

Chlamy Sequence Optimizer





Table of Contents

1. Introduction	3
2. Pipeline.....	3
3. GUI	3
i. Installation.....	3
ii. Input	4
iii. Process and output	5
4. Using the source code.....	5
Acknowledgments.....	5



1. Introduction

Chlamy Sequence Optimizer is an application built to allow a simple one-stop-shop for designing coding DNA sequences for high expression in the model microalga *Chlamydomonas reinhardtii*. The optimization pipeline follows the procedures described in **Weiner et al., The Plant Journal, 2018**.

This package contains both a graphical user interface (GUI) and the MATLAB source code. All resources mentioned in this guide can be found freely on GitHub:

<https://github.com/iddoweiner/Coding-Sequence-optimization-for-Chlamydomonas-reinhardtii>

2. Pipeline

The optimization is composed of three main steps:

- A. Codon selection
- B. Elimination of splicing signals
- C. Maximization of mRNA folding energy in the translation initiation vicinity

3. GUI

i. Installation

The GUI is available for both Windows and Mac.

For windows: download and run the **Windows_64bit.exe**

For Mac: download the folder **MyAppInstaller_web.app/Contents**, move it to the applications folder and run it.

* Important Note: While downloading and / or running these files you may come across security alerts protecting against installation of applications downloaded from the web. In this case you can modify your security preferences to accept this software. You can be assured it is safe 😊

In order for the software to work, MATLAB runtime – which can be downloaded freely – is required. If you do not already have MATLAB runtime, the installation pipeline will ask permission to automatically download it from the web (recommended). Alternatively, you can download it yourself at:

<https://www.mathworks.com/products/compiler/matlab-runtime.html>

Once installed, windows users can simply open the application manually.

Mac users will need to open the application from the terminal in order to include the MATLAB runtime package in their path:

- Open the terminal
- Type the following in a continuous line:
 - Full path to the shell script: `run_Chlamy_sequence_optimizer.sh`,
 - one space,
 - Full path to the directory in which MATLAB runtime is installed

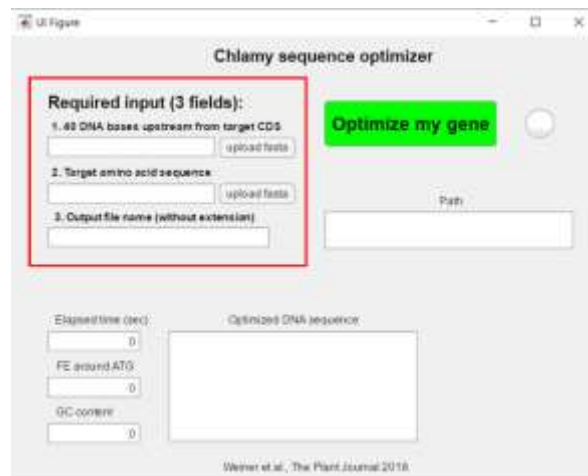
For example:

`~/Desktop/Applications/Tel_Aviv_University/Chlamy_sequence_optimizer/application/run_Chlamy_sequence_optimizer.sh ~/Desktop/Applications/MATLAB/MATLAB_Runtime/v93`

Executing this script will open the GUI with full MATLAB runtime permissions (note that simply opening the application manually might not work because MATLAB runtime will not be available).

ii. Input

The GUI has three input fields:



A. Forty (40) bases upstream from your target gene

This can be considered as the 5' UTR region of your target gene. The sequence in this region is taken into consideration while selecting codons for your target gene.

You can either upload a FASTA file containing your sequence or type / paste it in the field

B. Target amino acid sequence



Use 1-letter amino acid symbols (<http://www.fao.org/docrep/004/Y2775E/y2775e0e.htm>).

Include the stop codon (represented by: *).

You can either upload a FASTA file containing your sequence or type / paste it in the field

C. Output file name (without extension)

The program creates an output FASTA file with your optimized DNA sequence, together with some other information about the optimization. In this field you can enter the desired name of this file (e.g. My optimized gene). There is no need to write the file extension.

*This file will be created by default in the directory where the app is running. If you wish to change this, you can give your file a name specifying the full path to where you want it to be saved (e.g. C:\Users\user\Desktop\My optimized gene).

*If a file with the name you specified already exists, the data will be appended to it.

*If you leave this field empty, the default name of the output file will be 'optimization_output'.

iii. Process and output

Once the input fields are properly filled, hit the green 'Optimize my gene' button. The lamp right next to it will turn yellow to indicate that the process has commenced, and a wait-bar will appear and show you the progress of your run.

Besides the output file (see section 3.ii) which will be created at the end of your run, you will also be able to see your optimized DNA sequence (together with some additional information about the optimization) on the GUI screen.

4. Using the source code

If you are a MATLAB user and you wish to directly run the code without the GUI, this is possible as well. Download all the files in **MATLAB source code** and place them on your working path. Open the script: **run_optimization.m**. Simply running this script will now work with random data as input. Exchange the random data with your own and run the code. The output file is the same as the one generated by the GUI (see section 3.iii).

Acknowledgments

We would like to thank Mr. Gerd Guenther, who took the fascinating *Chlamydomonas* picture used as a cover picture for this application.

His work is available at: https://www.allposters.com/-st/Gerd-Guenther-Posters_c180530_.htm