Development and Validation of Deep Learning Models for Ovarian Clear Cell Carcinoma Survival

Yan Liu  
Qilu Hospital of Shandong University

Yang yang  
Qilu Hospital of Shandong University

Wenna Zhao  
Qilu Hospital of Shandong University

Yuan Zhang  
Qilu Hospital of Shandong University

Changzhen Huang  
Qilu Hospital of Shandong University

Yuanjian Wang  
Qilu Hospital of Shandong University

Ran Chu  
Qilu Hospital of Shandong University

Li Li  
Qilu Hospital of Shandong University

Yu Wang  (✉ wy_med@sdu.edu.cn)  
Qilu Hospital of Shandong University

Research Article

Keywords: ovarian clear cell carcinoma, survival analysis, machine learning, deep learning

Posted Date: August 21st, 2023

DOI: https://doi.org/10.21203/rs.3.rs-3266140/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License. Read Full License
Abstract

Background

Ovarian clear cell carcinoma (OCCC) is a rare and distinct histologic subtype of epithelial ovarian carcinomas. Few studies have explored the use of deep learning models for predicting survival in OCCC. Our study aims to compare the performance of deep learning models with a multivariate Cox regression model in predicting survival for OCCC patients.

Methods

In this population-based cohort study, we extracted 926 patients diagnosed with OCCC between 2010 and 2017 from the Surveillance, epidemiology, and end results (SEER) database. Three algorithms, including DeepSurv and neural multi-task logistic regression (NMTLR) based on neural networks, and RSF based on ensemble learning, were chosen for training. Additionally, a Cox proportional hazard model was constructed for comparison purposes. The algorithm was externally validated on an independent test cohort, comprising 134 OCCC patients diagnosed between January 2005 and July 2021 in Qilu Hospital of Shandong University. The model's performance was assessed using the C-index and IBS (Integrated Brier Score), while the accuracy of predicting 1-, 3-, and 5-year survival was evaluated using ROC and AUC. Furthermore, a user-friendly interface was developed to facilitate the use of deep learning models for predicting survival.

Results

The deep learning model has demonstrated promising results in predicting overall survival (OS) for OCCC patients, outperforming the Cox proportional hazard model. DeepSurv consistently exhibited superior prediction performance compared to the Cox proportional hazard model in both the SEER training set (C-index: 0.781 vs. 0.724) and the independent China test set (C-index: 0.836 vs. 0.829). Additionally, the DeepSurv model displayed significantly higher AUC values for 3-year and 5-year OS in the China cohort when compared to the Cox proportional hazard model (AUC for 3-year OS: 0.844 vs. 0.836; AUC for 5-year OS: 0.821 vs. 0.817). Moreover, we developed a user-friendly graphical interface that allows for visualization of the deep learning model.

Conclusions

This study appears that deep learning models hold more promising than traditional linear regression models in predicting OS in OCCC patients. However, it is important to note that further large-scale, real-world studies are required to validate and substantiate this model.
**Introduction**

Ovarian clear cell carcinoma (OCCC) is a relatively uncommon variant of ovarian cancer, which represents approximately 10% of all ovarian malignancies. Its occurrence varies from 5–25% depending on geographic and ethnic factors, with the highest incidence observed among Asian women [1–3]. Patients with early-stage OCCC generally exhibit favorable prognosis, whereas those diagnosed with advanced disease have poorer clinical outcomes compared with high-grade serous ovarian carcinoma [4, 5]. The prognosis for OCCC patients is particularly challenging due to its inherent resistance to platinum-based chemotherapy, highlighting the urgent need for more precise therapies [6, 7]. Stratifying OCCC patients based on survival outcomes is a critical step in treatment. Previous studies have identified independent prognostic factors such as tumor stage, residual tumor, lymph node metastasis, and treatment choice, which contribute to the personalized prediction of survival [8–11].

