Computational Representation of Metabolic Networks

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Monday L2



This is *not* a programming course.

- No assumption of previous programming experience.
- Basic usage of a language as a tool no technical details.
- Fundamental mathematical concepts as relevant to network analysis.

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Why use a language for modelling?

- Flexibility define what you want to do.
- Repeatability apply the actions same actions to many models.
- Reliability errors are less likely to go unnoticed, code can be analysed.
- Abstract concepts or large data-sets can't always be visualised.

Why Python?

- Easy to learn.
- Forgiving.
- Flexible.
- Interactive.
- High level lets you concentrate on the problem, not the computer.
- Wide range of existing software and libraries.
- Free (As in Beer and Freedom).

What's in a program?

- A collection of data representing some real-world entity.
- A set of actions that can be performed on that data.
- Some means by which the user can specify which actions to perform.

In Python (and other languages) the data and actions are both defined by *Objects* (aka *types*).

An object is a computational representation of something that exists in the real world.

The type (or class) of an object is defined by its properties.

- Cats:
 - Fur colour,
 - Length of whiskers.

- Proteins:
 - AA sequence,
 - Iso-electric point.

The type of an object defines what it can do, e.g.

- Cats can:
 - Sleep
 - Go miaow

- Proteins can:
 - Precipitate
 - Catalyse a reaction

The type of an object defines what can be done to it, e.g.

- Cats can be:
 - Stroked
 - Chased

- Proteins can be:
 - Crystallised
 - Digested

The type of an object defines its interactions with other objects.

- Cats can:
 - Reproduce with other cats
 - Digest a protein

- Proteins can:
 - Bind to other proteins
 - Poison a cat

Types and Classes - Summary

The concept of objects that have known properties, can be acted upon and can interact with other objects is central.

Objects are abstract representations of their real-world equivalents (including proteins and cats).

These can be combined to represent data of arbitrary size and structure, including metabolic models and databases.

Types and Classes in Python

Python defines a number of built-in fundamental classes, which can be used to create more complex representations of real-world entities.

Simple Python types - strings

Strings are sequences of characters, often used for names and simple descriptions, but could also represent an entire document.

Create an object called text of type string:

```
>>> text = "My_cat_plays_with_string"
```

It has properties, e.g. length:

```
>>> len(text)
24
```

It can be acted upon, e.g. printed:

```
>>> print text
My cat plays with string
```

It can interact with other objects:

```
print text + "_and_mice"
My cat plays with string and mice
```



Simple Python types - numbers

Numbers come in two main types: integer and float.

They behave mainly as expected

But see practical.

Compound types

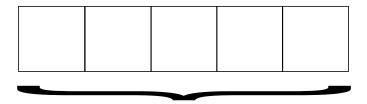
Compound types allow arbitrary collections of objects to be held together. The two major compound types are:

• Lists: Items are stored in order and are referenced (indexed) by an integer.

 Dictionaries: Items have no implicit order and can be indexed by a variety of types (commonly strings)

Lists hold collections of objects in order:

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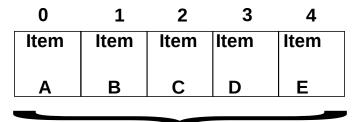


Lists hold collections of objects in order:

Item	Item	Item	Item	Item
Α	В	С	D	E

Lists hold collections of objects in order:

Index



Lists hold collections of objects in order:

Index

-5

-4

-3

-2

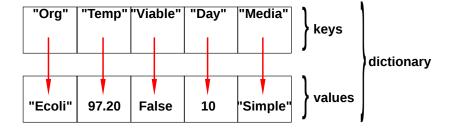
-1

Item	Item	Item	Item	Item
Α	В	С	D	E

Example:

```
>>> ExampleList = ["A","B","C","D","E"]
>>> ExampleList[0]
'A'
>>> ExampleList[1]
'B'
>>> ExampleList[4]
'E'
>>> ExampleList[-1]
'E'
>>> ExampleList[-5]
'A'
```

Similar in concept to lists, but items held as *key/value* pairs, are not ordered, and key types are not restricted to integer.



Creating a dictionary:

```
>>> ExampleDict={"Org":"Ecoli",
        "Temp":97.2,
        "Viable":False,
        "Day":10,
        "Media":"Simple"
}
>>> print ExampleDict
{'Media': 'Simple',
        'Org': 'Ecoli',
        'Viable': False,
        'Temp':97.2,
        'Day': 10
}
```

Changing existing values in a dictionary:

```
>>> ExampleDict["Media"] = "Complex"
>>> ExampleDict["Temp"] = 30
>>> ExampleDict["Viable"] = True
>>> print ExampleDict
{'Media': 'Complex',
  'Org': 'Ecoli',
  'Viable': True,
  'Temp': 30,
  'Day': 10
}
```

Adding new key/value pairs to a dictionary:

```
>>> ExampleDict["Recorded_by"] = "Mark"
>>> print ExampleDict
{'Media': 'Complex',
  'Org': 'Ecoli',
  'Viable': True,
  'Temp': 30,
  'Recorded_by': 'Mark',
  'Day': 10
}
```

More about objects - composition

Objects are collections (i.e. are composed) of Members

- Members contain:
 - Data or
 - Actions (Method or Function members).

- Members are accessed using "dot" notation see next slide.
- Data members can also be objects.

