
pycropml Documentation

Release 1.1.0

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1.1 Module description

1.1.1 What is PyCrop2ML?

PyCrop2ML is a free, open-source library for defining and exchanging CropML models. It is used to generate components of modeling and simulation platforms from the CropML specification and allow component exchange between different platform.

It allows to parse the models described in CropML format and automatically generate the equivalent executable Python, java, C#, C++ components and packages usable from existing crop simulation platform.

1.1.2 What is Crop2ML ?

CropML is a XML-(JSON-)based language used to represent different biological processes involved in the crop models.

CropML project aims to provide common framework for defining and exchanging descriptions of crop growth models between crop simulation frameworks.

Objectives

Our main objectives are:

- define a **declarative language** to describe either an atomic model or a composition of models
- add semantic dimension to CropML language by annotation of the models to allow the composition of components of different platforms by using the standards of the semantic web
- develop a library to allow the transformation and the exchange of CropML model between different Crop modelling and simulation platform
- provide a **web repository** enabling registration, search and discovery of CropML Models

- facilitate Agricultural Model Exchange Initiative

Context

Nowadays, we observe the emergence of plant growth models which are built in different platforms. Although standard platform development initiatives are emerged, there is a lack of transparency, reusability, and exchange code between platforms due to the high diversity of modeling languages leading to a lack of benchmarking between the different platforms.

This project aims to gather developers and plant growth modelers to define a standard framework based on the development of declarative language and libraries to improve exchange model components between platforms.

Motivation

Our motivation is to:

- Strengthen the synergy between crop modelers, users and scientific researchers
- Facilitate model intercomparison (at the process level) and model improvement through the exchange of model components (algorithms) and code reuse between platforms/models.
- Bridge the gap between ecophysiologicals who develop models at the process level with crop modelers and model users and facilitate the integration in crop models of new knowledge in plant science (i.e. we are seeking the exchange of knowledge rather than black box models).
- Increase capabilities and responsiveness to stakeholder' needs.
- Propose a solution to the AgMIP community for NexGen crop modeling tools.

Vision

- Facilitate the development of complex models
- Use modular modelling to share knowledge and rapidly develop operational tools.
- Reuse model parts to leverage the expertise of third parties;
- Renovate legacy code.
- Realize the benefit of sharing and complementing different expertise.
- Promote model sharing and reuse

1.1.3 CropML Description

In CropML, a model is either a model unit or a composition of models. A ModelUnit represents the atomic unit of a crop model define by the modelers. A model composition is a model resulting from the composition of two or more atomic model or composite models.

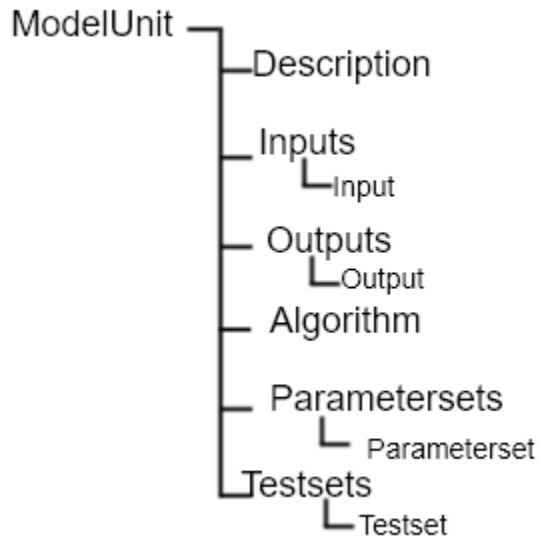
These models have a specific formal definition in CropML.

Formal definition of a Model Unit in CropML

The structure of a Model Unit in CropML MUST be conform to a specific Document Type Definition named [ModelUnit.dtd](#) .

So a Model Unit CropML document is a XML document well-formed and also obeys the rules given in the ModelUnit structure.