A comprehensive prognostic evaluation system would be helpful to guide the selection of treatment options, accurately answer OCCC patients’ concerns about survival and optimize their management. Cox proportional hazard (CoxPH) models have gained popularity for outcome prediction. Nomograms, predictive tools based on the Cox proportional hazard model that integrate important predictors, have been widely utilized for risk quantification and prognosis assessment in various cancer types [12–14]. However, the CoxPH model assumes that each predictive variable has a consistent effect at every follow-up time point, disregarding the potential variation in the impact of predictors on individual patients over time. Additionally, these models rely on linear assumptions rather than performing nonlinear analyses that can better represent the diverse clinical characteristics found in the real world. Consequently, there is a need for a novel method capable of performing nonlinear analyses [15].

Artificial intelligence (AI) has proven to have great potential in many areas of healthcare [16, 17]. Deep learning, a subset of machine learning, involves the identification of increasingly complex features within a multi-layer model. Deep learning is particularly effective in solving multi-factor and nonlinear problems [18, 19]. The continuous advancement of Deep learning research methods has paved the way for the application of machine learning in complex medical scenarios. Katzman et al [20] conducted a study where they combined the CoxPH model with a neural network called DeepSurv, and this approach could potentially improve the survival time of a specific group of patients. Avesani et al [21] used a multicentric database of advanced serous ovarian cancer to develop predictive radiological and Deep learning models for early recurrence and BRCA mutations, while validating them in a diverse group of cases from other institutions.

Our study aims to evaluate the predictive performance of machine learning models in estimating the survival of OCCC patients. Additionally, we intend to develop user-friendly web-based applications that utilize the most effective algorithms for clinical use. Through these effects, we aim to propel the field of clinical AI models and provide valuable prognostic assessments for OCCC patients.

**Materials and methods**
Patient population and data collection

For this retrospective cohort study, we obtained medical records of patients diagnosed with OCCC from the Surveillance, Epidemiology, and End Results (SEER) registry, covering the year of 2010–2017. The SEER database comprises data from 18 registries, representing approximately 27.8% of the total US population. We utilized the SEER*Stat software (Version 8.4.0; National Cancer Institute, Bethesda, MD) to extract relevant information. We collected the demographic information of cases (year of diagnosis, age, race, marital status), tumor characteristics (laterality, grade, stage (American Joint Commission on Cancer [AJCC] 7th version), tumor size, CA-125 level, tumor extension, distant metastasis), treatment-specific details (radiotherapy, chemotherapy, number of examined lymph nodes [LNs], LN status, surgical type, residual tumor). The initial staging information of the recruited patients was determined using the AJCC 7th edition and the SEER combined stage group. Subsequently, we restaged the original staging information based on the Federation of International of Gynecologists and Obstetricians (FIGO) 2018 staging guidelines.

The exclusion criteria were as follows: (1) not the primary tumor; (2) without histologic confirmation; (3) survival time shorter than 1 month; (4) no surgery; and (5) unknown information about LN, tumor size, stage, carbohydrate antigen-125 (CA-125) level, residual tumor and organ metastasis.

To validate these models, we collected an external test cohort provided by the China database. The cohort was composed of 134 patients with stage I to IV OCCC diagnosed between January 2005 and July 2021 in Qilu Hospital of Shandong University, which are completely distinct from the patients in SEER database. This study was approved by the Qilu Hospital of Shandong University ethics committee (KYLL-202301-012) and conducted according to the guidelines of the Declaration of Helsinki. Cohort selection is illustrated in Fig. 1.

Feature Selection

Collinearity occurs when two features are strongly related to each other. In order to avoid highly correlated features and reduce computational costs, we need to avoid over-fitting the model. Therefore, we employed the cor function from the stats R package to calculate the correlation between the features. A Pearson correlation coefficient of 0.7 indicates a high degree of collinearity between the features. Furthermore, we utilized univariate and multivariate Cox regression to assess the underlying features. This approach allows us to evaluate the impact of individual features on the outcome while considering the influence of other covariates.

