FastCPH: Efficient Survival Analysis for Neural Networks

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Abstract

The Cox proportional hazards model is a canonical method in survival analysis for prediction of the life expectancy of a patient given clinical or genetic covariates – it is a linear model in its original form. In recent years, several methods have been proposed to generalize the Cox model to neural networks, but none of these are both numerically correct and computationally efficient. We propose FastCPH, a new method that runs in linear time and supports both the standard Breslow and Efron methods for tied events. We also demonstrate the performance of FastCPH combined with LassoNet, a neural network that provides interpretability through feature sparsity, on survival datasets. The final procedure is efficient, selects useful covariates and outperforms existing CoxPH approaches.

1 Introduction

Survival analysis is a domain in statistics that studies the dependency of the time to the occurrence of an event on predictor variables. We usually call the estimated period “duration” and the event of interest “death” or “failure.” Censored data, where the endpoint of observation is not a failure, is an important component in this field and requires specialized techniques. The Cox proportional hazards model (CoxPH) is a classic semi-parametric method to handle censored data (Cox 1972). It was originally used as a linear regression model, supposing the log risk of failure is a linear combination of the clinical or genetic predictor variables. Its core idea is that the dependency of hazard rate on covariates is time-invariant and multiplicative. The formulation of CoxPH likelihood is explained in Section 2. A major advantage of CoxPH models over methods like Kaplan-Meier curves and the log-rank test is their ability to work easily with quantitative predictor variables and ability to generalize patterns from censored data (Efron 1988). Therefore, they are particularly suitable for survival analysis and predictions and are applied extensively in the biomedical field including in analyzing gene expressions and the likelihood of various diseases including liver diseases, coronary heart disease, diabetes, etc (Chang et al. 1990). Beyond that, CoxPH models also have a variety of applications. When compared with the results of the multiple discriminant analysis methods, the CoxPH model gives lower type I errors (Lane, Looney, and Wansley 1986).

In classical survival studies using CoxPH, a lot of effort is needed in feature engineering to make the model work well. Over the years, several methods were proposed to generalize it to nonlinear situations, allowing more complex formulation for the log-risk function, yet having mixed results (Mariani et al. 1997; Xiang et al. 2000; Sargent 2001).

1.1 Related work

Deep learning in survival analysis With the rise of deep learning applications in many scientific fields, some studies have tried to combine CoxPH functions with deep neural networks for better time-to-event predictions for larger datasets. Several methods have been proposed to deal with instances where there are ties, including the exact partial likelihood, the Breslow approximation, and the Efron approximation, the latter two being well-tested in theory and widely used practice (Breslow 1975; Efron 1977, Therneau and Grambsch 2000). The most commonly used approach is the Breslow method which simply uses the number of tied events as the exponent in the denominator of the relative risk. The Efron method is thought to produce superior outcomes, yet the formulation is more complicated to implement efficiently. The difference with the Breslow approach is minor when the number of ties is not large (Therneau 1997). Our work focuses on the deep learning method to model the survival hazards using CoxPH.

Handling ties CoxPH is developed under the assumption of continuous data, but there are often tied event times in real datasets. Several ways have been offered to deal with instances where there are ties, including the exact partial likelihood, the Breslow approximation, and the Efron approximation, the latter two being well-tested in theory and widely used practice (Breslow 1975; Efron 1977, Therneau and Grambsch 2000). The most commonly used approach is the Breslow method which simply uses the number of tied events as the exponent in the denominator of the relative risk. The Efron method is thought to produce superior outcomes, yet the formulation is more complicated to implement efficiently. The difference with the Breslow approach is minor when the number of ties is not large (Therneau 1997). Our work use with both Breslow and Efron methods to break ties.