This structure MAY be described by the below tree:



Element	Description
ModelUnit	The root of an atomic model in CropML which make the difference from a composite model.
Description	some basic information related to the name of the model, its authors and others elements used to reference it.
Inputs	A list of inputs characterized by their names, initial states, the range of values and others. Its input variables are related to climate, soil and cropping system
Outputs	A list of outputs defining the processes involved, the variables whose dynamics we want to observe.
Algorithm	The description of the behaviour of the model made by the mathematical relationship between the inputs and the outputs with some control structure.
Parametersets	Some sets of parameters which are invariant and used for the simulation of the models.
Testsets	Set of model configuration used to compare estimated and desired outputs .

In the next, we define the major elements of a CropML model unit.

ModelUnit element

An atomic model in CropML is declared with `<<ModelUnit>>` element, the usual root of CropML ModelUnit document.

```
<?xml version="1.0" encoding="utf-8"?>
<!DOCTYPE ModelUnit PUBLIC "-//SIMPLACE/DTD SOL 1.0//EN" "https://raw.
↪githubusercontent.com/AgriculturalModelExchangeInitiative/xml_representation/master/
↪ModelUnit.dtd">
<ModelUnit modelid=" " timestep=" " name=" " version=" ">
    ....
</ModelUnit>
```

This element MUST contain a Description, an Algorithm, Parametersets and Testsets elements and MAY optionally have Inputs and Outputs elements. The restriction of the length of different lists is not imposed.

ModelUnit element MUST have an modelid and name attributes which are used to reference an atomic model. It MUST also contain a timestep attribute to define the temporality of the model and a version attribute for each version of the model.

Description element

This element gives the general information on the model and is composed by a set of character elements. It MUST contain Title, Authors, Institution and abstract elements and MAY optionally contain URI and Reference elements.

```
<ModelUnit modelid=" " timestep=" " name=" " version = " ">
    <Description>
        <Title>title</Title>
        <Authors>authors</Authors>
        <Institution>institution</Institution>
        <URI>uri</URI>
        <Abstract><![CDATA[abstract]]></Abstract>
    </Description>
    ...
</ModelUnit>
```

Inputs elements

The inputs of Model are listed inside an XML element called Inputs within a [dictionary structure](#) composed by their attributes which declarations are optional(default, max, min, parametercategory, variablecategory and uri) or required(name, datatype, description, inputtype, unit) and their corresponding value. *Inputs* element MUST contain one or more *Input* elements.

```
<ModelUnit modelid=" " timestep=" " name=" " version = " ">
    ...
    <Inputs>
        <Input name=" " description=" " parametercategory=" " datatype=" " min=" " max=
↪" " default=" " unit=" " uri=" " inputtype=" "/>
```

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```

    <Input name=" " description=" " parametercategory=" " datatype=" " min=" " max="
↪ " " default=" " unit=" " uri=" " inputtype=" "/>
    ...
  </Inputs>
  ...
</ModelUnit>

```

- The required *datatype* attribute is the type of input value specified in *default* (the default value in the input), *min* (the minimum value in the input) and *max* (the maximum value in the input). It MAY be one type of the set of types used in the existing crop modeling platform.
- The *inputtype* attribute makes it possible to distinguish the variables and the parameters of the model. So it MUST take one of two possible values: *parameter* and *variable*.
- The *parametercategory* attribute defines the category of parameter which is specified by one of the following values: *constant*, *species*, *soil* and *genotypic*.
- The *variablecategory* defines the category of variable depending on whether it is a *state*, a *rate* or an “auxiliary” variable. State variable characterize the behavior of the model and rate variable characterizes the changes in state variables.

Outputs element

The outputs of Model are listed inside an XML element called Outputs within a [dictionary structure](#) composed by their attributes which declarations are:

- optional(variabletype and URI)
- required(name, datatype, description, unit, max and min)
- and their corresponding value

Outputs MUST contain zero or more output elements.