Model development

In this study, the patients in the SEER database were randomly divided into a training and test dataset, with a sample ratio of 7:3. The China dataset was utilized for external validation. Three commonly employed machine learning methods were implemented using Python version 3.7 and the PySurvival package. These methods include two neural network-based models (DeepSurv [20] and neural network multitask logistic regression [NMLTR]) and one ensemble learning model (RSF [22]). Each model has
several hyperparameters that can impact prediction accuracy, such as the learning rate. To determine the optimal hyperparameters for each model, a random hyperparameter search was conducted with 5-fold cross-validation on the training dataset. The performance of models with different combinations of hyperparameters was evaluated using the concordance index (C-index). Additionally, a multivariable CoxPH model was constructed for comparison purposes. Eleven variables were utilized as input data, while 1, 3, and 5-year overall survival were used as the output data for training and evaluation.

**Model evaluation**

The predictive performance of the three machine learning models was evaluated using the C-index and the integrated Brier score (IBS). The C-index measures the prediction accuracy of the model, with a value of 0.5 or lower indicating suboptimal performance and higher values indicating better accuracy. The IBS, on the other hand, is a measure of prediction error. A value of 0.5 or higher suggests poorer predictive performance, while lower values indicate better performance. The IBS was calculated using prediction error curves ranging from 0 (perfect performance) to 0.25 [23]. To assess the time-dependent sensitivity and specificity of the model, receiver operating characteristic (ROC) curves were generated, and the area under the curve (AUC) values were calculated for 1-year, 3-year, and 5-year survival. The AUC provides a measure of the model's discriminatory power, with higher values indicating better performance in distinguishing between positive and negative outcomes.

**Feature importance**

To evaluate the correlation between individual features and model accuracy, we calculate the importance of each feature by substituting its data in the test set. The model's accuracy, measured by the C-index, is then recalculated using the permuted data to determine the importance of each feature [24].

**Model visualization**

We deployed the best-performing algorithm using Python's Streamlit package, creating an interactive web application for practical use.

**Statistical analysis**

We utilized the R programming language (version 4.1.2) for data preprocessing and visualization. For model development, we employed three machine learning algorithms implemented using the PySurvival package in the Python programming language (version 3.6.8). A p-value of < 0.05 was deemed statistically significant.

**Results**

**Baseline characteristics of the OCCC patients**

A total of 1060 patients diagnosed with OCCC were enrolled in this study. We collected data of 2,470 patients in the SEER program between 2010 and 2017. Based on the inclusion and exclusion criteria,
1,544 patients were excluded because there were missing data for one or more of 11 variables. Therefore, the analysis was conducted on 926 patients with OCCC using various machine learning algorithms. Additionally, we reviewed data from 134 patients at Qilu Hospital of Shandong University in China (Fig. 1). The main baseline clinical data are summarized in Table 1. The majority of patients (791, 74.6%) were diagnosed at the early stage of the disease, and most were unilateral (930, 87.7%). Of these patients, 845 (79.7%) patients underwent lymph node dissection and 914 (86.2%) received chemotherapy. The increase of CA-125 level (786, 74.2%) may suggest the diagnosis of disease to some extent. During the follow-up period, 274 (29.6%) patients in the SEER database and 32 (23.9%) patients in the China cohort experienced events (deaths from OCCC).
Table 1
Main characteristics of patients in the whole data sets of survival analysis.

