Orange Data Mining Library Documentation

Release 3

Orange Data Mining

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CONTENTS

CHAPTER

ONE

TUTORIAL

This is a gentle introduction on scripting in Orange , a Python 3 data mining library. We here assume you have already downloaded and installed Orange from its github repository and have a working version of Python. In the command line or any Python environment, try to import Orange. Below, we used a Python shell:

```
% python
>>> import Orange
>>> Orange.version.version
'3.25.0.dev0+3bdef92'
>>>
```

If this leaves no error and warning, Orange and Python are properly installed and you are ready to continue with the tutorial.

1.1 The Data

This section describes how to load the data in Orange. We also show how to explore the data, perform some basic statistics, and how to sample the data.

1.1.1 Data Input

Orange can read files in proprietary tab-delimited format, or can load data from any of the major standard spreadsheet file types, like CSV and Excel. Native format starts with a header row with feature (column) names. The second header row gives the attribute type, which can be numeric, categorical, time, or string. The third header line contains meta information to identify dependent features (class), irrelevant features (ignore) or meta features (meta). More detailed specification is available in *Loading and saving data (io)*. Here are the first few lines from a dataset `lenses.tab`:

```
age       prescription  astigmatic    tear_rate     lenses
discrete  discrete      discrete      discrete      discrete
                                                    class
young     myope         no            reduced       none
young     myope         no            normal        soft
young     myope         yes           reduced       none
young     myope         yes           normal        hard
young     hypermetrope  no            reduced       none
```

Values are tab-limited. This dataset has four attributes (age of the patient, spectacle prescription, notion on astigmatism, and information on tear production rate) and an associated three-valued dependent variable encoding lens prescription for the patient (hard contact lenses, soft contact lenses, no lenses). Feature descriptions could use one letter only, so the header of this dataset could also read:

```
age       prescription  astigmatic    tear_rate     lenses
d         d             d             d             d
                                                    c
```

The rest of the table gives the data. Note that there are 5 instances in our table above. For the full dataset, check out or download `lenses.tab`) to a target directory. You can also skip this step as Orange comes preloaded with several demo datasets, lenses being one of them. Now, open a python shell, import Orange and load the data:

```
>>> import Orange
>>> data = Orange.data.Table("lenses")
>>>
```

Note that for the file name no suffix is needed, as Orange checks if any files in the current directory are of a readable type. The call to `Orange.data.Table` creates an object called `data` that holds your dataset and information about the lenses domain:

```
>>> data.domain.attributes
(DiscreteVariable('age', values=('pre-presbyopic', 'presbyopic', 'young')),
 DiscreteVariable('prescription', values=('hypermetrope', 'myope')),
 DiscreteVariable('astigmatic', values=('no', 'yes')),
 DiscreteVariable('tear_rate', values=('normal', 'reduced')))
>>> data.domain.class_var
DiscreteVariable('lenses', values=('hard', 'none', 'soft'))
>>> for d in data[:3]:
   ...:     print(d)
   ...:
[young, myope, no, reduced | none]
[young, myope, no, normal | soft]
[young, myope, yes, reduced | none]
>>>
```

The following script wraps-up everything we have done so far and lists first 5 data instances with `soft` prescription:

```
import Orange

data = Orange.data.Table("lenses")
print("Attributes:", ", ".join(x.name for x in data.domain.attributes))
print("Class:", data.domain.class_var.name)
print("Data instances", len(data))

target = "soft"
print("Data instances with %s prescriptions:" % target)
atts = data.domain.attributes
for d in data:
    if d.get_class() == target:
        print(" ".join(["%14s" % str(d[a]) for a in atts]))
```

Note that data is an object that holds both the data and information on the domain. We show above how to access attribute and class names, but there is much more information there, including that on feature type, set of values for categorical features, and other.

1.1.2 Creating a Data Table

To create a data table from scratch, one needs two things, a domain and the data. The domain is the description of the variables, i.e. column names, types, roles, etc.

First, we create the said domain. We will create three types of variables, numeric (ContiniousVariable), categorical (DiscreteVariable) and text (StringVariable). Numeric and categorical variables will be used a features (also known as X), while the text variable will be used as a meta variable.

```
>>> from Orange.data import Domain, ContinuousVariable,
    DiscreteVariable, StringVariable
>>>
>>> domain = Domain([ContinuousVariable("col1"),
                     DiscreteVariable("col2", values=["red", "blue"])],
                     metas=[StringVariable("col3")])
```

Now, we will build the data with numpy.

```
>>> import numpy as np
>>>
>>> column1 = np.array([1.2, 1.4, 1.5, 1.1, 1.2])
>>> column2 = np.array([0, 1, 1, 1, 0])
>>> column3 = np.array(["U13", "U14", "U15", "U16", "U17"], dtype=object)
```

Two things to note here. column2 has values 0 and 1, even though we specified it will be a categorical variable with values "red" and "blue". X (features in the data) can only be numbers, so the numpy matrix will contain numbers, while Orange will handle the categorical representation internally. 0 will be mapped to the value "red" and 1 to "blue" (in the order, specified in the domain).

Text variable requires `dtype=object` for numpy to handle it correctly.

Next, variables have to be transformed to a matrix.

```
>>> X = np.column_stack((column1, column2))
>>> M = column3.reshape(-1, 1)
```

Finally, we create a table. We need a domain and variables, which can be passed as X (features), Y (class variable) or metas.

```
>>> table = Table.from_numpy(domain, X=X, metas=M)
>>> print(table)
>>> [[1.2, red] {U13},
[1.4, blue] {U14},
[1.5, blue] {U15},
[1.1, blue] {U16},
[1.2, red] {U17}]
```

To add a class variable to the table, the procedure would be the same, with the class variable passed as Y (e.g. `table = Table.from_numpy(domain, X=X, Y=Y, metas=M)`).

To add a single column to the table, one can use the `Table.add_column()` method.

```
>>> new_var = DiscreteVariable("var4", values=["one", "two"])
>>> var4 = np.array([0, 1, 0, 0, 1]) # no reshaping necessary
>>> table = table.add_column(new_var, var4)
>>> print(table)
```

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```
>>> [[1.2, red, one] {U13},
[1.4, blue, two] {U14},
[1.5, blue, one] {U15},
[1.1, blue, one] {U16},
[1.2, red, two] {U17}]
```

1.1.3 Saving the Data

Data objects can be saved to a file:

```
>>> data.save("new_data.tab")
>>>
```

This time, we have to provide the file extension to specify the output format. An extension for native Orange's data format is ".tab". The following code saves only the data items with myope perscription:

```
import Orange

data = Orange.data.Table("lenses")
myope_subset = [d for d in data if d["prescription"] == "myope"]
new_data = Orange.data.Table(data.domain, myope_subset)
new_data.save("lenses-subset.tab")
```

We have created a new data table by passing the information on the structure of the data (`data.domain`) and a subset of data instances.

1.1.4 Exploration of the Data Domain

Data table stores information on data instances as well as on data domain. Domain holds the names of attributes, optional classes, their types and, and if categorical, the value names. The following code:

```
import Orange

data = Orange.data.Table("imports-85.tab")
n = len(data.domain.attributes)
n_cont = sum(1 for a in data.domain.attributes if a.is_continuous)
n_disc = sum(1 for a in data.domain.attributes if a.is_discrete)
print("%d attributes: %d continuous, %d discrete" % (n, n_cont, n_disc))

print(
    "First three attributes:",
    ", ".join(data.domain.attributes[i].name for i in range(3)),
)

print("Class:", data.domain.class_var.name)
```

outputs:

```
25 attributes: 14 continuous, 11 discrete
First three attributes: symboling, normalized-losses, make
Class: price
```

Orange's objects often behave like Python lists and dictionaries, and can be indexed or accessed through feature names:

```
print("First attribute:", data.domain[0].name)
name = "fuel-type"
print("Values of attribute '%s': %s" % (name, ", ".join(data.domain[name].values)))
```

The output of the above code is:

```
First attribute: symboling
Values of attribute 'fuel-type': diesel, gas
```

1.1.5 Data Instances

Data table stores data instances (or examples). These can be indexed or traversed as any Python list. Data instances can be considered as vectors, accessed through element index, or through feature name.

```
import Orange

data = Orange.data.Table("iris")
print("First three data instances:")
for d in data[:3]:
    print(d)

print("25-th data instance:")
print(data[24])

name = "sepal width"
print("Value of '%s' for the first instance:" % name, data[0][name])
print("The 3rd value of the 25th data instance:", data[24][2])
```

The script above displays the following output:

```
First three data instances:
[5.100, 3.500, 1.400, 0.200 | Iris-setosa]
[4.900, 3.000, 1.400, 0.200 | Iris-setosa]
[4.700, 3.200, 1.300, 0.200 | Iris-setosa]
25-th data instance:
[4.800, 3.400, 1.900, 0.200 | Iris-setosa]
Value of 'sepal width' for the first instance: 3.500
The 3rd value of the 25th data instance: 1.900
```

The Iris dataset we have used above has four continuous attributes. Here's a script that computes their mean:

```
average = lambda x: sum(x) / len(x)

data = Orange.data.Table("iris")
print("%-15s %s" % ("Feature", "Mean"))
for x in data.domain.attributes:
    print("%-15s %.2f" % (x.name, average([d[x] for d in data])))
```

The above script also illustrates indexing of data instances with objects that store features; in `d[x]` variable `x` is an Orange object. Here's the output:

```
Feature         Mean
sepal length    5.84
sepal width     3.05
petal length    3.76
petal width     1.20
```

A slightly more complicated, but also more interesting, code that computes per-class averages:

```
average = lambda xs: sum(xs) / float(len(xs))

data = Orange.data.Table("iris")
targets = data.domain.class_var.values
print("%-15s %s" % ("Feature", " ".join("%15s" % c for c in targets)))
for a in data.domain.attributes:
    dist = [
        "%15.2f" % average([d[a] for d in data if d.get_class() == c]) for c in targets
    ]
    print("%-15s" % a.name, " ".join(dist))
```

Of the four features, petal width and length look quite discriminative for the type of iris:

```
Feature             Iris-setosa Iris-versicolor  Iris-virginica
sepal length               5.01            5.94            6.59
sepal width                3.42            2.77            2.97
petal length               1.46            4.26            5.55
petal width                0.24            1.33            2.03
```

Finally, here is a quick code that computes the class distribution for another dataset:

```
import Orange
from collections import Counter

data = Orange.data.Table("lenses")
print(Counter(str(d.get_class()) for d in data))
```

1.1.6 Orange Datasets and NumPy

Orange datasets are actually wrapped NumPy arrays. Wrapping is performed to retain the information about the feature names and values, and NumPy arrays are used for speed and compatibility with different machine learning toolboxes, like scikit-learn, on which Orange relies. Let us display the values of these arrays for the first three data instances of the iris dataset:

```
>>> data = Orange.data.Table("iris")
>>> data.X[:3]
array([[ 5.1,  3.5,  1.4,  0.2],
       [ 4.9,  3. ,  1.4,  0.2],
       [ 4.7,  3.2,  1.3,  0.2]])
>>> data.Y[:3]
array([ 0.,  0.,  0.])
```

Notice that we access the arrays for attributes and class separately, using `data.X` and `data.Y`. Average values of attributes can then be computed efficiently by:

```
>>> import np as numpy
>>> np.mean(data.X, axis=0)
array([ 5.84333333,  3.054     ,  3.75866667,  1.19866667])
```

We can also construct a (classless) dataset from a numpy array:

```
>>> X = np.array([[1,2], [4,5]])
>>> data = Orange.data.Table(X)
>>> data.domain
[Feature 1, Feature 2]
```

If we want to provide meaninful names to attributes, we need to construct an appropriate data domain:

```
>>> domain = Orange.data.Domain([Orange.data.ContinuousVariable("lenght"),
                                 Orange.data.ContinuousVariable("width")])
>>> data = Orange.data.Table(domain, X)
>>> data.domain
[lenght, width]
```

Here is another example, this time with the construction of a dataset that includes a numerical class and different types of attributes:

```
size = Orange.data.DiscreteVariable("size", ["small", "big"])
height = Orange.data.ContinuousVariable("height")
shape = Orange.data.DiscreteVariable("shape", ["circle", "square", "oval"])
speed = Orange.data.ContinuousVariable("speed")

domain = Orange.data.Domain([size, height, shape], speed)

X = np.array([[1, 3.4, 0], [0, 2.7, 2], [1, 1.4, 1]])
Y = np.array([42.0, 52.2, 13.4])

data = Orange.data.Table(domain, X, Y)
print(data)
```

Running of this scripts yields:

```
[[big, 3.400, circle | 42.000],
 [small, 2.700, oval | 52.200],
 [big, 1.400, square | 13.400]
```

1.1.7 Meta Attributes

Often, we wish to include descriptive fields in the data that will not be used in any computation (distance estimation, modeling), but will serve for identification or additional information. These are called meta attributes, and are marked with `meta` in the third header row:

```
name        hair        eggs        milk        backbone        legs        type
string        d         d           d           d         d
meta                                            class
aardvark        1         0         1           1         4         mammal
antelope        1         0         1           1         4         mammal
```

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```
bass        0        1        0        1        0        fish
bear        1        0        1        1        4        mammal
```

Values of meta attributes and all other (non-meta) attributes are treated similarly in Orange, but stored in separate numpy arrays:

```
>>> data = Orange.data.Table("zoo")
>>> data[0]["name"]
>>> data[0]["type"]
>>> for d in data:
    ...:     print("{}/{}: {}".format(d["name"], d["type"], d["legs"]))
    ...:
aardvark/mammal: 4
antelope/mammal: 4
bass/fish: 0
bear/mammal: 4
>>> data.X
array([[ 1.,  0.,  1.,  1.,  2.],
       [ 1.,  0.,  1.,  1.,  2.],
       [ 0.,  1.,  0.,  1.,  0.],
       [ 1.,  0.,  1.,  1.,  2.]]))
>>> data.metas
array([['aardvark'],
       ['antelope'],
       ['bass'],
       ['bear']], dtype=object))
```

Meta attributes may be passed to `Orange.data.Table` after providing arrays for attribute and class values:

```
from Orange.data import Table, Domain
from Orange.data import ContinuousVariable, DiscreteVariable, StringVariable
import numpy as np

X = np.array([[2.2, 1625], [0.3, 163]])
Y = np.array([0, 1])
M = np.array([["houston", 10], ["ljubljana", -1]])

domain = Domain(
    [ContinuousVariable("population"), ContinuousVariable("area")],
    [DiscreteVariable("snow", ("no", "yes"))],
    [StringVariable("city"), StringVariable("temperature")],
)
data = Table(domain, X, Y, M)
print(data)
```

The script outputs:

```
[[2.200, 1625.000 | no] {houston, 10},
 [0.300, 163.000 | yes] {ljubljana, -1}
```

To construct a classless domain we could pass `None` for the class values.

1.1.8 Missing Values

Consider the following exploration of the dataset on votes of the US senate:

```
>>> import numpy as np
>>> data = Orange.data.Table("voting.tab")
>>> data[2]
[?, y, y, ?, y, ... | democrat]
>>> np.isnan(data[2][0])
True
>>> np.isnan(data[2][1])
False
```

The particular data instance included missing data (represented with '?') for the first and the fourth attribute. In the original dataset file, the missing values are, by default, represented with a blank space. We can now examine each attribute and report on proportion of data instances for which this feature was undefined:

```
data = Orange.data.Table("voting.tab")
for x in data.domain.attributes:
    n_miss = sum(1 for d in data if np.isnan(d[x]))
    print("%4.1f%% %s" % (100.0 * n_miss / len(data), x.name))
```

First three lines of the output of this script are:

```
 2.8% handicapped-infants
11.0% water-project-cost-sharing
 2.5% adoption-of-the-budget-resolution
```

A single-liner that reports on number of data instances with at least one missing value is:

```
>>> sum(any(np.isnan(d[x]) for x in data.domain.attributes) for d in data)
203
```

1.1.9 Data Selection and Sampling

Besides the name of the data file, `Orange.data.Table` can accept the data domain and a list of data items and returns a new dataset. This is useful for any data subsetting:

```
data = Orange.data.Table("iris.tab")
print("Dataset instances:", len(data))
subset = Orange.data.Table(data.domain, [d for d in data if d["petal length"] > 3.0])
print("Subset size:", len(subset))
```

The code outputs:

```
Dataset instances: 150
Subset size: 99
```

and inherits the data description (domain) from the original dataset. Changing the domain requires setting up a new domain descriptor. This feature is useful for any kind of feature selection:

```
data = Orange.data.Table("iris.tab")
new_domain = Orange.data.Domain(
```

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```
    list(data.domain.attributes[:2]),
    data.domain.class_var
)
new_data = Orange.data.Table(new_domain, data)

print(data[0])
print(new_data[0])
```

We could also construct a random sample of the dataset:

```
>>> sample = Orange.data.Table(data.domain, random.sample(data, 3))
>>> sample
[[6.000, 2.200, 4.000, 1.000 | Iris-versicolor],
 [4.800, 3.100, 1.600, 0.200 | Iris-setosa],
 [6.300, 3.400, 5.600, 2.400 | Iris-virginica]
]
```

or randomly sample the attributes:

```
>>> atts = random.sample(data.domain.attributes, 2)
>>> domain = Orange.data.Domain(atts, data.domain.class_var)
>>> new_data = Orange.data.Table(domain, data)
>>> new_data[0]
[5.100, 1.400 | Iris-setosa]
```

1.2 Classification

Much of Orange is devoted to machine learning methods for classification, or supervised data mining. These methods rely on data with class-labeled instances, like that of senate voting. Here is a code that loads this dataset, displays the first data instance and shows its predicted class (`republican`):

```
>>> import Orange
>>> data = Orange.data.Table("voting")
>>> data[0]
[n, y, n, y, y, ... | republican]
```

Orange implements functions for construction of classification models, their evaluation and scoring. In a nutshell, here is the code that reports on cross-validated accuracy and AUC for logistic regression and random forests:

```
import Orange

data = Orange.data.Table("voting")
lr = Orange.classification.LogisticRegressionLearner()
rf = Orange.classification.RandomForestLearner(n_estimators=100)
res = Orange.evaluation.CrossValidation(data, [lr, rf], k=5)

print("Accuracy:", Orange.evaluation.scoring.CA(res))
print("AUC:", Orange.evaluation.scoring.AUC(res))
```

It turns out that for this domain logistic regression does well:

```
Accuracy: [ 0.96321839  0.95632184]
AUC: [ 0.96233796  0.95671252]
```

For supervised learning, Orange uses learners. These are objects that receive the data and return classifiers. Learners are passed to evaluation routines, such as cross-validation above.

1.2.1 Learners and Classifiers

Classification uses two types of objects: learners and classifiers. Learners consider class-labeled data and return a classifier. Given the first three data instances, classifiers return the indexes of predicted class:

```
>>> import Orange
>>> data = Orange.data.Table("voting")
>>> learner = Orange.classification.LogisticRegressionLearner()
>>> classifier = learner(data)
>>> classifier(data[:3])
array([ 0.,  0.,  1.])
```

Above, we read the data, constructed a logistic regression learner, gave it the dataset to construct a classifier, and used it to predict the class of the first three data instances. We also use these concepts in the following code that predicts the classes of the selected three instances in the dataset:

```
learner = Orange.classification.LogisticRegressionLearner()
classifier = learner(data)
c_values = data.domain.class_var.values
for d in data[5:8]:
    c = classifier(d)
    print("{}, originally {}".format(c_values[int(classifier(d))], d.get_class()))
```

The script outputs:

```
democrat, originally democrat
republican, originally democrat
republican, originally republican
```

Logistic regression has made a mistake in the second case, but otherwise predicted correctly. No wonder, since this was also the data it trained from. The following code counts the number of such mistakes in the entire dataset:

```
data = Orange.data.Table("voting")
learner = Orange.classification.LogisticRegressionLearner()
classifier = learner(data)
x = np.sum(data.Y != classifier(data))
```

1.2.2 Probabilistic Classification

To find out what is the probability that the classifier assigns to, say, democrat class, we need to call the classifier with an additional parameter that specifies the classification output type.

```
data = Orange.data.Table("voting")
learner = Orange.classification.LogisticRegressionLearner()
classifier = learner(data)
target_class = 1
print("Probabilities for %s:" % data.domain.class_var.values[target_class])
probabilities = classifier(data, 1)
for p, d in zip(probabilities[5:8], data[5:8]):
    print(p[target_class], d.get_class())
```

The output of the script also shows how badly the logistic regression missed the class in the second case:

```
Probabilities for democrat:
0.999506847581 democrat
0.201139534658 democrat
0.042347504805 republican
```

1.2.3 Cross-Validation

Validating the accuracy of classifiers on the training data, as we did above, serves demonstration purposes only. Any performance measure that assesses accuracy should be estimated on the independent test set. Such is also a procedure called cross-validation, which averages the evaluation scores across several runs, each time considering a different training and test subsets as sampled from the original dataset:

```
data = Orange.data.Table("titanic")
lr = Orange.classification.LogisticRegressionLearner()
res = Orange.evaluation.CrossValidation(data, [lr], k=5)
print("Accuracy: %.3f" % Orange.evaluation.scoring.CA(res)[0])
print("AUC:      %.3f" % Orange.evaluation.scoring.AUC(res)[0])
```

Cross-validation is expecting a list of learners. The performance estimators also return a list of scores, one for every learner. There was just one learner (*lr*) in the script above, hence an array of length one was returned. The script estimates classification accuracy and area under ROC curve:

```
Accuracy: 0.779
AUC:      0.704
```

1.2.4 Handful of Classifiers

Orange includes a variety of classification algorithms, most of them wrapped from scikit-learn, including:

- logistic regression (`Orange.classification.LogisticRegressionLearner`)
- k-nearest neighbors (`Orange.classification.knn.KNNLearner`)
- support vector machines (say, `Orange.classification.svm.LinearSVMLearner`)
- classification trees (`Orange.classification.tree.SklTreeLearner`)
- random forest (`Orange.classification.RandomForestLearner`)

Some of these are included in the code that estimates the probability of a target class on a testing data. This time, training and test datasets are disjoint:

```
import Orange
import random

random.seed(42)
data = Orange.data.Table("voting")
test = Orange.data.Table(data.domain, random.sample(data, 5))
train = Orange.data.Table(data.domain, [d for d in data if d not in test])

tree = Orange.classification.tree.TreeLearner(max_depth=3)
knn = Orange.classification.knn.KNNLearner(n_neighbors=3)
lr = Orange.classification.LogisticRegressionLearner(C=0.1)

learners = [tree, knn, lr]
classifiers = [learner(train) for learner in learners]

target = 0
print("Probabilities for %s:" % data.domain.class_var.values[target])
print("original class ", " ".join("%-5s" % l.name for l in classifiers))

c_values = data.domain.class_var.values
for d in test:
    print(
        ("{:<15}" + " {:.3f}" * len(classifiers)).format(
            c_values[int(d.get_class())], *(c(d, 1)[target] for c in classifiers)
        )
    )
```

For these five data items, there are no major differences between predictions of observed classification algorithms:

```
Probabilities for republican:
original class  tree  knn   logreg
republican      0.991 1.000 0.966
republican      0.991 1.000 0.985
democrat        0.000 0.000 0.021
republican      0.991 1.000 0.979
republican      0.991 0.667 0.963
```

The following code cross-validates these learners on the titanic dataset.