```

<ModelUnit modelid=" " timestep=" " name=" " version =" ">
  ...
  <Outputs>
    <Output name=" " description=" " datatype=" " min=" " max=" " unit=" " uri=" "/
↪ >
    <Output name=" " description=" " datatype=" " min=" " max=" " unit=" " uri=" "/
↪ >
    ...
  </Outputs>
  ...
</ModelUnit>

```

The definition of different attributes is same as Input’s attributes.

Algorithm element

The *Algorithm* element defines the building block of CropML model unit and shows the computational method to determine the outputs from the inputs.

It consists of a set of mathematical equations (relation between inputs), loops and conditional instructions which are well structured in a specific *language*, the algorithm’s attribute.

```

<ModelUnit modelid=" " timestep=" " name=" " version = " ">
...
  <Algorithm language = "><![CDATA[
    ...
    ]]>
  </Algorithm>
...
</ModelUnit>

```

Parametersets element

Parametersets element contains one or more *Parameterset* elements that define the different ways of setting the model. Each *Parameterset* element MUST have *name* and *description* attributes that respectively represents the name and the description of each setting.

The different parameterset MUST contain a list of *Param* elements that show in attribute the name of the parameter (an input which inputtype equals *parameter*) and the fixed value of this one.

```

<ModelUnit modelid=" " timestep=" " name=" " version = " ">
...
  <Parametersets>
    <Parameterset name=" " description=" " uri = ""/>
    <Parameterset name=" " description=" " >
      <Param name=" ">value</Param>
      <Param name=" ">value</Param>
      ...
    </Parameterset>
    ...
  </Parametersets>
...
</ModelUnit>

```

Testsets element

Testsets element contains one or more *Testset* elements that define the different run for evaluating the outputs of the model.

Each *Testset* element MUST have *name*, *description* and *parameterset* attributes that respectively represents the name, the description of each run and the name of the parameterset related to the Testset. This one allow to retrieve the name and the value of different parameters includes in this parameterset.

The different Testset MUST contain a list of *InputValue* and *OutputValue* elements corresponding respectively to the values of inputs used in the run and the values of Outputs that will be asserted.

```

<ModelUnit modelid=" " timestep=" " name=" " version = " ">
...
  <Testsets>

```

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```

<Testset name="" parameterset = "" description="" uri = ""/>
<Testset name="" parameterset = "" description="" >
  <Test name="">
    <InputValue name="">value</InputValue>
    ...
    <OutputValue name="" precision = "">value</OutputValue>
    ...
  </Test>
  ...
</Testset>
...
</Testsets>
...
</ModelUnit>

```

Formal definition of a Composite Model in CropML

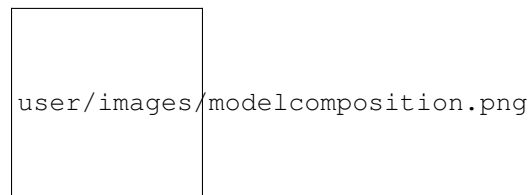
A Composite Model CropML is an assembly of processes which are described by a set of model units or a composition of models. Given a composite model is a model, this one has also inputs, outputs and internal state which describe the orchestration of different independent models composed.

The structure of a Composite Model in CropML MUST conform to a specific Document Type Definition named [ModelComposition.dtd](#) .

The composition is represented as a directed port graph of models:

- Vertices are the different models that form the composition.
- Ports are the inputs and outputs of each model.
- Edges are directed and connect one output port to an input port of another model.

It contains in addition to all Elements of a model unit a Composition Element for the composition of models. This structure MAY be described by the below tree:



In the next, we define the major elements of a CropML model unit.

Inputs element

It MUST contain one or more *input* element which provide a set of independent models entries. If two or more input variables of independent models are the same (same unit, interval, description) a link should be made to one input variable of the composite model.

Outputs element

It MUST contain one or more *output* element which provide a set of independent models outputs or a result of a combination of models .

Composition element

It's a list of *models* elements which contains a list of *links* elements. Link provides the mechanism for mapping inputs declared within one modelUnit to output in another modelUnit, allowing information to be exchanged between the various atomic models in the composite model.