Implementations of CoxPH When most studies focus on the application of linear and nonlinear CoxPH to survival datasets, few of them emphasize the implementation of the Cox partial likelihood function itself, which is the foundation of CoxPH-based methods. We review the four most popular
implementations of the CoxPH model in neural networks as in Table 1:

- **DeepSurv** (Katzman et al. 2018) implements a deep learning generalization of the Cox proportional hazards model using Theano and Lasagne. It supports tensor operation, runs in $O(n)$ by vectorized cumulative sums over the entire input, but assumes there are no tied events.

- **Pycox** (Kvamme, Borgan, and Schell 2019) provides a Python package for survival analysis and time-to-event prediction with PyTorch. It computes in $O(n)$ a cumulative sum of all input hazards but not the true risk sets of the CoxPH function.

- **PySurvival** (Fotso et al. 2019) is an open-source Python package for Survival Analysis modeling published in 2019 and compatible with PyTorch. The implementation of the nonlinear CoxPH model is based on Deepsurv (Katzman et al. 2018), while adding an $O(n^2)$ index matrix for Efron’s method to handle ties.

- **Scikit-survival** (Pölsterl 2020a) (sksurv) is a Python library for survival analysis compatible with scikit-learn (Pedregosa et al. 2011), published in 2020. It implements Breslow and Efron approximation of the CoxPH model in $O(n)$ using an inner for-loop at each distinct event time when going through all events. However, it does not support deep learning.

It is important for CoxPH-based methods to properly handle ties, support efficient computation, and use the correct approximation at the same time. Simply assuming the absence of ties or ignoring all tied cases is statistically inappropriate. Failure to handle ties and oversimplifications may cause unexpected consequences, especially when the behaviors of neural networks possess randomness and the results can be hard to interpret (Theerneu and Grambsch 2000; Borucka 2014). However, none of the existing popular survival analysis packages have CoxPH implemented in both an efficient and correct way for neural networks.

In recent years, people use the CoxPH model on survival datasets with larger scales and data complexity (Spooner et al. 2020). Existing methods sacrifice the correct formula for computational simplicity or the other way around, but why not use a method that strictly follows the well-tested approximations and possesses efficiency at the same time? Here we present the Fast Cox Proportional Hazard model (**FastCPH**), a computationally efficient and statistically correct method for survival analysis using neural networks.

### Table 1: Comparisons for different Cox PH implementations

|                      | Sksurv | PyCox | DeepSurv | PySurvival | **FastCPH (Ours)** |
|----------------------|--------|-------|----------|------------|-------------------|
| Time complexity      | $O(n)$ | $O(n)$ | $O(n)$   | $O(n^2)$   | $O(n)$            |
| Deep learning        | ×      | ✓     | ✓        | ×          | ✓                 |
| Handling ties        | Tie-awareness | ✓ | ✓ | ✓ | ✓ |
|                      | Efron approximation | ✓ | ✓ | ✓ | ✓ |
|                      | Breslow approximation | ✓ | ✓ | ✓ | ✓ |

### 1.2 Our contribution

We propose **FastCPH** to overcome the limitations of existing CoxPH methods in machine learning. It is a fully vectorized method that runs in $O(n)$ and yields both standard Breslow and Efron methods for tied events. We implement it with PyTorch and it can be easily used for any other machine learning research requiring the CoxPH model, allowing computationally efficient deep learning training for a larger scale of data.

As a demonstration of **FastCPH**, we combine it with LassoNet to present **FastCPH-LassoNet**, a simple neural network that provides interpretability through feature sparsity in survival analysis. We evaluate **FastCPH-LassoNet** on multiple survival datasets, and **FastCPH-LassoNet** outperforms existing CoxPH approaches.

### 2 Fast Cox Proportional Hazards Model

We propose **FastCPH** as the linear time implementation following the exact formula of CoxPH with Breslow Approximation for neural networks. As noted in Table 1, **FastCPH** is the first CoxPH method that is both computationally efficient for neural networks and supports Efron and Breslow approximation in handling tied events. We also provide a step-by-step proof verifying the correctness of our tensor-based implementation.

