# **CNApy Users Guide**

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#### **Abstract**

## Introduction

This is the user manual of CNApy. CNApy is a graphical interface for the modelling and analysis of metabolic networks on the basis of constraint-based (stoichiometric) modeling approaches. It allows

- the import/export of SBML models
- creating COBRApy/CNA models
- linking a graphical representation to the model data
- convenient exploration and editing of the model
- model analysis with standard and advanced constraint-based methods
- and saving everything as a CNApy \*.cna project

The methods provided for model analysis (some of them are part of CNApy but most are functions from CNA and COBRApy) include:

- Flux balance analysis
- · Parsimonious flux balance analysis
- Flux variability analysis
- · Minimal cut sets
- · Elementary modes
- Phase plane analysis
- Yield optimization

CNApy is available at https://github.com/cnapy-org/CNApy under the <a href="Apache-2.0 License">Apache-2.0 License</a>.

We appreciate any comments or suggestions for improvements and we are greatly interested in your feedback which you can give at our <u>User Forum</u>.

For feature requests and bug reports please use our <u>Issue tracker</u>

Thank you for using CNApy!

# Installation

The easiest way to install CNApy is using conda. First install conda and then:

Create a conda environment with all dependencies

```
conda create -n cnapy-1.0.0 -c conda-forge -c cnapy cnapy=1.0.0
```

Activate the cnapy conda environment

```
conda activate cnapy-1.0.0
```

Run CNApy

cnapy

On windows you may also use the graphical installer.

# **Configuration**

When we start CNApy for the first time we are greeted with a dialog like this.

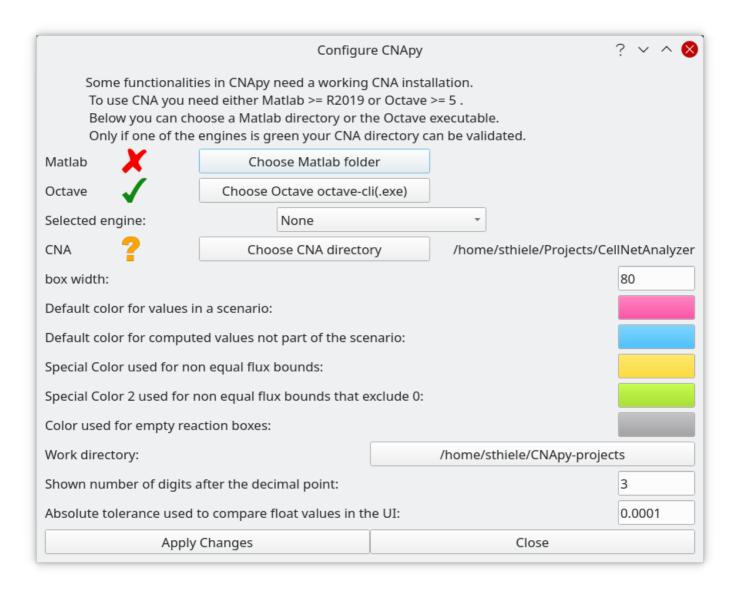


Figure 1: CNApy Configuration dialog.

With this dialog you can configure which Matlab/Octave installation CNApy should use.

The minimal cut set computation in CNApy uses functions that are provided by CellNetAnalyzer. To be able to use these functions you have to provide CNApy with either a path to a Matlab installation >R2019 or the path to an Octave executable >4, and of course with a path to a recent CellNetAnalyzer installation. You can do this by clicking these buttons (1). If you change the settings CNApy performs some basic tests to make sure everything is working. If all checks are successful green check marks are shown, if a check fails a red cross is shown.

If no check can be performed, a yellow question mark is shown. For example, the check of the CNA directory needs a working Matlab or Octave installation.

You can also configure which colors CNApy should use to highlight reactions on the map or in the reaction list.

# **User interface overview**

This section gives an introduction to the CNApy UI and its components and functions.

When we have finished our first configuration we are greeted with a window like this.

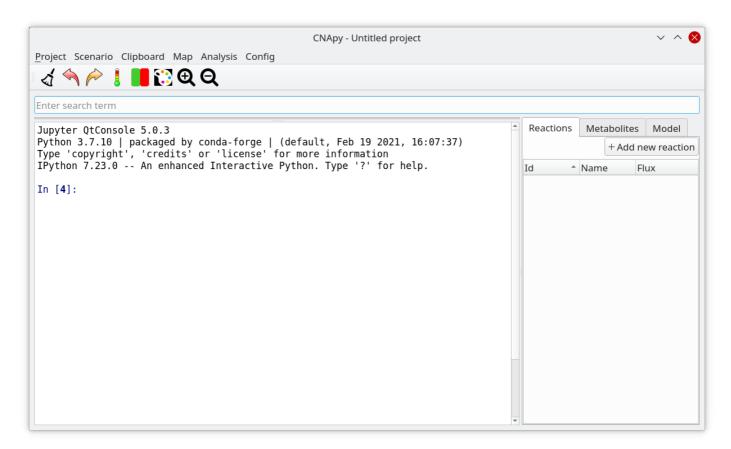


Figure 2: CNApy with an empty project.