Algorithm element

The implementation differs from the platform:

- Discrete Events Models and Formalisms (RECORD)
- Actor model framework (OpenAlea)
- A sequence of algorithmic instructions witch implement the control flow (BIOMA)

1.1.4 PyCROPML User Guide

Version 1.1.0

Release 1.1.0

Date May 05, 2020

This reference manual details functions, modules, and objects included in OpenAlea.Core, describing what they are and what they do. For a complete reference guide, see `core_reference`.

<p>Warning: This “Reference Guide” is still very much in progress. Many aspects of OpenAlea.Core are not covered.</p>
--

Manual

Note: The following examples assume you have installed the packages and setup your python path correctly.

Installation

```
conda install -c openalea pycropml
```

or

```
python setup.py install
```

Overview of the different classes

1.1.5 src

pycropml package

Subpackages

pycropml.interface package

Submodules

pycropml.interface.design module

pycropml.interface.version module

Module contents

pycropml.transpiler package

Subpackages

pycropml.transpiler.generators package

Submodules

pycropml.transpiler.generators.checkGenerator module

pycropml.transpiler.generators.cppGenerator module

pycropml.transpiler.generators.csharpGenerator module

pycropml.transpiler.generators.docGenerator module

pycropml.transpiler.generators.fortranGenerator module

pycropml.transpiler.generators.javaGenerator module

pycropml.transpiler.generators.openaleaGenerator module

pycropml.transpiler.generators.pythonGenerator module

pycropml.transpiler.generators.rGenerator module

pycropml.transpiler.generators.recordGenerator module

```
<vle_project version="1.1.x" date="2012-Oct-03 13:01:13" author="Eric Casellas">
```

```
  <structures>
```

```
    <model width="2184" height="1280" name="2CV_parcelle" type="coupled">
```

```
      <submodels> <model observables="vueDecision" conditions="condDecFSA" dynam-
        ics="dynDecFSA" debug="false" width="100" height="75" x="132" y="26" name="Decision"
        type="atomic"></model> <model width="100" height="165" x="316" y="127" name="2CV"
        type="coupled"></model>
```

```
    </submodels> <connections> </connections>
```

```
  </model>
```

```
</structures> <dynamics> </dynamics> <experiment name="2CV_parcelle"> </experiment>
```

```
</vle_project>
```

pycropml.transpiler.generators.simplaceGenerator module

pycropml.transpiler.generators.siriusGenerator module

Module contents

pycropml.transpiler.lib package

Module contents

pycropml.transpiler.rules package

Submodules

pycropml.transpiler.rules.cppRules module

pycropml.transpiler.rules.csharpRules module

pycropml.transpiler.rules.fortranRules module

pycropml.transpiler.rules.generalRule module

```
class pycropml.transpiler.rules.generalRule.GeneralRule
  Bases: object
```


” Abstract class of Rules

pycropml.transpiler.rules.javaRules module

pycropml.transpiler.rules.pythonRules module

pycropml.transpiler.rules.rRules module

pycropml.transpiler.rules.sqlRules module

Module contents

Submodules

pycropml.transpiler.Parser module

pycropml.transpiler.api_transform module

pycropml.transpiler.ast_transform module

pycropml.transpiler.builtin_typed_api module

pycropml.transpiler.checkingModel module

class `pycropml.transpiler.checkingModel.Checking`

Module used to check units validity in model equation based on model xml files. This checking can also use for python code with metadata

pycropml.transpiler.codeGenerator module

pycropml.transpiler.env module

class `pycropml.transpiler.env.Env` (*values=None, parent=None*)

child_env (*values=None*)

pycropml.transpiler.errors module

exception `pycropml.transpiler.errors.PseudoCythonNotTranslatableError` (*message, suggestions=None, right=None, wrong=None*)

Bases: `pycropml.transpiler.errors.PseudoError`

exception `pycropml.transpiler.errors.PseudoCythonTypeCheckError` (*message*,
suggestions=None,
right=None,
wrong=None)

