

Cesar is a script that allows the execution of various classification algorithms in combination of bio-inspired algorithms from already processed EEG signals. To do this, the script has a line with various libraries that can be installed using the Python pip command. To do this, its version must be equal to or greater than 3.0.9.

At the time of executing the script, several options can be passed to it depending on the classifier that will be used:

- --clasificador KNN
- --clasificador SVC
- --clasificador MLP
- --clasificador LGBM
- --clasificador XGBM

To select the bioinspired algorithm with which to combine the previous classifier:

- --MW GA
- --MW PSO
- --MW ES
- --MW BEE
- --MW ANT

To select the number of features with which to train the classifier, use: --features [numFeatures].

If the KNN classifier has been selected, the parameter can be used --vecinos [numVecinos] to establish the number of neighbors.

If the SVC classifier has been selected, the parameter can be set C, with --C [numC].

If the GA bioinspired algorithm has been selected, the parameters can be used --NGeneracion y --NGenes to establish the number of generations and numbers of genes.

Independently of these commands, you can change some values of the algorithms such XGBM or MLP to adjust it to the needs of the data provided.

On the other hand, for each execution the time and energy consumed, among other measurements, are obtained. These are in the “emissions.csv” file created by the CodeCarbon API.