```
import Orange

data = Orange.data.Table("titanic")
tree = Orange.classification.tree.TreeLearner(max_depth=3)
knn = Orange.classification.knn.KNNLearner(n_neighbors=3)
lr = Orange.classification.LogisticRegressionLearner(C=0.1)
learners = [tree, knn, lr]

print(" " * 9 + " ".join("%-4s" % learner.name for learner in learners))
res = Orange.evaluation.CrossValidation(data, learners, k=5)
print("Accuracy %s" % " ".join("%.2f" % s for s in Orange.evaluation.CA(res)))
print("AUC      %s" % " ".join("%.2f" % s for s in Orange.evaluation.AUC(res)))
```

Logistic regression wins in area under ROC curve:

```
         tree knn  logreg
Accuracy 0.79 0.47 0.78
AUC      0.68 0.56 0.70
```

1.3 Regression

Regression in Orange is, from the interface, very similar to classification. These both require class-labeled data. Just like in classification, regression is implemented with learners and regression models (regressors). Regression learners are objects that accept data and return regressors. Regression models are given data items to predict the value of continuous class:

```
import Orange

data = Orange.data.Table("housing")
learner = Orange.regression.LinearRegressionLearner()
model = learner(data)

print("predicted, observed:")
for d in data[:3]:
    print("%.1f, %.1f" % (model(d), d.get_class()))
```

1.3.1 Handful of Regressors

Let us start with regression trees. Below is an example script that builds a tree from data on housing prices and prints out the tree in textual form:

```
data = Orange.data.Table("housing")
tree_learner = Orange.regression.SimpleTreeLearner(max_depth=2)
tree = tree_learner(data)
print(tree.to_string())
```

The script outputs the tree:

```
RM<=6.941: 19.9
RM>6.941
|    RM<=7.437
|    |    CRIM>7.393: 14.4
|    |    CRIM<=7.393
|    |    |    DIS<=1.886: 45.7
|    |    |    DIS>1.886: 32.7
|    RM>7.437
|    |    TAX<=534.500: 45.9
|    |    TAX>534.500: 21.9
```

Following is the initialization of a few other regressors and their prediction of the first five data instances in the housing price dataset:

```

random.seed(42)
```

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```
data = Orange.data.Table("housing")
test = Orange.data.Table(data.domain, random.sample(data, 5))
train = Orange.data.Table(data.domain, [d for d in data if d not in test])

lin = Orange.regression.linear.LinearRegressionLearner()
rf = Orange.regression.random_forest.RandomForestRegressionLearner()
rf.name = "rf"
ridge = Orange.regression.RidgeRegressionLearner()

learners = [lin, rf, ridge]
regressors = [learner(train) for learner in learners]

print("y    ", " ".join("%5s" % l.name for l in regressors))

for d in test:
    print(
        ("{:<5}" + " {:5.1f}" * len(regressors)).format(
            d.get_class(), *(r(d) for r in regressors)
        )
    )
```

Looks like the housing prices are not that hard to predict:

```
y    linreg    rf ridge
22.2   19.3  21.8  19.5
31.6   33.2  26.5  33.2
21.7   20.9  17.0  21.0
10.2   16.9  14.3  16.8
14.0   13.6  14.9  13.5
```

1.3.2 Cross Validation

Evaluation and scoring methods are available at `Orange.evaluation`:

```
data = Orange.data.Table("housing.tab")

lin = Orange.regression.linear.LinearRegressionLearner()
rf = Orange.regression.random_forest.RandomForestRegressionLearner()
rf.name = "rf"
ridge = Orange.regression.RidgeRegressionLearner()
mean = Orange.regression.MeanLearner()

learners = [lin, rf, ridge, mean]

res = Orange.evaluation.CrossValidation(data, learners, k=5)
rmse = Orange.evaluation.RMSE(res)
r2 = Orange.evaluation.R2(res)

print("Learner  RMSE  R2")
for i in range(len(learners)):
    print("{:8s} {:.2f} {:5.2f}".format(learners[i].name, rmse[i], r2[i]))
```

We have scored the regression with two measures for goodness of fit: root-mean-square error and coefficient of determination, or R squared. Random forest has the lowest root mean squared error:

```
Learner  RMSE  R2
linreg   4.88  0.72
rf       4.70  0.74
ridge    4.91  0.71
mean     9.20 -0.00
```

Not much difference here. Each regression method has a set of parameters. We have been running them with default parameters, and parameter fitting would help. Also, we have included `MeanLearner` in the list of our regressors; this regressor simply predicts the mean value from the training set, and is used as a baseline.

CHAPTER

TWO

REFERENCE

Available classes and methods.

2.1 Data model (data)

Orange stores data in `Orange.data.Storage` classes. The most commonly used storage is *Orange.data.Table*, which stores all data in two-dimensional numpy arrays. Each row of the data represents a data instance.

Individual data instances are represented as instances of *Orange.data.Instance*. Different storage classes may derive subclasses of *Instance* to represent the retrieved rows in the data more efficiently and to allow modifying the data through modifying data instance. For example, if *table* is *Orange.data.Table*, *table[0]* returns the row as *Orange.data.RowInstance*.

Every storage class and data instance has an associated domain description *domain* (an instance of *Orange.data.Domain*) that stores descriptions of data columns. Every column is described by an instance of a class derived from *Orange.data.Variable*. The subclasses correspond to continuous variables (*Orange.data.ContinuousVariable*), discrete variables (*Orange.data.DiscreteVariable*) and string variables (*Orange.data.StringVariable*). These descriptors contain the variable's name, symbolic values, number of decimals in printouts and similar.

The data is divided into attributes (features, independent variables), class variables (classes, targets, outcomes, dependent variables) and meta attributes. This division applies to domain descriptions, data storages that contain separate arrays for each of the three parts of the data and data instances.

Attributes and classes are represented with numeric values and are used in modelling. Meta attributes contain additional data which may be of any type. (Currently, only string values are supported in addition to continuous and numeric.)

In indexing, columns can be referred to by their names, descriptors or an integer index. For example, if *inst* is a data instance and *var* is a descriptor of type `Continuous`, referring to the first column in the data, which is also names "petal length", then *inst[var]*, *inst[0]* and *inst["petal length"]* refer to the first value of the instance. Negative indices are used for meta attributes, starting with -1.

Continuous and discrete values can be represented by any numerical type; by default, Orange uses double precision (64-bit) floats. Discrete values are represented by whole numbers.

2.1.1 Data Storage (storage)

`Orange.data.storage.Storage` is an abstract class representing a data object in which rows represent data instances (examples, in machine learning terminology) and columns represent variables (features, attributes, classes, targets, meta attributes).

Data is divided into three parts that represent independent variables (*X*), dependent variables (*Y*) and meta data (*metas*). If practical, the class should expose those parts as properties. In the associated domain (*Orange.data.Domain*), the three parts correspond to lists of variable descriptors *attributes*, *class_vars* and *metas*.

Any of those parts may be missing, dense, sparse or sparse boolean. The difference between the later two is that the sparse data can be seen as a list of pairs (variable, value), while in the latter the variable (item) is present or absent, like in market basket analysis. The actual storage of sparse data depends upon the storage type.

There is no uniform constructor signature: every derived class provides one or more specific constructors.

There are currently two derived classes *Orange.data.Table* and `Orange.data.sql.Table`, the former storing the data in-memory, in numpy objects, and the latter in SQL (currently, only PostreSQL is supported).

Derived classes must implement at least the methods for getting rows and the number of instances (*__getitem__* and *__len__*). To make storage fast enough to be practically useful, it must also reimplement a number of filters, preprocessors and aggregators. For instance, method *_filter_values(self, filter)* returns a new storage which only contains the rows that match the criteria given in the filter. *Orange.data.Table* implements an efficient method based on numpy indexing, and `Orange.data.sql.Table`, which "stores" a table as an SQL query, converts the filter into a WHERE clause.

`Orange.data.storage.`**domain**(*:obj: `Orange.data.Domain `*)
The domain describing the columns of the data

Data access

`Orange.data.storage.`**__getitem__**(*self*, *index*)
Return one or more rows of the data.

- If the index is an int, e.g. *data[7]*; the corresponding row is returned as an instance of *Instance*. Concrete implementations of *Storage* use specific derived classes for instances.
- If the index is a slice or a sequence of ints (e.g. *data[7:10]* or *data[[7, 42, 15]]*, indexing returns a new storage with the selected rows.
- If there are two indices, where the first is an int (a row number) and the second can be interpreted as columns, e.g. *data[3, 5]* or *data[3, 'gender']* or *data[3, y]* (where *y* is an instance of *Variable*), a single value is returned as an instance of `Value`.
- In all other cases, the first index should be a row index, a slice or a sequence, and the second index, which represent a set of columns, should be an int, a slice, a sequence or a numpy array. The result is a new storage with a new domain.

.__len__(*self*)
Return the number of data instances (rows)

Inspection

Storage.X_density, Storage.Y_density, Storage.metas_density
Indicates whether the attributes, classes and meta attributes are dense (*Storage.DENSE*) or sparse (*Storage.SPARSE*). If they are sparse and all values are 0 or 1, it is marked as (*Storage.SPARSE_BOOL*). The Storage class provides a default DENSE. If the data has no attibutes, classes or meta attributes, the corresponding method should re

Filters

Storage should define the following methods to optimize the filtering operations as allowed by the underlying data structure. *Orange.data.Table* executes them directly through numpy (or bottleneck or related) methods, while Orange.data.sql.Table appends them to the WHERE clause of the query that defines the data.

These methods should not be called directly but through the classes defined in *Orange.data.filter*. Methods in *Orange.data.filter* also provide the slower fallback functions for the functions not defined in the storage.

Orange.data.storage.**_filter_is_defined**(*self*, *columns=None*, *negate=False*)
Extract rows without undefined values.

Parameters

- **columns** (*sequence of ints, variable names or descriptors*) – optional list of columns that are checked for unknowns
- **negate** (*bool*) – invert the selection

Returns a new storage of the same type or *Table*

Return type Orange.data.storage.Storage

Orange.data.storage.**_filter_has_class**(*self*, *negate=False*)
Return rows with known value of the target attribute. If there are multiple classes, all must be defined.

Parameters **negate** (*bool*) – invert the selection

Returns a new storage of the same type or *Table*

Return type Orange.data.storage.Storage

Orange.data.storage.**_filter_same_value**(*self*, *column*, *value*, *negate=False*)
Select rows based on a value of the given variable.

Parameters

- **column** (*int, str or Orange.data.Variable*) – the column that is checked
- **value** (*int, float or str*) – the value of the variable
- **negate** (*bool*) – invert the selection

Returns a new storage of the same type or *Table*

Return type Orange.data.storage.Storage

Orange.data.storage.**_filter_values**(*self*, *filter*)
Apply a the given filter to the data.

Parameters **filter** (*Orange.data.Filter*) – A filter for selecting the rows

Returns a new storage of the same type or *Table*

Return type Orange.data.storage.Storage

Aggregators

Similarly to filters, storage classes should provide several methods for fast computation of statistics. These methods are not called directly but by modules within `Orange.statistics`.

_compute_basic_stats(
self, columns=None, include_metas=False, compute_variance=False)

Compute basic statistics for the specified variables: minimal and maximal value, the mean and a varianca (or a zero placeholder), the number of missing and defined values.

Parameters

- **columns** (list of ints, variable names or descriptors of type *Orange.data.Variable*) – a list of columns for which the statistics is computed; if *None*, the function computes the data for all variables
- **include_metas** (*bool*) – a flag which tells whether to include meta attributes (applicable only if *columns* is *None*)
- **compute_variance** (*bool*) – a flag which tells whether to compute the variance

Returns a list with tuple (min, max, mean, variance, #nans, #non-nans) for each variable

Return type list

Orange.data.storage.**_compute_distributions**(*self*, *columns=None*)

Compute the distribution for the specified variables. The result is a list of pairs containing the distribution and the number of rows for which the variable value was missing.

For discrete variables, the distribution is represented as a vector with absolute frequency of each value. For continuous variables, the result is a 2-d array of shape (2, number-of-distinct-values); the first row contains (distinct) values of the variables and the second has their absolute frequencies.

Parameters **columns** (list of ints, variable names or descriptors of type *Orange.data.Variable*) – a list of columns for which the distributions are computed; if *None*, the function runs over all variables

Returns a list of distributions

Return type list of numpy arrays

Storage.**_compute_contingency**(*col_vars=None*, *row_var=None*)

Compute contingency matrices for one or more discrete or continuous variables against the specified discrete variable.

The resulting list contains a pair for each column variable. The first element contains the contingencies and the second elements gives the distribution of the row variables for instances in which the value of the column variable is missing.

The format of contingencies returned depends on the variable type:

- for discrete variables, it is a numpy array, where element (i, j) contains count of rows with i-th value of the row variable and j-th value of the column variable.
- for continuous variables, contingency is a list of two arrays, where the first array contains ordered distinct values of the column_variable and the element (i,j) of the second array contains count of rows with i-th value of the row variable and j-th value of the ordered column variable.

Parameters

- **col_vars** (list of ints, variable names or descriptors of type *Orange.data.Variable*) – variables whose values will correspond to columns of contingency matrices

- **row_var** (int, variable name or *Orange.data.DiscreteVariable*) – a discrete variable whose values will correspond to the rows of contingency matrices

2.1.2 Data Table (table)

class Orange.data.**Table**(**args*, ***kwargs*)

Stores data instances as a set of 2d tables representing the independent variables (attributes, features) and dependent variables (classes, targets), and the corresponding weights and meta attributes.

The data is stored in 2d numpy arrays `X`, `Y`, `W`, `metas`. The arrays may be dense or sparse. All arrays have the same number of rows. If certain data is missing, the corresponding array has zero columns.

Arrays can be of any type; default is *float* (that is, double precision). Values of discrete variables are stored as whole numbers. Arrays for meta attributes usually contain instances of *object*.

The table also stores the associated information about the variables as an instance of *Domain*. The number of columns must match the corresponding number of variables in the description.

There are multiple ways to get values or entire rows of the table.

- The index can be an int, e.g. *table[7]*; the corresponding row is returned as an instance of *RowInstance*.
- The index can be a slice or a sequence of ints (e.g. *table[7:10]* or *table[[7, 42, 15]]*, indexing returns a new data table with the selected rows.
- If there are two indices, where the first is an int (a row number) and the second can be interpreted as columns, e.g. *table[3, 5]* or *table[3, 'gender']* or *table[3, y]* (where *y* is an instance of *Variable*), a single value is returned as an instance of `Value`.
- In all other cases, the first index should be a row index, a slice or a sequence, and the second index, which represent a set of columns, should be an int, a slice, a sequence or a numpy array. The result is a new table with a new domain.

Rules for setting the data are as follows.

- If there is a single index (an *int*, *slice*, or a sequence of row indices) and the value being set is a single scalar, all attributes (not including the classes) are set to that value. That is, *table[r] = v* is equivalent to *table.X[r] = v*.
- If there is a single index and the value is a data instance (*Orange.data.Instance*), it is converted into the table's domain and set to the corresponding rows.
- Final option for a single index is that the value is a sequence whose length equals the number of attributes and target variables. The corresponding rows are set; meta attributes are set to unknowns.
- **For two indices, the row can again be given as a single *int*, a** *slice* or a sequence of indices. Column indices can be a single *int*, *str* or *Orange.data.Variable*, a sequence of them, a *slice* or any iterable. The value can be a single value, or a sequence of appropriate length.

domain

Description of the variables corresponding to the table's columns. The domain is used for determining the variable types, printing the data in human-readable form, conversions between data tables and similar.

property columns

A class whose attributes contain attribute descriptors for columns. For a table *table*, setting *c = table.columns* will allow accessing the table's variables with, for instance *c.gender*, *c.age* ets. Spaces are replaced with underscores.

Constructors

The preferred way to construct a table is to invoke a named constructor.

classmethod Table.**from_domain**(*domain*, *n_rows=0*, *weights=False*)

Construct a new *Table* with the given number of rows for the given domain. The optional vector of weights is initialized to 1's.

Parameters

- **domain** (Orange.data.Domain) – domain for the *Table*
- **n_rows** (*int*) – number of rows in the new table
- **weights** (*bool*) – indicates whether to construct a vector of weights

Returns a new table

Return type *Orange.data.Table*

classmethod Table.**from_table**(*domain*, *source*, *row_indices=Ellipsis*)

Create a new table from selected columns and/or rows of an existing one. The columns are chosen using a domain. The domain may also include variables that do not appear in the source table; they are computed from source variables if possible.

The resulting data may be a view or a copy of the existing data.

Parameters

- **domain** (Orange.data.Domain) – the domain for the new table
- **source** (Orange.data.Table) – the source table
- **row_indices** (*a slice or a sequence*) – indices of the rows to include

Returns a new table

Return type *Orange.data.Table*

classmethod Table.**from_table_rows**(*source*, *row_indices*)

Construct a new table by selecting rows from the source table.

Parameters

- **source** (Orange.data.Table) – an existing table
- **row_indices** (*a slice or a sequence*) – indices of the rows to include

Returns a new table

Return type *Orange.data.Table*

classmethod Table.**from_numpy**(*domain*, *X*, *Y=None*, *metas=None*, *W=None*, *attributes=None*, *ids=None*)

Construct a table from numpy arrays with the given domain. The number of variables in the domain must match the number of columns in the corresponding arrays. All arrays must have the same number of rows. Arrays may be of different numpy types, and may be dense or sparse.

Parameters

- **domain** (Orange.data.Domain) – the domain for the new table
- **X** (*np.array*) – array with attribute values
- **Y** (*np.array*) – array with class values
- **metas** (*np.array*) – array with meta attributes
- **W** (*np.array*) – array with weights

Returns

classmethod Table.**from_file**(*filename*, *sheet=None*)
Read a data table from a file. The path can be absolute or relative.

Parameters

- **filename** (*str*) – File name
- **sheet** (*str*) – Sheet in a file (optional)

Returns a new data table

Return type *Orange.data.Table*

Inspection

Table.**is_view**()
Return *True* if all arrays represent a view referring to another table

Table.**is_copy**()
Return *True* if the table owns its data

Table.**ensure_copy**()
Ensure that the table owns its data; copy arrays when necessary.

Table.**has_missing**()
Return *True* if there are any missing attribute or class values.

Table.**has_missing_class**()
Return *True* if there are any missing class values.

Table.**checksum**(*include_metas=True*)
Return a checksum over X, Y, metas and W.

Row manipulation

Note: Methods that change the table length (*append*, *extend*, *insert*, *clear*, and resizing through deleting, slicing or by other means), were deprecated and removed in Orange 3.24.

Table.**shuffle**()
Randomly shuffle the rows of the table.

Weights

Table.**has_weights**()
Return *True* if the data instances are weighed.

Table.**set_weights**(*weight=1*)
Set weights of data instances; create a vector of weights if necessary.

Table.**total_weight**()
Return the total weight of instances in the table, or their number if they are unweighted.

2.1.3 SQL table (data.sql)

class Orange.data.sql.table.**SqlTable**(**args*, ***kwargs*)

SqlTable represents a table with the data which is stored in the database. Besides the inherited attributes, the object stores a connection to the database and row filters.

Constructor connects to the database, infers the variable types from the types of the columns in the database and constructs the corresponding domain description. Discrete and continuous variables are put among attributes, and string variables are meta attributes. The domain does not have a class.

SqlTable overloads the data access methods for random access to rows and for iteration (*__getitem__* and *__iter__*). It also provides methods for fast computation of basic statistics, distributions and contingency matrices, as well as for filtering the data. Filtering the data returns a new instance of *SqlTable*. The new instances however differs only in that an additional filter is added to the row_filter.

All evaluation is lazy in the sense that most operations just modify the domain and the list of filters. These are used to construct an SQL query when the data is actually needed, for instance to retrieve a data row or compute a distribution of values for a certain column.

connection
The object that holds the database connection. An instance of a class compatible with Python DB API 2.0.

host
The host name of the database server

database
The name of the database

table_name
The name of the table in the database

row_filters
A list of filters that are applied when constructing the query. The filters in the should have a method *to_sql*. Module Orange.data.sql.filter contains classes derived from filters in *Orange.data.filter* with the appropriate implementation of the method.

static __new__(*cls*, **args*, ***kwargs*)

__init__(*connection_params*, *table_or_sql*, *backend=None*, *type_hints=None*, *inspect_values=False*)
Create a new proxy for sql table.

To create a new SqlTable, specify the connection parameters for psycopg2 and the name of the table/sql query used to fetch the data.

> table = SqlTable('database_name', 'table_name') table = SqlTable('database_name', 'SELECT * FROM table')

For complex configurations, dictionary of connection parameters can be used instead of the database name. For documentation about connection parameters, see: http://www.postgresql.org/docs/current/static/libpq-connect.html#LIBPQ-PARAMKEYWORDS

Data domain is inferred from the columns of the table/query.

The (very quick) default setting is to treat all numeric columns as continuous variables and everything else as strings and placed among meta attributes.

If inspect_values parameter is set to True, all column values are inspected and int/string columns with less than 21 values are intepreted as discrete features.

Domains can be constructed by the caller and passed in type_hints parameter. Variables from the domain are used for the columns with the matching names; for columns without the matching name in the domain, types are inferred as described above.

__getitem__(*key*)
Indexing of SqlTable is performed in the following way:

If a single row is requested, it is fetched from the database and returned as a SqlRowInstance.

A new SqlTable with appropriate filters is constructed and returned otherwise.

__iter__()
Iterating through the rows executes the query using a cursor and then yields resulting rows as SqlRowInstances as they are requested.

copy()
Return a copy of the SqlTable

__bool__()
Return True if the SqlTable is not empty.

__len__()
Return number of rows in the table. The value is cached so it is computed only the first time the length is requested.

download_data(*limit=None*, *partial=False*)
Download SQL data and store it in memory as numpy matrices.

property X
Numpy array with attribute values.

property Y
Numpy array with class values.

property metas
Numpy array with class values.

property W
Numpy array with class values.

property ids
Numpy array with class values.

has_weights()
Return *True* if the data instances are weighed.

classmethod from_table(*domain*, *source*, *row_indices=Ellipsis*)
Create a new table from selected columns and/or rows of an existing one. The columns are chosen using a domain. The domain may also include variables that do not appear in the source table; they are computed from source variables if possible.

