GFA version 1.0

The MATLAB subroutines in GFA (v.1.0) have been successfully tested on MATLAB® 2016a. Please refer to the GFA manuscript for more detailed information about the algorithm. Any questions regarding GFA usage can be addressed to rudi.gunawan@chem.ethz.ch.

Installation instruction:

Unzip the package GFA\_1.0.zip (XX MB) to a preferred folder.

Set the current working directory to GFA in MATLAB.

The GFA package includes the following:

1. Input.xlsx

An Excel® file specifying the glycosylation network as well as the glycan measurements with the following Sheets:

‘Overview’: Contains the overall model specifications

‘Stoichiometry’: Contains the glycosylation network stoichiometry formatted as in the given example

‘VCD’: The viable cell density measurements formatted as in the given example

‘Titer’: The protein production measurements formatted as in the given example

‘Fractions’: The glycan fractions formatted as in the given example.

2. GFA\_v1.m

This is the main Matlab file of GFA. It runs GFA for a given dataset of a fed-batch experiment as specified in Input.xlsx.

3. GFA\_xlsxread.m

Extracts data from an EXCEL file and saves them in a form that can be used by GFA.

4. GFA\_main.m

Calls the GFA fixed point optimization and evaluates the GFA outputs.

5.GFA\_fixedpoint.m

Solves the GFA based on a fixed point iteration.

6. GFA\_plots.m

Generates plots of all GFA results.