The input is given as a feature matrix $x$ where each row is a sample, and each column is a feature. Each row is associated with an event time $t_i$ (that can produce ties) and an indicator $\delta_i$ indicating whether the event is censored or not (1 if uncensored).

#### 2.1 Without ties

**Definition 2.1.** Given a regression model that gives a real number $g(x_i)$ for each sample, the CoxPH likelihood that is maximized in the absence of ties is:

$$L(g) = \prod_{i=1}^{n} \frac{\exp(g(x_i))}{\sum_{j \mid \delta_j = 1 \land t_j \geq t_i} \exp(g(x_j))}$$  

The negative log likelihood (loss function) is

$$LL(g) = \sum_{i \in J} \log \left( \sum_{j \in R_i} \exp(g(x_j)) \right) - g(x_i)$$  

In implementation, assuming the event times $t$ are sorted in decreasing order (which is a $O(n \log n)$ preprocessing), we
can compute all values of \( \log \left( \sum_{j \in R_i} \exp [g(x_j)] \right) \) in \( O(n) \) by using the \texttt{logcumsumexp} function\(^\text{1}\) (as implemented in PyTorch \cite{paszke2019pytorch}): \[
\sum_{i \in J} \log \text{cumsumexp}(g(x_i))_i - g(x_i) \tag{3}
\]

2.2 Breslow’s method
When there are ties, the theoretical best solution would assume that the events still happened in some order and sum the formula without ties over all orders. This is not efficient because there are \( d_i! \) possible orders for each tie, thus rarely used in applications.

Breslow approximation assumes that all \( d_i \) elements were selected from the same risk set. Thus, the above formula stays unchanged. The implementation simply indexes the logcumsumexp terms so that events with the same failure time have the same denominator.

2.3 Efron’s method
Efron’s method observes that the denominator is too big in Breslow’s approximation, as when multiples elements are selected from the same risk set, that risk set gets smaller.

\textbf{Definition 2.2.} Efron’s approximation results in the following likelihood:

\[
L(g) = \prod_{i \in J'} \frac{\prod_{j \in D_i} \exp(g(x_j))}{\prod_{k=0}^{d_i-1} \left( \sum_{j \in R_i} \exp(g(x_j)) - \frac{k}{d_i} \sum_{j \in D_i} \exp(g(x_j)) \right)}
\]

where \( J' \) is a subset of \( J \) with unique event times. The idea is to discount the denominator over the whole risk set \( \sum_{j \in R_i} \exp(g(x_j)) \) by the average risk over \( D_i \):

\[
\frac{1}{d_i} \sum_{j \in D_i} \exp(g(x_j)), \text{ } k \text{ indexes the set } D_i.
\]

Compared with Equation\(^2\) the numerator did not change (it is still the product over all uncensored events). The denominator has three terms:

- \( \sum_{j \in R_i} \exp(g(x_j)) \) can be computed for all \( j \) in linear time as before.
- \( \frac{k}{d_i} \) is trivial to compute for all elements of \( J \) (which is the union of all \( D_i \) for \( i \in J' \)).
- \( \sum_{j \in D_i} \exp(g(x_j)) \) can also be computed in linear time with a vectorized scatter operation.

Finally, those terms are easy to combine in linear time with vectorized operations. All computations are realized in the log space to avoid numerical errors, using tricks similar to those used to implement the log-sum-exp operation.

We provide \texttt{FastCPH} as an efficient, vectorized and linear-time function implemented in PyTorch that can be conveniently used by any neural network.

\footnote{\texttt{logcumsumexp}(g(x))_i \text{ is a slight abuse of notation as \texttt{logcumsumexp} is applied on all events, not just those from \( J \), then indexed on the elements of \( J \).}}

3 Experiments
We want to evaluate the following three aspects of \texttt{FastCPH}:

1. Is the implementation of \texttt{FastCPH} computationally efficient for neural networks?
2. Can \texttt{FastCPH-LassoNet} obtain feature sparsity along the regularization path?
3. Does \texttt{FastCPH-LassoNet} have promising performance compared to other CoxPH-based models on real-world survival datasets?