The resulting data may be a view or a copy of the existing data.

Parameters

- **domain** (Orange.data.Domain) – the domain for the new table
- **source** (Orange.data.Table) – the source table
- **row_indices** (*a slice or a sequence*) – indices of the rows to include

Returns a new table

Return type *Orange.data.Table*

checksum(*include_metas=True*)
Return a checksum over X, Y, metas and W.

2.1.4 Domain description (domain)

Description of a domain stores a list of features, class(es) and meta attribute descriptors. A domain descriptor is attached to all tables in Orange to assign names and types to the corresponding columns. Columns in the *Orange.data.Table* have the roles of attributes (features, independent variables), class(es) (targets, outcomes, dependent variables) and meta attributes; in parallel to that, the domain descriptor stores their corresponding descriptions in collections of variable descriptors of type *Orange.data.Variable*.

Domain descriptors are also stored in predictive models and other objects to facilitate automated conversions between domains, as described below.

Domains are most often constructed automatically when loading the data or wrapping the numpy arrays into Orange's *Table*.

```
>>> from Orange.data import Table
>>> iris = Table("iris")
>>> iris.domain
[sepal length, sepal width, petal length, petal width | iris]
```

class Orange.data.**Domain**(*attributes*, *class_vars=None*, *metas=None*, *source=None*)

attributes

A tuple of descriptors (instances of *Orange.data.Variable*) for attributes (features, independent variables).

```
>>> iris.domain.attributes
(ContinuousVariable('sepal length'), ContinuousVariable('sepal width'),
ContinuousVariable('petal length'), ContinuousVariable('petal width'))
```

class_var

Class variable if the domain has a single class; *None* otherwise.

```
>>> iris.domain.class_var
DiscreteVariable('iris')
```

class_vars

A tuple of descriptors for class attributes (outcomes, dependent variables).

```
>>> iris.domain.class_vars
(DiscreteVariable('iris'),)
```

variables

A list of attributes and class attributes (the concatenation of the above).

```
>>> iris.domain.variables
(ContinuousVariable('sepal length'), ContinuousVariable('sepal width'),
ContinuousVariable('petal length'), ContinuousVariable('petal width'),
DiscreteVariable('iris'))
```

metas

List of meta attributes.

anonymous

True if the domain was constructed when converting numpy array to *Orange.data.Table*. Such domains can be converted to and from other domains even if they consist of different variable descriptors for as long as their number and types match.

__init__(*attributes*, *class_vars=None*, *metas=None*, *source=None*)

Initialize a new domain descriptor. Arguments give the features and the class attribute(s). They can be described by descriptors (instances of *Variable*), or by indices or names if the source domain is given.

Parameters

- **attributes** (list of *Variable*) – a list of attributes
- **class_vars** (*Variable* or list of *Variable*) – target variable or a list of target variables
- **metas** (list of *Variable*) – a list of meta attributes
- **source** (Orange.data.Domain) – the source domain for attributes

Returns a new domain

Return type *Domain*

The following script constructs a domain with a discrete feature *gender* and continuous feature *age*, and a continuous target *salary*.

```
>>> from Orange.data import Domain, DiscreteVariable, ContinuousVariable
>>> domain = Domain([DiscreteVariable.make("gender"),
...                  ContinuousVariable.make("age")],
...                 ContinuousVariable.make("salary"))
>>> domain
[gender, age | salary]
```

This constructs a new domain with some features from the Iris dataset and a new feature *color*.

```
>>> new_domain = Domain(["sepal length",
...                      "petal length",
...                      DiscreteVariable.make("color")],
...                     iris.domain.class_var,
...                     source=iris.domain)
>>> new_domain
[sepal length, petal length, color | iris]
```

classmethod from_numpy(*X*, *Y=None*, *metas=None*)

Create a domain corresponding to the given numpy arrays. This method is usually invoked from *Orange.data.Table.from_numpy()*.

All attributes are assumed to be continuous and are named "Feature <n>". Target variables are discrete if the only two values are 0 and 1; otherwise they are continuous. Discrete targets are named "Class <n>" and continuous are named "Target <n>". Domain is marked as *anonymous*, so data from any other domain of the same shape can be converted into this one and vice-versa.

Parameters

- **X** (*numpy.ndarray*) – 2-dimensional array with data
- **Y** (*numpy.ndarray* or None) – 1- of 2- dimensional data for target
- **metas** (*numpy.ndarray* or None) – meta attributes

Returns a new domain

Return type *Domain*

```
>>> import numpy as np
>>> from Orange.data import Domain
```

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```
>>> X = np.arange(20, dtype=float).reshape(5, 4)
>>> Y = np.arange(5, dtype=int)
>>> domain = Domain.from_numpy(X, Y)
>>> domain
[Feature 1, Feature 2, Feature 3, Feature 4 | Class 1]
```

__getitem__(*idx*)

Return a variable descriptor from the given argument, which can be a descriptor, index or name. If *var* is a descriptor, the function returns this same object.

Parameters **idx** (int, str or *Variable*) – index, name or descriptor

Returns an instance of *Variable* described by *var*

Return type *Variable*

```
>>> iris.domain[1:3]
(ContinuousVariable('sepal width'), ContinuousVariable('petal length'))
```

__len__()

The number of variables (features and class attributes).

The current behavior returns the length of only features and class attributes. In the near future, it will include the length of metas, too, and __iter__ will act accordingly.

__contains__(*item*)

Return *True* if the item (*str*, *int*, *Variable*) is in the domain.

```
>>> "petal length" in iris.domain
True
>>> "age" in iris.domain
False
```

index(*var*)

Return the index of the given variable or meta attribute, represented with an instance of *Variable*, *int* or *str*.

```
>>> iris.domain.index("petal length")
2
```

has_discrete_attributes(*include_class=False*, *include_metas=False*)

Return *True* if domain has any discrete attributes. If *include_class* is set, the check includes the class attribute(s). If *include_metas* is set, the check includes the meta attributes.

```
>>> iris.domain.has_discrete_attributes()
False
>>> iris.domain.has_discrete_attributes(include_class=True)
True
```

has_continuous_attributes(*include_class=False*, *include_metas=False*)

Return *True* if domain has any continuous attributes. If *include_class* is set, the check includes the class attribute(s). If *include_metas* is set, the check includes the meta attributes.

```
>>> iris.domain.has_continuous_attributes()
True
```

Domain conversion

Domain descriptors also convert data instances between different domains.

In a typical scenario, we may want to discretize some continuous data before inducing a model. Discretizers (`Orange.preprocess`) construct a new data table with attribute descriptors (*Orange.data.variable*), that include the corresponding functions for conversion from continuous to discrete values. The trained model stores this domain descriptor and uses it to convert instances from the original domain to the discretized one at prediction phase.

In general, instances are converted between domains as follows.

- If the target attribute appears in the source domain, the value is copied; two attributes are considered the same if they have the same descriptor.
- If the target attribute descriptor defines a function for value transformation, the value is transformed.
- Otherwise, the value is marked as missing.

An exception to this rule are domains in which the anonymous flag is set. When the source or the target domain is anonymous, they match if they have the same number of variables and types. In this case, the data is copied without considering the attribute descriptors.

2.1.5 Variable Descriptors (`variable`)

Every variable is associated with a descriptor that stores its name and other properties. Descriptors serve three main purposes:

- conversion of values from textual format (e.g. when reading files) to the internal representation and back (e.g. when writing files or printing out);
- identification of variables: two variables from different datasets are considered to be the same if they have the same descriptor;
- conversion of values between domains or datasets, for instance from continuous to discrete data, using a precomputed transformation.

Descriptors are most often constructed when loading the data from files.

```
>>> from Orange.data import Table
>>> iris = Table("iris")

>>> iris.domain.class_var
DiscreteVariable('iris')
>>> iris.domain.class_var.values
['Iris-setosa', 'Iris-versicolor', 'Iris-virginica']

>>> iris.domain[0]
ContinuousVariable('sepal length')
>>> iris.domain[0].number_of_decimals
1
```

Some variables are derived from others. For instance, discretizing a continuous variable gives a new, discrete variable. The new variable can compute its values from the original one.

```
>>> from Orange.preprocess import DomainDiscretizer
>>> discretizer = DomainDiscretizer()
>>> d_iris = discretizer(iris)
```

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```
>>> d_iris[0]
DiscreteVariable('D_sepal length')
>>> d_iris[0].values
['<5.2', '[5.2, 5.8)', '[5.8, 6.5)', '>=6.5']
```

See *Derived variables* for a detailed explanation.

Constructors

Orange maintains lists of existing descriptors for variables. This facilitates the reuse of descriptors: if two datasets refer to the same variables, they should be assigned the same descriptors so that, for instance, a model trained on one dataset can make predictions for the other.

Variable descriptors are seldom constructed in user scripts. When needed, this can be done by calling the constructor directly or by calling the class method *make*. The difference is that the latter returns an existing descriptor if there is one with the same name and which matches the other conditions, such as having the prescribed list of discrete values for *DiscreteVariable*:

```
>>> from Orange.data import ContinuousVariable
>>> age = ContinuousVariable.make("age")
>>> age1 = ContinuousVariable.make("age")
>>> age2 = ContinuousVariable("age")
>>> age is age1
True
>>> age is age2
False
```

The first line returns a new descriptor after not finding an existing desciptor for a continuous variable named "age". The second reuses the first descriptor. The last creates a new one since the constructor is invoked directly.

The distinction does not matter in most cases, but it is important when loading the data from different files. Orange uses the *make* constructor when loading data.

Base class

class Orange.data.**Variable**(*name=''*, *compute_value=None*, *, *sparse=False*)

The base class for variable descriptors contains the variable's name and some basic properties.

name

The name of the variable.

unknown_str

A set of values that represent unknowns in conversion from textual formats. Default is *{"?", ".", "", "NA", "~", None}*.

compute_value

A function for computing the variable's value when converting from another domain which does not contain this variable. The function will be called with a data set (*Orange.data.Table*) and has to return an array of computed values for all its instances. The base class defines a static method *compute_value*, which returns *Unknown*. Non-primitive variables must redefine it to return *None*.

sparse

A flag about sparsity of the variable. When set, the variable suggests it should be stored in a sparse matrix.

source_variable
An optional descriptor of the source variable - if any - from which this variable is derived and computed via *compute_value*.

attributes
A dictionary with user-defined attributes of the variable

classmethod is_primitive(*var=None*)
True if the variable's values are stored as floats. Non-primitive variables can appear in the data only as meta attributes.

static str_val(*val*)
Return a textual representation of variable's value *val*. Argument *val* must be a float (for primitive variables) or an arbitrary Python object (for non-primitives).

Derived classes must overload the function.

to_val(*s*)
Convert the given argument to a value of the variable. The argument can be a string, a number or *None*. For primitive variables, the base class provides a method that returns `Unknown` if *s* is found in *unknown_str*, and raises an exception otherwise. For non-primitive variables it returns the argument itself.

Derived classes of primitive variables must overload the function.

Parameters **s** (*str, float or None*) – value, represented as a number, string or *None*

Return type float or object

val_from_str_add(*s*)
Convert the given string to a value of the variable. The method is similar to *to_val* except that it only accepts strings and that it adds new values to the variable's domain where applicable.

The base class method calls *to_val*.

Parameters **s** (*str*) – symbolic representation of the value

Return type float or object

Continuous variables

class Orange.data.**ContinuousVariable**(*name=''*, *number_of_decimals=None*, *compute_value=None*, ***, *sparse=False*)
Descriptor for continuous variables.

number_of_decimals
The number of decimals when the value is printed out (default: 3).

adjust_decimals
A flag regulating whether the *number_of_decimals* is being adjusted by *to_val*.

The value of *number_of_decimals* is set to 3 and *adjust_decimals* is set to 2. When *val_from_str_add* is called for the first time with a string as an argument, *number_of_decimals* is set to the number of decimals in the string and *adjust_decimals* is set to 1. In the subsequent calls of *to_val*, the nubmer of decimals is increased if the string argument has a larger number of decimals.

If the *number_of_decimals* is set manually, *adjust_decimals* is set to 0 to prevent changes by *to_val*.

classmethod make(*name*, **args*, ***kwargs*)
Return an existing continuous variable with the given name, or construct and return a new one.

classmethod is_primitive(*var=None*)
True if the variable's values are stored as floats. Non-primitive variables can appear in the data only as meta attributes.

str_val(*val*)
Return the value as a string with the prescribed number of decimals.

to_val(*s*)
Convert a value, given as an instance of an arbitrary type, to a float.

val_from_str_add(*s*)
Convert a value from a string and adjust the number of decimals if *adjust_decimals* is non-zero.

Discrete variables

class Orange.data.**DiscreteVariable**(*name=''*, *values=()*, *compute_value=None*, *, *sparse=False*)
Descriptor for symbolic, discrete variables. Values of discrete variables are stored as floats; the numbers corresponds to indices in the list of values.

values
A list of variable's values.

classmethod make(*name*, **args*, ***kwargs*)
Return an existing continuous variable with the given name, or construct and return a new one.

classmethod is_primitive(*var=None*)
True if the variable's values are stored as floats. Non-primitive variables can appear in the data only as meta attributes.

str_val(*val*)
Return a textual representation of the value (*self.values[int(val)]*) or "?" if the value is unknown.

Parameters **val** (*float (should be whole number)*) – value

Return type str

to_val(*s*)
Convert the given argument to a value of the variable (*float*). If the argument is numeric, its value is returned without checking whether it is integer and within bounds. *Unknown* is returned if the argument is one of the representations for unknown values. Otherwise, the argument must be a string and the method returns its index in *values*.

Parameters **s** – values, represented as a number, string or *None*

Return type float

val_from_str_add(*s*)
Similar to *to_val*, except that it accepts only strings and that it adds the value to the list if it does not exist yet.

Parameters **s** (*str*) – symbolic representation of the value

Return type float

String variables

class Orange.data.**StringVariable**(*name=''*, *compute_value=None*, *, *sparse=False*)
Descriptor for string variables. String variables can only appear as meta attributes.

classmethod make(*name*, **args*, ***kwargs*)
Return an existing continuous variable with the given name, or construct and return a new one.

classmethod is_primitive(*var=None*)
True if the variable's values are stored as floats. Non-primitive variables can appear in the data only as meta attributes.

static str_val(*val*)
Return a string representation of the value.

to_val(*s*)
Return the value as a string. If it is already a string, the same object is returned.

val_from_str_add(*s*)
Return the value as a string. If it is already a string, the same object is returned.

Time variables

Time variables are continuous variables with value 0 on the Unix epoch, 1 January 1970 00:00:00.0 UTC. Positive numbers are dates beyond this date, and negative dates before. Due to limitation of Python `datetime` module, only dates in 1 A.D. or later are supported.

class Orange.data.**TimeVariable**(**args*, *have_date=0*, *have_time=0*, ***kwargs*)
TimeVariable is a continuous variable with Unix epoch (1970-01-01 00:00:00+0000) as the origin (0.0). Later dates are positive real numbers (equivalent to Unix timestamp, with microseconds in the fraction part), and the dates before it map to the negative real numbers.

Unfortunately due to limitation of Python datetime, only dates with year >= 1 (A.D.) are supported.

If time is specified without a date, Unix epoch is assumed.

If time is specified without an UTC offset, localtime is assumed.

parse(*datestr*)
Return *datestr*, a datetime provided in one of ISO 8601 formats, parsed as a real number. Value 0 marks the Unix epoch, positive values are the dates after it, negative before.

If date is unspecified, epoch date is assumed.

If time is unspecified, 00:00:00.0 is assumed.

If timezone is unspecified, local time is assumed.

Derived variables

The *compute_value* mechanism is used throughout Orange to compute all preprocessing on training data and applying the same transformations to the testing data without hassle.

Method *compute_value* is usually invoked behind the scenes in conversion of domains. Such conversions are are typically implemented within the provided wrappers and cross-validation schemes.

Derived variables in Orange

Orange saves variable transformations into the domain as *compute_value* functions. If Orange was not using *compute_value*, we would have to manually transform the data:

```
>>> from Orange.data import Domain, ContinuousVariable
>>> data = Orange.data.Table("iris")
>>> train = data[::2]  # every second row
>>> test = data[1::2]  # every other second instance
```

We will create a new data set with a single feature, "petals", that will be a sum of petal lengths and widths:

```
>>> petals = ContinuousVariable("petals")
>>> derived_train = train.transform(Domain([petals],
...                                        data.domain.class_vars))
>>> derived_train.X = train[:, "petal width"].X + \
...                   train[:, "petal length"].X
```

We have set *Table*'s *X* directly. Next, we build and evaluate a classification tree:

```
>>> learner = Orange.classification.TreeLearner()
>>> from Orange.evaluation import CrossValidation, TestOnTestData
>>> res = CrossValidation(derived_train, [learner], k=5)
>>> Orange.evaluation.scoring.CA(res)[0]
0.88
>>> res = TestOnTestData(derived_train, test, [learner])
>>> Orange.evaluation.scoring.CA(res)[0]
0.3333333333333333
```

A classification tree shows good accuracy with cross validation, but not on separate test data, because Orange can not reconstruct the "petals" feature for test data—we would have to reconstruct it ourselves. But if we define *compute_value* and therefore store the transformation in the domain, Orange could transform both training and test data:

```
>>> petals = ContinuousVariable("petals",
...     compute_value=lambda data: data[:, "petal width"].X + \
...                                data[:, "petal length"].X)
>>> derived_train = train.transform(Domain([petals],
                                           data.domain.class_vars))
>>> res = TestOnTestData(derived_train, test, [learner])
>>> Orange.evaluation.scoring.CA(res)[0]
0.9733333333333334
```

All preprocessors in Orange use *compute_value*.

Example with discretization

The following example converts features to discrete:

```
>>> iris = Orange.data.Table("iris")
>>> iris_1 = iris[::2]
>>> discretizer = Orange.preprocess.DomainDiscretizer()
>>> d_iris_1 = discretizer(iris_1)
```

A dataset is loaded and a new table with every second instance is created. On this dataset, we compute discretized data, which uses the same data to set proper discretization intervals.

The discretized variable "D_sepal length" stores a function that can derive continous values into discrete:

```
>>> d_iris_1[0]
DiscreteVariable('D_sepal length')
>>> d_iris_1[0].compute_value
<Orange.feature.discretization.Discretizer at 0x10d5108d0>
```

The function is used for converting the remaining data (as automatically happens within model validation in Orange):

```
>>> iris_2 = iris[1::2]  # previously unselected
>>> d_iris_2 = iris_2.transform(d_iris_1.domain)
>>> d_iris_2[0]
[<5.2, [2.8, 3), <1.6, <0.2 | Iris-setosa]
```

The code transforms previously unused data into the discrete domain *d_iris_1.domain*. Behind the scenes, the values for the destination domain that are not yet in the source domain (*iris_2.domain*) are computed with the destination variables' *compute_value*.

Optimization for repeated computation

Some transformations share parts of computation across variables. For example, *PCA* uses all input features to compute the PCA transform. If each output PCA component was implemented with ordinary *compute_value*, the PCA transform would be repeatedly computed for each PCA component. To avoid repeated computation, set *compute_value* to a subclass of *SharedComputeValue*.

class Orange.data.util.**SharedComputeValue**(*compute_shared*, *variable=None*)

A base class that separates compute_value computation for different variables into shared and specific parts.

Parameters

- **compute_shared** (*Callable[[Orange.data.Table], object]*) – A callable that performs computation that is shared between multiple variables. Variables sharing computation need to set the same instance.
- **variable** (Orange.data.Variable) – The original variable on which this compute value is set. Optional.

compute(*data*, *shared_data*)

Given precomputed shared data, perform variable-specific part of computation and return new variable values. Subclasses need to implement this function.

The following example creates normalized features that divide values by row sums and then tranforms the data. In the example the function *row_sum* is called only once; if we did not use *SharedComputeValue*, *row_sum* would be called four times, once for each feature.

```
iris = Orange.data.Table("iris")

def row_sum(data):
    return data.X.sum(axis=1, keepdims=True)

class DivideWithMean(Orange.data.util.SharedComputeValue):

    def __init__(self, var, fn):
        super().__init__(fn)
        self.var = var

    def compute(self, data, shared_data):
        return data[:, self.var].X / shared_data

divided_attributes = [
    Orange.data.ContinuousVariable(
        "Divided " + attr.name,
        compute_value=DivideWithMean(attr, row_sum)
    ) for attr in iris.domain.attributes]

divided_domain = Orange.data.Domain(
    divided_attributes,
    iris.domain.class_vars
)

divided_iris = iris.transform(divided_domain)
```

2.1.6 Values (value)

class Orange.data.variable.**Value**(*variable*, *value=nan*)

The class representing a value. The class is not used to store values but only to return them in contexts in which we want the value to be accompanied with the descriptor, for instance to print the symbolic value of discrete variables.

The class is derived from *float*, with an additional attribute *variable* which holds the descriptor of type *Orange.data.Variable*. If the value continuous or discrete, it is stored as a float. Other types of values, like strings, are stored in the attribute *value*.

The class overloads the methods for printing out the value: *variable.repr_val* and *variable.str_val* are used to get a suitable representation of the value.

Equivalence operator is overloaded as follows:

- unknown values are equal; if one value is unknown and the other is not, they are different;
- if the value is compared with the string, the value is converted to a string using *variable.str_val* and the two strings are compared
- if the value is stored in attribute *value*, it is compared with the given other value
- otherwise, the inherited comparison operator for *float* is called.

Finally, value defines a hash, so values can be put in sets and appear as keys in dictionaries.

variable(*:obj:`Orange.data.Variable`*)

Descriptor; used for printing out and for comparing with strings

value
Value; the value can be of arbitrary type and is used only for variables that are neither discrete nor continuous. If *value* is *None*, the derived *float* value is used.

2.1.7 Data Instance (instance)

Class *Instance* represents a data instance, typically retrieved from a *Orange.data.Table* or Orange.data.sql.SqlTable. The base class contains a copy of the data; modifying does not change the data in the storage from which the instance was retrieved. Derived classes (e.g. *Orange.data.table.RowInstance*) can represent views into various data storages, therefore changing them actually changes the data.

Like data tables, every data instance is associated with a domain and its data is split into attributes, classes, meta attributes and the weight. Its constructor thus requires a domain and, optionally, data. For the following example, we borrow the domain from the Iris dataset.

```
>>> from Orange.data import Table, Instance
>>> iris = Table("iris")
>>> inst = Instance(iris.domain, [5.2, 3.8, 1.4, 0.5, "Iris-virginica"])
>>> inst
[5.2, 3.8, 1.4, 0.5 | Iris-virginica]
>>> inst0 = Instance(iris.domain)
>>> inst0
[?, ?, ?, ? | ?]
```

The instance's data can be retrieved through attributes x, y and metas.

```
>>> inst.x
array([ 5.2,  3.8,  1.4,  0.5])
>>> inst.y
array([ 2.])
>>> inst.metas
array([], dtype=object)
```

Other utility functions provide for easier access to the instances data.

```
>>> inst.get_class()
Value('iris', Iris-virginica)
>>> for e in inst.attributes():
...     print(e)
...
5.2
3.8
1.4
0.5
```

class Orange.data.**Instance**(*domain*, *data=None*, *id=None*)
Constructor requires a domain and the data as numpy array, an existing instance from the same or another domain or any Python iterable.