<table>
<thead>
<tr>
<th>Characteristic*</th>
<th>Data set, No (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Training (n = 648)</td>
</tr>
<tr>
<td>Age, years</td>
<td></td>
</tr>
<tr>
<td>50</td>
<td>170 (26.2)</td>
</tr>
<tr>
<td>50–60</td>
<td>244 (37.7)</td>
</tr>
<tr>
<td>60</td>
<td>234 (36.1)</td>
</tr>
<tr>
<td>Marriage</td>
<td></td>
</tr>
<tr>
<td>Single</td>
<td>166 (25.6)</td>
</tr>
<tr>
<td>Married</td>
<td>376 (58.0)</td>
</tr>
<tr>
<td>Divorced</td>
<td>60 (9.3)</td>
</tr>
<tr>
<td>Widowed</td>
<td>46 (7.1)</td>
</tr>
<tr>
<td>Laterality</td>
<td></td>
</tr>
<tr>
<td>Unilateral</td>
<td>572 (88.3)</td>
</tr>
<tr>
<td>Bilateral</td>
<td>76 (11.7)</td>
</tr>
<tr>
<td>FIGO 2018 stage</td>
<td></td>
</tr>
<tr>
<td>I</td>
<td>392 (60.5)</td>
</tr>
<tr>
<td>II</td>
<td>84 (13.0)</td>
</tr>
<tr>
<td>III</td>
<td>144 (22.2)</td>
</tr>
<tr>
<td>IV</td>
<td>28 (4.3)</td>
</tr>
<tr>
<td>CA 125</td>
<td></td>
</tr>
<tr>
<td>Normal</td>
<td>185 (28.5)</td>
</tr>
<tr>
<td>Elevated</td>
<td>463 (71.5)</td>
</tr>
<tr>
<td>Chemotherapy</td>
<td></td>
</tr>
<tr>
<td>None/unknown</td>
<td>93 (14.4)</td>
</tr>
<tr>
<td>Yes</td>
<td>555 (85.6)</td>
</tr>
</tbody>
</table>

SEER, Surveillance, Epidemiology and End Results cancer registry; CA-125, carbohydrate antigen-125; LN, lymph node.

*Other detailed clinical characteristics can be found in Tables S1 in Additional file 1.
<table>
<thead>
<tr>
<th>Characteristic*</th>
<th>Data set, No (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Training (n = 648)</td>
</tr>
<tr>
<td>Residual tumor</td>
<td></td>
</tr>
<tr>
<td>No surgery</td>
<td>149 (23.0)</td>
</tr>
<tr>
<td>Macroscopic residual tumor or residual tumor greater than 1 cm</td>
<td>27 (4.2)</td>
</tr>
<tr>
<td>Optimal debulking surgery or no gross residual tumor or residual tumor less than 1 cm</td>
<td>472 (72.8)</td>
</tr>
<tr>
<td>LN examined</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>124 (19.1)</td>
</tr>
<tr>
<td>1–10</td>
<td>186 (28.7)</td>
</tr>
<tr>
<td>10</td>
<td>338 (52.2)</td>
</tr>
<tr>
<td>LN positive</td>
<td></td>
</tr>
<tr>
<td>No dissection</td>
<td>124 (19.1)</td>
</tr>
<tr>
<td>Negative</td>
<td>438 (67.6)</td>
</tr>
<tr>
<td>Positive</td>
<td>86 (13.3)</td>
</tr>
<tr>
<td>Metastasis</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>639 (98.6)</td>
</tr>
<tr>
<td>Yes</td>
<td>9 (1.4)</td>
</tr>
<tr>
<td>Surgery</td>
<td></td>
</tr>
<tr>
<td>Oophorectomy</td>
<td>139 (21.5)</td>
</tr>
<tr>
<td>Oophorectomy + omentectomy</td>
<td>317 (48.9)</td>
</tr>
<tr>
<td>Debulking surgery</td>
<td>185 (28.5)</td>
</tr>
<tr>
<td>Pelvic exenteration</td>
<td>7 (1.1)</td>
</tr>
<tr>
<td>Survival status</td>
<td></td>
</tr>
<tr>
<td>Death</td>
<td>199 (30.7)</td>
</tr>
<tr>
<td>Alive</td>
<td>449 (69.3)</td>
</tr>
</tbody>
</table>

SEER, Surveillance, Epidemiology and End Results cancer registry; CA-125, carbohydrate antigen-125; LN, lymph node.

