
GECKO Documentation

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SysBioChalmers

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CHAPTER 1

About GECKO

The **GECKO** toolbox is a Matlab/Python package for enhancing a **G**enome-scale model to account for **E**nzyme **C**onstraints, using **K**inetics and **O**mics. It is the companion software to the publication:

Benjamin J. Sanchez, Cheng Zhang, Avlant Nilsson, Petri-Jaan Lahtvee, Eduard J. Kerkhoven, Jens Nielsen (2017). *Improving the phenotype predictions of a yeast genome-scale metabolic model by incorporating enzymatic constraints.* *Molecular Systems Biology*, 13(8):935

The software comes in two flavors, Python and Matlab scripts to fetch online data and build the published ecYeast7 GECKO models, and a Python package which can be used with `cobrapy` to obtain a ecYeast7 model object, optionally adjusted for provided proteomics data.

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2.1 Required software - Python module

- Python 2.7
- setuptools for python 2.7
- SOAPpy:

```
easy_install-2.7 SOAPpy
```

2.2 Required software - Matlab module

- **MATLAB** (7.5 or higher) + Optimization Toolbox.
- The **COBRA toolbox for MATLAB**. Note that **libSBML** and the **SBML toolbox** should both be installed. Both of them are free of charge for academic users. Additionally, you should add the cobra folder to your MATLAB search path.

2.3 Usage

See the supporting information of Sanchez et al. (2017)

Integrating proteomic data to the yeast GECKO model

If all you need is the ecYeast7 model to use together with cobrapy you can use the `geckopy` Python package.

3.1 Required software

- Python 2.7, 3.4, 3.5 or 3.6
- cobrapy

3.2 Installation

```
pip install geckopy
```

3.3 Usage

```
from geckopy import GeckoModel
import pandas
some_measurements = pandas.Series({'P00549': 0.1, 'P31373': 0.1, 'P31382': 0.1})
model = GeckoModel('multi-pool')
model.limit_proteins(some_measurements)
model.optimize()
```


CHAPTER 4

Contributors

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