# Relative flux trade-offs and optimization of metabolic network functionalities

# Publication

## OS

* Code was tested on Fedora 31

## Dependencies

* Matlab -tested with 2019b
* [COBRA toolbox 3.0](https://github.com/opencobra/cobratoolbox)
* GNU Linear Programming Kit(glpk) solver -tested with version 5.0
* [Gurobi solver](https://www.gurobi.com/)(tested with version 9.1.1)

## Setup

* Set up the COBRA toolbox following the [installation instructions](https://opencobra.github.io/cobratoolbox/stable/installation.html) that can be found [here](https://opencobra.github.io/cobratoolbox/stable/installation.html)
* Set up the glpk solver toolbox following the [installation instruction](https://opencobra.github.io/cobratoolbox/stable/installation.html) that can be found [here](https://de.mathworks.com/matlabcentral/fileexchange/75318-glpkmex-gnu-linear-programming-kit-glpk-mex-generator)
* Set up the Gurobi solver and connect it with the COBRA toolbox using install instructions that can be found [here](https://opencobra.github.io/cobratoolbox/stable/installation.html#gurobi)

## Run FluTOr

### To reproduce the results presented in the paper run the following scripts

* E. coli: Trade\_offs\_ecoliijo1366
* S. cerevisiae: Trade\_offs\_serevisiae
* A. thaliana: Trade\_offs\_athaliana

## How to apply FluTOr to another model

1. create a model which will be using to find tradeoffs. The output of the function must be a model named “model” and the name of the biomass reaction from the field “model.rxns”.
2. Give a name to the string variable “file\_name” to the results you want to save it as
3. flux accuracy must be defined as an integer variable names “rnd” (default value is 1e-5).
4. Then run the following codes respectively

model = CPR(model, rnd,file\_name);

tradeoff\_seaker(file\_name, model, biomass);