*Other detailed clinical characteristics can be found in Tables S1 in Additional file 1.
Feature analysis and selection

According to the Cox regression analysis (Additional file 1: Table S1), the following variables were included in model development: age, marital status, laterality, stage, CA-125 level, distant metastasis, surgical type, residual tumor, the number of LN examined, LN status, chemotherapy. Collinearity analysis revealed that there was no significant collinearity among the 11 variables included (Fig. 2). The estimated correlation values are distributed within the range of -1 to +1. They are represented by color depth, with a number closer to either end value implying a stronger negative or positive correlation.

Model development and validation

Based on the included variables, we conducted 1000 repeated random searches with 5-fold cross validation on the training data set, and then selected the parameter that showed the highest average C-index in the cross validation as the optimal parameter. Figure S1 in Additional file 2 demonstrated the loss convergence of two neural network models (DeepSurv and NMTLR). Performance evaluation of the models generated by the three machine learning algorithms and CoxPH is presented in Table 2. In the China test dataset, both machine learning models showed significantly better discrimination compared to the CoxPH model (C-index of DeepSurv vs. RSF vs. CoxPH: 0.836 vs. 0.850 vs. 0.829). In the SEER test dataset, the NMTLR model exhibited better predictions than the CoxPH model (C-index of NMTLR vs CoxPH: 0.744 vs 0.729). The IBS of the four models in the two test datasets is shown in the Figure S2 of Additional file 3. IBS values were well below 0.25 across the entire model time axis, indicating good predictive performance for the models.

Table 2
Performance of four survival models.

<table>
<thead>
<tr>
<th>Models</th>
<th>C index</th>
<th></th>
<th></th>
<th>IBS</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Train</td>
<td>SEER test dataset</td>
<td>China test dataset</td>
<td>Train</td>
<td>SEER test dataset</td>
</tr>
<tr>
<td>CoxPH</td>
<td>0.724</td>
<td>0.729</td>
<td>0.829</td>
<td>0.140</td>
<td>0.130</td>
<td>0.120</td>
</tr>
<tr>
<td>DeepSurv</td>
<td>0.781</td>
<td>0.718</td>
<td>0.836</td>
<td>0.120</td>
<td>0.130</td>
<td>0.130</td>
</tr>
<tr>
<td>NMTLR</td>
<td>0.716</td>
<td>0.744</td>
<td>0.818</td>
<td>0.150</td>
<td>0.140</td>
<td>0.150</td>
</tr>
<tr>
<td>RSF(^a)</td>
<td>0.732</td>
<td>0.706</td>
<td>0.850</td>
<td>0.160</td>
<td>0.160</td>
<td>0.140</td>
</tr>
</tbody>
</table>

CoxPH, Cox proportional hazards; NMLTR, Neural multi-task logistic regression; RSF, Random survival forest; IBS, Integrated Brier Score; C index, Concordance index.

Overall, the AUC values of the three machine learning algorithms outperformed the CoxPH model on both test datasets, as shown in Fig. 3 and Table S2 of Additional file 1. Specifically, for the SEER test dataset, the NMTLR model achieved optimal performance with the highest 1-, 3-, 5-year AUC values (1-year AUC: 0.894 [0.842–0.945]; 3-year AUC: 0.798 [0.725–0.870]; 5-year AUC: 0.796 [0.727–0.865]). In China test
dataset, the DeepSurv model demonstrated the best AUC values of 3-,5-year (3-year AUC: 0.844 [0.749–0.940]; 5-year AUC: 0.821 [0.712–0.931]). These results indicate that the deep learning models were more accurate in predicting the survival prognosis of patients with OCCC compared to the CoxPH model.

**Feature importance**

Feature importance evaluation (Additional file 4: Figure S3) determined the importance of characteristics for model accuracy. On average, the C-index of alternative data for variables such as stage, surgery, LN examined, LN positive, CA-125, age, residual tumor, chemotherapy, and metastasis decreased by more than 1%. A higher value indicates greater importance in predicting the accuracy of the respective model.