3.1 Experiment 1: Runtime analysis of \texttt{FastCPH}
\textbf{Baselines} To analyze the computational efficiency of \texttt{FastCPH}, we compare its runtime with 4 other popular vec-
weighted terms in denominator. The experimental results To evaluate FastCPH-LassoNet we use the following four datasets:

3.2 Dataset settings

Table 3: Hyperparameters and run time of FastCPH-LassoNet (95% CI if indicated). Run time is in seconds for per run per CPU. Training FastCPH-LassoNet is performed on 2.8 GHz Quad-Core Intel Core i7 with 16 GB memory. As shown in the table, training FastCPH only requires a few minutes, demonstrating its computational efficiency.

Table 2: Performance of different CoxPH models on survival datasets (in percentage, 95% CI if indicated)

3.2 Dataset settings

To evaluate FastCPH-LassoNet on real world scenarios, we use the following four datasets:

- **Breast cancer dataset (Desmedt et al. 2007):** This dataset comes from experiments set up to validate a certain gene signature in primary breast tumors. It contains data points from 198 patients, with 80 features each. The endpoint of this dataset is distant metastases. Of all patients, 51 of them (25.8%) exhibited the symptom.
- **WHAS500 dataset (Muche 2001):** The Worcester Heart Attack Study dataset is an observational dataset set up to track trends in acute myocardial infarction and out-of-hospital coronary heart disease deaths in Worcester, Massachusetts. The endpoint of this dataset is death. Out of 500 patients in the dataset with 14 features each, the endpoint occurred for 215 patients (43.0%).
- **Veteran’s lung cancer dataset (Kabbeleisch and Prentice 2011):** This dataset comes from a lung cancer trial by the Department of Veterans Affairs. The endpoint of this dataset is death. Out of 137 patients in the dataset with 6 features each, the endpoint occurred for 128 patients (93.4%).
- **HNSCC (Grossberg et al. 2020):** This dataset is composed of 451 head and neck squamous cell carcinoma (HNSCC) patients treated with curative-intent intensity modulated radiotherapy (IMRT). This dataset was previously used to predict local recurrence and HPV status (Head, Group et al. 2018). Survival analysis is done in data exploration, but nothing predictive. We include it as a showcase of our method. The endpoint used for our analysis is death.

Data preprocessing: For the breast cancer dataset, WHAS500, and veteran’s lung cancer dataset, we retrieve the data from Scikit-survival package (Pölsterl 2020b) and obtain one-hot encodings to quantify entries such as treatment received, cell types, prior therapy, etc. The number of final entries is shown in the last row of Table 1. The HNSCC dataset is publicly available via the Cancer Imaging Archive with TCIA Limited Access License (Grossberg et al. 2020). The DICOM imaging data is processed using the MedImageTools pipeline (Sejin 2022) to extract the computed tomography (CT) images and gross tumor volume (GTV) segmentation masks with uniform voxel spacing for consistent feature extraction. These images and masks are processed into the NIfTI file format, which is a common standard for 3D medical images, and compatible with PyRadiomics. The processed image and GTV masks into PyRadiomics to ex-
Table 4: Results of FastCPH-LassoNet and DeepSurv with more complex architectures (in percentage, 95% CI)

