Orange: Data Mining Toolbox in Python

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Abstract

Orange is a machine learning and data mining suite for data analysis through Python scripting and visual programming. Here we report on the scripting part, which features interactive data analysis and component-based assembly of data mining procedures. In the selection and design of components, we focus on the flexibility of their reuse: our principal intention is to let the user write simple and clear scripts in Python, which build upon C++ implementations of computationally-intensive tasks. Orange is intended both for experienced users and programmers, as well as for students of data mining.

Keywords: Python, data mining, machine learning, toolbox, scripting

1. Introduction

Scripting languages have recently risen in popularity in all fields of computer science. Within the context of explorative data analysis, they offer advantages like interactivity and fast prototyping by gluing together existing components or adapting them for new tasks. Python is a scripting language with clear and simple syntax, which also made it popular in education. Its relatively slow execution can be circumvented by using libraries that implement the computationally intensive tasks in low-level languages.

Python offers a huge number of extension libraries. Many are related to machine learning, including several general packages like scikit-learn (Pedregosa et al., 2011), PyBrain (Schaul et al., 2010) and mlpy (Albanese et al., 2012). Orange was conceived in late 1990s and is among the oldest of such tools. It focuses on simplicity, interactivity through scripting, and component-based design.
2. Toolbox Overview

Orange library is a hierarchically-organized toolbox of data mining components. The low-level procedures at the bottom of the hierarchy, like data filtering, probability assessment and feature scoring, are assembled into higher-level algorithms, such as classification tree learning. This allows developers to easily add new functionality at any level and fuse it with the existing code. The main branches of the component hierarchy are:

**data management and preprocessing** for data input and output, data filtering and sampling, imputation, feature manipulation (discretization, continuization, normalization, scaling and scoring), and feature selection,

**classification** with implementations of various supervised machine learning algorithms (trees, forests, instance-based and Bayesian approaches, rule induction), borrowing from some well-known external libraries such as LIBSVM (Chang and Lin, 2011),

**regression** including linear and lasso regression, partial least square regression, regression trees and forests, and multivariate regression splines,

**association** for association rules and frequent itemsets mining,

**ensembles** implemented as wrappers for bagging, boosting, forest trees, and stacking,

**clustering**, which includes $k$-means and hierarchical clustering approaches,

**evaluation** with cross-validation and other sampling-based procedures, functions for scoring the quality of prediction methods, and procedures for reliability estimation,

**projections** with implementations of principal component analysis, multi-dimensional scaling and self-organizing maps.

The library is designed to simplify the assembly of data analysis workflows and crafting of data mining approaches from a combination of existing components. Besides broader range of features, Orange differs from most other Python-based machine learning libraries by its maturity (over 15 years of active development and use), a large user community supported through an active forum, and extensive documentation that includes tutorials, scripting examples, data set repository, and documentation for developers. Orange scripting library is also a foundation for its visual programming platform with graphical user interface components for interactive data visualization.

The two major packages that are similar to Orange and are still actively developed are scikit-learn (Pedregosa et al., 2011) and mlpy (Albanese et al., 2012). Both are more tightly integrated with numpy and at present better blend into Python’s numerical computing habitat. Orange was on the other hand inspired by classical machine learning that focuses on symbolic methods. Rather than supporting only numerical arrays, Orange data structures combine symbolic, string and numerical attributes and meta data information. User can for instance refer to variables and values by their names. Variables store mapping functions, a mechanism which for instance allows classifiers to define transformations on training data that are then automatically applied when making predictions. These features also make Orange more suitable for interactive, explorative data analysis.
3. Scripting Examples

Let us illustrate the utility of Orange through an example of data analysis in Python shell:

```python
>>> import Orange
>>> data = Orange.data.Table("titanic")
>>> len(data)
2201
>>> nbc = Orange.classification.bayes.NaiveLearner()
>>> svm = Orange.classification.svm.SVM Learner()
>>> stack = Orange.ensemble.stacking.StackedClassificationLearner([nbc, svm])
>>> res = Orange.evaluation.testing.cross_validation([nbc, svm, stack], data)
>>> Orange.evaluation.scoring.AUC(res)
[0.7148500435874006, 0.731873352343742, 0.7635593576372478]
```

We first read the data on survival of 2,201 passengers from HMS Titanic and construct a set of learning algorithms: a naive Bayesian and SVM learner, and a stacked combination of the two (Wolpert, 1992). We then cross-validate the learners and report the area under ROC curves.