Bases: `pycropml.transpiler.errors.PseudoError`

exception `pycropml.transpiler.errors.PseudoError` (*message*, *suggestions=None*,
right=None, *wrong=None*)

Bases: `exceptions.Exception`

`pycropml.transpiler.errors.beautiful_error` (*exception*)

`pycropml.transpiler.errors.cant_infer_error` (*name*, *line*)

`pycropml.transpiler.errors.tab_aware` (*location*, *code*)

if tabs in beginning of code, add tabs for them, otherwise spaces

`pycropml.transpiler.errors.translation_error` (*data*, *location=None*, *code=None*,
wrong_type=None, ***options*)

`pycropml.transpiler.errors.type_check_error` (*data*, *location=None*, *code=None*,
wrong_type=None, ***options*)

pycropml.transpiler.helpers module

`pycropml.transpiler.helpers.prepare_table` (*types*, *original_methods=None*)

`pycropml.transpiler.helpers.safe_serialize_type` (*l*)
serialize only with letters, numbers and _

`pycropml.transpiler.helpers.serialize_type` (*l*)

pycropml.transpiler.interface module

pycropml.transpiler.main module

pycropml.transpiler.nodeVisitor module

pycropml.transpiler.pseudo_tree module

pycropml.transpiler.version module

Maintain version for this package. Do not edit this file, use 'version' section of config.

`pycropml.transpiler.version.MAJOR = 0`
(int) Version major component.

`pycropml.transpiler.version.MINOR = 0`
(int) Version minor component.

`pycropml.transpiler.version.POST = 2`
(int) Version post or bugfix component.

Module contents

Submodules

pycropml.algorithm module

```
class pycropml.algorithm.Algorithm (language, development, platform, filename=None)
    Bases: object
```

pycropml.checking module

```
class pycropml.checking.Test (name)
    Bases: pycropml.checking.Testset
```

```
class pycropml.checking.Testset (name, parameterset, description, uri=None)
    Bases: object
```

Test

```
pycropml.checking.testset (model, name, kwds)
```

pycropml.code2nbk module

pycropml.composition module

pycropml.cyaml module

pycropml.description module

```
class pycropml.description.Description
    Bases: object
```

Model Unit Description.

A description is defined by:

- Title
- Author
- Institution
- Reference
- Abstract

pycropml.error module

Created on Wed Apr 10 17:01:34 2019

@author: midingoy

```
exception pycropml.error.Error (message)
    Bases: exceptions.Exception
```

pycropml.formater_f90 module

pycropml.formater_f90.**formater** (*code*)
pycropml.formater_f90.**formaterNext** (*line*)

pycropml.function module

class pycropml.function.**Function** (*name, language, filename, type, description*)
Bases: `object`

pycropml.initialization module

class pycropml.initialization.**Initialization** (*name, language, filename*)
Bases: `object`
Function

pycropml.inout module

class pycropml.inout.**Input** (*kwds*)
Bases: `pycropml.inout.InputOutput`

class pycropml.inout.**InputOutput** (*kwds*)
Bases: `object`

class pycropml.inout.**Output** (*kwds*)
Bases: `pycropml.inout.InputOutput`

pycropml.main module

pycropml.model module

pycropml.modelunit module

Model Description and Model Unit.

class pycropml.modelunit.**ModelDefinition** (*kwds*)
Bases: `object`

class pycropml.modelunit.**ModelUnit** (*kwds*)
Bases: `pycropml.modelunit.ModelDefinition`
Formal description of a Model Unit.

add_description (*description*)
TODO

pycropml.package module

pycropml.parameterset module

class pycropml.parameterset.**Parameterset** (*name, description, uri=None*)

Bases: `object`

Parameter set

pycropml.parameterset.**parameterset** (*model, name, kwds*)

pycropml.pparse module

pycropml.render_R module

pycropml.render_cpp module

pycropml.render_csharp module

pycropml.render_cyml module

pycropml.render_fortran module

pycropml.render_java module

pycropml.render_notebook module

pycropml.render_notebook_csharp module

pycropml.render_notebook_java module

pycropml.render_python module

pycropml.test_generator module

pycropml.topology module

pycropml.version module

Maintain version for this package. Do not edit this file, use 'version' section of config.