**Model visualization**

We have created a user-friendly web application using streamlit (https://survival-of-ovarian-clear-cell-carcinoma.streamlit.app/) to support researchers and doctors in utilizing our predictive model. Users can enter clinical parameters of a new sample into a web interface (Fig. 4), and the online application can subsequently estimate the survival probability based on data from OCCC patients.

**Discussion**

OCCC is considered to have different biological features from other types of epithelial ovarian cancer, but few attempts have been made to develop predictive models. However, the development of an accurate prognostic model is crucial for clinical decision-making and improving the survival outcomes of advanced OCCC patients, given its poor prognosis. Thus, our study aimed to develop deep learning network models and validate their prognostic performance using an independent external cohort. Importantly, the Deepsurv model consistently demonstrated superior performance in the external dataset, highlighting its clinical applicability.

Previous studies have reported several linear models for predicting the survival in patients with OCCC. For instance, Chen et al. [14] utilized the SEER database to develop and validate a nomogram for predicting overall survival and cancer-specific survival in patients diagnosed with this type of cancer. Their nomogram outperformed the AJCC staging system, achieving C-index values of 0.746 and 0.770 for overall survival and cancer-specific survival, respectively, in the validation cohort. However, this model was only internally validated and lacks external validation using cohorts from other countries to assess its performance. Similarly, Li et al. [25] established a nomogram for predicting progression-free survival and overall survival in OCCC patients at a large ovarian cancer center in China. They demonstrated that their nomogram outperformed the FIGO system, but external validation will still be necessary in future studies. In our study, we validated our model using an external cohort and observed superior predictive performance compared to the traditional linear regression models.

Nomograms have been widely used as the preferred method for individualized predictions in numerous model building studies [14, 25, 26]. However, nomograms have limitations in time-event prediction and fail to capture the nonlinear relationships among clinical features. In contrast, we chose deep learning...
models to account for the complex interactions between clinically relevant factors and survival outcomes. While deep learning models have been extensively used in diagnostic work, their application in survival prediction for cancer patients is still limited. Matsuo et al. [27] compared the performance of the deep learning model with the traditional CoxPH model in the survival analysis of women with newly diagnosed cervical cancer and found that the deep learning model showed superior performance. A similar conclusion was reached in our study. Deep learning models offer several advantages for cancer research. Firstly, they have higher adaptability to nonlinearly correlated variables, which are commonly observed in clinical practice. This makes deep learning models more suitable for addressing clinical problems compared to linear regression models. Secondly, deep learning models possess the capability to automatically learn relevant features and analyze censored factors. Lastly, as the size of the dataset increases, the advantages of deep neural network models become more apparent, leading to improved prediction accuracy.

The factors analyzed in our constructed model are clinically relevant and readily available, requiring no complex data processing. These factors encompass the patient's clinical characteristics and treatment information, which have been widely recognized in the literature for their impact on prognosis [5, 28–32]. Therefore, these factors are practical and applicable to most clinicians. In our study, patients with distant metastases or lymph node involved, advanced stage, macroscopic residual tumors, and positive lymph node had a relatively poor prognosis. A 10-year retrospective study in China showed that positive lymph nodes were an independent prognostic factor [5]. Another retrospective study in Korea reported that early stage and optimal debulking were considered a favorable prognostic factor [4]. According to the study based on the SEER database, LN dissection was an independent prognostic factor for OS [31]. Our study included these relevant prognostic factors and even incorporated more comprehensive factors than previous studies.

Furthermore, we have explored the model's utility in a China cohort, where it exhibited a C-index of 0.836 compared to 0.718 in the SEER database. This discrepancy may be attributed to environmental factors, economic differences, ethnicity, and other variables, highlighting the need for developing specific models tailored to different races or regions. Additionally, incorporating more factors based on large cohort studies would enhance the model's accuracy. Moreover, the user-friendly graphical interface we developed in this study facilitates effective doctor-patient communication and assists in conveying individualized postoperative outcomes to patients.

