 to +1, where +1 indicates a perfect prediction, 0 suggests no better than random, and –1 implies total disagreement between prediction and reality.

Example: Imagine we have a predictive model that aims to predict whether a cancer patient will survive or not after a specific treatment. MCC takes into account all four scenarios: TPs (correctly predicted survivors), TNs (correctly predicted nonsurvivors), FPs (predicted survivors who did not survive), and FNs (predicted nonsurvivors who survived).

If our MCC score is +0.8, it indicates that our model has strong predictive power, correctly classifying many survivors and nonsurvivors. On the other hand, an MCC score of –0.2 would imply that the model's predictions are inconsistent with actual outcomes.

$$\mathrm{MCC} = \frac{(\mathrm{TP} * \mathrm{TN}) - (\mathrm{FP} * \mathrm{FN})}{\sqrt{(\mathrm{TP} + \mathrm{FP})(\mathrm{TP} + \mathrm{FN})(\mathrm{TN} + \mathrm{FP})(\mathrm{TN} + \mathrm{FN})}} \tag{15.6}$$

15.3.2.2 Threat score (Critical Success Index)

The Threat score, also known as the Critical Success Index, assesses the accuracy of a predictive model in cancer survival prediction. It measures how well the model predicts actual survival outcomes in cancer patients.

Example: Consider a scenario where our predictive model forecasts that 80 out of 100 cancer patients will survive based on their medical data. Out of these 80 predicted survivors, 75 patients indeed survive (TPs), while 5 do not (FPs). Additionally, out of the 20 predicted nonsurvivors, 18 patients did not survive (TNs), and 2 patients unexpectedly survived (FNs).

Using the threat score formula, if we calculate a score of 0.85, it suggests that our model has a high degree of success in accurately predicting survival outcomes. In this case, it aligns with the observed events closely.

$$\mathrm{ThreatScore} = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN} + \mathrm{FP}} \tag{15.7}$$

15.3.2.3 Area under the receiver operating characteristic curve

The area under the receiver operating characteristic curve (AUC-ROC) is a metric that evaluates how well a predictive model can differentiate between patients who survived and those who did not. It is valuable in cancer survival prediction as it quantifies the model's ability to rank patients by their survival probabilities. It's often depicted as a curve on a graph, with the AUC providing a numerical representation of the model's discriminatory power.

Example: Imagine you have a diagnostic test for a disease. If the test effectively distinguishes between healthy (negative) and diseased (positive) individuals and the AUC-ROC is close to 1, it means the test is excellent at classifying people correctly. Conversely, if the AUC-ROC is closer to 0.5, it suggests that the test performs no better than random guessing.

15.3.2.4 Area under the precision-recall curve

The area under the precision-recall curve (AUC-PR) metric measures the trade-off between precision and recall for different classification thresholds. It is particularly useful in cancer survival prediction when dealing with imbalanced datasets, where one class (survivors) significantly outnumbers the other (nonsurvivors).

Example: Suppose we have a dataset with 90% survivors and 10% nonsurvivors. In such cases, precision-recall analysis becomes crucial. A high AUC-PR value, say 0.85, indicates that our model can make precise predictions (few FPs) while maintaining high recall (capturing most of the actual survivors).

15.3.2.5 Concordance index

The concordance index, often referred to as the C-Index, evaluates the predictive accuracy of a survival model by comparing predicted survival times with observed survival times among cancer patients.

Example: In a real-world scenario, suppose our predictive model estimates the survival times for a group of cancer patients after treatment. The C-index, if calculated as 0.82, indicates that our model's predictions closely align with the actual survival times for these patients, signifying its effectiveness in ranking them by survival probabilities.

15.3.3 Explainability metrics

15.3.3.1 Local interpretable model-agnostic explanations

In the context of cancer survival prediction, local interpretable model-agnostic explanations (LIME) plays a crucial role in offering precise insights into individual predictions. Instead of providing generic explanations, LIME focuses on the specifics of each prediction, making it highly relevant for healthcare professionals to gain a deeper understanding of the model's decision-making process and make the predictions more transparent and interpretable (Lundberg & Lee, 2017; Ribeiro et al., 2016). It achieves this by creating a local interpretable model based on data points resembling the one being analyzed. By doing so, LIME highlights the significance of each feature for that specific prediction (Gramegna Alex, 2021).

Example: Think of LIME as a personalized interpreter for cancer survival predictions. Suppose we have a patient whose data suggest a favorable prognosis. LIME dives into this specific case, highlighting which patient characteristics, such as age, tumor size, or treatment type, influence the prediction the most. This patient-centered approach empowers healthcare providers with valuable insights into why a particular prognosis was made for this specific individual.

15.3.3.2 Shapley additive explanations

Shapley additive explanations (SHAPs) offers a versatile framework for interpreting MI models, including those used in cancer survival prediction. It employs Shapley values, derived from game theory, to quantify the contribution of each feature to a prediction (Lundberg & Lee, 2017; Shapley, 1953). This approach helps us grasp how different factors impact predictions, making it particularly useful in understanding cancer survival prognosis (Gramegna Alex, 2021).

