
sklearn-genetic

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sklearn-genetic is a genetic feature selection module for scikit-learn.

Genetic algorithms mimic the process of natural selection to search for optimal values of a function.

INSTALLATION

1.1 Dependencies

sklearn-genetic requires:

- Python (≥ 3.7)
- scikit-learn (≥ 1.0)
- deap ($\geq 1.0.2$)
- numpy
- multiprocessing

1.2 User installation

The easiest way to install sklearn-genetic is using `pip`

```
pip install sklearn-genetic
```

or `conda`

```
conda install -c conda-forge sklearn-genetic
```


EXAMPLES

Noisy (non informative) features are added to the iris data and genetic feature selection is applied.

```
import random
import numpy as np
from sklearn import datasets, linear_model
from genetic_selection import GeneticSelectionCV

# When using multiple processes (n_jobs != 1), protect the entry point of the program if
↪necessary
if __name__ == "__main__":

    # Set seed for reproducibility
    random.seed(42)
    np.random.seed(42)

    iris = datasets.load_iris()

    # Some noisy data not correlated
    E = np.random.uniform(0, 0.1, size=(len(iris.data), 20))

    X = np.hstack((iris.data, E))
    y = iris.target

    estimator = linear_model.LogisticRegression(solver="liblinear", multi_class="ovr")

    selector = GeneticSelectionCV(
        estimator,
        cv=5,
        verbose=1,
        scoring="accuracy",
        max_features=5,
        n_population=50,
        crossover_proba=0.5,
        mutation_proba=0.2,
        n_generations=40,
        crossover_independent_proba=0.5,
        mutation_independent_proba=0.05,
        tournament_size=3,
        n_gen_no_change=10,
        caching=True,
```

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```
        n_jobs=-1,  
    )  
    selector = selector.fit(X, y)  
  
    print(selector.support_)
```

API REFERENCE

```
class genetic_selection.GeneticSelectionCV(estimator, cv=None, scoring=None, fit_params=None,  
                                           max_features=None, verbose=0, n_jobs=1,  
                                           n_population=300, crossover_proba=0.5,  
                                           mutation_proba=0.2, n_generations=40,  
                                           crossover_independent_proba=0.1,  
                                           mutation_independent_proba=0.05, tournament_size=3,  
                                           n_gen_no_change=None, caching=False)
```

Feature selection with genetic algorithm.

Parameters

- **estimator** (*object*) – A supervised learning estimator with a *fit* method.
- **cv** (*int*, *cross-validation generator or an iterable*, *optional*) – Determines the cross-validation splitting strategy. Possible inputs for *cv* are:
 - *None*, to use the default 3-fold cross-validation,
 - *integer*, to specify the number of folds.
 - An object to be used as a cross-validation generator.
 - An iterable yielding train/test splits.For integer/*None* inputs, if *y* is binary or multiclass, *StratifiedKfold* used. If the estimator is a classifier or if *y* is neither binary nor multiclass, *Kfold* is used.
- **scoring** (*string*, *callable or None*, *optional*, *default: None*) – A string (see model evaluation documentation) or a scorer callable object / function with signature *scorer(estimator, X, y)*.
- **fit_params** (*dict*, *optional*) – Parameters to pass to the *fit* method.
- **max_features** (*int or None*, *optional*) – The maximum number of features selected.
- **verbose** (*int*, *default=0*) – Controls verbosity of output.
- **n_jobs** (*int*, *default 1*) – Number of cores to run in parallel. Defaults to 1 core. If *n_jobs=-1*, then number of jobs is set to number of cores.
- **n_population** (*int*, *default=300*) – Number of population for the genetic algorithm.
- **crossover_proba** (*float*, *default=0.5*) – Probability of crossover for the genetic algorithm.
- **mutation_proba** (*float*, *default=0.2*) – Probability of mutation for the genetic algorithm.
- **n_generations** (*int*, *default=40*) – Number of generations for the genetic algorithm.

- **crossover_independent_proba** (*float*, *default=0.1*) – Independent probability for each attribute to be exchanged, for the genetic algorithm.
- **mutation_independent_proba** (*float*, *default=0.05*) – Independent probability for each attribute to be mutated, for the genetic algorithm.
- **tournament_size** (*int*, *default=3*) – Tournament size for the genetic algorithm.
- **n_gen_no_change** (*int*, *default=None*) – If set to a number, it will terminate optimization when best individual is not changing in all of the previous **n_gen_no_change** number of generations.
- **caching** (*boolean*, *default=False*) – If True, scores of the genetic algorithm are cached.

n_features_

The number of selected features with cross-validation.

Type

int

support_

The mask of selected features.

Type

array of shape [n_features]

generation_scores_

The maximum cross-validation score for each generation.

Type

array of shape [n_generations]

estimator_

The external estimator fit on the reduced dataset.

Type

object

Examples

An example showing genetic feature selection.

