Writing bibliographic tools with *pybliographer*

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Chapter 1

Introduction

pybliographer is a developer-oriented framework for manipulating bibliographic data. It is written in *python*¹, and uses extensively the dynamic nature of this language.

pybliographer does not try to define another standard format for bibliographic data, nor does it solely rely on a single existing standards. Standards are important in order to allow for interoperability and durability. Unfortunately, real-world data often contain a great number of mistakes, or reflect certain local conventions. pybliographer is on the pragmatic side of considering these issues as part of its business: most of the parsing tasks can be easily overriden and specialized in order to fit the code to the data, and not the other way around.

1.1 Basic concepts

pybliographer deals with sets of Records, stored in a so-called Database. This database can be actually implemented on top of different systems. Two are available today, one based on a single XML file, using a custom XML dialect, the other based on Berkeley DB², a very efficient database system.

Each record represents an elementary object you want to describe, and has a number of *attributes*. For instance, if you are describing a book, one attribute will be its *title*, another its *ISBN*, etc. Each of these attributes can contain one or more values, all of the same *type*. To continue the description of our book, we probably have the *author* attribute, which contains as many Person values as there are authors for the book. All the values of a given attribute are of the same type.

In some cases, simply having this flat key/value model to describe an object is not enough. *pybliographer* allows, for every value of every attribute, to provide a set of *qualifiers*. These qualifiers are also attributes which can hold one or more values. If my book, or information about the book, is available via the internet, I can provide a *link* attribute, but for each of the actual URLs provided, I might wish to add a *description* qualifier, which will indicate, say, if the URL points to the editor's website, or to a review, etc.

This nesting of objects is best described in figure 1.1.

 $^{^{1}}$ see http://python.org/

²see http://www.sleepycat.com/

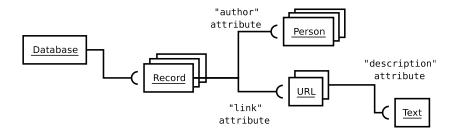


Figure 1.1: Objects manipulated in pybliographer

pybliographer comes with a set of defined attribute types, like Person, Text, Date, ID (see the Pyblio.Attribute module for a complete list), and can be extended to support your own types.

1.1.1 The database schema

Even though attributes are typed, the data model described above is quite flexible. In order for *pybliographer* to help you checking that your records are properly typed, it needs to know the database schema you are using. This schema, usually stored in an XML file with the extension <code>.sip</code>, simply lists the known attributes with their type and the qualifiers it allows for its values. Some <code>.sip</code> files are distributed with *pybliographer*, and can be seen in the <code>Pyblio.RIP</code> directory.

In addition to validation information, the schema contains human-readable description of the different fields, possibly in several languages, so that it can be automatically extracted by user interfaces to provide up-to-date information.

1.1.2 Taxonomies

Taxonomies can be used as *enumerated values*, say for listing the possible types of a document, or the language in which a text is written. They have however the extra capability of being hierarchical: you can define subcategories of a main category. For instance, imagine a doctype taxonomy with the following values:

- Published
 - Article
 - * Peer-reviewed
 - * Non peer-reviewed
 - Book

You can tag an article as Peer-reviewed, but in the case you don't know its status, you can use Article. If you search for all the Published documents, you will retrieve all those that have the Published tag, but also those that are articles (either peer-reviewed or not), books,...

pybliographer uses the Pyblio. Attribute. Txo object to represent a logical value in a given taxonomy. Then, a record can be tagged with this Txo

object by adding a Pyblio. Attribute. TxoItem value in the corresponding attribute.

Taxonomies can be declared and pre-filled in a database schema, so that any database created from the schema will at least contain the specified taxonomies.

To see how these taxonomies can be further created and modified, please have a look at the txo member of a Database object, which is an instance of the Pyblio.Store.TxoGroup class.

