

COVID-19 mortality prediction using the in-silico test of cytokines based on the blood routine data

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The experiments in study were carried out on a Windows 10 computer with 8 GB system memory and one Intel Xeon I5-1234 CPU. All the experiments were programmed using the Python version 3.8.8, the scikit-learn version 1.0.2 and the pytorch version 1.10.1.

Directory: Cytokines_predict

This directory contains two sub-directories Cytokines_predict (first blood routine) and Cytokines_predict (final blood routine).

- Cytokines_predict (first blood routine): contains a model for predicting cytokines using the blood routine data from the first test after admission.
- Cytokines_predict (final blood routine): contains a model for predicting cytokines using the blood routine data from the final test after admission.

Command syntax of the main script:

```
python PredictCytokine.py BloodRoutine.csv Cytokine.csv
```

- BloodRoutine.csv is the input file. A row in the document represents a sample, while a column is a blood routine index.
- Cytokine.csv is the output file. A row in the document represents a sample, while a column is a cytokine index.

Directory: Cytokines_predict _mortality

This directory contains two sub-directories Cytokines_predict _mortality (first blood routine) and Cytokines_predict _mortality (final blood routine).

- Cytokines_predict _mortality(first blood routine) folder contains the predicted cytokines to predict the mortality model. These cytokines were predicted using routine blood data from the first test at admission.
- Cytokines_predict _mortality(final blood routine) folder contains the predicted cytokines to predict the mortality model. These cytokines were predicted using blood routine data from the final test at admission.

Command syntax of the main script:

```
python PredictCytokine_mortality.py BloodRoutine.csv Cytokine_mortality.csv
```

- BloodRoutine.csv is the input file. A row in the document represents a sample, while a column is a blood routine index.
- Cytokine_mortality.csv is the output file. A row in the document represents a sample. Columns represent predicted patient outcomes, while 0 is alive and 1 is dead

Directory: Blood_Cytokines_predict _mortality

This directory contains two sub-directories Blood_Cytokines_predict _mortality (first blood routine) and Blood_Cytokines_predict _mortality (final blood routine).

- Blood_Cytokines_predict _mortality(first blood routine) folder contains a mortality prediction model. The data used are the blood routine data of the first test at admission and the cytokines predicted by these blood routine data
- Blood_Cytokines_predict _mortality(final blood routine) folder contains a mortality prediction model. The data used are the blood routine data of the final test at admission and the cytokines predicted by these blood routine data

Command syntax of the main script:

```
python Blood_PredictCytokine_mortality.py BloodRoutine.csv Blood_Cytokine_mortality.csv
```

- BloodRoutine.csv is the input file. A row in the document represents a sample, while a column is a blood routine index.
- Blood_Cytokine_mortality.csv is the output file. A row in the document represents a sample. Columns represent predicted patient outcomes, while 0 is alive and 1 is dead