Domain can be omitted it the data is given as an existing data instances.

When the instance is not from the given domain, Orange converts it.

```
>>> from Orange.preprocess import DomainDiscretizer
>>> discretizer = DomainDiscretizer()
```

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```
>>> d_iris = discretizer(iris)
>>> d_inst = Instance(d_iris, inst)
```

property domain
The domain describing the instance's values.

property x
Instance's attributes as a 1-dimensional numpy array whose length equals *len(self.domain.attributes)*.

property y
Instance's classes as a 1-dimensional numpy array whose length equals *len(self.domain.attributes)*.

property metas
Instance's meta attributes as a 1-dimensional numpy array whose length equals *len(self.domain.attributes)*.

property list
All instance's values, including attributes, classes and meta attributes, as a list whose length equals *len(self.domain.attributes)* + *len(self.domain.class_vars)* + *len(self.domain.metas)*.

property weight
The weight of the data instance. Default is 1.

attributes()
Return iterator over the instance's attributes

classes()
Return iterator over the instance's class attributes

get_class()
Return the class value as an instance of `Orange.data.Value`. Throws an exception if there are multiple classes.

get_classes()
Return the class value as a list of instances of `Orange.data.Value`.

set_class(*value*)
Set the instance's class. Throws an exception if there are multiple classes.

Rows of Data Tables

class Orange.data.**RowInstance**(*table*, *row_index*)
RowInstance is a specialization of *Instance* that represents a row of *Orange.data.Table*. *RowInstance* is returned by indexing a *Table*.

The difference between *Instance* and *RowInstance* is that the latter represents a view into the table: changing the *RowInstance* changes the data in the table:

```
>>> iris[42]
[4.4, 3.2, 1.3, 0.2 | Iris-setosa]
>>> inst = iris[42]
>>> inst.set_class("Iris-virginica")
>>> iris[42]
[4.4, 3.2, 1.3, 0.2 | Iris-virginica]
```

Dense tables can also be modified directly through `x`, `y` and `metas`.

```
>>> inst.x[0] = 5
>>> iris[42]
[5.0, 3.2, 1.3, 0.2 | Iris-virginica]
```

Sparse tables cannot be changed in this way.

property weight
The weight of the data instance. Default is 1.

set_class(*value*)
Set the instance's class. Throws an exception if there are multiple classes.

2.1.8 Data Filters (filter)

Instances of classes derived from *Filter* are used for filtering the data.

When called with an individual data instance (*Orange.data.Instance*), they accept or reject the instance by returning either *True* or *False*.

When called with a data storage (e.g. an instance of *Orange.data.Table*) they check whether the corresponding class provides the method that implements the particular filter. If so, the method is called and the result should be of the same type as the storage; e.g., filter methods of *Orange.data.Table* return new instances of *Orange.data.Table*, and filter methods of SQL proxies return new SQL proxies.

If the class corresponding to the storage does not implement a particular filter, the fallback computes the indices of the rows to be selected and returns *data[indices]*.

class Orange.data.filter.**IsDefined**(*columns=None*, *negate=False*)
Select the data instances with no undefined values. The check can be restricted to a subset of columns.

The filter's behaviour may depend upon the storage implementation.

In particular, *Table* with sparse matrix representation will select all data instances whose values are defined, even if they are zero. However, if individual columns are checked, it will select all rows with non-zero entries for this columns, disregarding whether they are stored as zero or omitted.

columns
The columns to be checked, given as a sequence of indices, names or *Orange.data.Variable*.

class Orange.data.filter.**HasClass**(*negate=False*)
Return all rows for which the class value is known.

Orange.data.Table implements the filter on the sparse data so that it returns all rows for which all class values are defined, even if they equal zero.

class Orange.data.filter.**Random**(*prob=None*, *negate=False*)
Return a random selection of data instances.

prob
The proportion (if below 1) or the probability (if 1 or above) of selected instances

class Orange.data.filter.**SameValue**(*column*, *value*, *negate=False*)
Return the data instances with the given value in the specified column.

column
The column, described by an index, a string or *Orange.data.Variable*.

value
The reference value

class Orange.data.filter.**Values**(*conditions*, *conjunction=True*, *negate=False*)
Select the data instances based on conjunction or disjunction of filters derived from `ValueFilter` that check values of individual features or another (nested) Values filter.

conditions
A list of conditions, derived from `ValueFilter` or *Values*

conjunction
If *True*, the filter computes a conjunction, otherwise a disjunction

negate
Revert the selection

class Orange.data.filter.**FilterDiscrete**(*column*, *values*)
Subfilter for discrete variables, which selects the instances whose value matches one of the given values.

column
The column to which the filter applies (int, str or *Orange.data.Variable*).

values
The list (or a set) of accepted values. If None, it checks whether the value is defined.

class Orange.data.filter.**FilterContinuous**(*position*, *oper*, *ref=None*, *max=None*, *min=None*)
Subfilter for continuous variables.

column
The column to which the filter applies (int, str or *Orange.data.Variable*).

ref
The reference value; also aliased to *min* for operators *Between* and *Outside*.

max
The upper threshold for operators *Between* and *Outside*.

oper
The operator; should be *FilterContinuous.Equal*, *NotEqual*, *Less*, *LessEqual*, *Greater*, *GreaterEqual*, *Between*, *Outside* or *IsDefined*.

Type
alias of *Orange.data.filter.FilterContinuous*

class Orange.data.filter.**FilterString**(*position*, *oper*, *ref=None*, *max=None*, *case_sensitive=True*, ***a*)
Subfilter for string variables.

column
The column to which the filter applies (int, str or *Orange.data.Variable*).

ref
The reference value; also aliased to *min* for operators *Between* and *Outside*.

max
The upper threshold for operators *Between* and *Outside*.

oper
The operator; should be *FilterString.Equal*, *NotEqual*, *Less*, *LessEqual*, *Greater*, *GreaterEqual*, *Between*, *Outside*, *Contains*, *StartsWith*, *EndsWith* or *IsDefined*.

case_sensitive
Tells whether the comparisons are case sensitive

Type
alias of *Orange.data.filter.FilterString*

class Orange.data.filter.**FilterStringList**(*column*, *values*, *case_sensitive=True*)
Subfilter for strings variables which checks whether the value is in the given list of accepted values.

column
The column to which the filter applies (int, str or *Orange.data.Variable*).

values
The list (or a set) of accepted values.

case_sensitive
Tells whether the comparisons are case sensitive

class Orange.data.filter.**FilterRegex**(*column*, *pattern*, *flags=0*)
Filter that checks whether the values match the regular expression.

2.1.9 Loading and saving data (io)

Orange.data.Table supports loading from several file formats:

- Comma-separated values (*.csv) file,
- Tab-separated values (*.tab, *.tsv) file,
- Excel spreadsheet (*.xls, *.xlsx),
- Python pickle.

In addition, the text-based files (CSV, TSV) can be compressed with gzip, bzip2 or xz (e.g. *.csv.gz).

Header Format

The data in CSV, TSV, and Excel files can be described in an extended three-line header format, or a condensed single-line header format.

Three-line header format

A three-line header consists of:

1. **Feature names** on the first line. Feature names can include any combination of characters.
2. **Feature types** on the second line. The type is determined automatically, or, if set, can be any of the following:
   - `discrete` (or `d`) — imported as *Orange.data.DiscreteVariable*,
   - a space-separated **list of discrete values**, like "`male female`", which will result in *Orange.data.DiscreteVariable* with those values and in that order. If the individual values contain a space character, it needs to be escaped (prefixed) with, as common, a backslash ('\') character.
   - `continuous` (or `c`) — imported as *Orange.data.ContinuousVariable*,
   - `string` (or `s`, or `text`) — imported as *Orange.data.StringVariable*,
   - `time` (or `t`) — imported as *Orange.data.TimeVariable*, if the values parse as ISO 8601 date/time formats,
3. **Flags** (optional) on the third header line. Feature's flag can be empty, or it can contain, space-separated, a consistent combination of:
   - `class` (or `c`) — feature will be imported as a class variable. Most algorithms expect a single class variable.

- `meta` (or `m`) — feature will be imported as a meta-attribute, just describing the data instance but not actually used for learning,
- `weight` (or `w`) — the feature marks the weight of examples (in algorithms that support weighted examples),
- `ignore` (or `i`) — feature will not be imported,
- <key>=<value> are custom attributes recognized in specific contexts, for instance `color`, which defines the color palette when the variable is visualized, or `type=image` which signals that the variable contains a path to an image.

Example of iris dataset in Orange's three-line format (`iris.tab`).

```
sepal length        sepal width        petal length        petal width        iris
c        c        c        c        d
                                    class
5.1        3.5        1.4        0.2        Iris-setosa
4.9        3.0        1.4        0.2        Iris-setosa
4.7        3.2        1.3        0.2        Iris-setosa
4.6        3.1        1.5        0.2        Iris-setosa
```

Single-line header format

Single-line header consists of feature names prefixed by an optional "<flags>#" string, i.e. flags followed by a hash ('#') sign. The flags can be a consistent combination of:

- `c` for class feature (also known as a target variable or dependent variable),
- `i` for feature to be ignored,
- `m` for meta attributes (not used in learning),
- `C` for features that are continuous (numeric),
- `D` for features that are discrete (categorical),
- `T` for features that represent date and/or time in one of the ISO 8601 formats,
- `S` for string features.

If some (all) names or flags are omitted, the names, types, and flags are discerned automatically, and correctly (most of the time).

2.2 Data Preprocessing (`preprocess`)

Preprocessing module contains data processing utilities like data discretization, continuization, imputation and transformation.

2.2.1 Impute

Imputation replaces missing values with new values (or omits such features).

```
from Orange.data import Table
from Orange.preprocess import Impute

data = Table("heart-disease.tab")
imputer = Impute()

impute_heart = imputer(data)
```

There are several imputation methods one can use.

```
from Orange.data import Table
from Orange.preprocess import Impute, Average

data = Table("heart_disease.tab")
imputer = Impute(method=Average())
impute_heart = imputer(data)
```

2.2.2 Discretization

Discretization replaces continuous features with the corresponding categorical features:

```
import Orange

iris = Orange.data.Table("iris.tab")
disc = Orange.preprocess.Discretize()
disc.method = Orange.preprocess.discretize.EqualFreq(n=3)
d_iris = disc(iris)

print("Original dataset:")
for e in iris[:3]:
    print(e)

print("Discretized dataset:")
for e in d_iris[:3]:
    print(e)
```

The variable in the new data table indicate the bins to which the original values belong.

```
Original dataset:
[5.1, 3.5, 1.4, 0.2 | Iris-setosa]
[4.9, 3.0, 1.4, 0.2 | Iris-setosa]
[4.7, 3.2, 1.3, 0.2 | Iris-setosa]
Discretized dataset:
[<5.5, >=3.2, <2.5, <0.8 | Iris-setosa]
[<5.5, [2.8, 3.2), <2.5, <0.8 | Iris-setosa]
[<5.5, >=3.2, <2.5, <0.8 | Iris-setosa]
```

Default discretization method (four bins with approximatelly equal number of data instances) can be replaced with other methods.

```
iris = Orange.data.Table("iris.tab")
disc = Orange.preprocess.Discretize()
disc.method = Orange.preprocess.discretize.EqualFreq(n=2)
```

Discretization Algorithms

class Orange.preprocess.discretize.**EqualWidth**(*n=4*)
Discretization into a fixed number of bins with equal widths.

n
Number of bins (default: 4).

class Orange.preprocess.discretize.**EqualFreq**(*n=4*)
Discretization into bins with approximately equal number of data instances.

n
Number of bins (default: 4). The actual number may be lower if the variable has less than n distinct values.

class Orange.preprocess.discretize.**EntropyMDL**(*force=False*)
Discretization into bins inferred by recursively splitting the values to minimize the class-entropy. The procedure stops when further splits would decrease the entropy for less than the corresponding increase of minimal description length (MDL). [FayyadIrani93].

If there are no suitable cut-off points, the procedure returns a single bin, which means that the new feature is constant and can be removed.

force
Induce at least one cut-off point, even when its information gain is lower than MDL (default: False).

To add a new discretization, derive it from `Discretization`.

class Orange.preprocess.discretize.**Discretization**
Abstract base class for discretization classes.

2.2.3 Continuization

class Orange.preprocess.**Continuize**
Given a data table, return a new table in which the discretize attributes are replaced with continuous or removed.

- binary variables are transformed into 0.0/1.0 or -1.0/1.0 indicator variables, depending upon the argument `zero_based`.
- multinomial variables are treated according to the argument `multinomial_treatment`.
- discrete attribute with only one possible value are removed;

```
import Orange
titanic = Orange.data.Table("titanic")
continuizer = Orange.preprocess.Continuize()
titanic1 = continuizer(titanic)
```

The class has a number of attributes that can be set either in constructor or, later, as attributes.

zero_based
Determines the value used as the "low" value of the variable. When binary variables are transformed into continuous or when multivalued variable is transformed into multiple variables, the transformed variable can either have values 0.0 and 1.0 (default, `zero_based=True`) or -1.0 and 1.0 (`zero_based=False`).

multinomial_treatment
Defines the treatment of multinomial variables.

`Continuize.Indicators`

The variable is replaced by indicator variables, each corresponding to one value of the original variable. For each value of the original attribute, only the corresponding new attribute will have a value of one and others will be zero. This is the default behaviour.

Note that these variables are not independent, so they cannot be used (directly) in, for instance, linear or logistic regression.

For example, dataset "titanic" has feature "status" with values "crew", "first", "second" and "third", in that order. Its value for the 15th row is "first". Continuization replaces the variable with variables "status=crew", "status=first", "status=second" and "status=third". After

```
continuizer = Orange.preprocess.Continuize()
titanic1 = continuizer(titanic)
```

we have

```
>>> titanic.domain
[status, age, sex | survived]
>>> titanic1.domain
[status=crew, status=first, status=second, status=third,
 age=adult, age=child, sex=female, sex=male | survived]
```

For the 15th row, the variable "status=first" has value 1 and the values of the other three variables are 0:

```
>>> print(titanic[15])
[first, adult, male | yes]
>>> print(titanic1[15])
[0.000, 1.000, 0.000, 0.000, 1.000, 0.000, 0.000, 1.000 | yes]
```

Continuize.FirstAsBase Similar to the above, except that it creates indicators for all values except the first one, according to the order in the variable's *values* attribute. If all indicators in the transformed data instance are 0, the original instance had the first value of the corresponding variable.

Continuizing the variable "status" with this setting gives variables "status=first", "status=second" and "status=third". If all of them were 0, the status of the original data instance was "crew".

```
>>> continuizer.multinomial_treatment = continuizer.FirstAsBase
>>> continuizer(titanic).domain
[status=first, status=second, status=third, age=child, sex=male | survived]
```

Continuize.FrequentAsBase Like above, except that the most frequent value is used as the base. If there are multiple most frequent values, the one with the lowest index in *values* is used. The frequency of values is extracted from data, so this option does not work if only the domain is given.

Continuizing the Titanic data in this way differs from the above by the attributes sex: instead of "sex=male" it constructs "sex=female" since there were more females than males on Titanic.

```
>>> continuizer.multinomial_treatment = continuizer.FrequentAsBase
>>> continuizer(titanic).domain
[status=first, status=second, status=third, age=child, sex=female |␣
↪survived]
```

Continuize.Remove Discrete variables are removed.

```
>>> continuizer.multinomial_treatment = continuizer.Remove
>>> continuizer(titanic).domain
[ | survived]
```

Continuize.RemoveMultinomial Discrete variables with more than two values are removed. Binary variables are treated the same as in *FirstAsBase*.

```
>>> continuizer.multinomial_treatment = continuizer.RemoveMultinomial
>>> continuizer(titanic).domain
[age=child, sex=male | survived]
```

Continuize.ReportError Raise an error if there are any multinomial variables in the data.

Continuize.AsOrdinal Multinomial variables are treated as ordinal and replaced by continuous variables with indices within *values*, e.g. 0, 1, 2, 3…

```
>>> continuizer.multinomial_treatment = continuizer.AsOrdinal
>>> titanic1 = continuizer(titanic)
>>> titanic[700]
[third, adult, male | no]
>>> titanic1[700]
[3.000, 0.000, 1.000 | no]
```

Continuize.AsNormalizedOrdinal As above, except that the resulting continuous value will be from range 0 to 1, e.g. 0, 0.333, 0.667, 1 for a four-valued variable:

```
>>> continuizer.multinomial_treatment = continuizer.AsNormalizedOrdinal
>>> titanic1 = continuizer(titanic)
>>> titanic1[700]
[1.000, 0.000, 1.000 | no]
>>> titanic1[15]
[0.333, 0.000, 1.000 | yes]
```

transform_class
If `True` the class is replaced by continuous attributes or normalized as well. Multiclass problems are thus transformed to multitarget ones. (Default: `False`)

class Orange.preprocess.**DomainContinuizer**
Construct a domain in which discrete attributes are replaced by continuous.

```
domain_continuizer = Orange.preprocess.DomainContinuizer()
domain1 = domain_continuizer(titanic)
```

Orange.preprocess.Continuize calls *DomainContinuizer* to construct the domain.

Domain continuizers can be given either a dataset or a domain, and return a new domain. When given only the domain, use the most frequent value as the base value.

By default, the class does not change continuous and class attributes, discrete attributes are replaced with N attributes (`Indicators`) with values 0 and 1.

2.2.4 Normalization

class Orange.preprocess.**Normalize**(*zero_based=True*, *norm_type=Normalize.NormalizeBySD*, *transform_class=False*, *center=True*, *normalize_datetime=False*)

Construct a preprocessor for normalization of features. Given a data table, preprocessor returns a new table in which the continuous attributes are normalized.

Parameters

- **zero_based** (*bool (default=True)*) – Only used when *norm_type=NormalizeBySpan*.

  Determines the value used as the "low" value of the variable. It determines the interval for normalized continuous variables (either [-1, 1] or [0, 1]).

- **norm_type** (*NormTypes (default: Normalize.NormalizeBySD)*) – Normalization type. If Normalize.NormalizeBySD, the values are replaced with standardized values by subtracting the average value and dividing by the standard deviation. Attribute zero_based has no effect on this standardization.

  If Normalize.NormalizeBySpan, the values are replaced with normalized values by subtracting min value of the data and dividing by span (max - min).

- **transform_class** (*bool (default=False)*) – If True the class is normalized as well.

- **center** (*bool (default=True)*) – Only used when *norm_type=NormalizeBySD*.

  Whether or not to center the data so it has mean zero.

- **normalize_datetime** (*bool (default=False)*) –

Examples

```
>>> from Orange.data import Table
>>> from Orange.preprocess import Normalize
>>> data = Table("iris")
>>> normalizer = Normalize(norm_type=Normalize.NormalizeBySpan)
>>> normalized_data = normalizer(data)
```

2.2.5 Randomization

class Orange.preprocess.**Randomize**(*rand_type=Randomize.RandomizeClasses*, *rand_seed=None*)

Construct a preprocessor for randomization of classes, attributes and/or metas. Given a data table, preprocessor returns a new table in which the data is shuffled.

Parameters

- **rand_type** (*RandTypes (default: Randomize.RandomizeClasses)*) – Randomization type. If Randomize.RandomizeClasses, classes are shuffled. If Randomize.RandomizeAttributes, attributes are shuffled. If Randomize.RandomizeMetas, metas are shuffled.

- **rand_seed** (*int (optional)*) – Random seed

Examples

```
>>> from Orange.data import Table
>>> from Orange.preprocess import Randomize
>>> data = Table("iris")
>>> randomizer = Randomize(Randomize.RandomizeClasses)
>>> randomized_data = randomizer(data)
```

2.2.6 Remove

class Orange.preprocess.**Remove**(*attr_flags=0*, *class_flags=0*, *meta_flags=0*)

Construct a preprocessor for removing constant features/classes and unused values. Given a data table, preprocessor returns a new table and a list of results. In the new table, the constant features/classes and unused values are removed. The list of results consists of two dictionaries. The first one contains numbers of 'removed', 'reduced' and 'sorted' features. The second one contains numbers of 'removed', 'reduced' and 'sorted' features.

Parameters

- **attr_flags** (*int (default: 0)*) – If SortValues, values of discrete attributes are sorted. If RemoveConstant, unused attributes are removed. If RemoveUnusedValues, unused values are removed from discrete attributes. It is possible to merge operations in one by summing several types.
- **class_flags** (*int (default: 0)*) – If SortValues, values of discrete class attributes are sorted. If RemoveConstant, unused class attributes are removed. If RemoveUnusedValues, unused values are removed from discrete class attributes. It is possible to merge operations in one by summing several types.

Examples

```
>>> from Orange.data import Table
>>> from Orange.preprocess import Remove
>>> data = Table("zoo")[:10]
>>> flags = sum([Remove.SortValues, Remove.RemoveConstant, Remove.
↪RemoveUnusedValues])
>>> remover = Remove(attr_flags=flags, class_flags=flags)
>>> new_data = remover(data)
>>> attr_results, class_results = remover.attr_results, remover.class_results
```

2.2.7 Feature selection

Feature scoring

Feature scoring is an assessment of the usefulness of features for prediction of the dependant (class) variable. Orange provides classes that compute the common feature scores for classification and regression.

The code below computes the information gain of feature "tear_rate" in the Lenses dataset:

```
>>> data = Orange.data.Table("lenses")
>>> Orange.preprocess.score.InfoGain(data, "tear_rate")
0.54879494069539858
```

An alternative way of invoking the scorers is to construct the scoring object and calculate the scores for all the features at once, like in the following example:

```
>>> gain = Orange.preprocess.score.InfoGain()
>>> scores = gain(data)
>>> for attr, score in zip(data.domain.attributes, scores):
...     print('%.3f' % score, attr.name)
0.039 age
0.040 prescription
0.377 astigmatic
0.549 tear_rate
```

Feature scoring methods work on different feature types (continuous or discrete) and different types of target variables (i.e. in classification or regression problems). Refer to method's *feature_type* and *class_type* attributes for intended type or employ preprocessing methods (e.g. discretization) for conversion between data types.

class Orange.preprocess.score.**ANOVA**

A wrapper for *sklearn.feature_selection._univariate_selection.f_classif*. The following is the documentation from scikit-learn.

Compute the ANOVA F-value for the provided sample.

Read more in the User Guide.

feature_type
alias of *Orange.data.variable.ContinuousVariable*

class_type
alias of *Orange.data.variable.DiscreteVariable*

class Orange.preprocess.score.**Chi2**

A wrapper for *sklearn.feature_selection._univariate_selection.chi2*. The following is the documentation from scikit-learn.

Compute chi-squared stats between each non-negative feature and class.

This score can be used to select the n_features features with the highest values for the test chi-squared statistic from X, which must contain only non-negative features such as booleans or frequencies (e.g., term counts in document classification), relative to the classes.

Recall that the chi-square test measures dependence between stochastic variables, so using this function "weeds out" the features that are the most likely to be independent of class and therefore irrelevant for classification.

Read more in the User Guide.

feature_type
alias of *Orange.data.variable.DiscreteVariable*

class_type
alias of *Orange.data.variable.DiscreteVariable*

class Orange.preprocess.score.**GainRatio**
Information gain ratio is the ratio between information gain and the entropy of the feature's value distribution. The score was introduced in [Quinlan1986] to alleviate overestimation for multi-valued features. See Wikipedia entry on gain ratio.

feature_type
alias of *Orange.data.variable.DiscreteVariable*

class_type
alias of *Orange.data.variable.DiscreteVariable*

class Orange.preprocess.score.**Gini**
Gini impurity is the probability that two randomly chosen instances will have different classes. See Wikipedia entry on Gini impurity.

feature_type
alias of *Orange.data.variable.DiscreteVariable*

class_type
alias of *Orange.data.variable.DiscreteVariable*

class Orange.preprocess.score.**InfoGain**
Information gain is the expected decrease of entropy. See Wikipedia entry on information gain.

feature_type
alias of *Orange.data.variable.DiscreteVariable*

class_type
alias of *Orange.data.variable.DiscreteVariable*

class Orange.preprocess.score.**UnivariateLinearRegression**

A wrapper for *sklearn.feature_selection._univariate_selection.f_regression*. The following is the documentation from scikit-learn.

Univariate linear regression tests returning F-statistic and p-values.

Quick linear model for testing the effect of a single regressor, sequentially for many regressors.

This is done in 2 steps:

1. The cross correlation between each regressor and the target is computed, that is, ((X[:, i] - mean(X[:, i])) * (y - mean_y)) / (std(X[:, i]) * std(y)) using r_regression function.
2. It is converted to an F score and then to a p-value.

`f_regression()` is derived from `r_regression()` and will rank features in the same order if all the features are positively correlated with the target.

Note however that contrary to `f_regression()`, `r_regression()` values lie in [-1, 1] and can thus be negative. `f_regression()` is therefore recommended as a feature selection criterion to identify potentially predictive feature for a downstream classifier, irrespective of the sign of the association with the target variable.

Furthermore `f_regression()` returns p-values while `r_regression()` does not.

Read more in the User Guide.

feature_type
alias of *Orange.data.variable.ContinuousVariable*

class_type
alias of *Orange.data.variable.ContinuousVariable*

class Orange.preprocess.score.**FCBF**
Fast Correlation-Based Filter. Described in:

Yu, L., Liu, H., Feature selection for high-dimensional data: A fast correlation-based filter solution. 2003. http://www.aaai.org/Papers/ICML/2003/ICML03-111.pdf

feature_type
alias of *Orange.data.variable.DiscreteVariable*

class_type
alias of *Orange.data.variable.DiscreteVariable*

class Orange.preprocess.score.**ReliefF**(*n_iterations=50*, *k_nearest=10*, *random_state=None*)
ReliefF algorithm. Contrary to most other scorers, Relief family of algorithms is not as myoptic but tends to give unreliable results with datasets with lots (hundreds) of features.

Robnik-Šikonja, M., Kononenko, I. Theoretical and empirical analysis of ReliefF and RReliefF. 2003. http://lkm.fri.uni-lj.si/rmarko/papers/robnik03-mlj.pdf

feature_type
alias of *Orange.data.variable.Variable*

class_type
alias of *Orange.data.variable.DiscreteVariable*

class Orange.preprocess.score.**RReliefF**(*n_iterations=50*, *k_nearest=50*, *random_state=None*)
feature_type
alias of *Orange.data.variable.Variable*

class_type
alias of *Orange.data.variable.ContinuousVariable*

Additionally, you can use the `score_data()` method of some learners (`Orange.classification.LinearRegressionLearner`, `Orange.regression.LogisticRegressionLearner`, *Orange.classification.RandomForestLearner*, and *Orange.regression.RandomForestRegressionLearner*) to obtain the feature scores as calculated by these learners. For example:

```
>>> learner = Orange.classification.LogisticRegressionLearner()
>>> learner.score_data(data)
[0.31571299907366146,
 0.28286199971877485,
 0.67496525667835794,
 0.99930286901257692]
```

Feature selection

We can use feature selection to limit the analysis to only the most relevant or informative features in the dataset.

Feature selection with a scoring method that works on continuous features will retain all discrete features and vice versa.

The code below constructs a new dataset consisting of two best features according to the ANOVA method:

```
>>> data = Orange.data.Table("wine")
>>> anova = Orange.preprocess.score.ANOVA()
>>> selector = Orange.preprocess.SelectBestFeatures(method=anova, k=2)
>>> data2 = selector(data)
>>> data2.domain
[Flavanoids, Proline | Wine]
```

class Orange.preprocess.**SelectBestFeatures**(*method=None*, *k=None*, *threshold=None*, *decreasing=True*)
A feature selector that builds a new dataset consisting of either the top *k* features (if *k* is an *int*) or a proportion (if *k* is a *float* between 0.0 and 1.0), or all those that exceed a given *threshold*. Features are scored using the provided feature scoring *method*. By default it is assumed that feature importance decreases with decreasing scores.

If both *k* and *threshold* are set, only features satisfying both conditions will be selected.

If *method* is not set, it is automatically selected when presented with the dataset. Datasets with both continuous and discrete features are scored using a method suitable for the majority of features.

Parameters

- **method** (*Orange.preprocess.score.ClassificationScorer, Orange.preprocess.score.SklScorer*) – Univariate feature scoring method.
- **k** (*int or float*) – The number or propotion of top features to select.
- **threshold** (*float*) – A threshold that a feature should meet according to the provided method.
- **decreasing** (*boolean*) – The order of feature importance when sorted from the most to the least important feature.

2.2.8 Preprocessors

2.3 Outlier detection (classification)

2.3.1 One Class Support Vector Machines

class Orange.classification.**OneClassSVMLearner**(*kernel='rbf', degree=3, gamma='auto', coef0=0.0, tol=0.001, nu=0.5, shrinking=True, cache_size=200, max_iter=- 1, preprocessors=None*)

A wrapper for *sklearn.svm._classes.OneClassSVM*. The following is its documentation:

Unsupervised Outlier Detection.

Estimate the support of a high-dimensional distribution.

The implementation is based on libsvm.

Read more in the User Guide.

2.3.2 Elliptic Envelope

class Orange.classification.**EllipticEnvelopeLearner**(*store_precision=True, assume_centered=False, support_fraction=None, contamination=0.1, random_state=None, preprocessors=None*)

A wrapper for *sklearn.covariance._elliptic_envelope.EllipticEnvelope*. The following is its documentation:

An object for detecting outliers in a Gaussian distributed dataset.

Read more in the User Guide.

2.3.3 Local Outlier Factor

class Orange.classification.**LocalOutlierFactorLearner**(*n_neighbors=20*, *algorithm='auto'*, *leaf_size=30*, *metric='minkowski'*, *p=2*, *metric_params=None*, *contamination='auto'*, *novelty=True*, *n_jobs=None*, *preprocessors=None*)

A wrapper for *sklearn.neighbors._lof.LocalOutlierFactor*. The following is its documentation:

Unsupervised Outlier Detection using the Local Outlier Factor (LOF).

The anomaly score of each sample is called the Local Outlier Factor. It measures the local deviation of the density of a given sample with respect to its neighbors. It is local in that the anomaly score depends on how isolated the object is with respect to the surrounding neighborhood. More precisely, locality is given by k-nearest neighbors, whose distance is used to estimate the local density. By comparing the local density of a sample to the local densities of its neighbors, one can identify samples that have a substantially lower density than their neighbors. These are considered outliers.

New in version 0.19.

2.3.4 Isolation Forest

class Orange.classification.**IsolationForestLearner**(*n_estimators=100*, *max_samples='auto'*, *contamination='auto'*, *max_features=1.0*, *bootstrap=False*, *n_jobs=None*, *behaviour='deprecated'*, *random_state=None*, *verbose=0*, *warm_start=False*, *preprocessors=None*)

A wrapper for *sklearn.ensemble._iforest.IsolationForest*. The following is its documentation:

Isolation Forest Algorithm.

Return the anomaly score of each sample using the IsolationForest algorithm

The IsolationForest 'isolates' observations by randomly selecting a feature and then randomly selecting a split value between the maximum and minimum values of the selected feature.

Since recursive partitioning can be represented by a tree structure, the number of splittings required to isolate a sample is equivalent to the path length from the root node to the terminating node.

This path length, averaged over a forest of such random trees, is a measure of normality and our decision function.

Random partitioning produces noticeably shorter paths for anomalies. Hence, when a forest of random trees collectively produce shorter path lengths for particular samples, they are highly likely to be anomalies.

Read more in the User Guide.

New in version 0.18.

2.4 Classification (classification)

2.4.1 Logistic Regression

class Orange.classification.**LogisticRegressionLearner**(*penalty='l2'*, *dual=False*, *tol=0.0001*, *C=1.0*, *fit_intercept=True*, *intercept_scaling=1*, *class_weight=None*, *random_state=None*, *solver='auto'*, *max_iter=100*, *multi_class='auto'*, *verbose=0*, *n_jobs=1*, *preprocessors=None*)

A wrapper for *sklearn.linear_model._logistic.LogisticRegression*. The following is its documentation:

Logistic Regression (aka logit, MaxEnt) classifier.

In the multiclass case, the training algorithm uses the one-vs-rest (OvR) scheme if the 'multi_class' option is set to 'ovr', and uses the cross-entropy loss if the 'multi_class' option is set to 'multinomial'. (Currently the 'multinomial' option is supported only by the 'lbfgs', 'sag', 'saga' and 'newton-cg' solvers.)

This class implements regularized logistic regression using the 'liblinear' library, 'newton-cg', 'sag', 'saga' and 'lbfgs' solvers. **Note that regularization is applied by default**. It can handle both dense and sparse input. Use C-ordered arrays or CSR matrices containing 64-bit floats for optimal performance; any other input format will be converted (and copied).

The 'newton-cg', 'sag', and 'lbfgs' solvers support only L2 regularization with primal formulation, or no regularization. The 'liblinear' solver supports both L1 and L2 regularization, with a dual formulation only for the L2 penalty. The Elastic-Net regularization is only supported by the 'saga' solver.

Read more in the User Guide.

2.4.2 Random Forest

class Orange.classification.**RandomForestLearner**(*n_estimators=10*, *criterion='gini'*, *max_depth=None*, *min_samples_split=2*, *min_samples_leaf=1*, *min_weight_fraction_leaf=0.0*, *max_features='auto'*, *max_leaf_nodes=None*, *bootstrap=True*, *oob_score=False*, *n_jobs=1*, *random_state=None*, *verbose=0*, *class_weight=None*, *preprocessors=None*)

A wrapper for *sklearn.ensemble._forest.RandomForestClassifier*. The following is its documentation:

A random forest classifier.

A random forest is a meta estimator that fits a number of decision tree classifiers on various sub-samples of the dataset and uses averaging to improve the predictive accuracy and control over-fitting. The sub-sample size is controlled with the *max_samples* parameter if *bootstrap=True* (default), otherwise the whole dataset is used to build each tree.

Read more in the User Guide.

2.4.3 Simple Random Forest

class Orange.classification.**SimpleRandomForestLearner**(*n_estimators=10*, *min_instances=2*, *max_depth=1024*, *max_majority=1.0*, *skip_prob='sqrt'*, *seed=42*)

A random forest classifier, optimized for speed. Trees in the forest are constructed with *SimpleTreeLearner* classification trees.

Parameters

- **n_estimators** (*int, optional (default = 10)*) – Number of trees in the forest.
- **min_instances** (*int, optional (default = 2)*) – Minimal number of data instances in leaves. When growing the three, new nodes are not introduced if they would result in leaves with fewer instances than min_instances. Instance count is weighed.
- **max_depth** (*int, optional (default = 1024)*) – Maximal depth of tree.
- **max_majority** (*float, optional (default = 1.0)*) – Maximal proportion of majority class. When this is exceeded, induction stops (only used for classification).
- **skip_prob** (*string, optional (default = "sqrt")*) – Data attribute will be skipped with probability skip_prob.
  - if float, then skip attribute with this probability.
  - if "sqrt", then *skip_prob = 1 - sqrt(n_features) / n_features*
  - if "log2", then *skip_prob = 1 - log2(n_features) / n_features*
- **seed** (*int, optional (default = 42)*) – Random seed.

fit_storage(*data*)

Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

2.4.4 Softmax Regression

class Orange.classification.**SoftmaxRegressionLearner**(*lambda_=1.0*, *preprocessors=None*, ***fmin_args*)

L2 regularized softmax regression classifier. Uses the L-BFGS algorithm to minimize the categorical cross entropy cost with L2 regularization. This model is suitable when dealing with a multi-class classification problem.

When using this learner you should:

- choose a suitable regularization parameter lambda_,
- consider using many logistic regression models (one for each value of the class variable) instead of softmax regression.

Parameters

- **lambda_** (*float, optional (default=1.0)*) – Regularization parameter. It controls trade-off between fitting the data and keeping parameters small. Higher values of lambda_ force parameters to be smaller.
- **preprocessors** (*list, optional*) – Preprocessors are applied to data before training or testing. Default preprocessors: *[RemoveNaNClasses(), RemoveNaNColumns(), Impute(), Continuize(), Normalize()]*
  - remove columns with all values as NaN
  - replace NaN values with suitable values

  - continuize all discrete attributes,
  - transform the dataset so that the columns are on a similar scale,
- **fmin_args** (*dict, optional*) – Parameters for L-BFGS algorithm.

2.4.5 k-Nearest Neighbors

class Orange.classification.**KNNLearner**(*n_neighbors=5*, *metric='euclidean'*, *weights='uniform'*, *algorithm='auto'*, *metric_params=None*, *preprocessors=None*)

A wrapper for *sklearn.neighbors._classification.KNeighborsClassifier*. The following is its documentation:

Classifier implementing the k-nearest neighbors vote.

Read more in the User Guide.

2.4.6 Naive Bayes

class Orange.classification.**NaiveBayesLearner**(*preprocessors=None*)

Naive Bayes classifier. Works only with discrete attributes. By default, continuous attributes are discretized.

Parameters **preprocessors** (*list, optional (default="[Orange.preprocess.Discretize]")*) – An ordered list of preprocessors applied to data before training or testing.

fit_storage(*table*)

Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

The following code loads lenses dataset (four discrete attributes and discrete class), constructs naive Bayesian learner, uses it on the entire dataset to construct a classifier, and then applies classifier to the first three data instances:

```
>>> import Orange
>>> lenses = Orange.data.Table('lenses')
>>> nb = Orange.classification.NaiveBayesLearner()
>>> classifier = nb(lenses)
>>> classifier(lenses[0:3], True)
array([[ 0.04358755,  0.82671726,  0.12969519],
       [ 0.17428279,  0.20342097,  0.62229625],
       [ 0.18633359,  0.79518516,  0.01848125]])
```

2.4.7 Support Vector Machines

class Orange.classification.**SVMLearner**(*C=1.0*, *kernel='rbf'*, *degree=3*, *gamma='auto'*, *coef0=0.0*, *shrinking=True*, *probability=False*, *tol=0.001*, *cache_size=200*, *max_iter=- 1*, *preprocessors=None*)

A wrapper for *sklearn.svm._classes.SVC*. The following is its documentation:

C-Support Vector Classification.

The implementation is based on libsvm. The fit time scales at least quadratically with the number of samples and may be impractical beyond tens of thousands of samples. For large datasets consider using `LinearSVC` or `SGDClassifier` instead, possibly after a `Nystroem` transformer.

The multiclass support is handled according to a one-vs-one scheme.

For details on the precise mathematical formulation of the provided kernel functions and how *gamma*, *coef0* and *degree* affect each other, see the corresponding section in the narrative documentation: svm_kernels.

Read more in the User Guide.

2.4.8 Linear Support Vector Machines

class Orange.classification.**LinearSVMLearner**(*penalty='l2'*, *loss='squared_hinge'*, *dual=True*, *tol=0.0001*, *C=1.0*, *multi_class='ovr'*, *fit_intercept=True*, *intercept_scaling=True*, *random_state=None*, *preprocessors=None*)

A wrapper for *sklearn.svm._classes.LinearSVC*. The following is its documentation:

Linear Support Vector Classification.

Similar to SVC with parameter kernel='linear', but implemented in terms of liblinear rather than libsvm, so it has more flexibility in the choice of penalties and loss functions and should scale better to large numbers of samples.

This class supports both dense and sparse input and the multiclass support is handled according to a one-vs-the-rest scheme.

Read more in the User Guide.

2.4.9 Nu-Support Vector Machines

class Orange.classification.**NuSVMLearner**(*nu=0.5*, *kernel='rbf'*, *degree=3*, *gamma='auto'*, *coef0=0.0*, *shrinking=True*, *probability=False*, *tol=0.001*, *cache_size=200*, *max_iter=- 1*, *preprocessors=None*)

A wrapper for *sklearn.svm._classes.NuSVC*. The following is its documentation:

Nu-Support Vector Classification.

Similar to SVC but uses a parameter to control the number of support vectors.

The implementation is based on libsvm.

Read more in the User Guide.

2.4.10 Classification Tree

Orange includes three implemenations of classification trees. *TreeLearner* is home-grown and properly handles multinominal and missing values. The one from scikit-learn, *SklTreeLearner*, is faster. Another home-grown, *SimpleTreeLearner*, is simpler and still faster.

The following code loads iris dataset (four numeric attributes and discrete class), constructs a decision tree learner, uses it on the entire dataset to construct a classifier, and then prints the tree:

```
>>> import Orange
>>> iris = Orange.data.Table('iris')
>>> tr = Orange.classification.TreeLearner()
>>> classifier = tr(data)
>>> printed_tree = classifier.print_tree()
>>> for i in printed_tree.split('\n'):
>>>     print(i)
[50.  0.  0.] petal length  1.9
```

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```
[ 0. 50. 50.] petal length > 1.9
[ 0. 49.  5.]     petal width  1.7
[ 0. 47.  1.]         petal length  4.9
   [0. 2. 4.]         petal length > 4.9
   [0. 0. 3.]             petal width  1.5
   [0. 2. 1.]             petal width > 1.5
   [0. 2. 0.]                 sepal length  6.7
   [0. 0. 1.]                 sepal length > 6.7
[ 0.  1. 45.]     petal width > 1.7
```

class Orange.classification.**TreeLearner**(**args*, *binarize=False*, *max_depth=None*, *min_samples_leaf=1*, *min_samples_split=2*, *sufficient_majority=0.95*, *preprocessors=None*, ***kwargs*)

Tree inducer with proper handling of nominal attributes and binarization.

The inducer can handle missing values of attributes and target. For discrete attributes with more than two possible values, each value can get a separate branch (*binarize=False*), or values can be grouped into two groups (*binarize=True*, default).

The tree growth can be limited by the required number of instances for internal nodes and for leafs, the sufficient proportion of majority class, and by the maximal depth of the tree.

If the tree is not binary, it can contain zero-branches.

Parameters

- **binarize** (*bool*) – if *True* the inducer will find optimal split into two subsets for values of discrete attributes. If *False* (default), each value gets its branch.
- **min_samples_leaf** (*float*) – the minimal number of data instances in a leaf
- **min_samples_split** (*float*) – the minimal nubmer of data instances that is split into subgroups
- **max_depth** (*int*) – the maximal depth of the tree
- **sufficient_majority** (*float*) – a majority at which the data is not split further

Returns instance of OrangeTreeModel

fit_storage(*data*)

Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

class Orange.classification.**SklTreeLearner**(*criterion='gini'*, *splitter='best'*, *max_depth=None*, *min_samples_split=2*, *min_samples_leaf=1*, *max_features=None*, *random_state=None*, *max_leaf_nodes=None*, *preprocessors=None*)

Wrapper for SKL's tree inducer

2.4.11 Simple Tree

class Orange.classification.**SimpleTreeLearner**(*min_instances=2*, *max_depth=32*, *max_majority=0.95*, *skip_prob=0.0*, *bootstrap=False*, *seed=42*)

Classification or regression tree learner. Uses gain ratio for classification and mean square error for regression. This learner was developed to speed-up random forest construction, but can also be used as a standalone tree learner.

min_instances [int, optional (default = 2)] Minimal number of data instances in leaves. When growing the three, new nodes are not introduced if they would result in leaves with fewer instances than min_instances. Instance count is weighed.

max_depth [int, optional (default = 1024)] Maximal depth of tree.

max_majority [float, optional (default = 1.0)] Maximal proportion of majority class. When this is exceeded, induction stops (only used for classification).

skip_prob [string, optional (default = 0.0)] Data attribute will be skipped with probability `skip_prob`.

- if float, then skip attribute with this probability.
- if "sqrt", then *skip_prob = 1 - sqrt(n_features) / n_features*
- if "log2", then *skip_prob = 1 - log2(n_features) / n_features*

bootstrap [data table, optional (default = False)] A bootstrap dataset.

seed [int, optional (default = 42)] Random seed.

fit_storage(*data*)

Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

2.4.12 Majority Classifier

class Orange.classification.**MajorityLearner**(*preprocessors=None*)

A majority classifier. Always returns most frequent class from the training set, regardless of the attribute values from the test data instance. Returns class value distribution if class probabilities are requested. Can be used as a baseline when comparing classifiers.

In the special case of uniform class distribution within the training data, class value is selected randomly. In order to produce consistent results on the same dataset, this value is selected based on hash of the class vector.

fit_storage(*dat*)

Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

2.4.13 Neural Network

class Orange.classification.**NNClassificationLearner**(*hidden_layer_sizes=(100,)*, *activation='relu'*, *solver='adam'*, *alpha=0.0001*, *batch_size='auto'*, *learning_rate='constant'*, *learning_rate_init=0.001*, *power_t=0.5*, *max_iter=200*, *shuffle=True*, *random_state=None*, *tol=0.0001*, *verbose=False*, *warm_start=False*, *momentum=0.9*, *nesterovs_momentum=True*, *early_stopping=False*, *validation_fraction=0.1*, *beta_1=0.9*, *beta_2=0.999*, *epsilon=1e-08*, *preprocessors=None*)

A wrapper for *Orange.classification.neural_network.MLPClassifierWCallback*. The following is its documentation:

Multi-layer Perceptron classifier.