Getting information about objects

The members of an object can be identified using the built-in **dir**() function:

and are accessed using dot notation:

```
>>> ExampleList.reverse()
>>> print ExampleList
['D', 'E', 'A', 'B', 'C']
>>> ExampleList.sort()
>>> print ExampleList
['A', 'B', 'C', 'D', 'E']
```

Here's one I made earlier - Modules

Modules are used to store pre-written python code for later re-use. They must be *imported* in order to be used:

```
>>> import math
>>> dir (math)
[...,
'pi',...
'sqrt'...]
```

Modules can then be accessed with dot notation:

```
>>> print math.pi
3.14159265359
>>> print math.sqrt(2)
1.41421356237
```

Here's one I made earlier - Modules

Alternatively selection of items can be imported instead:

```
>>> from math import pi, \sin >>> print \sin(pi/4)
0.707106781187
```

For loops (other loops are available)

We frequently wish to act upon each item in a list in turn. The **for** loop provides a convenient way of doing this.

```
In general:
    for Item in MyList :
        # do something

Example:
>>> for letter in ExampleList:
    print letter
C
B
A
E
D
```

For loops (other loops are available)

For loops provide a convenient way of scanning across a range of numbers, using, for example the built in **range** function:

```
>>> for x in range(10):
    print x, x**2, x**3
0 0 0
1 1 1
2 4 8
3 9 27
4 16 64
5 25 125
6 36 216
7 49 343
8 64 512
9 81 729
```

End of Part 1

We have now covered enough fundamentals to think about how to use it for modelling.

What do we want to represent and act upon?

What is ScrumPy?

A collection of modules (a **package**) providing the ability to define and analyse models.

Everything revolves around the use of model objects:

```
>>> m = ScrumPy.Model("FileName.spy")
```

Where "FileName.spy" is the name of file describing the model.

The ".spy" extension is conventional and convenient, but not mandatory.

and "m" is the model object. In these talks, "m" will always be used to denote the model.

Model Definition

In ScrumPy, a model is defined by one or more text files, defining:

Comments Ignored by ScrumPy, but are useful to the human reader.

Directives Not part of the model *per se*, but specify how the model is to be read.

Reactions Define the metabolic network.

Initialisations Define parameter values and initial metabolite concentrations (only in kinetic models)

Model Definition

```
# comment, everything from #
# to the end of the line is ignored
Structural()
# a Directive. Do not do any kinetic processing.
Rubisco:
                                    # a reaction name
    x CO2 + RuBP ch -> 2 PGA ch # stoichiometry
                                    # default kinetic
PGK:
    PGA_ch + ATP_ch <> BPGA_ch + ADP_ch
G3Pdh:
    BPGA ch + x NADPH ch + x Proton ch <>
                         x NADP_ch + GAP_ch + Pi_ch
```

Model Definition - identifiers

Identifiers = Names

Either:

Any sequence of alphanumeric characters and _ (underscore), not starting with a number e.g. Valid:

Fructose6_Phosphate AlphaAnaline

Invalid:

2,3—bisphosphoglycerate TRANS-23-DEHYDROADIPYL-COA

Or:

Any quoted (") sequence of characters.

```
"Saturated-Fatty-Acyl-CoA"
```

"3-oxo-cis-vaccenoyl-ACPs"

Accessed as m.sm (internal) and m.smx (external):

	Ru5Pk	Aldo2	TPT_DHAP	Light_react	TKL
RuBP_ch	1/1	0/1	0/1	0/1	0/1
ATP_ch	-1/1	0/1	0/1	1/1	0/1
ADP_ch	1/1	0/1	0/1	-1/1	0/1
GAP_ch	0/1	0/1	0/1	0/1	-1/1
Pi_ch	0/1	0/1	1/1	-1/1	0/1
DHAP_ch	0/1	-1/1	-1/1	0/1	0/1
F6P_ch	0/1	0/1	0/1	0/1	-1/1
E4P_ch	0/1	-1/1	0/1	0/1	1/1
X5P_ch	0/1	0/1	0/1	0/1	1/1
SBP_ch	0/1	1/1	0/1	0/1	0/1
Ru5P_ch	-1/1	0/1	0/1	0/1	0/1

By default values in the stoichiometry matrices are rational numbers (ie fractions).

They can are represented as (e.g) 1/2 or mpq(1,2).

This can be changed with the ElType() directive (earlier slide).

For large (genome scale) models it is more common to use *real* numbers (EIType(**float**))

Stoichiometry matrices behave as a list of rows:

```
>>> print m.sm[0] [mpq(1,1), mpq(0,1), mpq(0,1), mpq(0,1), ...]
```

Or as a dictionary of rows:

```
>>> print m.sm["RuBP_ch"]
[mpq(1,1), mpq(0,1), mpq(0,1), mpq(0,1), ...]
```

Individual elements can be accessed as matrix[row,col]:

```
>>> print m.sm[0,0]
1/1
>>> print m.sm["RuBP_ch","Ru5Pk"]
1/1
```

The null-space is obtained the matrix.NullSpace() method:

```
>>> k = m.sm.NullSpace()
>>> print k
```

	c_0	c_1	c_2	c_3	c_4
Ru5Pk	0/1	0/1	0/1	0/1	-3/1
Aldo2	0/1	0/1	0/1	0/1	-1/1
TPT_DHAP	0/1	2/1	1/1	1/1	-1/1
Light_react	-1/1	-1/1	0/1	1/1	-9/1
TKL	0/1	0/1	0/1	0/1	-1/1
G3Pdh	0/1	0/1	0/1	1/1	-6/1
PGK	0/1	0/1	0/1	1/1	-6/1
TPI	0/1	1/1	1/1	1/1	-3/1
TKL2	0/1	0/1	0/1	0/1	-1/1

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And now

We have covered enough to start the practical.