Running stacking on the subset of about 470 female passengers improves AUC score:

```python
>>> females = Orange.data.Table([d for d in data if d["sex"]=='female'])
>>> len(females)
470
>>> res = Orange.evaluation.testing.cross_validation([stack], females)
>>> Orange.evaluation.scoring.AUC(res)
[0.8124014221073045]
```

We can use existing machine learning components to craft new ones. For instance, learning algorithms must implement a `__call__` operator that accepts the training data and, optionally, data instance weights, and has to return a model. The following example defines a new learner that encloses another learner into a feature selection wrapper: it sorts the features by their information gain (as implemented in `Orange.feature.scoring.InfoGain`), constructs a new data set with only the m best features and calls the `base_learner`.

```python
class FSSLearner(Orange.classification.PyLearner):
    def __init__(self, base_learner, m=5):
        self.m = m
        self.base_learner = base_learner

    def __call__(self, data, weights=None):
        gain = Orange.feature.scoring.InfoGain()
        best = sorted(data.domain.features, key=lambda x: -gain(x, data))[:self.m]
        domain = Orange.data.Domain(best + [data.domain.class_var])
        new_data = Orange.data.Table(domain, data)
        model = self.base_learner(new_data, weights)
        return Orange.classification.PyClassifier(classifier=model)
```

Below we compare the original and wrapped naive Bayesian classifier on a data set with 106 instances and 57 features:

```python
>>> data = Orange.data.Table("promoters")
>>> len(data), len(data.domain.features)
(106, 57)
```
>>> bayes = Orange.classification.bayes.NaiveLearner()
>>> res = Orange.evaluation.testing.cross_validation([bayes, FSSLearner(bayes)], data)
>>> Orange.evaluation.scoring.AUC(res)
[0.9329999999999998, 0.945]

4. Code Design

Orange’s core is a collection of nearly 200 C++ classes that cover the basic data structures and majority of preprocessing and modeling algorithms. The C++ part is self-contained, without any calls to Python that would induce unnecessary overhead. The core includes several open source libraries, including LIBSVM (Chang and Lin, 2011), LIBLINEAR (Rong-En et al., 2008), Earth (see http://www.milbo.users.sonic.net/earth), QHull (Barber et al., 1996) and a subset of BLAS (Blackford et al., 2002). The Python layer also uses popular Python libraries numpy for linear algebra, networkx (Hagberg et al., 2008) for working with networks and matplotlib (Hunter, 2007) for basic visualization.

The upper layer of Orange is written in Python and includes procedures that are not time-critical. This is also the place at which users outside the core development group most easily contribute to the project.

Automated testing of the system relies on over 1,500 regression tests that are mostly based on code snippets from extensive documentation. A part of the code is also covered with stricter unit tests.

5. Availability, Requirements and Plans for the Future

Orange is free software released under GPL. The code is hosted on Bitbucket repository (https://bitbucket.org/biolab/orange). Orange runs on Windows, Mac OS X and Linux, and can also be installed from the Python Package Index repository (pip install Orange). Binary installer for Windows and application bundle for Mac OS X are available on project’s web site (http://orange.biolab.si).

Orange currently runs on Python 2.6 and 2.7. A version for Python 3 and higher is under development. There, we will switch to numpy-based data structures and scrap the C++ core in favor of using routines from numpy and scipy (Jones et al., 2001–), scikit-learn (Pedregosa et al., 2011) and similar libraries that did not exist when Orange was first conceived. Despite planned changes in the core, we will maintain backward compatibility. For existing users, the changes of the Python interface will be minor.

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References