This is an empty project on the right hand side we see the empty lists of reactions and metabolites. On the left we see the embedded Jupyter Console where one can interact programmatically with the model and UI. We can create a new project by importing SBML models, editing the reactions and adding graphical maps. We can also load one of the projects included in our projects repository.

Let's go to Project in our menubar and open the ECC2comp.cna project.



Figure 3: CNApy with the ECC2comp project.

In this picture we see CNApy with the open ECC2comp project. On the right hand side (1) we see the populated reactions and metabolites lists with the color coded current values and corresponding details for the selected reaction/metabolite. The reactions list contains buttons that lets us add/delete reactions to/from the model. The console (2) now shows the output of some computations, and above the console we have a map view (3) with a graphical representation of our network. On top (4) we have the menu bar which gives us access to the various functionalities of CNApy and a Toolbar for quick access to often used functions.

We can add new maps via the Map menu, and drag reactions from the reaction list onto the desired position on the map.

The rest of this document is a full list of formatting elements/features supported by Manubot. Compare the input ( .md files in the /content directory) to the output you see below.

# **Basic formatting**

#### Centered text

Right-aligned text

Italic text

Combined italics and bold

#### Strikethrough

- 1. Ordered list item
- 2. Ordered list item
  - a. Sub-item
  - b. Sub-item
    - i. Sub-sub-item
- 3. Ordered list item
  - a. Sub-item
- List item
- · List item
- · List item

subscript: H<sub>2</sub>O is a liquid

superscript: 2<sup>10</sup> is 1024.

unicode superscripts<sup>0123456789</sup>

#### unicode subscripts<sub>0123456789</sub>

A long paragraph of text. Lorem ipsum dolor sit amet, consectetur adipiscing elit, sed do eiusmod tempor incididunt ut labore et dolore magna aliqua. Ut enim ad minim veniam, quis nostrud exercitation ullamco laboris nisi ut aliquip ex ea commodo consequat. Duis aute irure dolor in reprehenderit in voluptate velit esse cillum dolore eu fugiat nulla pariatur. Excepteur sint occaecat cupidatat non proident, sunt in culpa qui officia deserunt mollit anim id est laborum.

Putting each sentence on its own line has numerous benefits with regard to <u>editing</u> and <u>version</u> <u>control</u>.

Line break without starting a new paragraph by putting two spaces at end of line.

# **Document organization**

Document section headings:

# **Heading 1**

# **Heading 2**

**Heading 3** 

Heading 4

Heading 5

Heading 6



Horizontal rule:

Heading 1's are recommended to be reserved for the title of the manuscript.

Heading 2's are recommended for broad sections such as Abstract, Methods, Conclusion, etc.

Heading 3's and Heading 4's are recommended for sub-sections.

### Links

Bare URL link: <a href="https://manubot.org">https://manubot.org</a>

<u>Long link with lots of words and stuff and junk and bleep and blah and stuff and other stuff and more stuff yeah</u>

Link with text

Link with hover text

Link by reference

## **Citations**

Citation by DOI [1].

Citation by PubMed Central ID [2].

Citation by PubMed ID [3].

Citation by Wikidata ID [4].

Citation by ISBN [5].

Citation by URL [6].

Citation by alias [7].

Multiple citations can be put inside the same set of brackets [1,5,7]. Manubot plugins provide easier, more convenient visualization of and navigation between citations [2,3,7,8].

Citation tags (i.e. aliases) can be defined in their own paragraphs using Markdown's reference link syntax:

# Referencing figures, tables, equations

Figure 4

Figure 5

```
Figure 6

Figure 7

Table 1

Equation 1

Equation 2
```

# **Quotes and code**

Quoted text

Quoted block of text

Two roads diverged in a wood, and I—I took the one less traveled by, And that has made all the difference.

Code in the middle of normal text, aka inline code.

Code block with Python syntax highlighting:

```
from manubot.cite.doi import expand_short_doi

def test_expand_short_doi():
    doi = expand_short_doi("10/c3bp")
    # a string too long to fit within page:
    assert doi == "10.25313/2524-2695-2018-3-vliyanie-enhansera-copia-i-
        insulyatora-gypsy-na-sintez-ernk-modifikatsii-hromatina-i-
        svyazyvanie-insulyatornyh-belkov-vtransfetsirovannyh-geneticheskih-
        konstruktsiyah"
```

Code block with no syntax highlighting:

```
Exporting HTML manuscript
Exporting DOCX manuscript
Exporting PDF manuscript
```

# **Figures**



**Figure 4:** A square image at actual size and with a bottom caption. Loaded from the latest version of image on GitHub.



**Figure 5: An image too wide to fit within page at full size.** Loaded from a specific (hashed) version of the image on GitHub.



Figure 6: A tall image with a specified height. Loaded from a specific (hashed) version of the image on GitHub.