|                       | Breast cancer | WHAS500 | Veteran’s lung cancer | HNSCC |
|-----------------------|---------------|---------|-----------------------|-------|
| FastCPH-LassoNet      | 69.7 (±5.35)  | 76.6 (±1.35) | 73.0 (±2.49) | 63.7 (±5.89) |
| DeepSurv              | 68.2 (±2.47)  | 64.5 (±1.06) | 66.3 (±1.47) | 61.6 (±3.05) |
|                       | (32)          |         |                       |       |
| FastCPH-LassoNet      | 67.4 (±4.90)  | 76.8 (±1.29) | 72.6 (±2.12) | 69.3 (±4.68) |
| DeepSurv              | 66.6 (±1.27)  | 65.8 (±0.68) | 69.3 (±0.72) | 58.9 (±2.56) |
|                       | (32, 16)      |         |                       |       |
| FastCPH-LassoNet      | 69.0 (±3.47)  | 75.4 (±2.49) | 71.9 (±3.23) | 65.3 (±5.38) |
| DeepSurv              | 68.7 (±1.20)  | 66.1 (±1.07) | 66.2 (±1.46) | 57.1 (±2.39) |
|                       | (64)          |         |                       |       |
| FastCPH-LassoNet      | 68.6 (±5.11)  | 76.8 (±1.40) | 72.9 (±2.50) | 69.0 (±4.22) |
| DeepSurv              | 67.0 (±1.24)  | 64.8 (±0.63) | 67.3 (±1.13) | 58.5 (±2.00) |

Figure 2: Demonstration of the training behavior of FastCPH-LassoNet on the breast cancer dataset. The y-axis of the first two rows represents the test score, which is calculated as the C-index. The model starts from a given $\lambda$. At each iteration, $\lambda$ increases at a fixed geometric rate, the model is retrained based on the model selected at the last $\lambda$. At each $\lambda$, the iterated model can select a subset of features in the input, that is supposed to decrease. The first figure is the number of selected features versus the test C-index. The second figure represents the change in test score when $\lambda$ increases during training. The third figure is the number of features selected when $\lambda$ increases during training. We can see that the test score reaches a peak when $\lambda$ is between $10^2$ and $10^3$. The test C-index fluctuates when the number of selected features decreases, and it reaches the global optimal when the number of features is 19.

Metric We use Harrell’s concordance index (C-index) as a metric to evaluate the performance of our model and other baselines. It is a generalization of Area under ROC curve (AUC) regarding censored data, reflecting the accuracy of pairwise orders of the risk function as the output of the model (Harrell et al. 1982; Uno et al. 2011; James et al. 2013).

For input $x_i$, duration $t_i$ and events $\delta_i$ (1 if uncensored, 0 otherwise), the C-index is computed as:

$$C = \frac{\sum_{i,j, t_j < t_i, \delta_j} 1(g(x_j) > g(x_i)) \delta_j}{\sum_{i,j, t_j < t_i} \delta_j}.$$  \hspace{1cm} (5)

We also provide an $O(n \log n)$ implementation of the C-index using ordered data structures.

3.3 Experiment 2: FastCPH-LassoNet with a linear architecture

Baselines We first compare FastCPH-LassoNet with other CoxPH-based methods using linear structures. We use CoxPH linear model (Cox 1972), CoxNet (Simon et al. 2011), GlmNet (Friedman, Hastie, and Tibshirani 2010) and DeepSurv (Katzman et al. 2018) as baselines. The first three are classical CoxPH-based models with different regularizations. DeepSurv is considered the most advanced deep learning CoxPH-based method (Katzman et al. 2018; Spooner et al. 2020).

Implementation details The implementations of the Cox linear model and CoxNet are from Scikit-survival (Pölsterl 2020a). For the CoxPH linear model, we set $\alpha = 10^{-6}$ as the regularization parameter in the ridge regression penalty. CoxNet is the CoxPH model with an elastic net penalty. We use cross-validation for choosing the best $\alpha$ of the regularization path from $10^{-1}$ to $10^{-5}$. For GlmNet, we use the R built-in cross-validation cv.glmnet with the Breslow method to select the model for testing. The number of folds in cross-validation (if used) is 5 for breast cancer and veteran’s lung cancer dataset and 10 for WHAS500 and HNSCC dataset. For FastCPH-LassoNet and DeepSurv, we fix the number of hidden dimensions to 1 and the number of hidden layers

