Figure 1. Comparison of clinic characteristics of COVID-19 patients in Mild-Moderate and Severe-Critically Severe groups (n=196).

COVID-19 were divided into Mild-Moderate and Severe-Critically Severe groups according to the 8th edition of the China Guidelines for the Diagnosis and Treatment Plan of COVID-19 Infection by the National Health Commission (Trial Version 8). **A.** Gender differences between the two groups, P-value was calculated according to chi-square test. **B.** Age differences between the two groups. Each plot graphically displays the central position and scatter/dispersion of the values of each group. P-value was calculated according to student t-test. **C.** WBC differences between the two groups, P-value was calculated according to Wilcoxon-test. **D.** LYMC differences between the two groups, P-value was calculated according to Wilcoxon-test. **E.** LYMPH differences between the two groups, P-value was calculated according to Wilcoxon-test. **F.** NEUT differences between the two groups, P-value was calculated according to Wilcoxon-test. **G.** NEU differences between the two groups, P-value was calculated according to Wilcoxon-test. **H.** NLR differences between the two groups, P-value was calculated according to Wilcoxon-test.

*P <0.05, **P <0.01, ***P <0.001

Figure 2. The correlation between clinic characteristics and severity of COVID-2019 and the predictive value of clinic characteristics for the severity of COVID-19.

A. Correlation analysis: Characteristics of the COVID-19 patient including Gender, Age WBC, LYMC, LYMPH, NEUT, NEU, NLR and Severity. WBC, LYMC, LYMPH, NEUT, NEU and NLR were extracted form patients' initial blood test results. Patients were divided into Mild-Moderate and Severe-Critically Severe groups according to the 8th edition of the China Guidelines for the Diagnosis and Treatment Plan of COVID-19 Infection by the National Health Commission (Trial Version 8). According to the characteristics of the data, the correlation was calculated based on the Kendall correlation coefficient (Gender-severity) or Spearman correlation coefficient. P <0.05 was considered statistically significant. **B.** P-values of correlation. **C.** ROC curve used to evaluate the predictive value of Age for the severity of COVID-19 based on stratified random sampling: 80% as the training set and 20% as the testing set. **D.** ROC curve used to evaluate the predictive value of Age, WBC, LYMC for the severity of COVID-19 based on stratified random sampling: 80% as the training set and 20% as the testing set.

Figure 3. Design and implementation of the Multiple Criteria Decision Making (MCDM)

algorithm for predicting the severity of COVID-19.

A. The MCDM algorithm-Stage 1. Preprocessing, this stage is the process of refining the collected raw data to eliminate noise, including correlation analysis and feature selection based on P values. Correlation was calculated according to Spearman correlation coefficient. $P < 0.05$ was considered statistically significant. **B.** The MCDM algorithm-Stage 2. Feature Ranking, this stage is the process of using the TOPSIS method to rank features. TOPSIS method: according to the severity-relevance, we defined the top 20% as the core features and the other 80% as the auxiliary feature. For key features: First, select the first feature that is most relevant to the severity; Second, select the remaining key features in turn by ranking. The ranking criteria are as relevant as possible to severity, and not relevant to the selected key features. For auxiliary features: score and rank auxiliary features according to the degree of irrelevance to key features. **C.** The MCDM algorithm-Stage 3. Feature Selection, this stage is to select a subset of the features ranked by the TOPSIS method to remove irrelevant, redundant, or noisy features. EVAL1: The correlation between input features $x \in X$ and output features $y \in Y$, $R[x,y]$ or $R[y,x]$; EVAL2: The correlation between input features $x \in X$ and labeled features $v \in L$, $R[x,v]$ or $R[v,x]$; Subset: The optimal input feature subset. **D.** The MCDM algorithm-Stage 4. Performance evaluation, this stage is to measure the performance of the binary classification by Accuracy (ACC), True Positive Rate (TPR), False Positive Rate (FPR) and F1 score.

Figure 4. The subset of features selected by the MCDM algorithm to predict the severity of COVID-19.

Data set was divided 100 times (80% training set and 20% test set) and repeatedly run the algorithm to test the stability of the algorithm and observe the influence of the dataset uncertainty on feature selection. **A.** the average number of features selected by 3 different criteria. EVAL1: The correlation between input features $x \in X$ and output features $y \in Y$, $R[x,y]$ or $R[y,x]$; EVAL2: The correlation between input features $x \in X$ and labeled features $v \in L$, $R[x,v]$ or $R[v,x]$; Subset: The optimal input feature subset. Error bars represents 95% CI. **B.** The metrics (ACC, TPR, FPR and F1 score) of 3 different criteria. Error bars represents 95% CI. **C.** Different feature selection rates of EVAL1+ EVAL2 subsets.

Figure 5. ROC curve used to evaluate the predictive value of the features selected by the MCDM algorithm for the severity of COVID-19.

A. ROC curve used to evaluate the predictive value of {Age, WBC, LYMC, NEUT} for the severity of COVID-19. **B.** ROC curve used to evaluate the predictive value of {Age, NEUT, LYMC} for the severity of COVID-19. **C.** ROC curve used to evaluate the predictive value of {Age, WBC, LYMC} for the severity of COVID-19. Stratified random sampling: 80% for the "training set" and 20% for the "testing set".