

BIO334 – Practical Bioinformatics

Wagner's module



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Day	Date	Time morning	Professor	Time
Thu	09.05.19	09:00 - 12:00	von Mering	13:
Fri	10.05.19	09:00 - 12:00	von Mering	13:
Tue	14.05.19			13:
Wed	15.05.19	09:00 - 12:00	Shimizu	13:
Thu	16.05.19	09:00 - 12:00	Shimizu	13:
Fri	17.05.19	09:00 - 12:00	Shimizu	13:
Tue	21.05.19			13:
Wed	22.05.19	09:00 - 12:00	Wagner	13:
Thu	23.05.19	09:00 - 12:00	Wagner	13:

Metabolic network analysis

With:

- Python (version 2.7 and later ones)
 OLAT: Python_trainer

Metabolic network analysis

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- Python (version 2.7 and later ones)

OLAT: Python_trainer_2016

- Cobrapy (python package)

OLAT: cobrapy_documentation.pdf

<https://cobrapy.readthedocs.io/en/latest/>

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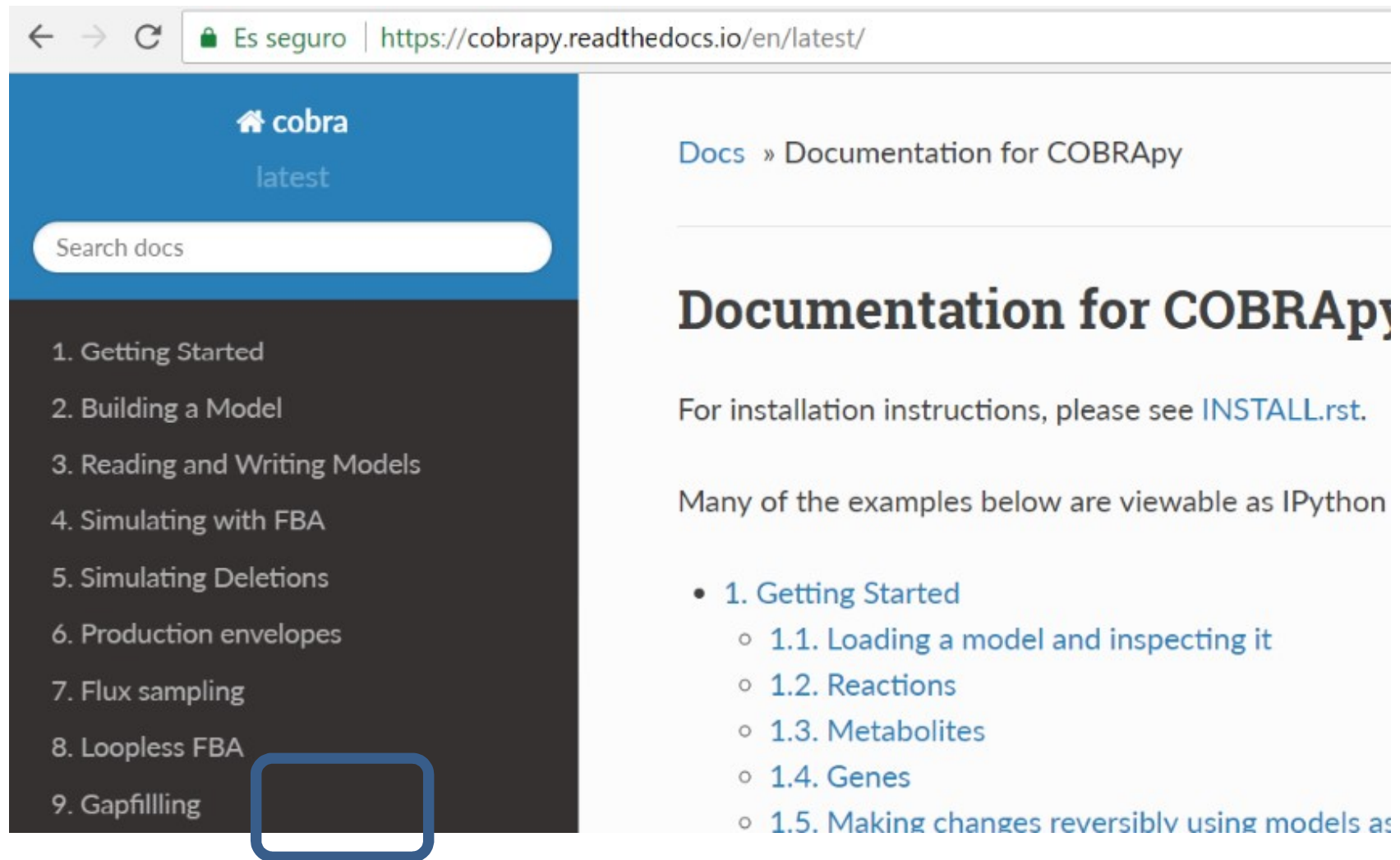
<https://cobrapy.readthedocs.io/en/latest/>

OLAT: software_requirements_bio334_AW.txt
and cobrapy_installationInstructions.txt

Import COBRApy and check version

```
1 # -*- coding: utf-8 -*-  
2 """  
3 Created on Thu May 17 09  
4  
5 @author: sanro  
6 """  
7  
8 import cobra
```

Import COBRApy and check version



The screenshot shows a web browser window with the URL <https://cobrapy.readthedocs.io/en/latest/>. The page title is "Documentation for COBRApy". The left sidebar contains a list of topics, with "1. Getting Started" highlighted. A blue box is drawn around the "1. Getting Started" link in the sidebar. The main content area shows the "Getting Started" section, which includes a link to "INSTALL.rst" for installation instructions and a list of sub-topics: "1.1. Loading a model and inspecting it", "1.2. Reactions", "1.3. Metabolites", "1.4. Genes", and "1.5. Making changes reversibly using models as".

← → ↻ Es seguro | <https://cobrapy.readthedocs.io/en/latest/>

cobra
latest

Search docs

1. Getting Started
2. Building a Model
3. Reading and Writing Models
4. Simulating with FBA
5. Simulating Deletions
6. Production envelopes
7. Flux sampling
8. Loopless FBA
9. Gapfilling

Docs » Documentation for COBRApy

Documentation for COBRApy

For installation instructions, please see [INSTALL.rst](#).

Many of the examples below are viewable as IPython

- 1. Getting Started
 - 1.1. Loading a model and inspecting it
 - 1.2. Reactions
 - 1.3. Metabolites
 - 1.4. Genes
 - 1.5. Making changes reversibly using models as

Exercises

Exercise 1 - Introduction to metabolic networks and metabolic network analysis

Exercise 2 - Analyzing simple biological networks

Exercise 3 - Biomass reaction constituents

Exercise 4 - Carbon sources of *E. coli*

Exercise 5 - Drug design

Exercises

Exercise 1 - Introduction to metabolic networks and metabolic network analysis (1.2 - 1.8)

Exercise 2 - Analyzing simple biological networks (2.1, 2.3 2.5 - 2.9)

Exercise 3 - Biomass reaction constituents (3.1, 3.2)

Exercise 4 - Carbon sources of *E. coli*

Exercise 5 - Drug design

How to..?

Build model and include external reactions - **1.3**

Read model and optimize - **1.5**

Essential reactions - **1.6**

Active reactions - **1.7**

Flux Variability Analysis (FVA) - **1.8**

Modify constraints on reactions - **1.9**

Plot - **2.6**

Last comments

- Take breaks when needed
- Fill the sheet with the exercises you have done before leaving
- Check COBRApy version before you start