This model optimizes the log-loss function using LBFGS or stochastic gradient descent.

New in version 0.18.

2.4.14 CN2 Rule Induction

Induction of rules works by finding a rule that covers some learning instances, removing these instances, and repeating this until all instances are covered. Rules are scored by heuristics such as impurity of class distribution of covered instances. The module includes common rule-learning algorithms, and allows for replacing rule search strategies, scoring and other components.

class Orange.classification.rules.**CN2Learner**(*preprocessors=None*, *base_rules=None*)

Classic CN2 inducer that constructs a list of ordered rules. To evaluate found hypotheses, entropy measure is used. Returns a CN2Classifier if called with data.

References

"The CN2 Induction Algorithm", Peter Clark and Tim Niblett, Machine Learning Journal, 3 (4), pp261-283, (1989)

fit_storage(*data*)

Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

class Orange.classification.rules.**CN2UnorderedLearner**(*preprocessors=None*, *base_rules=None*)

Construct a set of unordered rules.

Rules are learnt for each class individually and scored by the relative frequency of the class corrected by the Laplace correction. After adding a rule, only the covered examples of that class are removed.

The code below loads the *iris* dataset (four continuous attributes and a discrete class) and fits the learner.

```
import Orange

data = Orange.data.Table("iris")
learner = Orange.classification.CN2UnorderedLearner()

# consider up to 10 solution streams at one time
learner.rule_finder.search_algorithm.beam_width = 10
```

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```
# continuous value space is constrained to reduce computation time
learner.rule_finder.search_strategy.constrain_continuous = True

# found rules must cover at least 15 examples
learner.rule_finder.general_validator.min_covered_examples = 15

# found rules may combine at most 2 selectors (conditions)
learner.rule_finder.general_validator.max_rule_length = 2

classifier = learner(data)
```

References

"Rule Induction with CN2: Some Recent Improvements", Peter Clark and Robin Boswell, Machine Learning - Proceedings of the 5th European Conference (EWSL-91), pp151-163, 1991

fit_storage(*data*)
Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

class Orange.classification.rules.**CN2SDLearner**(*preprocessors=None*, *base_rules=None*)
Ordered CN2SD inducer that constructs a list of ordered rules. To evaluate found hypotheses, Weighted relative accuracy measure is used. Returns a CN2SDClassifier if called with data.

In this setting, ordered rule induction refers exclusively to finding best rule conditions and assigning the majority class in the rule head (target class is set to None). To later predict instances, rules will be regarded as unordered.

Notes

A weighted covering algorithm is applied, in which subsequently induced rules also represent interesting and sufficiently large subgroups of the population. Covered positive examples are not deleted from the learning set, rather their weight is reduced.

The algorithm demonstrates how classification rule learning (predictive induction) can be adapted to subgroup discovery, a task at the intersection of predictive and descriptive induction.

References

"Subgroup Discovery with CN2-SD", Nada Lavrač et al., Journal of Machine Learning Research 5 (2004), 153-188, 2004

fit_storage(*data*)
Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

class Orange.classification.rules.**CN2SDUnorderedLearner**(*preprocessors=None*, *base_rules=None*)
Unordered CN2SD inducer that constructs a set of unordered rules. To evaluate found hypotheses, Weighted relative accuracy measure is used. Returns a CN2SDUnorderedClassifier if called with data.

Notes

A weighted covering algorithm is applied, in which subsequently induced rules also represent interesting and sufficiently large subgroups of the population. Covered positive examples are not deleted from the learning set, rather their weight is reduced.

The algorithm demonstrates how classification rule learning (predictive induction) can be adapted to subgroup discovery, a task at the intersection of predictive and descriptive induction.

References

"Subgroup Discovery with CN2-SD", Nada Lavrač et al., Journal of Machine Learning Research 5 (2004), 153-188, 2004

fit_storage(*data*)
Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

2.4.15 Calibration and threshold optimization

class Orange.classification.calibration.**ThresholdClassifier**(*base_model*, *threshold*)
A model that wraps a binary model and sets a different threshold.

The target class is the class with index 1. A data instances is classified to class 1 it the probability of this class equals or exceeds the threshold

base_model
base mode

Type Orange.classification.Model

threshold
decision threshold

Type float

class Orange.classification.calibration.**ThresholdLearner**(*base_learner*, *threshold_criterion=0*)
A learner that runs another learner and then finds the optimal threshold for CA or F1 on the training data.

base_leaner
base learner

Type Learner

threshold_criterion
ThresholdLearner.OptimizeCA or *ThresholdLearner.OptimizeF1*

Type int

fit_storage(*data*)
Induce a model using the provided *base_learner*, compute probabilities on training data and the find the optimal decision thresholds. In case of ties, select the threshold that is closest to 0.5.

class Orange.classification.calibration.**CalibratedClassifier**(*base_model*, *calibrators*)
A model that wraps another model and recalibrates probabilities

base_model
base mode

Type Mode

calibrators
list of functions that get a vector of probabilities and return calibrated probabilities

Type list of callable

class Orange.classification.calibration.**CalibratedLearner**(*base_learner*, *calibration_method=0*)
Probability calibration for learning algorithms

This learner that wraps another learner, so that after training, it predicts the probabilities on training data and calibrates them using sigmoid or isotonic calibration. It then returns a `CalibratedClassifier`.

base_learner
base learner

Type Learner

calibration_method
CalibratedLearner.Sigmoid or *CalibratedLearner.Isotonic*

Type int

fit_storage(*data*)
Induce a model using the provided *base_learner*, compute probabilities on training data and use scipy's *_SigmoidCalibration* or *IsotonicRegression* to prepare calibrators.

2.4.16 Gradient Boosted Trees

class Orange.classification.gb.**GBClassifier**(*loss='deviance'*, *learning_rate=0.1*, *n_estimators=100*, *subsample=1.0*, *criterion='friedman_mse'*, *min_samples_split=2*, *min_samples_leaf=1*, *min_weight_fraction_leaf=0.0*, *max_depth=3*, *min_impurity_decrease=0.0*, *min_impurity_split=None*, *init=None*, *random_state=None*, *max_features=None*, *verbose=0*, *max_leaf_nodes=None*, *warm_start=False*, *presort='deprecated'*, *validation_fraction=0.1*, *n_iter_no_change=None*, *tol=0.0001*, *ccp_alpha=0.0*, *preprocessors=None*)
A wrapper for *sklearn.ensemble._gb.GradientBoostingClassifier*. The following is its documentation:

Gradient Boosting for classification.

GB builds an additive model in a forward stage-wise fashion; it allows for the optimization of arbitrary differentiable loss functions. In each stage `n_classes_` regression trees are fit on the negative gradient of the binomial or multinomial deviance loss function. Binary classification is a special case where only a single regression tree is induced.

Read more in the User Guide.

class Orange.classification.catgb.**CatGBClassifier**(*iterations=None*, *learning_rate=None*, *depth=None*, *l2_leaf_reg=None*, *model_size_reg=None*, *rsm=None*, *loss_function=None*, *border_count=None*, *feature_border_type=None*, *per_float_feature_quantization=None*, *input_borders=None*, *output_borders=None*, *fold_permutation_block=None*, *od_pval=None*, *od_wait=None*, *od_type=None*, *nan_mode=None*, *counter_calc_method=None*, *leaf_estimation_iterations=None*, *leaf_estimation_method=None*, *thread_count=None*, *random_seed=None*, *use_best_model=None*, *verbose=False*, *logging_level=None*, *metric_period=None*, *ctr_leaf_count_limit=None*, *store_all_simple_ctr=None*, *max_ctr_complexity=None*, *has_time=None*, *allow_const_label=None*, *classes_count=None*, *class_weights=None*, *one_hot_max_size=None*, *random_strength=None*, *name=None*, *ignored_features=None*, *train_dir='/home/docs/.cache/Orange/3.32.0.dev'*, *custom_loss=None*, *custom_metric=None*, *eval_metric=None*, *bagging_temperature=None*, *save_snapshot=None*, *snapshot_file=None*, *snapshot_interval=None*, *fold_len_multiplier=None*, *used_ram_limit=None*, *gpu_ram_part=None*, *allow_writing_files=False*, *final_ctr_computation_mode=None*, *approx_on_full_history=None*, *boosting_type=None*, *simple_ctr=None*, *combinations_ctr=None*, *per_feature_ctr=None*, *task_type=None*, *device_config=None*, *devices=None*, *bootstrap_type=None*, *subsample=None*, *sampling_unit=None*, *dev_score_calc_obj_block_size=None*, *max_depth=None*, *n_estimators=None*, *num_boost_round=None*, *num_trees=None*, *colsample_bylevel=None*, *random_state=None*, *reg_lambda=None*, *objective=None*, *eta=None*, *max_bin=None*, *scale_pos_weight=None*, *gpu_cat_features_storage=None*, *data_partition=None*, *metadata=None*, *early_stopping_rounds=None*, *cat_features=None*, *grow_policy=None*, *min_data_in_leaf=None*, *min_child_samples=None*, *max_leaves=None*, *num_leaves=None*, *score_function=None*, *leaf_estimation_backtracking=None*, *ctr_history_unit=None*, *monotone_constraints=None*, *feature_weights=None*, *penalties_coefficient=None*, *first_feature_use_penalties=None*, *model_shrink_rate=None*, *model_shrink_mode=None*, *langevin=None*, *diffusion_temperature=None*, *posterior_sampling=None*, *boost_from_average=None*, *text_features=None*, *tokenizers=None*, *dictionaries=None*,

Implementation of the scikit-learn API for CatBoost classification.

class Orange.classification.xgb.**XGBClassifier**(*max_depth=None*, *learning_rate=None*, *n_estimators=100*, *verbosity=None*, *objective='binary:logistic'*, *booster=None*, *tree_method=None*, *n_jobs=None*, *gamma=None*, *min_child_weight=None*, *max_delta_step=None*, *subsample=None*, *colsample_bytree=None*, *colsample_bylevel=None*, *colsample_bynode=None*, *reg_alpha=None*, *reg_lambda=None*, *scale_pos_weight=None*, *base_score=None*, *random_state=None*, *missing=nan*, *num_parallel_tree=None*, *monotone_constraints=None*, *interaction_constraints=None*, *importance_type='gain'*, *gpu_id=None*, *validate_parameters=None*, *preprocessors=None*)

A wrapper for *xgboost.sklearn.XGBClassifier*. The following is its documentation:

Implementation of the scikit-learn API for XGBoost classification.

class Orange.classification.xgb.**XGBRFClassifier**(*max_depth=None*, *learning_rate=None*, *n_estimators=100*, *verbosity=None*, *objective='binary:logistic'*, *booster=None*, *tree_method=None*, *n_jobs=None*, *gamma=None*, *min_child_weight=None*, *max_delta_step=None*, *subsample=None*, *colsample_bytree=None*, *colsample_bylevel=None*, *colsample_bynode=None*, *reg_alpha=None*, *reg_lambda=None*, *scale_pos_weight=None*, *base_score=None*, *random_state=None*, *missing=nan*, *num_parallel_tree=None*, *monotone_constraints=None*, *interaction_constraints=None*, *importance_type='gain'*, *gpu_id=None*, *validate_parameters=None*, *preprocessors=None*)

A wrapper for *xgboost.sklearn.XGBRFClassifier*. The following is its documentation:

scikit-learn API for XGBoost random forest classification.

2.5 Regression (regression)

2.5.1 Linear Regression

Linear regression is a statistical regression method which tries to predict a value of a continuous response (class) variable based on the values of several predictors. The model assumes that the response variable is a linear combination of the predictors, the task of linear regression is therefore to fit the unknown coefficients.

Example

```
>>> from Orange.regression.linear import LinearRegressionLearner
>>> mpg = Orange.data.Table('auto-mpg')
>>> mean_ = LinearRegressionLearner()
>>> model = mean_(mpg[40:110])
>>> print(model)
LinearModel LinearRegression(copy_X=True, fit_intercept=True, normalize=False)
>>> mpg[20]
Value('mpg', 25.0)
>>> model(mpg[0])
Value('mpg', 24.6)
```

class Orange.regression.linear.**LinearRegressionLearner**(*preprocessors=None*, *fit_intercept=True*)

A wrapper for *sklearn.linear_model._base.LinearRegression*. The following is its documentation:

Ordinary least squares Linear Regression.

LinearRegression fits a linear model with coefficients w = (w1, ..., wp) to minimize the residual sum of squares between the observed targets in the dataset, and the targets predicted by the linear approximation.

class Orange.regression.linear.**RidgeRegressionLearner**(*alpha=1.0*, *fit_intercept=True*, *normalize=False*, *copy_X=True*, *max_iter=None*, *tol=0.001*, *solver='auto'*, *preprocessors=None*)

A wrapper for *sklearn.linear_model._ridge.Ridge*. The following is its documentation:

Linear least squares with l2 regularization.

Minimizes the objective function:

```
||y - Xw||^2_2 + alpha * ||w||^2_2
```

This model solves a regression model where the loss function is the linear least squares function and regularization is given by the l2-norm. Also known as Ridge Regression or Tikhonov regularization. This estimator has built-in support for multi-variate regression (i.e., when y is a 2d-array of shape (n_samples, n_targets)).

Read more in the User Guide.

class Orange.regression.linear.**LassoRegressionLearner**(*alpha=1.0*, *fit_intercept=True*, *normalize=False*, *precompute=False*, *copy_X=True*, *max_iter=1000*, *tol=0.0001*, *warm_start=False*, *positive=False*, *preprocessors=None*)

A wrapper for *sklearn.linear_model._coordinate_descent.Lasso*. The following is its documentation:

Linear Model trained with L1 prior as regularizer (aka the Lasso).

The optimization objective for Lasso is:

```
(1 / (2 * n_samples)) * ||y - Xw||^2_2 + alpha * ||w||_1
```

Technically the Lasso model is optimizing the same objective function as the Elastic Net with `l1_ratio=1.0` (no L2 penalty).

Read more in the User Guide.

class Orange.regression.linear.**SGDRegressionLearner**(*loss='squared_error'*, *penalty='l2'*, *alpha=0.0001*, *l1_ratio=0.15*, *fit_intercept=True*, *max_iter=5*, *tol=0.001*, *shuffle=True*, *epsilon=0.1*, *n_jobs=1*, *random_state=None*, *learning_rate='invscaling'*, *eta0=0.01*, *power_t=0.25*, *class_weight=None*, *warm_start=False*, *average=False*, *preprocessors=None*)

A wrapper for *sklearn.linear_model._stochastic_gradient.SGDRegressor*. The following is its documentation:

Linear model fitted by minimizing a regularized empirical loss with SGD.

SGD stands for Stochastic Gradient Descent: the gradient of the loss is estimated each sample at a time and the model is updated along the way with a decreasing strength schedule (aka learning rate).

The regularizer is a penalty added to the loss function that shrinks model parameters towards the zero vector using either the squared euclidean norm L2 or the absolute norm L1 or a combination of both (Elastic Net). If the parameter update crosses the 0.0 value because of the regularizer, the update is truncated to 0.0 to allow for learning sparse models and achieve online feature selection.

This implementation works with data represented as dense numpy arrays of floating point values for the features.

Read more in the User Guide.

class Orange.regression.linear.**LinearModel**(*skl_model*)

2.5.2 Polynomial

Polynomial model is a wrapper that constructs polynomial features of a specified degree and learns a model on them.

class Orange.regression.linear.**PolynomialLearner**(*learner=LinearRegressionLearner()*, *degree=2*, *preprocessors=None*, *include_bias=True*)

Generate polynomial features and learn a prediction model

Parameters

- **learner** (*LearnerRegression*) – learner to be fitted on the transformed features
- **degree** (*int*) – degree of used polynomial
- **preprocessors** (*List[Preprocessor]*) – preprocessors to be applied on the data before learning

2.5.3 Mean

Mean model predicts the same value (usually the distribution mean) for all data instances. Its accuracy can serve as a baseline for other regression models.

The model learner (*MeanLearner*) computes the mean of the given data or distribution. The model is stored as an instance of MeanModel.

Example

```
>>> from Orange.data import Table
>>> from Orange.regression import MeanLearner
>>> data = Table('auto-mpg')
>>> learner = MeanLearner()
>>> model = learner(data)
>>> print(model)
MeanModel(23.51457286432161)
>>> model(data[:4])
array([ 23.51457286,  23.51457286,  23.51457286,  23.51457286])
```

class Orange.regression.**MeanLearner**(*preprocessors=None*)

Fit a regression model that returns the average response (class) value.

fit_storage(*data*)

Construct a MeanModel by computing the mean value of the given data.

Parameters **data** (Orange.data.Table) – data table

Returns regression model, which always returns mean value

Return type MeanModel

2.5.4 Random Forest

class Orange.regression.**RandomForestRegressionLearner**(*n_estimators=10*, *criterion='squared_error'*, *max_depth=None*, *min_samples_split=2*, *min_samples_leaf=1*, *min_weight_fraction_leaf=0.0*, *max_features='auto'*, *max_leaf_nodes=None*, *bootstrap=True*, *oob_score=False*, *n_jobs=1*, *random_state=None*, *verbose=0*, *preprocessors=None*)

A wrapper for *sklearn.ensemble._forest.RandomForestRegressor*. The following is its documentation:

A random forest regressor.

A random forest is a meta estimator that fits a number of classifying decision trees on various sub-samples of the dataset and uses averaging to improve the predictive accuracy and control over-fitting. The sub-sample size is controlled with the *max_samples* parameter if *bootstrap=True* (default), otherwise the whole dataset is used to build each tree.

Read more in the User Guide.

2.5.5 Simple Random Forest

class Orange.regression.**SimpleRandomForestLearner**(*n_estimators=10*, *min_instances=2*, *max_depth=1024*, *max_majority=1.0*, *skip_prob='sqrt'*, *seed=42*)

A random forest regressor, optimized for speed. Trees in the forest are constructed with SimpleTreeLearner classification trees.

Parameters

- **n_estimators** (*int, optional (default = 10)*) – Number of trees in the forest.

- **min_instances** (*int, optional (default = 2)*) – Minimal number of data instances in leaves. When growing the three, new nodes are not introduced if they would result in leaves with fewer instances than min_instances. Instance count is weighed.
- **max_depth** (*int, optional (default = 1024)*) – Maximal depth of tree.
- **max_majority** (*float, optional (default = 1.0)*) – Maximal proportion of majority class. When this is exceeded, induction stops (only used for classification).
- **skip_prob** (*string, optional (default = "sqrt")*) – Data attribute will be skipped with probability skip_prob.
  - if float, then skip attribute with this probability.
  - if "sqrt", then *skip_prob = 1 - sqrt(n_features) / n_features*
  - if "log2", then *skip_prob = 1 - log2(n_features) / n_features*
- **seed** (*int, optional (default = 42)*) – Random seed.

fit_storage(*data*)
Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

2.5.6 Regression Tree

Orange includes two implemenations of regression tres: a home-grown one, and one from scikit-learn. The former properly handles multinominal and missing values, and the latter is faster.

class Orange.regression.**TreeLearner**(**args*, *binarize=False*, *min_samples_leaf=1*, *min_samples_split=2*, *max_depth=None*, ***kwargs*)
Tree inducer with proper handling of nominal attributes and binarization.

The inducer can handle missing values of attributes and target. For discrete attributes with more than two possible values, each value can get a separate branch (*binarize=False*), or values can be grouped into two groups (*binarize=True*, default).

The tree growth can be limited by the required number of instances for internal nodes and for leafs, and by the maximal depth of the tree.

If the tree is not binary, it can contain zero-branches.

Parameters

- **binarize** – if *True* the inducer will find optimal split into two subsets for values of discrete attributes. If *False* (default), each value gets its branch.
- **min_samples_leaf** – the minimal number of data instances in a leaf
- **min_samples_split** – the minimal number of data instances that is split into subgroups
- **max_depth** – the maximal depth of the tree

Return type instance of OrangeTreeModel

fit_storage(*data*)
Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

class Orange.regression.**SklTreeRegressionLearner**(*criterion='squared_error'*, *splitter='best'*, *max_depth=None*, *min_samples_split=2*, *min_samples_leaf=1*, *max_features=None*, *random_state=None*, *max_leaf_nodes=None*, *preprocessors=None*)
A wrapper for *sklearn.tree._classes.DecisionTreeRegressor*. The following is its documentation:

A decision tree regressor.

Read more in the User Guide.

2.5.7 Neural Network

class Orange.regression.**NNRegressionLearner**(*hidden_layer_sizes=(100,)*, *activation='relu'*, *solver='adam'*, *alpha=0.0001*, *batch_size='auto'*, *learning_rate='constant'*, *learning_rate_init=0.001*, *power_t=0.5*, *max_iter=200*, *shuffle=True*, *random_state=None*, *tol=0.0001*, *verbose=False*, *warm_start=False*, *momentum=0.9*, *nesterovs_momentum=True*, *early_stopping=False*, *validation_fraction=0.1*, *beta_1=0.9*, *beta_2=0.999*, *epsilon=1e-08*, *preprocessors=None*)

A wrapper for *Orange.regression.neural_network.MLPRegressorWCallback*. The following is its documentation:

Multi-layer Perceptron regressor.

This model optimizes the squared error using LBFGS or stochastic gradient descent.

New in version 0.18.

2.5.8 Gradient Boosted Trees

class Orange.regression.gb.**GBRegressor**(*loss='squared_error'*, *learning_rate=0.1*, *n_estimators=100*, *subsample=1.0*, *criterion='friedman_mse'*, *min_samples_split=2*, *min_samples_leaf=1*, *min_weight_fraction_leaf=0.0*, *max_depth=3*, *min_impurity_decrease=0.0*, *min_impurity_split=None*, *init=None*, *random_state=None*, *max_features=None*, *alpha=0.9*, *verbose=0*, *max_leaf_nodes=None*, *warm_start=False*, *presort='deprecated'*, *validation_fraction=0.1*, *n_iter_no_change=None*, *tol=0.0001*, *ccp_alpha=0.0*, *preprocessors=None*)

A wrapper for *sklearn.ensemble._gb.GradientBoostingRegressor*. The following is its documentation:

Gradient Boosting for regression.

GB builds an additive model in a forward stage-wise fashion; it allows for the optimization of arbitrary differentiable loss functions. In each stage a regression tree is fit on the negative gradient of the given loss function.

Read more in the User Guide.

class Orange.regression.catgb.**CatGBRegressor**(*iterations=None*, *learning_rate=None*, *depth=None*, *l2_leaf_reg=None*, *model_size_reg=None*, *rsm=None*, *loss_function=None*, *border_count=None*, *feature_border_type=None*, *per_float_feature_quantization=None*, *input_borders=None*, *output_borders=None*, *fold_permutation_block=None*, *od_pval=None*, *od_wait=None*, *od_type=None*, *nan_mode=None*, *counter_calc_method=None*, *leaf_estimation_iterations=None*, *leaf_estimation_method=None*, *thread_count=None*, *random_seed=None*, *use_best_model=None*, *verbose=False*, *logging_level=None*, *metric_period=None*, *ctr_leaf_count_limit=None*, *store_all_simple_ctr=None*, *max_ctr_complexity=None*, *has_time=None*, *allow_const_label=None*, *classes_count=None*, *class_weights=None*, *one_hot_max_size=None*, *random_strength=None*, *name=None*, *ignored_features=None*, *train_dir='/home/docs/.cache/Orange/3.32.0.dev'*, *custom_loss=None*, *custom_metric=None*, *eval_metric=None*, *bagging_temperature=None*, *save_snapshot=None*, *snapshot_file=None*, *snapshot_interval=None*, *fold_len_multiplier=None*, *used_ram_limit=None*, *gpu_ram_part=None*, *allow_writing_files=False*, *final_ctr_computation_mode=None*, *approx_on_full_history=None*, *boosting_type=None*, *simple_ctr=None*, *combinations_ctr=None*, *per_feature_ctr=None*, *task_type=None*, *device_config=None*, *devices=None*, *bootstrap_type=None*, *subsample=None*, *sampling_unit=None*, *dev_score_calc_obj_block_size=None*, *max_depth=None*, *n_estimators=None*, *num_boost_round=None*, *num_trees=None*, *colsample_bylevel=None*, *random_state=None*, *reg_lambda=None*, *objective=None*, *eta=None*, *max_bin=None*, *scale_pos_weight=None*, *gpu_cat_features_storage=None*, *data_partition=None*, *metadata=None*, *early_stopping_rounds=None*, *cat_features=None*, *grow_policy=None*, *min_data_in_leaf=None*, *min_child_samples=None*, *max_leaves=None*, *num_leaves=None*, *score_function=None*, *leaf_estimation_backtracking=None*, *ctr_history_unit=None*, *monotone_constraints=None*, *feature_weights=None*, *penalties_coefficient=None*, *first_feature_use_penalties=None*, *model_shrink_rate=None*, *model_shrink_mode=None*, *langevin=None*, *diffusion_temperature=None*, *posterior_sampling=None*, *boost_from_average=None*, *text_features=None*, *tokenizers=None*, *dictionaries=None*, *feature_calcers=None*, *text_processing=None*, *preprocessors=None*)

A wrapper for *catboost.core.CatBoostRegressor*. The following is its documentation:

Implementation of the scikit-learn API for CatBoost regression.

class Orange.regression.xgb.**XGBRegressor**(*max_depth=None*, *learning_rate=None*, *n_estimators=100*, *verbosity=None*, *objective='reg:squarederror'*, *booster=None*, *tree_method=None*, *n_jobs=None*, *gamma=None*, *min_child_weight=None*, *max_delta_step=None*, *subsample=None*, *colsample_bytree=None*, *colsample_bylevel=None*, *colsample_bynode=None*, *reg_alpha=None*, *reg_lambda=None*, *scale_pos_weight=None*, *base_score=None*, *random_state=None*, *missing=nan*, *num_parallel_tree=None*, *monotone_constraints=None*, *interaction_constraints=None*, *importance_type='gain'*, *gpu_id=None*, *validate_parameters=None*, *preprocessors=None*)

A wrapper for *xgboost.sklearn.XGBRegressor*. The following is its documentation:

Implementation of the scikit-learn API for XGBoost regression.

class Orange.regression.xgb.**XGBRFRegressor**(*max_depth=None*, *learning_rate=None*, *n_estimators=100*, *verbosity=None*, *objective='reg:squarederror'*, *booster=None*, *tree_method=None*, *n_jobs=None*, *gamma=None*, *min_child_weight=None*, *max_delta_step=None*, *subsample=None*, *colsample_bytree=None*, *colsample_bylevel=None*, *colsample_bynode=None*, *reg_alpha=None*, *reg_lambda=None*, *scale_pos_weight=None*, *base_score=None*, *random_state=None*, *missing=nan*, *num_parallel_tree=None*, *monotone_constraints=None*, *interaction_constraints=None*, *importance_type='gain'*, *gpu_id=None*, *validate_parameters=None*, *preprocessors=None*)

A wrapper for *xgboost.sklearn.XGBRFRegressor*. The following is its documentation:

scikit-learn API for XGBoost random forest regression.

2.5.9 Curve Fit

class Orange.regression.curvefit.**CurveFitLearner**(*expression: Union[Callable, _ast.Expression, str]*, *parameters_names: Optional[List[str]] = None*, *features_names: Optional[List[str]] = None*, *available_feature_names: Optional[List[str]] = None*, *functions: Optional[List[str]] = None*, *sanitizer: Optional[Callable] = None*, *env: Optional[Dict[str, Any]] = None*, *p0: Optional[Union[List, Dict]] = None*, *bounds: Union[Tuple, Dict] = (- inf, inf)*, *preprocessors=None*)

Fit a function to data. It uses the scipy.curve_fit to find the optimal values of parameters.

Parameters

- **expression** (*callable or str*) – A modeling function. If callable, it must take the independent variable as the first argument and the parameters to fit as separate remaining arguments. If string, a lambda function is created, using *expression*, *available_feature_names*, *function* and *env* attributes. Should be string for pickling the model.

- **parameters_names** (*list of str*) – List of parameters names. Only needed when the expression is callable.
- **features_names** (*list of str*) – List of features names. Only needed when the expression is callable.
- **available_feature_names** (*list of str*) – List of all available features names. Only needed when the expression is string. Needed to distinguish between parameters and features when translating the expression into the lambda.
- **functions** (*list of str*) – List of all available functions. Only needed when the expression is string. Needed to distinguish between parameters and functions when translating the expression into the lambda.
- **sanitizer** (*callable*) – Function for sanitizing names.
- **env** (*dict*) – An environment to capture in the lambda's closure.
- **p0** (*list of floats, optional*) – Initial guess for the parameters.
- **bounds** (*2-tuple of array_like, optional*) – Lower and upper bounds on parameters.
- **preprocessors** (*tuple of Orange preprocessors, optional*) – The processors that will be used when data is passed to the learner.

Examples