1.1.3 Result sets

Result sets are used to manipulate an explicit list of records, among all the records kept in a database. They are returned from queries on the database, and can be manipulated by the user. Result sets are somewhat like mathematical sets, as you cannot put duplicate values in them, and they have no default ordering of their elements. You can create result sets via the rs attribute of your database, which is an instance of the Pyblio.Store.ResultSetStore.

A special result set is available as Pyblio.entries, and contains at every time all the records of the database.

1.1.4 Views

We have seen that result sets are **not** ordered. However, in many cases, one needs to provide the records in a specific order. To do so, you can create a *view* on top of a result set. This view is created by calling the view method of the result set, with an order parameter being the description of the sort order you wish to have. The module Pyblio.Sort provides elementary constructs to build such a description.

Once the view is created, modifying the corresponding result set leads to updating the view accordingly.

1.2 Manipulating data

This section describes some simple operations you can perform on some subset of a *pybliographer* database.

1.2.1 Loading and saving

The first thing you need to do is of course *actually having* a database available. The following code does the job:

```
from Pyblio import Store, Schema

schema = Schema.Schema('myschema.sip')
store = Store.get('file')

db = store.dbcreate('mydb.bip', schema)
```

This example relies on the fact that you already have a schema at hand. There are schemas available in the Pyblio.RIP directory. It the starts by reading the schema. The next step is to select the actual physical store which will hold your database. We choose to store it in a simple XML file, whose canonical extension is .bip. The last operation actually creates the database with the specified schema.

Independently of the selected store, it is always possible to *export* a database in the .sip format, by calling the db.xmlwrite(...) method of the database. Such a file can then be reused later on by using store.dbimport(...) instead of store..dbcreate(...).

When you have finished modifying your database, you can call db.save() method to ensure that it is properly saved.

Caution: the bsddb store for instance is updated at every actual modification, not only when you call the save method. Don't rely on it to provide some kind of *rollback* feature.

1.2.2 Using the registry

pybliographer has a mechanism to register known schemas, and specify which import and export filters can properly work with each schema. This mechanism can be used to create our database by asking for a specific schema, as shown below:

```
from Pyblio import Store, Registry

Registry.parse_default()

schema = Registry.getSchema("org.pybliographer/bibtex/0.1")
store = Store.get('file')

db = store.dbcreate('mydb.bip', schema)
```

The registry must be first initialized. Then you can ask for a specific schema, in that case a schema that supports BibTeX databases.

1.2.3 Updating records

The next example will loop over all the records in a database, and add a new author to the list of authors.

We use the itervalues() iterator to loop over all the records stored in the database. Then, we simply insert a new value in the author attribute. The record.add(...) method takes care of creating the attribute if it does not exist yet.

One thing not to forget is to store the record back in the database once the modification is performed. Without this step, you might experience weird behavior where some modifications are not properly kept.

We finish by saving the database.

1.2.4 Sorting

To sort records, you create *views* (see section 1.1.4 on page 4). You can of course create multiple views on top of a single result set. In order to sort the whole database, simply create the view on database.entries instead of a result set. If you want to sort your database by decreasing year and then by author, you can use a view like that:

So, sorting constraints can be arbitrarily chained with the & operator, and each constraint can be either *ascending* (the default), or *descending*. This defines a very simple *Domain Specific Language*, or DSL for short. Such languages also appear in other part of *pybliographer* (searching, citation formatting), as they are a convenient way to describe complex abstraction without having to reinvent a complete environment.

1.2.5 Searching

To search, you call the database.query(...) method. The method takes a query specification as argument, which is constructed with the help of another DSL, similar to the one used for sorting. You have access to a certain number of primitive queries, which are then linked together with the usual boolean operators, as in the following example:

We first get the taxonomy item corresponding to articles, and we then compose the following query: get all the documents that are *not* articles, and which contain the word *lazyness* in any attribute.

1.3 Importing and exporting

TODO

1.4 Citation formatting

TODO

Chapter 2

Extending pybliographer

TODO

2.1 Specializing a parser

TODO