pycropml.version.**MAJOR** = 1

(int) Version major component.

pycropml.version.**MINOR** = 1

(int) Version minor component.

pycropml.version.**POST** = 0

(int) Version post or bugfix component.

pycropml.wf2xml module

pycropml.writeTest module

pycropml.writeTest_f90 module

pycropml.xml2wf module

Module contents

1.1.6 Usecases

1.1.7 Licence

PyCropML is released under a MIT License.

1.1.8 Usecases

1.1.9 Glossary

Terminology

Model Simplified representation of the crop system within specific objectives.

Overview

1.2 Documentation

- A [PDF](#) version of **lcorel** documentation is available.

1.3 History

1.3.1 creation (2018-01-18)

- First release on PyPI.

1.4 Indices and tables

1.5 History

1.5.1 creation (2018-01-18)

- First release on PyPI.

1.6 License

PyCropML is released under a MIT License.

1.7 Welcome to CropML's documentation!

Contents:

1.7.1 Contributing Guide

This is a wiki for anything related to the contributing on [\[\[Crop2ML|https://github.com/AgriculturalModelExchangeInitiative/Crop2ML\]\]](https://github.com/AgriculturalModelExchangeInitiative/Crop2ML) which is a project of the Agricultural Model Exchange Initiative. For more information about this project, please visit CropML documentation [\[\[Crop2ML|https://cropmlformat.readthedocs.io/en/latest/?badge=latest#documentation\]\]](https://cropmlformat.readthedocs.io/en/latest/?badge=latest#documentation):

1.7.2 Quick Links

- [\[\[Project Git Repository|https://github.com/cython/cython|Git Repository\]\]](https://github.com/cython/cython) (and [\[\[Change Log|https://github.com/cython/cython/blob/master/CHANGES.rst|Change Log\]\]](https://github.com/cython/cython/blob/master/CHANGES.rst))
- [\[\[Differences between Cython and Pyrex|https://cython.readthedocs.io/en/latest/src/userguide/pyrex_differences.html|Differences between Cython and Pyrex\]\]](https://cython.readthedocs.io/en/latest/src/userguide/pyrex_differences.html)
- [\[\[Unsupported Python features|https://cython.readthedocs.io/en/latest/src/userguide/limitations.html|Unsupported Python features\]\]](https://cython.readthedocs.io/en/latest/src/userguide/limitations.html) (aka TODO list)
- [\[\[Hacker-Guide: How to work on the Cython compiler itself|HackerGuide| Hacker-Guide: How to work on the Cython compiler itself\]\]](#)
- [\[\[Enhancement proposals|enhancements| Enhancement proposals\]\]](#) (CEPs)
- [\[\[Projects using Cython|projects| Projects using Cython\]\]](#)
- [\[\[Comparison with SWIG|SWIG| Comparison with SWIG\]\]](#)
- [\[\[Automatic .pxd/.pyx generation|AutoPxd|Automatic .pxd/.pyx generation\]\]](#) from C or C++ header files.

Cython Installers

- [\[\[PyPi|http://pypi.python.org/pypi/Cython/|PyPi\]\]](http://pypi.python.org/pypi/Cython/) via `easy_install` or `pip`
- [\[\[Gentoo Ebuild|http://packages.gentoo.org/package/dev-python/cython|Gentoo Ebuild\]\]](http://packages.gentoo.org/package/dev-python/cython)
- [\[\[Debian package|http://packages.debian.org/sid/cython|Debian package\]\]](http://packages.debian.org/sid/cython) (not always up to date)
- [\[\[Installing Cython on Windows|InstallingOnWindows| Installing Cython on Windows\]\]](#)