Example: Imagine our MI model as a complex puzzle. SHAP breaks down this puzzle, revealing the influence of each piece (feature) on the final picture (prediction). For instance, it might show that a patient's family history of cancer has a more significant impact on their survival prediction than other factors. This “feature breakdown” simplifies the model's decision process, aiding both researchers and clinicians in comprehending the rationale behind predictions.

15.3.3.3 Faithfulness

Faithfulness metrics assess the accuracy of how an explanation method represents a model's decision-making process. It checks if the explanation faithfully reflects how the model arrives at its predictions (Xie et al., 2023).

Example: In the context of cancer survival prediction, faithfulness metrics ensure that the explanations we derive accurately reflect our model's decision-making process. We're talking about a connection between what the model says is important and what it truly does. Imagine using a correlation coefficient, like the familiar Pearson coefficient, to ascertain if the weight distribution in our explanation matches the model's behavior. A value close to 1 signifies harmony, while values close to 0 raise a flag for inconsistencies (Oblizanov et al., 2023).

15.3.3.4 Monotonicity

Monotonicity metrics focus on whether changes in a feature consistently impact the model's prediction in the expected direction. They validate if the explanation accurately captures the predictable relationship between features and predictions. These metrics also evaluate the correctness of a sequence of features ranked by their increasing importance obtained through explainable AI methods (Oblizanov et al., 2023). It is important to note that monotonicity metrics focus on assessing the correctness of the distribution of weights between features, rather than evaluating the accuracy of individual weight values (Nguyen et al., 2023).

15.3.3.5 Incompleteness

Incompleteness metrics measure the extent to which an explanation method falls short in explaining specific aspects of the model's behavior. They assess whether the explanation overlooks relevant features or fails to capture essential patterns in the model's decision process (Oblizanov et al., 2023).

Example: In cancer survival prediction, where every detail matters, incompleteness metrics help us understand if our explanation method misses any crucial aspects of the model's behavior. It's a way of checking if we've captured every essential pattern and relevant feature. It's like ensuring that the puzzle of our model's decision-making is fully assembled, leaving no piece unturned.

15.4 Challenges and limitations of using artificial intelligence techniques

Now we discuss some explanations of the challenges and limitations associated with the application of AI techniques in predicting cancer survival, along with the ethical considerations they bring:

15.4.1 Data availability and quality (the data dilemma)

Navigating the world of AI for cancer survival prediction poses a daunting challenge—the availability and quality of data. Despite the vast ocean of data available, obtaining data of high quality is an extremely difficult task. Often, data comes with imperfections—missing pieces, inconsistencies, and sometimes, hidden biases. Moreover, data from different sources might not speak the same language, making it challenging to combine and decipher effectively (Kelly et al., 2019).

15.4.2 Interpretation and explainability (the artificial intelligence enigma)

Another significant challenge is the interpretation and explainability of AI models. As AI models can be highly complex, this makes it tough to grasp how they make their predictions (Samek et al., 2017). This lack of transparency can be problematic for healthcare professionals who need to explain to patients why a particular treatment is being recommended (Holzinger et al., 2017).

15.4.3 Ethical considerations (guardian of privacy)

Think of AI as a powerful tool, capable of great good or potential harm. One of the most important concerns is privacy. Imagine you're sharing your deepest secrets with a confidant—you expect them to be kept safe. In healthcare, if the patient data falls into the wrong hands, it could lead to serious breaches of confidentiality. AI's hunger for data must be balanced with the need to protect individual privacy. Moreover, AI has the potential to propagate existing biases and inequalities in healthcare (Naik et al., 2022). It's like trying to create a fair race when some runners have a head start. Ensuring that AI benefits all, regardless of background or circumstance, is a moral obligation we must fulfill.

15.5 Conclusion and future direction

AI techniques hold significant potential in the field of cancer survival prediction. With the availability of massive-scale datasets and advancements in computational resources, AI models have evolved to be more accurate and robust. However, several challenges and constraints need to be addressed, related to data accessibility and quality, the interpretability of AI-driven models and explainability, and ethical considerations. Despite these challenges, there are several key takeaways and emerging trends in the field. Firstly, the use of multimodal data and the integration of diverse data sources are becoming increasingly popular and offer a holistic perspective. Secondly, the development of graph representation learning models is an exciting area with significant potential for improving cancer survival prediction. Lastly, the integration of AI models with clinical decision support systems is an important area for improving patient outcomes.

In terms of future directions, there is a need for more standardized and transparent evaluation metrics to compare the performance of various models. Additionally, there is a need for more studies that focus on the generalizability of AI models across diverse populations and clinical settings are essential. Finally, there is a need for more interdisciplinary collaborations between computer scientists, clinicians, and other stakeholders is essential to ensure that AI models are developed with a patient-centered approach and ethical considerations in mind.

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