**Figure 7:** A vector .svg image loaded from GitHub. The parameter sanitize=true is necessary to properly load SVGs hosted via GitHub URLs. White background specified to serve as a backdrop for transparent sections of the image.

# **Tables**

**Table 1:** A table with a top caption and specified relative column widths.

Bowling Scores	Jane	John	Alice	Bob
Game 1	150	187	210	105
Game 2	98	202	197	102
Game 3	123	180	238	134

**Table 2:** A table too wide to fit within page.

	Digits 1-33	Digits 34-66	Digits 67-99	Ref.
pi	3.14159265358979323 846264338327950	28841971693993751 0582097494459230	78164062862089986 2803482534211706	piday.org
е	2.71828182845904523 536028747135266	24977572470936999 5957496696762772	40766303535475945 7138217852516642	nasa.gov

 Table 3: A table with merged cells using the attributes plugin.

	Colors		
Size	Text Color	Background Color	
big	blue	orange	
small	black	white	

# **Equations**

A LaTeX equation:

$$\int_0^\infty e^{-x^2} dx = \frac{\sqrt{\pi}}{2} \tag{1}$$

An equation too long to fit within page:

$$x = a + b + c + d + e + f + g + h + i + j + k + l + m + n + o + p + q + r + s + t + u + v + w + x + y + z + 1 + 2 + 3 + 4 + 5 + 6 + 7 + 8 + 9$$
(2)

# **Special**

▲ WARNING The following features are only supported and intended for .html and .pdf exports. Journals are not likely to support them, and they may not display correctly when converted to other formats such as .docx .

LINK STYLED AS A BUTTON

Adding arbitrary HTML attributes to an element using Pandoc's attribute syntax:

Manubot Manubot Manubot Manubot Manubot. Manubot Manubot Manubot Manubot. Manubot Manubot Manubot. Manubot Manubot. Manubot.

Adding arbitrary HTML attributes to an element with the Manubot attributes plugin (more flexible than Pandoc's method in terms of which elements you can add attributes to):

Manubot Manubo

Available background colors for text, images, code, banners, etc:

white lightgrey grey darkgrey black lightred lightyellow lightgreen lightblue lightpurple red orange yellow green blue purple

Using the Font Awesome icon set:



Light Grey Banner
useful for general information - manubot.org

# **1** Blue Banner

useful for important information - manubot.org

**♦ Light Red Banner** useful for *warnings* - <u>manubot.org</u>

# References

#### 1. Sci-Hub provides access to nearly all scholarly literature

Daniel S Himmelstein, Ariel Rodriguez Romero, Jacob G Levernier, Thomas Anthony Munro, Stephen Reid McLaughlin, Bastian Greshake Tzovaras, Casey S Greene *eLife* (2018-03-01) <a href="https://doi.org/ckcj">https://doi.org/ckcj</a>

DOI: 10.7554/elife.32822 · PMID: 29424689 · PMCID: PMC5832410

### 2. Reproducibility of computational workflows is automated using continuous analysis

Brett K Beaulieu-Jones, Casey S Greene

Nature biotechnology (2017-04) <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6103790/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6103790/</a>

DOI: <u>10.1038/nbt.3780</u> · PMID: <u>28288103</u> · PMCID: <u>PMC6103790</u>

#### 3. **Bitcoin for the biological literature.**

Douglas Heaven

Nature (2019-02) https://www.ncbi.nlm.nih.gov/pubmed/30718888

DOI: 10.1038/d41586-019-00447-9 · PMID: 30718888

# 4. Plan S: Accelerating the transition to full and immediate Open Access to scientific publications

cOAlition S

(2018-09-04) https://www.wikidata.org/wiki/Q56458321

#### 5. **Open access**

Peter Suber

MIT Press (2012)

ISBN: 9780262517638

#### 6. Open collaborative writing with Manubot

Daniel S Himmelstein, Vincent Rubinetti, David R Slochower, Dongbo Hu, Venkat S Malladi, Casey S Greene, Anthony Gitter

Manubot (2020-05-25) https://greenelab.github.io/meta-review/

#### 7. Opportunities and obstacles for deep learning in biology and medicine

Travers Ching, Daniel S Himmelstein, Brett K Beaulieu-Jones, Alexandr A Kalinin, Brian T Do, Gregory P Way, Enrico Ferrero, Paul-Michael Agapow, Michael Zietz, Michael M Hoffman, ... Casey S Greene

Journal of The Royal Society Interface (2018-04-04) https://doi.org/gddkhn

DOI: <u>10.1098/rsif.2017.0387</u> · PMID: <u>29618526</u> · PMCID: <u>PMC5938574</u>

#### 8. Open collaborative writing with Manubot

Daniel S Himmelstein, Vincent Rubinetti, David R Slochower, Dongbo Hu, Venkat S Malladi, Casey S Greene, Anthony Gitter

PLOS Computational Biology (2019-06-24) https://doi.org/c7np

DOI: 10.1371/journal.pcbi.1007128 · PMID: 31233491 · PMCID: PMC6611653