Tips and Tricks

- [Getting started](http://docs.cython.org/src/quickstart/index.html)
- [Using early binding techniques to improve speed](http://docs.cython.org/en/latest/src/userguide/early_binding_for_speed.html)
- [Writing Cython programs in pure Python](http://docs.cython.org/src/tutorial/pure.html)
- [Helpful notes for wrapping C++ APIs](http://docs.cython.org/en/latest/src/userguide/wrapping_CPlusPlus.html)
- [Discussion of all the options how to wrap C/C++ code to Python](#)
- [WritingFastPyrexCode](http://www.sagemath.org:9001/WritingFastPyrexCode/)
- [Successful creation of a hierarchy of modules in a package](#)
- [One method for source-level debugging](http://docs.cython.org/en/latest/src/userguide/debugging.html)
- [Dynamic Memory Allocation \(malloc, realloc, free\)](http://docs.cython.org/en/latest/src/tutorial/memory_allocation.html)
- [Profiling](#)
- [Building a Windows Installer](#)
- [Embedding Python](#) to create standalone Cython programs.
- [List Subclass Example](#) Adding mathematical operations to subclassed built-in list.
- Working with Numpy
 - [Tutorial for NumPy users](http://docs.cython.org/en/latest/src/userguide/numpy_tutorial.html)
 - [Accessing a Numpy pointer for passing to C](http://docs.cython.org/en/latest/src/userguide/memoryviews.html#pass-data-from-a-c-function-via-pointer)

1.7.3 People

[Stefan Behnel](http://scoder.behnel.de/), [Robert Bradshaw](http://www.math.washington.edu/~robertwb/), [Dag Seljebotn](http://heim.ifi.uio.no/dagss/), Lisandro Dalcin.

1.7.4 Mailing Lists

Our development mailing list is [cython-devel](http://mail.python.org/mailman/listinfo/cython-devel) and user mailing list at <http://groups.google.com/group/cython-users>.

In the past we also used a [Google group](http://groups.google.com/group/cython) and a list at [BerliOS Developer](https://lists.berlios.de/mailman/listinfo/cython-dev). You can still read [the archives at Gmane](http://blog.gmane.org/gmane.comp.python.cython.devel).

1.7.5 Project Goals

- Fully supported easy-to-use test suite, including the normal CPython test suite.
- Easy installation and usage.
- Rich, accessible documentation. Make sure the examples are plenty and can be automatically tested.
- Make Cython part of the standard distribution of Python (like ctypes).
- Compile all Python code except for possibly some obvious exclusions, which will be worked out by developers.
- Very fast when the user explicitly declares types (but we're not going to make promises with type inference). Precise benchmarks.
- Mitigate or eliminate the need for users to invoke the Python/C API directly without sacrificing performance.

1.7.6 Documentation

- See <http://docs.cython.org/>.
- Official Pyrex [\[Language Overview\]](http://www.cosc.canterbury.ac.nz/greg.ewing/python/Pyrex/version/Doc/LanguageOverview/) (note the [\[changes\]](http://hg.cython.org/cython/changes) though).
- [\[\[Extension Types\]](http://www.cosc.canterbury.ac.nz/greg.ewing/python/Pyrex/version/Doc/Manual/extension_types.html)
- [\[\[Sharing Declarations Between Pyrex Modules\]](http://www.cosc.canterbury.ac.nz/greg.ewing/python/Pyrex/version/Doc/Manual/declarations_between_modules.html)
- [\[\[FAQ\]](http://www.cosc.canterbury.ac.nz/greg.ewing/python/Pyrex/version/Doc/FAQ.html)
- [\[\[Quick Guide to Pyrex\]](http://ldots.org/pyrex-guide/) from Michael Jason-Smith.
- CategoryCythonDoc lists pages that are related to Cython documentation.
- [\[\[Pure Python mode\]](#)
- SAGE Days 4 talk highlighting some of the [\[\[differences between Pyrex and SageX\]](http://cython.org/talks/SageX.pdf) (the predecessor of Cython).

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1.8 Indices and tables

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