```
>>> import numpy as np
>>> from Orange.data import Table
>>> from Orange.regression import CurveFitLearner
>>> data = Table("housing")
>>> # example with callable expression
>>> cfun = lambda x, a, b, c: a * np.exp(-b * x[:, 0] * x[:, 1]) + c
>>> learner = CurveFitLearner(cfun, ["a", "b", "c"], ["CRIM", "LSTAT"])
>>> model = learner(data)
>>> pred = model(data)
>>> coef = model.coefficients
>>> # example with str expression
>>> sfun = "a * exp(-b * CRIM * LSTAT) + c"
>>> names = [a.name for a in data.domain.attributes]
>>> learner = CurveFitLearner(sfun, available_feature_names=names,
...                           functions=["exp"])
>>> model = learner(data)
>>> pred = model(data)
>>> coef = model.coefficients
```

fit_storage(*data:* Orange.data.table.Table) → Orange.regression.curvefit.CurveFitModel

Default implementation of fit_storage defaults to calling fit. Derived classes must define fit_storage or fit

2.6 Clustering (clustering)

2.6.1 Hierarchical (hierarchical)

Example

The following example shows clustering of the Iris data with distance matrix computed with the Orange.distance.Euclidean distance and clustering using average linkage.

```
>>> from Orange import data, distance
>>> from Orange.clustering import hierarchical
>>> data = data.Table('iris')
>>> dist_matrix = distance.Euclidean(data)
>>> hierar = hierarchical.HierarchicalClustering(n_clusters=3)
>>> hierar.linkage = hierarchical.AVERAGE
>>> hierar.fit(dist_matrix)
>>> hierar.labels
array([ 1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,
        1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,
        1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,
        1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  0.,  0.,
        0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,
        0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,
        0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,
        0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  0.,  2.,  0.,  2.,  2.,
        2.,  2.,  0.,  2.,  2.,  2.,  2.,  2.,  2.,  0.,  0.,  2.,  2.,
        2.,  2.,  0.,  2.,  0.,  2.,  0.,  2.,  2.,  0.,  0.,  2.,  2.,
        2.,  2.,  2.,  0.,  2.,  2.,  2.,  2.,  0.,  2.,  2.,  2.,  0.,
        2.,  2.,  2.,  0.,  2.,  2.,  0.])
```

Hierarchical Clustering

class Orange.clustering.hierarchical.**HierarchicalClustering**(*n_clusters=2*, *linkage='average'*)

2.7 Distance (distance)

The following example demonstrates how to compute distances between all data instances from Iris:

```
>>> from Orange.data import Table
>>> from Orange.distance import Euclidean
>>> iris = Table('iris')
>>> dist_matrix = Euclidean(iris)
>>> # Distance between first two examples
>>> dist_matrix.X[0, 1]
0.53851648
```

To compute distances between all columns, we set *axis* to 0.

```
>>> Euclidean(iris, axis=0)
DistMatrix([[  0.        ,  36.17927584,  28.9542743 ,  57.1913455 ],
            [ 36.17927584,   0.        ,  25.73382987,  25.81259383],
            [ 28.9542743 ,  25.73382987,   0.        ,  33.87270287],
            [ 57.1913455 ,  25.81259383,  33.87270287,   0.        ]])
```

Finally, we can compute distances between all pairs of rows from two tables.

```
>>> iris1 = iris[:100]
>>> iris2 = iris[100:]
>>> dist = Euclidean(iris_even, iris_odd)
>>> dist.shape
(75, 100)
```

Most metrics can be fit on training data to normalize values and handle missing data. We do so by calling the constructor without arguments or with parameters, such as *normalize*, and then pass the data to method *fit*.

```
>>> dist_model = Euclidean(normalize=True).fit(iris1)
>>> dist = dist_model(iris2[:3])
>>> dist
DistMatrix([[ 0.        ,  1.36778277,  1.11352233],
            [ 1.36778277,  0.        ,  1.57810546],
            [ 1.11352233,  1.57810546,  0.        ]])
```

The above distances are computed on the first three rows of *iris2*, normalized by means and variances computed from *iris1*.

Here are five closest neighbors of *iris2[0]* from *iris1*:

```
>>> dist0 = dist_model(iris1, iris2[0])
>>> neigh_idx = np.argsort(dist0.flatten())[:5]
>>> iris1[neigh_idx]
[[5.900, 3.200, 4.800, 1.800 | Iris-versicolor],
 [6.700, 3.000, 5.000, 1.700 | Iris-versicolor],
 [6.300, 3.300, 4.700, 1.600 | Iris-versicolor],
 [6.000, 3.400, 4.500, 1.600 | Iris-versicolor],
 [6.400, 3.200, 4.500, 1.500 | Iris-versicolor]
]
```

All distances share a common interface.

class Orange.distance.**Distance**(*e1=None*, *e2=None*, *axis=1*, *impute=False*, *callback=None*, ***kwargs*)

Base class for construction of distances models (`DistanceModel`).

Distances can be computed between all pairs of rows in one table, or between pairs where one row is from one table and one from another.

If *axis* is set to *0*, the class computes distances between all pairs of columns in a table. Distances between columns from separate tables are probably meaningless, thus unsupported.

The class can be used as follows:

- Constructor is called only with keyword argument *axis* that specifies the axis over which the distances are computed, and with other subclass-specific keyword arguments.
- Next, we call the method *fit(data)* to produce an instance of `DistanceModel`; the instance stores any parameters needed for computation of distances, such as statistics for normalization and handling of missing data.

- We can then call the `DistanceModel` with data to compute the distance between its rows or columns, or with two data tables to compute distances between all pairs of rows.

The second, shorter way to use this class is to call the constructor with one or two data tables and any additional keyword arguments. Constructor will execute the above steps and return `DistMatrix`. Such usage is here for backward compatibility, practicality and efficiency.

Parameters

- **e1** (*Table* or *Instance* or `np.ndarray` or *None*) – data on which to train the model and compute the distances
- **e2** (*Table* or *Instance* or `np.ndarray` or *None*) – if present, the class computes distances with pairs coming from the two tables
- **axis** (*int*) – axis over which the distances are computed, 1 (default) for rows, 0 for columns
- **impute** (*bool*) – if *True* (default is *False*), nans in the computed distances are replaced with zeros, and infs with very large numbers.
- **callback** (*callable or None*) – callback function

axis
axis over which the distances are computed, 1 (default) for rows, 0 for columns

Type int

impute
if *True* (default is *False*), nans in the computed distances are replaced with zeros, and infs with very large numbers.

Type bool

normalize
if *True*, columns are normalized before computation. This attribute applies only if the distance supports normalization.

Type bool

The capabilities of the metrics are described with class attributes.

If class attribute *supports_discrete* is *True*, the distance also uses discrete attributes to compute row distances. The use of discrete attributes depends upon the type of distance; e.g. Jaccard distance observes whether the value is zero or non-zero, while Euclidean and Manhattan distance observes whether a pair of values is same or different.

Class attribute *supports_missing* indicates that the distance can cope with missing data. In such cases, letting the distance handle it should be preferred over pre-imputation of missing values.

Class attribute *supports_normalization* indicates that the constructor accepts an argument *normalize*. If set to *True*, the metric will attempt to normalize the values in a sense that each attribute will have equal influence. For instance, the Euclidean distance subtract the mean and divides the result by the deviation, while Manhattan distance uses the median and MAD.

If class attribute *supports_sparse* is *True*, the class will handle sparse data. Currently, all classes that do handle it rely on fallbacks to SKL metrics. These, however, do not support discrete data and missing values, and will fail silently.

2.7.1 Handling discrete and missing data

Discrete data is handled as appropriate for the particular distance. For instance, the Euclidean distance treats a pair of values as either the same or different, contributing either 0 or 1 to the squared sum of differences. In other cases – particularly in Jaccard and cosine distance, discrete values are treated as zero or non-zero.

Missing data is not simply imputed. We assume that values of each variable are distributed by some unknown distribution and compute - without assuming a particular distribution shape - the expected distance. For instance, for the Euclidean distance it turns out that the expected squared distance between a known and a missing value equals the square of the known value's distance from the mean of the missing variable, plus its variance.

2.7.2 Supported distances

Euclidean distance

For numeric values, the Euclidean distance is the square root of sums of squares of pairs of values from rows or columns. For discrete values, 1 is added if the two values are different.

To put all numeric data on the same scale, and in particular when working with a mixture of numeric and discrete data, it is recommended to enable normalization by adding *normalize=True* to the constructor. With this, numeric values are normalized by subtracting their mean and divided by deviation multiplied by the square root of two. The mean and deviation are computed on the training data, if the *fit* method is used. When computing distances between two tables and without explicitly calling *fit*, means and variances are computed from the first table only. Means and variances are always computed from columns, disregarding the axis over which we compute the distances, since columns represent variables and hence come from a certain distribution.

As described above, the expected squared difference between a known and a missing value equals the squared difference between the known value and the mean, plus the variance. The squared difference between two unknown values equals twice the variance.

For normalized data, the difference between a known and missing numeric value equals the square of the known value + 0.5. The difference between two missing values is 1.

For discrete data, the expected difference between a known and a missing value equals the probablity that the two values are different, which is 1 minus the probability of the known value. If both values are missing, the probability of them being different equals 1 minus the sum of squares of all probabilities (also known as the Gini index).

Manhattan distance

Manhattan distance is the sum of absolute pairwise distances.

Normalization and treatment of missing values is similar as in the Euclidean distance, except that medians and median absolute distance from the median (MAD) are used instead of means and deviations.

For discrete values, distances are again 0 or 1, hence the Manhattan distance for discrete columns is the same as the Euclidean.

Cosine distance

Cosine similarity is the dot product divided by the product of lengths (where the length is the square of dot product of a row/column with itself). Cosine distance is computed by subtracting the similarity from one.

In calculation of dot products, missing values are replaced by means. In calculation of lengths, the contribution of a missing value equals the square of the mean plus the variance. (The difference comes from the fact that in the former case the missing values are independent.)

Non-zero discrete values are replaced by 1. This introduces the notion of a "base value", which is the first in the list of possible values. In most cases, this will only make sense for indicator (i.e. two-valued, boolean attributes).

Cosine distance does not support any column-wise normalization.

Jaccard distance

Jaccard similarity between two sets is defined as the size of their intersection divided by the size of the union. Jaccard distance is computed by subtracting the similarity from one.

In Orange, attribute values are interpreted as membership indicator. In row-wise distances, columns are interpreted as sets, and non-zero values in a row (including negative values of numeric features) indicate that the row belongs to the particular sets. In column-wise distances, rows are sets and values indicate the sets to which the column belongs.

For missing values, relative frequencies from the training data are used as probabilities for belonging to a set. That is, for row-wise distances, we compute the relative frequency of non-zero values in each column, and vice-versa for column-wise distances. For intersection (union) of sets, we then add the probability of belonging to both (any of) the two sets instead of adding a 0 or 1.

SpearmanR, AbsoluteSpearmanR, PearsonR, AbsolutePearsonR

The four correlation-based distance measure equal (1 - the correlation coefficient) / 2. For *AbsoluteSpearmanR* and *AbsolutePearsonR*, the absolute value of the coefficient is used.

These distances do not handle missing or discrete values.

Mahalanobis distance

Mahalanobis distance is similar to cosine distance, except that the data is projected into the PCA space.

Mahalanobis distance does not handle missing or discrete values.

2.8 Evaluation (`evaluation`)

2.8.1 Sampling procedures for testing models (`testing`)

class Orange.evaluation.testing.**Results**(*data=None*, ***, *nmethods=None*, *nrows=None*, *nclasses=None*, *domain=None*, *row_indices=None*, *folds=None*, *score_by_folds=True*, *learners=None*, *models=None*, *failed=None*, *actual=None*, *predicted=None*, *probabilities=None*, *store_data=None*, *store_models=None*, *train_time=None*, *test_time=None*)

Class for storing predictions in model testing.

data
Data used for testing.

Type Optional[*Table*]

models
A list of induced models.

Type Optional[List[Model]]

row_indices
Indices of rows in *data* that were used in testing, stored as a numpy vector of length *nrows*. Values of *actual[i]*, *predicted[i]* and *probabilities[i]* refer to the target value of instance, that is, the i-th test instance is *data[row_indices[i]]*, its actual class is *actual[i]*, and the prediction by m-th method is *predicted[m, i]*.

Type np.ndarray

nrows
The number of test instances (including duplicates); *nrows* equals the length of *row_indices* and *actual*, and the second dimension of *predicted* and *probabilities*.

Type int

actual
true values of target variable in a vector of length *nrows*.

Type np.ndarray

predicted
predicted values of target variable in an array of shape (number-of-methods, *nrows*)

Type np.ndarray

probabilities
predicted probabilities (for discrete target variables) in an array of shape (number-of-methods, *nrows*, number-of-classes)

Type Optional[np.ndarray]

folds
a list of indices (or slice objects) corresponding to testing data subsets, that is, *row_indices[folds[i]]* contains row indices used in fold i, so *data[row_indices[folds[i]]]* is the corresponding testing data

Type List[Slice or List[int]]

train_time
training times of batches

Type np.ndarray

test_time
testing times of batches

Type np.ndarray

get_augmented_data(*model_names*, *include_attrs=True*, *include_predictions=True*, *include_probabilities=True*)
Return the test data table augmented with meta attributes containing predictions, probabilities (if the task is classification) and fold indices.

Parameters

- **model_names** (*list of str*) – names of models
- **include_attrs** (*bool*) – if set to *False*, original attributes are removed

- **include_predictions** (*bool*) – if set to *False*, predictions are not added
- **include_probabilities** (*bool*) – if set to *False*, probabilities are not added

Returns data augmented with predictions, probabilities and fold indices

Return type augmented_data (*Orange.data.Table*)

split_by_model()
Split evaluation results by models.

The method generates instances of *Results* containing data for single models

class Orange.evaluation.testing.**CrossValidation**(*data=None*, *learners=None*, *preprocessor=None*, *test_data=None*, ***, *callback=None*, *store_data=False*, *store_models=False*, *n_jobs=None*, ***kwargs*)

K-fold cross validation

k
number of folds (default: 10)

Type int

random_state
seed for random number generator (default: 0). If set to *None*, a different seed is used each time

Type int

stratified
flag deciding whether to perform stratified cross-validation. If *True* but the class sizes don't allow it, it uses non-stratified validataion and adds a list *warning* with a warning message(s) to the *Result*.

Type bool

get_indices(*data*)
Return a list of arrays of indices of test data instance

For example, in k-fold CV, the result is a list with *k* elements, each containing approximately *len(data) / k* nonoverlapping indices into *data*.

This method is abstract and must be implemented in derived classes unless they provide their own implementation of the *__call__* method.

Parameters **data** (Orange.data.Table) – test data

Returns a list of arrays of indices into *data*

Return type indices (list of np.ndarray)

class Orange.evaluation.testing.**LeaveOneOut**(*data=None*, *learners=None*, *preprocessor=None*, *test_data=None*, ***, *callback=None*, *store_data=False*, *store_models=False*, *n_jobs=None*, ***kwargs*)

Leave-one-out testing

get_indices(*data*)
Return a list of arrays of indices of test data instance

For example, in k-fold CV, the result is a list with *k* elements, each containing approximately *len(data) / k* nonoverlapping indices into *data*.

This method is abstract and must be implemented in derived classes unless they provide their own implementation of the *__call__* method.

Parameters **data** (Orange.data.Table) – test data

Returns a list of arrays of indices into *data*

Return type indices (list of np.ndarray)

static prepare_arrays(*data*, *indices*)
Prepare *folds*, *row_indices* and *actual*.

The method is used by *__call__*. While functional, it may be overriden in subclasses for speed-ups.

Parameters

- **data** (Orange.data.Table) – data use for testing
- **indices** (*list of vectors*) – indices of data instances in each test sample

Returns (np.ndarray): see class documentation row_indices: (np.ndarray): see class documentation actual: (np.ndarray): see class documentation

Return type folds

class Orange.evaluation.testing.**TestOnTrainingData**(*data=None*, *learners=None*, *preprocessor=None*, ***kwargs*)

Test on training data

class Orange.evaluation.testing.**ShuffleSplit**(*data=None*, *learners=None*, *preprocessor=None*, *test_data=None*, ***, *callback=None*, *store_data=False*, *store_models=False*, *n_jobs=None*, ***kwargs*)

Test by repeated random sampling

n_resamples
number of repetitions

Type int

test_size
If float, should be between 0.0 and 1.0 and represent the proportion of the dataset to include in the test split. If int, represents the absolute number of test samples. If None, the value is set to the complement of the train size. By default, the value is set to 0.1. The default will change in version 0.21. It will remain 0.1 only if `train_size` is unspecified, otherwise it will complement the specified `train_size`. (from documentation of scipy.sklearn.StratifiedShuffleSplit)

Type float, int, None

train_size
float, int, or None, default is None If float, should be between 0.0 and 1.0 and represent the proportion of the dataset to include in the train split. If int, represents the absolute number of train samples. If None, the value is automatically set to the complement of the test size. (from documentation of scipy.sklearn.StratifiedShuffleSplit)

stratified
flag deciding whether to perform stratified cross-validation.

Type bool

random_state
seed for random number generator (default: 0). If set to *None*, a different seed is used each time

Type int

get_indices(*data*)
Return a list of arrays of indices of test data instance

For example, in k-fold CV, the result is a list with *k* elements, each containing approximately *len(data) / k* nonoverlapping indices into *data*.

This method is abstract and must be implemented in derived classes unless they provide their own implementation of the *__call__* method.

Parameters **data** (Orange.data.Table) – test data

Returns a list of arrays of indices into *data*

Return type indices (list of np.ndarray)

class Orange.evaluation.testing.**TestOnTestData**(*data=None*, *test_data=None*, *learners=None*, *preprocessor=None*, ***kwargs*)

Test on separately provided test data

Note that the class has a different signature for *__call__*.

Orange.evaluation.testing.**sample**(*table*, *n=0.7*, *stratified=False*, *replace=False*, *random_state=None*)

Samples data instances from a data table. Returns the sample and a dataset from input data table that are not in the sample. Also uses several sampling functions from scikit-learn.

table [data table] A data table from which to sample.

n [float, int (default = 0.7)] If float, should be between 0.0 and 1.0 and represents the proportion of data instances in the resulting sample. If int, n is the number of data instances in the resulting sample.

stratified [bool, optional (default = False)] If true, sampling will try to consider class values and match distribution of class values in train and test subsets.

replace [bool, optional (default = False)] sample with replacement

random_state [int or RandomState] Pseudo-random number generator state used for random sampling.

class Orange.evaluation.testing.**CrossValidationFeature**(*data=None*, *learners=None*, *preprocessor=None*, *test_data=None*, ***, *callback=None*, *store_data=False*, *store_models=False*, *n_jobs=None*, ***kwargs*)

Cross validation with folds according to values of a feature.

feature

the feature defining the folds

Type *Orange.data.Variable*

get_indices(*data*)

Return a list of arrays of indices of test data instance

For example, in k-fold CV, the result is a list with *k* elements, each containing approximately *len(data) / k* nonoverlapping indices into *data*.

This method is abstract and must be implemented in derived classes unless they provide their own implementation of the *__call__* method.

Parameters **data** (Orange.data.Table) – test data

Returns a list of arrays of indices into *data*

Return type indices (list of np.ndarray)

2.8.2 Scoring methods (scoring)

CA

Orange.evaluation.**CA**(*results=None*, ***kwargs*)

A wrapper for *sklearn.metrics._classification.accuracy_score*. The following is its documentation:

Accuracy classification score.

In multilabel classification, this function computes subset accuracy: the set of labels predicted for a sample must *exactly* match the corresponding set of labels in y_true.

Read more in the User Guide.

Precision

Orange.evaluation.**Precision**(*results=None*, ***kwargs*)

A wrapper for *sklearn.metrics._classification.precision_score*. The following is its documentation:

Compute the precision.

The precision is the ratio `tp / (tp + fp)` where `tp` is the number of true positives and `fp` the number of false positives. The precision is intuitively the ability of the classifier not to label as positive a sample that is negative.

The best value is 1 and the worst value is 0.

Read more in the User Guide.

Recall

Orange.evaluation.**Recall**(*results=None*, ***kwargs*)

A wrapper for *sklearn.metrics._classification.recall_score*. The following is its documentation:

Compute the recall.

The recall is the ratio `tp / (tp + fn)` where `tp` is the number of true positives and `fn` the number of false negatives. The recall is intuitively the ability of the classifier to find all the positive samples.

The best value is 1 and the worst value is 0.

Read more in the User Guide.

F1

Orange.evaluation.**F1**(*results=None*, ***kwargs*)

A wrapper for *sklearn.metrics._classification.f1_score*. The following is its documentation:

Compute the F1 score, also known as balanced F-score or F-measure.

The F1 score can be interpreted as a harmonic mean of the precision and recall, where an F1 score reaches its best value at 1 and worst score at 0. The relative contribution of precision and recall to the F1 score are equal. The formula for the F1 score is:

```
F1 = 2 * (precision * recall) / (precision + recall)
```

In the multi-class and multi-label case, this is the average of the F1 score of each class with weighting depending on the `average` parameter.

Read more in the User Guide.

PrecisionRecallFSupport

Orange.evaluation.**PrecisionRecallFSupport**(*results=None*, ***kwargs*)

A wrapper for *sklearn.metrics._classification.precision_recall_fscore_support*. The following is its documentation:

Compute precision, recall, F-measure and support for each class.

The precision is the ratio `tp / (tp + fp)` where `tp` is the number of true positives and `fp` the number of false positives. The precision is intuitively the ability of the classifier not to label as positive a sample that is negative.

The recall is the ratio `tp / (tp + fn)` where `tp` is the number of true positives and `fn` the number of false negatives. The recall is intuitively the ability of the classifier to find all the positive samples.

The F-beta score can be interpreted as a weighted harmonic mean of the precision and recall, where an F-beta score reaches its best value at 1 and worst score at 0.

The F-beta score weights recall more than precision by a factor of `beta`. `beta == 1.0` means recall and precision are equally important.

The support is the number of occurrences of each class in `y_true`.

If `pos_label is None` and in binary classification, this function returns the average precision, recall and F-measure if `average` is one of `'micro'`, `'macro'`, `'weighted'` or `'samples'`.

Read more in the User Guide.

AUC

Orange.evaluation.**AUC**(*results=None*, ***kwargs*)

${sklpar}

Parameters

- **results** (*Orange.evaluation.Results*) – Stored predictions and actual data in model testing.
- **target** (*int, optional (default=None)*) – Value of class to report.

Log Loss

Orange.evaluation.**LogLoss**(*results=None*, ***kwargs*)

${sklpar}

Parameters

- **results** (*Orange.evaluation.Results*) – Stored predictions and actual data in model testing.
- **eps** (*float*) – Log loss is undefined for p=0 or p=1, so probabilities are clipped to max(eps, min(1 - eps, p)).
- **normalize** (*bool, optional (default=True)*) – If true, return the mean loss per sample. Otherwise, return the sum of the per-sample losses.
- **sample_weight** (*array-like of shape = [n_samples], optional*) – Sample weights.

Examples

```
>>> Orange.evaluation.LogLoss(results)
array([ 0.3...])
```

MSE

Orange.evaluation.**MSE**(*results=None*, ***kwargs*)

A wrapper for *sklearn.metrics._regression.mean_squared_error*. The following is its documentation:

Mean squared error regression loss.

Read more in the User Guide.

MAE

Orange.evaluation.**MAE**(*results=None*, ***kwargs*)

A wrapper for *sklearn.metrics._regression.mean_absolute_error*. The following is its documentation:

Mean absolute error regression loss.

Read more in the User Guide.

R2

Orange.evaluation.**R2**(*results=None*, ***kwargs*)

A wrapper for *sklearn.metrics._regression.r2_score*. The following is its documentation:

R^2 (coefficient of determination) regression score function.

Best possible score is 1.0 and it can be negative (because the model can be arbitrarily worse). A constant model that always predicts the expected value of y, disregarding the input features, would get a R^2 score of 0.0.

Read more in the User Guide.

CD diagram

Orange.evaluation.**compute_CD**(*avranks*, *n*, *alpha='0.05'*, *test='nemenyi'*)

Returns critical difference for Nemenyi or Bonferroni-Dunn test according to given alpha (either alpha="0.05" or alpha="0.1") for average ranks and number of tested datasets N. Test can be either "nemenyi" for for Nemenyi two tailed test or "bonferroni-dunn" for Bonferroni-Dunn test.

Orange.evaluation.**graph_ranks**(*avranks*, *names*, *cd=None*, *cdmethod=None*, *lowv=None*, *highv=None*, *width=6*, *textspace=1*, *reverse=False*, *filename=None*, ***kwargs*)

Draws a CD graph, which is used to display the differences in methods' performance. See Janez Demsar, Statistical Comparisons of Classifiers over Multiple Data Sets, 7(Jan):1–30, 2006.

Needs matplotlib to work.

The image is ploted on *plt* imported using *import matplotlib.pyplot as plt*.

Parameters

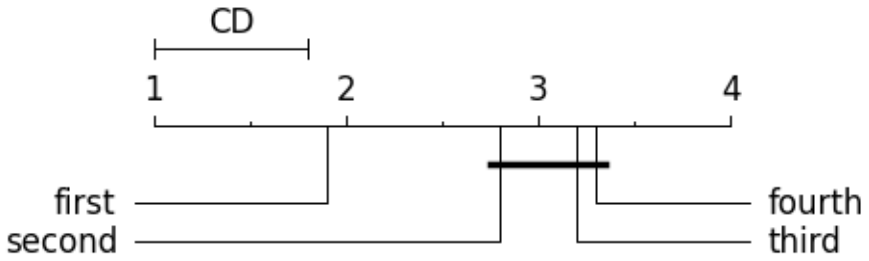
- **avranks** (*list of float*) – average ranks of methods.
- **names** (*list of str*) – names of methods.

- **cd** (*float*) – Critical difference used for statistically significance of difference between methods.
- **cdmethod** (*int, optional*) – the method that is compared with other methods If omitted, show pairwise comparison of methods
- **lowv** (*int, optional*) – the lowest shown rank
- **highv** (*int, optional*) – the highest shown rank
- **width** (*int, optional*) – default width in inches (default: 6)
- **textspace** (*int, optional*) – space on figure sides (in inches) for the method names (default: 1)
- **reverse** (*bool, optional*) – if set to *True*, the lowest rank is on the right (default: *False*)
- **filename** (*str, optional*) – output file name (with extension). If not given, the function does not write a file.

Example

```
>>> import Orange
>>> import matplotlib.pyplot as plt
>>> names = ["first", "third", "second", "fourth" ]
>>> avranks =  [1.9, 3.2, 2.8, 3.3 ]
>>> cd = Orange.evaluation.compute_CD(avranks, 30) #tested on 30 datasets
>>> Orange.evaluation.graph_ranks(avranks, names, cd=cd, width=6, textspace=1.5)
>>> plt.show()
```

The code produces the following graph:



2.8.3 Performance curves

class Orange.evaluation.performance_curves.**Curves**(*ytrue*, *probs*)

Computation of performance curves (ca, f1, precision, recall and the rest of the zoo) from test results.

The class works with binary classes. Attribute *probs* contains ordered probabilities and all curves represent performance statistics if an instance is classified as positive if it equals or exceeds the threshold in *probs*, that is, *sensitivity[i]* is the sensitivity of the classifier that classifies an instances as positive if the probability of being positive is at least *probs[i]*.

Class can be constructed by giving *probs* and *ytrue*, or from test results (see *Curves.from_results*). The latter removes instances with missing class values or predicted probabilities.

The class treats all results as obtained from a single run instead of computing separate curves and fancy averaging.

Parameters

- **probs** (*np.ndarray*) – vector of predicted probabilities
- **ytrue** (*np.ndarray*) – corresponding true classes

probs
ordered vector of predicted probabilities

Type np.ndarray

ytrue
corresponding true classes

Type np.ndarray

tot
total number of data instances

Type int

p
number of real positive instances

Type int

n
number of real negative instances

Type int

tp
number of true positives (property computed from *tn*)

Type np.ndarray

fp
number of false positives (property computed from *tn*)

Type np.ndarray

tn
number of true negatives (property computed from *tn*)

Type np.ndarray

fn
number of false negatives (precomputed, not a property)

Type np.ndarray

classmethod from_results(*results*, *target_class=None*, *model_index=None*)
Construct an instance of *Curves* from test results.

Parameters

- **results** (*Orange.evaluation.testing.Results*) – test results
- **target_class** (*int*) – target class index; if the class is binary, this defaults to *1*, otherwise it must be given
- **model_index** (*int*) – model index; if there is only one model, this argument can be omitted

Returns curves (*Curves*)

ca()
Classification accuracy curve

f1()
F1 curve

sensitivity()
Sensitivity curve

specificity()
Specificity curve

precision()
Precision curve

The last element represents precision at threshold 1. Unless such a probability appears in the data, the precision at this point is undefined. To avoid this, we copy the previous value to the last.

recall()
Recall curve

ppv()
PPV curve; see the comment at *precision*

npv()
NPV curve

The first value is undefined (no negative instances). To avoid this, we copy the second value into the first.

fpr()
FPR curve

tpr()
TPR curve

2.9 Projection (projection)

2.9.1 PCA

Principal component analysis is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components.

Example

```
>>> from Orange.projection import PCA
>>> from Orange.data import Table
>>> iris = Table('iris')
>>> pca = PCA()
>>> model = pca(iris)
>>> model.components_    # PCA components
array([[ 0.36158968, -0.08226889,  0.85657211,  0.35884393],
    [ 0.65653988,  0.72971237, -0.1757674 , -0.07470647],
    [-0.58099728,  0.59641809,  0.07252408,  0.54906091],
    [ 0.31725455, -0.32409435, -0.47971899,  0.75112056]])
>>> transformed_data = model(iris)    # transformed data
>>> transformed_data
```

(continues on next page)

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```
[[-2.684, 0.327, -0.022, 0.001 | Iris-setosa],
[-2.715, -0.170, -0.204, 0.100 | Iris-setosa],
[-2.890, -0.137, 0.025, 0.019 | Iris-setosa],
[-2.746, -0.311, 0.038, -0.076 | Iris-setosa],
[-2.729, 0.334, 0.096, -0.063 | Iris-setosa],
...
]
```

class Orange.projection.pca.**PCA**(*n_components=None*, *copy=True*, *whiten=False*, *svd_solver='auto'*, *tol=0.0*, *iterated_power='auto'*, *random_state=None*, *preprocessors=None*)

A wrapper for *Orange.projection.pca.ImprovedPCA*. The following is its documentation:

Patch sklearn PCA learner to include randomized PCA for sparse matrices.

Scikit-learn does not currently support sparse matrices at all, even though efficient methods exist for PCA. This class patches the default scikit-learn implementation to properly handle sparse matrices.

Notes

- This should be removed once scikit-learn releases a version which implements this functionality.

class Orange.projection.pca.**SparsePCA**(*n_components=None*, *alpha=1*, *ridge_alpha=0.01*, *max_iter=1000*, *tol=1e-08*, *method='lars'*, *n_jobs=1*, *U_init=None*, *V_init=None*, *verbose=False*, *random_state=None*, *preprocessors=None*)

A wrapper for *sklearn.decomposition._sparse_pca.SparsePCA*. The following is its documentation:

Sparse Principal Components Analysis (SparsePCA).

Finds the set of sparse components that can optimally reconstruct the data. The amount of sparseness is controllable by the coefficient of the L1 penalty, given by the parameter alpha.

Read more in the User Guide.

class Orange.projection.pca.**IncrementalPCA**(*n_components=None*, *whiten=False*, *copy=True*, *batch_size=None*, *preprocessors=None*)

A wrapper for *sklearn.decomposition._incremental_pca.IncrementalPCA*. The following is its documentation:

Incremental principal components analysis (IPCA).

Linear dimensionality reduction using Singular Value Decomposition of the data, keeping only the most significant singular vectors to project the data to a lower dimensional space. The input data is centered but not scaled for each feature before applying the SVD.

Depending on the size of the input data, this algorithm can be much more memory efficient than a PCA, and allows sparse input.

This algorithm has constant memory complexity, on the order of `batch_size * n_features`, enabling use of np.memmap files without loading the entire file into memory. For sparse matrices, the input is converted to dense in batches (in order to be able to subtract the mean) which avoids storing the entire dense matrix at any one time.

The computational overhead of each SVD is `O(batch_size * n_features ** 2)`, but only 2 * batch_size samples remain in memory at a time. There will be `n_samples / batch_size` SVD computations to get the principal components, versus 1 large SVD of complexity `O(n_samples * n_features ** 2)` for PCA.

Read more in the User Guide.

New in version 0.16.

2.9.2 FreeViz

FreeViz uses a paradigm borrowed from particle physics: points in the same class attract each other, those from different class repel each other, and the resulting forces are exerted on the anchors of the attributes, that is, on unit vectors of each of the dimensional axis. The points cannot move (are projected in the projection space), but the attribute anchors can, so the optimization process is a hill-climbing optimization where at the end the anchors are placed such that forces are in equilibrium.

Example

```
>>> from Orange.projection import FreeViz
>>> from Orange.data import Table
>>> iris = Table('iris')
>>> freeviz = FreeViz()
>>> model = freeviz(iris)
>>> model.components_    # FreeViz components
array([[  3.83487853e-01,   1.38777878e-17],
   [ -6.95058218e-01,   7.18953457e-01],
   [  2.16525357e-01,  -2.65741729e-01],
   [  9.50450079e-02,  -4.53211728e-01]])
>>> transformed_data = model(iris)    # transformed data
>>> transformed_data
[[-0.157, 2.053 | Iris-setosa],
[0.114, 1.694 | Iris-setosa],
[-0.123, 1.864 | Iris-setosa],
[-0.048, 1.740 | Iris-setosa],
[-0.265, 2.125 | Iris-setosa],
...
]
```

class Orange.projection.freeviz.**FreeViz**(*weights=None*, *center=True*, *scale=True*, *dim=2*, *p=1*, *initial=None*, *maxiter=500*, *alpha=0.1*, *atol=1e-05*, *preprocessors=None*)

2.9.3 LDA

Linear discriminant analysis is another way of finding a linear transformation of data that reduces the number of dimensions required to represent it. It is often used for dimensionality reduction prior to classification, but can also be used as a classification technique itself ([1]).

[1] Witten, I.H., Frank, E., Hall, M.A. and Pal, C.J., 2016. Data Mining: Practical machine learning tools and techniques. Morgan Kaufmann.

Example

```
>>> from Orange.projection import LDA
>>> from Orange.data import Table
>>> iris = Table('iris')
>>> lda = LDA()
>>> model = LDA(iris)
>>> model.components_    # LDA components
array([[ 0.20490976,  0.38714331, -0.54648218, -0.71378517],
   [ 0.00898234,  0.58899857, -0.25428655,  0.76703217],
   [-0.71507172,  0.43568045,  0.45568731, -0.30200008],
   [ 0.06449913, -0.35780501, -0.42514529,  0.828895  ]])
>>> transformed_data = model(iris)    # transformed data
>>> transformed_data
[[1.492, 1.905 | Iris-setosa],
[1.258, 1.608 | Iris-setosa],
[1.349, 1.750 | Iris-setosa],
[1.180, 1.639 | Iris-setosa],
[1.510, 1.963 | Iris-setosa],
...
]
```

class Orange.projection.lda.**LDA**(*solver='svd'*, *shrinkage=None*, *priors=None*, *n_components=None*, *store_covariance=False*, *tol=0.0001*, *preprocessors=None*)

A wrapper for *sklearn.discriminant_analysis.LinearDiscriminantAnalysis*. The following is its documentation:

Linear Discriminant Analysis.

A classifier with a linear decision boundary, generated by fitting class conditional densities to the data and using Bayes' rule.

The model fits a Gaussian density to each class, assuming that all classes share the same covariance matrix.

The fitted model can also be used to reduce the dimensionality of the input by projecting it to the most discriminative directions, using the *transform* method.

New in version 0.17: *LinearDiscriminantAnalysis*.

Read more in the User Guide.

2.9.4 References

2.10 Miscellaneous (misc)

2.10.1 Distance Matrix (distmatrix)

class Orange.misc.distmatrix.**DistMatrix**(*data*, *row_items=None*, *col_items=None*, *axis=1*)

Distance matrix. Extends `numpy.ndarray`.

row_items

Items corresponding to matrix rows.

col_items

Items corresponding to matrix columns.

axis
If axis=1 we calculate distances between rows, if axis=0 we calculate distances between columns.

property dim
Returns the single dimension of the symmetric square matrix.

property flat
A 1-D iterator over the array.

This is a *numpy.flatiter* instance, which acts similarly to, but is not a subclass of, Python's built-in iterator object.

See also:

flatten Return a copy of the array collapsed into one dimension.

flatiter

Examples

```
>>> x = np.arange(1, 7).reshape(2, 3)
>>> x
array([[1, 2, 3],
       [4, 5, 6]])
>>> x.flat[3]
4
>>> x.T
array([[1, 4],
       [2, 5],
       [3, 6]])
>>> x.T.flat[3]
5
>>> type(x.flat)
<class 'numpy.flatiter'>
```

An assignment example:

```
>>> x.flat = 3; x
array([[3, 3, 3],
       [3, 3, 3]])
>>> x.flat[[1,4]] = 1; x
array([[3, 1, 3],
       [3, 1, 3]])
```

submatrix(*row_items*, *col_items=None*)
Return a submatrix

Parameters

- **row_items** – indices of rows
- **col_items** – incides of columns

classmethod from_file(*filename*)
Load distance matrix from a file

The file should be preferrably encoded in ascii/utf-8. White space at the beginning and end of lines is ignored.

The first line of the file starts with the matrix dimension. It can be followed by a list flags

- *axis*=<*number*>: the axis number
- *symmetric*: the matrix is symmetric; when reading the element (i, j) it's value is also assigned to (j, i)
- *asymmetric*: the matrix is asymmetric
- *row_labels*: the file contains row labels
- *col_labels*: the file contains column labels

By default, matrices are symmetric, have axis 1 and no labels are given. Flags *labeled* and *labelled* are obsolete aliases for *row_labels*.

If the file has column labels, they follow in the second line. Row labels appear at the beginning of each row. Labels are arbitrary strings that cannot contain newlines and tabulators. Labels are stored as instances of *Table* with a single meta attribute named "label".

The remaining lines contain tab-separated numbers, preceded with labels, if present. Lines are padded with zeros if necessary. If the matrix is symmetric, the file contains the lower triangle; any data above the diagonal is ignored.

Parameters **filename** – file name

has_row_labels()
Returns *True* if row labels can be automatically determined from data

For this, the *row_items* must be an instance of *Orange.data.Table* whose domain contains a single meta attribute, which has to be a string. The domain may contain other variables, but not meta attributes.

has_col_labels()
Returns *True* if column labels can be automatically determined from data

For this, the *col_items* must be an instance of *Orange.data.Table* whose domain contains a single meta attribute, which has to be a string. The domain may contain other variables, but not meta attributes.

save(*filename*)
Save the distance matrix to a file in the file format described at *from_file*.

Parameters **filename** – file name

BIBLIOGRAPHY

[Quinlan1986] J R Quinlan: Induction of Decision Trees, Machine Learning, 1986.

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