tract shape, texture, and statistics features (Van Griethuysen et al. 2017).
to 1. They share the same architecture and setting (ReLU, Adam, \(1e=10^{-3}\)). For \textit{FastCPH-LassoNet}, we set \(M = 10\) and start at \(\lambda = 10^{-6}\). The \textit{prox} method of \textit{LassoNet} is called on the dense model following on a geometric path until the model becomes sparse. That value is divided by 10 to give \(\lambda_{\text{start}}\). 5-fold cross validation is used to select the best \(\lambda\) value from multiple runs. We use Efron’s method to break ties.

**Training and testing** We use stratified sampling w.r.t uncensored/censored events to split the training set (80%) and test set (20%) for each of the datasets. For models with randomness in training, we run 5 trails for each set of hyperparameters and obtain the average performance.

**Results** Firstly, \textit{FastCPH-LassoNet} obtains promising results in different datasets and generally outperform existing CoxPH-based methods as in Table 2. Its C-index is ranked 1, 1, 2, 4 for the breast cancer, WHAS500, Veteran’s lung cancer, and HNSCC datasets, respectively, showing its discrimination ability to provide reliable ranking of survival times based on risk scores. Comparing \textit{FastCPH-LassoNet} to DeepSurv, \textit{FastCPH-LassoNet} performs better in 4 datasets using the same architecture. Moreover, \textit{FastCPH-LassoNet} is able to attain an effective recovery of signals given a subset of features. As shown in Table 3 and 2, the model gives excellent performance with sparsity in covariates (C-index=0.70 for 10% feature selected and C-index=0.67 for 18% feature in the HNSCC and breast cancer dataset, respectively). It achieves highest validation accuracy with a low ratio of the number of total feature over the number of total feature. However, when the number of total features is small, the model may not be able to obtain sparsity over covariates, as shown by its result of WHAS500. Fig 2 gives an example of the training curve of \textit{FastCPH-LassoNet} on the breast cancer dataset. We can see \textit{LassoNet} optimized properly with \textit{FastCPH} as the loss function. The sparsity demonstrated in the experiments implies its potential on large-scale, more complicated real-world datasets.

### 3.4 Experiment 3: \textit{FastCPH-LassoNet} with more complex architectures

**Baselines** In the context of NN methods, we further analyze the performance of \textit{FastCPH-LassoNet} using more complex architectures. We use DeepSurv as the baseline because it is commonly recognized as the most advanced CoxPH-based deep learning method.

**Implementation details** We let \textit{FastCPH-LassoNet} and DeepSurv share the same architecture (as indicated in parentheses in Table 4 and setting (ReLU, Adam, \(1e=10^{-3}\)). For both methods, we run 15 trails to give 95% CI. The implementation of \textit{FastCPH-LassoNet} is the same as in Experiment 2.

**Results** \textit{FastCPH-LassoNet} outperforms DeepSurv with the same architecture on all datasets in our experiments. It is a more robust deep learning method with promising results in survival analysis. Looking at the results in Table 5 and 2 together, \textit{FastCPH-LassoNet} is the best CoxPH-based method on 3 out of 4 survival datasets we use. Notice that for the breast cancer and WHAS500 datasets, \textit{FastCPH-LassoNet} yields a significantly better C-index than DeepSurv and other existing methods in Table 2. These results reflect that \textit{FastCPH-LassoNet} has best overall performance than other CoxPH plus regularization models. To summarize, \textit{FastCPH-LassoNet} is an efficient and robust way to conduct survival analysis based on the \textit{FastCPH} and \(L^1\) penalty (Tibshirani 1996).