```
>>> import numpy as np
>>> from sklearn import datasets, linear_model
>>> from genetic_selection import GeneticSelectionCV
>>> iris = datasets.load_iris()
>>> E = np.random.uniform(0, 0.1, size=(len(iris.data), 20))
>>> X = np.hstack((iris.data, E))
>>> y = iris.target
>>> estimator = linear_model.LogisticRegression(solver="liblinear", multi_class="ovr",
↪)
>>> selector = GeneticSelectionCV(estimator, cv=5)
>>> selector = selector.fit(X, y)
>>> selector.support_
array([ True  True  True  True False False False False False False False False
       False False False False False False False False False False False],
↪dtype=bool)
```

fit(*X*, *y*, *groups=None*)

Fit the GeneticSelectionCV model and the underlying estimator on the selected features.

Parameters

- **X** (*array-like, sparse matrix*), *shape = [n_samples, n_features]*) – The training input samples.
- **y** (*array-like*, *shape = [n_samples]*) – The target values.
- **groups** (*array-like, shape = [n_samples]*, *optional*) – Group labels for the samples used while splitting the dataset into train/test set. Only used in conjunction with a “Group” *cv* instance (e.g., *GroupKFold*).

predict(*X*)

Reduce *X* to the selected features and then predict using the underlying estimator.

Parameters

X (*array of shape [n_samples, n_features]*) – The input samples.

Returns

y – The predicted target values.

Return type

array of shape [n_samples]

score(*X*, *y*)

Reduce *X* to the selected features and return the score of the underlying estimator.

Parameters

- **X** (*array of shape [n_samples, n_features]*) – The input samples.
- **y** (*array of shape [n_samples]*) – The target values.

set_fit_request(**, groups: bool | None | str = '\$UNCHANGED\$'*) → *GeneticSelectionCV*

Request metadata passed to the `fit` method.

Note that this method is only relevant if `enable_metadata_routing=True` (see `sklearn.set_config()`). Please see User Guide on how the routing mechanism works.

The options for each parameter are:

- **True**: metadata is requested, and passed to `fit` if provided. The request is ignored if metadata is not provided.
- **False**: metadata is not requested and the meta-estimator will not pass it to `fit`.
- **None**: metadata is not requested, and the meta-estimator will raise an error if the user provides it.
- **str**: metadata should be passed to the meta-estimator with this given alias instead of the original name.

The default (`sklearn.utils.metadata_routing.UNCHANGED`) retains the existing request. This allows you to change the request for some parameters and not others.

New in version 1.3.

Note: This method is only relevant if this estimator is used as a sub-estimator of a meta-estimator, e.g. used inside a `pipeline.Pipeline`. Otherwise it has no effect.

Parameters

groups (*str, True, False, or None, default=sklearn.utils.metadata_routing.UNCHANGED*) – Metadata routing for groups parameter in fit.

Returns

self – The updated object.

Return type

object

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