Despite the good accuracy of our developed survival prediction models, there are several limitations to consider in our study. Firstly, the generalization of the model to different populations is uncertain, despite initial validation in a China patient cohort. Secondly, the retrospective nature of the study limits the comprehensiveness of some clinical variables, thereby impacting the model's performance to some extent. Thirdly, although our sample size is relatively large compared to similar studies, it is still relatively small. Since deep learning models perform better with larger sample sizes, expanding the number of training and validation cohorts would further enhance the model's performance and stability. Fourthly, interpreting the predictions of deep learning models can be challenging. The reliability of deep learning
models is a noteworthy concern, and further verification and model development are necessary to ensure their reliability. These methods are still in the exploratory stage and require complex analysis and data processing, which may also restrict their utilization and generalizability.

**Conclusion**

In conclusion, deep learning models have the potential to predict survival risk in individual OCCC patients, guiding personalized treatment and resource allocation in line with personalized precision medicine. Their application is expected to become more widespread in the near future. However, a valuable research direction is to explore methods for providing clinically meaningful explanations from deep learning models, improving their interpretability and trustworthiness in clinical settings. For future research directions, how to provide clinically meaningful explanations from deep learning models would be valuable and promising.

**Abbreviations**

OCCC Ovarian clear cell carcinoma  
SEER Surveillance, epidemiology, and end results  
NMTLR neural multi-task logistic regression  
RSF random survival forest  
CoxPH Cox proportional hazards  
C-index concordance index  
IBS Integrated Brier Score  
ROC Receiver operating curves  
AUC Area under the curve  
OS Overall survival  
AJCC American Joint Commission on Cancer  
LN Lymph node  
FIGO The International Federation of Gynecology and Obstetrics  
CA-125: Carbohydrate antigen-125

**Declarations**
**Ethics approval and consent to participate**

The retrospective study was approved by Ethics Committees of the Qilu Hospital of Shandong University and conducted according to the guidelines of the Declaration of Helsinki.

**Consent for publication**

Not applicable.

**Competing interests**

The authors declare that they have no competing interests.

**Availability of data and materials**

All SEER data here are publicly available in the SEER database [https://seer.cancer.gov/]. The China dataset used during this study are available from the corresponding author on reasonable request.

**Funding**

The work was supported by the National Key Technology R&D Program of China (grant numbers 2022YFC2704200 and 2022YFC2704202).

**Author contributions**

Conception and design: YL, YZ, LL, YW. Administrative support: YW, LL. Provision of study materials or patients: CH, WZ, YW. Collection and assembly of data: YL, RC, YY. Data analysis and interpretation: YL, YY, YZ, RC, WZ, CH, YW, YW. Manuscript writing: All authors. All authors read and approved the final manuscript.

**Acknowledgements**

We thank all staff of the SEER database for their contribution in data collection, maintenance, distribution and so on. We would like also to thank all the developers of the Python programming package for selflessly sharing their code.

**References**


Figures


**Figure 1**

Flow chart of datasets construction.
Figure 2

Correlation coefficients for variables in the data set.
Figure 3
The receiver operating curves (ROC) for 1-, 3-, 5-year survival predictions in two test sets. ROC curves for (A) 1-, (B) 3-, (C) 5-year survival predictions in SEER test dataset. ROC curves for (D) 1-, (E) 3-, (F) 5-year survival predictions in China test dataset.
DeepSurv-based model for predicting survival of ovarian clear cell carcinoma

Figure 4

A screenshot of the online web-based application of DeepSurv model.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- Additionalfile1.docx
- Additionalfile2FigureS1.docx
- Additionalfile3FigureS2.docx
- Additionalfile4FigureS3.docx