### 4 Discussion

In this paper, we have proposed \textit{FastCPH}, an efficient CoxPH method for survival analysis in neural networks that follows the exact formula of well-tested methods to handle tied events. \textit{FastCPH} is an efficient and numerically correct solution for neural networks in survival analysis. It can be quickly adapted to other deep learning methods and used in more real-world scenarios with censored data such as (Lane, Looney, and Wansley 1986; Liang, Self, and Liu 1983; Bendell, Wightman, and Walker 1991). We have shown \textit{FastCPH-LassoNet} outperformed other CoxPH-based methods in various survival datasets. More study can be done to provide applications of \textit{FastCPH} as an objective function in more complex neural network architectures. It will be interesting to see the effect of tied events on the behavior of neural networks. In addition, it is worth pointing out the importance of following the exact formulae of classic statistical methods in implementation and avoiding oversimplifications in the machine learning community.

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Appendix

This supplementary document is organized as the following. Firstly, we give distributions of ties presented in each dataset. We then provide additional information on datasets we used in the experiments, including an illustration of covariate breakdown, pipeline, and the correlation matrix of HNSCC dataset. We also supplement the code for FastCPH and experiments on https://github.com/lasso-net/lassonet.

Datasets statistics

Ties are common in the datasets we use, listed as in Table [6] Breslow and Efron methods give the same log likelihood when no ties are present in the dataset. Our method in Table [2] using Breslow approximation is capable of handling datasets with and without ties.

HNSCC dataset is a challenging prediction dataset when adapting it for survival analysis. Fig [4] is a visualization of the correlation matrix of clinical covariates in HNSCC dataset generated by PySurvival (Fotso et al. 2019–). As we can see in the figure, many of the covariates are heavily correlated with each other, posing a need of selecting useful features for constructing an efficient solution. According to a single value decomposition computation, the matrix is rank deficient. Despite that, FastCPH-LassoNet can successfully select a subset of covariates (11.04 out of 107) and attain a good and stable performance as shown in Table [2].

| # of patients | 451 |
|--------------|-----|
| Outcome      |     |
| Alive / Censored | 395 (88%) |
| Death        | 56 (12%) |
| Sex          |     |
| Male         | 387 (86%) |
| Female       | 64 (14%) |
| Disease subsite |       |
| Base of Tongue | 238 (53%) |
| Tonsil       | 174 (39%) |
| Glossopharyngeal sulcus | 10 (2%) |
| Other        | 29 (6%) |
| HPV Status   |     |
| Positive     | 232 (51%) |
| Negative / Unknown | 219 (49%) |
| Stage        |     |
| I            | 3 (1%) |
| II           | 14 (3%) |
| III          | 63 (14%) |
| IV           | 371 (83%) |
| Tumor Laterality |     |
| R            | 222 (49%) |
| L            | 215 (48%) |
| Other        | 14 (3%) |

Table 5: Event and clinical variable distribution of HNSCC.
Figure 3: The pipeline of obtaining HNSCC features for survival analysis. HNSCC dataset was curated by the University of Texas MD Anderson Cancer Center, approved by the institutional review board, and written informed consent was obtained from all study participants. This dataset is available publicly upon submission of a limited data access agreement to safeguard patient privacy. While the dataset has been thoroughly de-identified in accordance with HIPAA, it is theoretically possible to reconstruct the face, head, or body using volumetric images. For our analysis, we ensured the data was processed on a HIPAA-compliant encrypted server and the radiomics features extracted for our analysis do not contain any identifiable information or offensive content.

|                     | Breast cancer | WHAS500 | Veteran’s lung cancer | HNSCC |
|---------------------|---------------|---------|-----------------------|-------|
| # total observations| 198           | 500     | 137                   | 451   |
| # total tied events | 6             | 178     | 64                    | 232   |
| # uncensored events | 51            | 215     | 128                   | 56    |
| # uncensored tied events | 0    | 80 | 55 | 4 |

Table 6: Statistics on tied events in different datasets
Figure 4: Correlation matrix of covariates in HNSCC. The red color at the bottom of the spectrum indicates $-1$ and blue color at the top means $1$. 