
sklearn-genetic

Manuel Calzolari

Apr 10, 2022

CONTENTS

1	Installation	3
1.1	Dependencies	3
1.2	User installation	3
2	Examples	5
3	API Reference	7
4	Indices and tables	11
	Python Module Index	13
	Index	15

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 (≥ 3.6)
- scikit-learn (≥ 0.23)
- 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,
```

(continues on next page)

(continued from previous page)

```
        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],
↪      dtype=bool)
```

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

Fit the GeneticSelectionCV model and then 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 then 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.

INDICES AND TABLES

- `genindex`
- `modindex`
- `search`

PYTHON MODULE INDEX

g

`genetic_selection`, [7](#)

INDEX

E

`estimator_` (*genetic_selection.GeneticSelectionCV* attribute), 8

F

`fit()` (*genetic_selection.GeneticSelectionCV* method), 8

G

`generation_scores_` (*genetic_selection.GeneticSelectionCV* attribute), 8

`genetic_selection`
module, 7

`GeneticSelectionCV` (class in *genetic_selection*), 7

M

module
 genetic_selection, 7

N

`n_features_` (*genetic_selection.GeneticSelectionCV* attribute), 8

P

`predict()` (*genetic_selection.GeneticSelectionCV* method), 9

S

`score()` (*genetic_selection.GeneticSelectionCV* method), 9

`support_` (*genetic_selection.GeneticSelectionCV* attribute), 8