Novel Prognostication of Patients with Spinal and Pelvic Chondrosarcoma Using Deep Survival Neural Networks:An analysis of the Surveillance, Epidemiology, and End Results (SEER) Database

Sun-Ho Lee MD; Sung Wook Seo

Department of Neurosurgery, Samsung Medical Center, Sungkyunkwan University School of Medicine

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Introduction The Surveillance, Epidemiology, and End Results (SEER) database has been queried to include all malignant osseous spinal tumors, including chondrosarcoma. Machine learning (ML) techniques to predict disease have shown higher diagnostic accuracy than classical methods. We sought to develop and validate deep survival neural network ML algorithms to predict survival following diagnosis of chondrosarcoma, using a SEER database.

Methods With the SEER 18 registries, Risk Estimate Distance Survival Neural Network (RED_SNN) was applied for modeling. Our prediction model was evaluated at each time window with receiver operating characteristic curves and areas under the curve (AUCs), as was the concordance index (c-index).

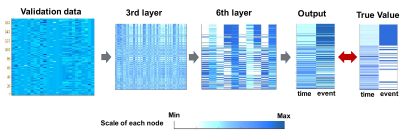
Results The subjects (n=1088) were separated into training (80%, n=870) and test sets (20%, n=218). The training data were randomly sorted into training and validation sets

The median c-index of the five validation sets was 0.84 (95% confidence interval 0.7919 to 0.8677) The median AUC of the five validation subsets was 0.838. This model was evaluated with the previously separated test set. The c-index was 0.818 and the mean AUC of the 30 different time windows was 0.85 (standard deviation 0.016). According to estimated survival probability (by 62 months), we divided the test group into five subgroups. The survival curves of the subgroups showed statistically significant separation (log-rank test: P < .001).

Conclusions This study is the first to analyze population-level data using artificial neural network ML algorithms for the role and outcomes of surgical resection and radiation therapy in spinal and pelvic chondrosarcoma.

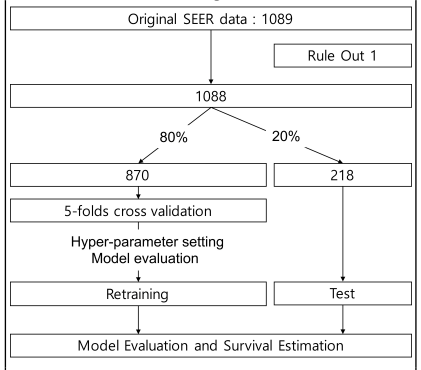
Learning Objectives RED_SNN is a valid method of predicting survival for spinal chondrosarcoma.

Figure 2. The architecture of the basic learning unit of the RED_SNN model



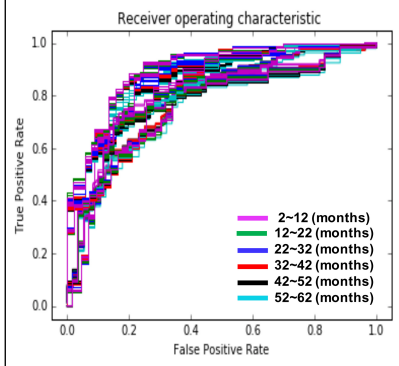
The validation data (N=169) were inputted to the pre-trained network. The number of nodes was gradually reduced across the hidden layers. The output time and event were compared to the true target values.

Figure 1. Enrolled Study Population and Pipeline of Data Analysis



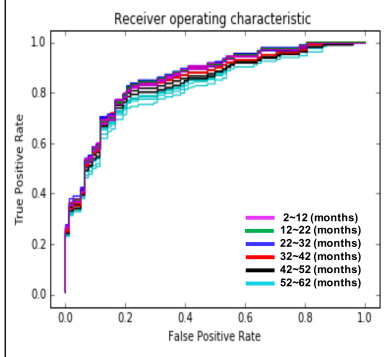
The training data were validated using 5-fold cross validation.

Figure 3. Optimization and validation of RED_SNN model using 5-fold cross validation



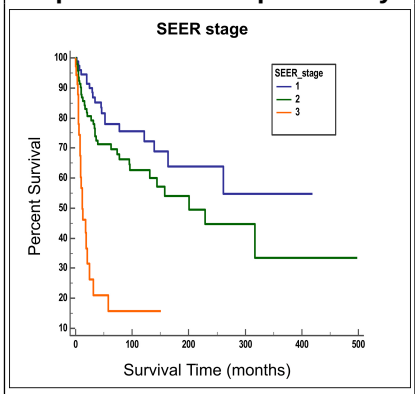
The model was serially trained to learn patient's survival status within a 10-month time interval, until 62 months from the initial observation.

Figure 4. Performance evaluation of RED_SNN using test data set

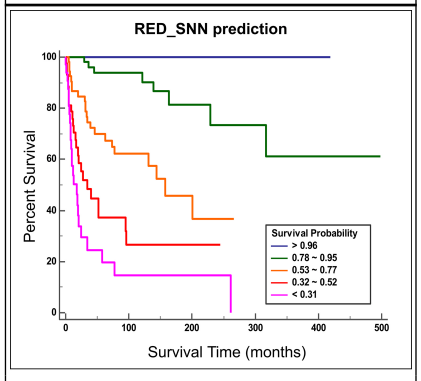


ROC curves to evaluate the prediction with test data set.

Figure 5. Kaplan Meier curves of subgroups according to SEER stage vs our model expected survival probability



A. SEER stage identified three prognostic subgroups in Kaplan Meier survival analysis.



B. RED_SNN identified five prognostic subgroups in Kaplan Meier survival analysis.