

Introduction

The problematic of greenhouse gas (GHG) emissions is a global environmental challenge that has raised concerns in the past few decades. Particularly, the increase in atmospheric concentrations of carbon dioxide, methane, and other damaging gases can lead to catastrophic repercussions to life as we know it. Therefore, reducing GHG emissions and fomenting strategies for their mitigation are crucial steps that need to be taken in order to meet the Paris Agreement and ultimately ensure a sustainable future for our planet and those that inhabit it [1]. Taking this into account, our work aims at identifying the metabolic capabilities of photosynthetic microorganisms to reduce methane emissions.

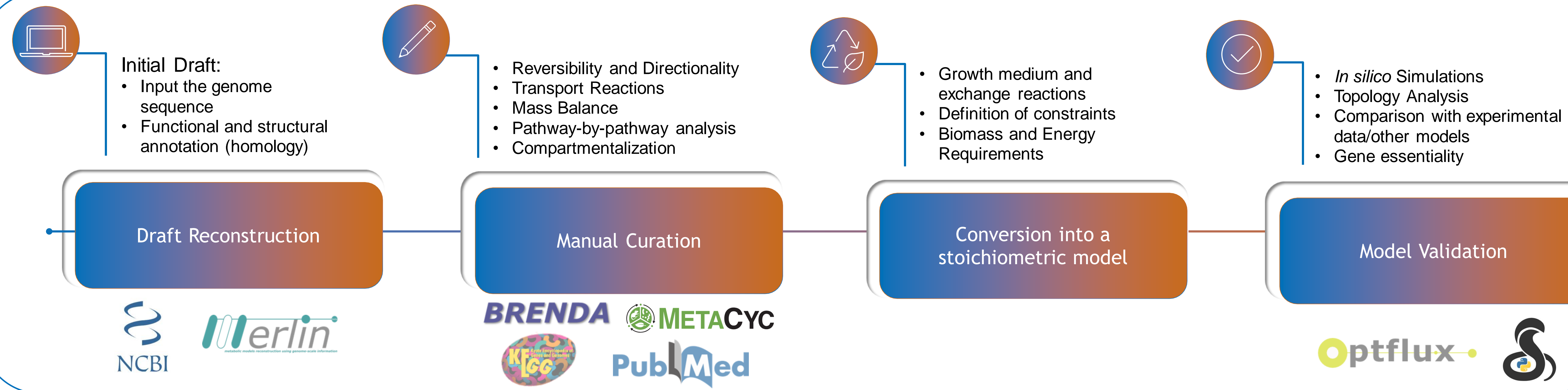
Genome-scale metabolic (GSM) models allow the *in silico* simulation and prediction of metabolic fluxes on a large scale, providing a powerful tool for optimizing and designing metabolic engineering methods. By integrating high-throughput data with GSM models, a comprehensive understanding of cellular metabolism and identification of strategies to improve a certain objective function can be obtained. The importance of this emerging technology in industry stems from its ability to offer a faster and more cost-effective approach, surpassing the efficiency of traditional methods [2].

Herein, we describe the reconstruction of GSM models for the microalga *Chlorella vulgaris* sp. – iGA1305 –, and for the cyanobacterium *Synechocystis* sp. – iJG708. Both GSM models provide a powerful tool for metabolic improvement, allowing predictions and simulations of CH₄ metabolism in response to different culture conditions and genetic modifications.

Both *C.vulgaris* and *Synechocystis* already have GSM models. **So, why should we reconstruct a model for an organism that already has one?**

- Genomic information is continuously updated on databases.
- Previous models don't incorporate methane in their reconstruction.

Methods



Results

Chlorella vulgaris – iGA1305

Model Overview

Table 1: Experimental and predicted growth rates reported for *C. vulgaris* (iGA1305/iCZ843) and *C. reinhardtii* (iRC1080) shown for comparison

Conditions	iGA1305 (This work)	iCZ843	iRC1080		
	Growth rate	Growth rate	Experimental	Growth rate	Experimental
Photoautotrophy	0.103	0.025	0.014–0.025 ^a	0.154	0.035–0.09 ^b
Heterotrophy	0.023 ^c	0.017 ^c	0.018–0.025 ^a	0.029 ^d	0.059–0.084 ^b
Mixotrophy	0.127 ^c	0.041 ^c	0.02–0.03 ^a	0.182 ^d	0.066 ^b

^a Data from [3]. ^b Data from [4]. ^c glucose used as organic carbon source. ^d Acetate used as organic carbon source.

Table 2: Properties of the GSM model for *C. vulgaris* (iGA1305), for the previous *Chlorella* model (iCZ843) and for the *C. reinhardtii* model (iRC1080) shown for comparison

Organism	Model	Genes	Reactions	Metabolites
<i>C. vulgaris</i> (This work)	iGA1305	1305	2659	2027
<i>C. vulgaris</i> (UTEX-395)	iCZ843	843	2286	1770
<i>C. reinhardtii</i>	iRC1080	1080	2191	1706

Synechocystis – iJG706

Model Overview

Table 3: Experimental and predicted growth rates reported for *Synechocystis* shown for comparison

Conditions	iJG706 (This work)	iJN678 [7]	Experimental
	Growth Rate	Growth Rate	
Photoautotrophy	0.085	0.088	0.085 [5]
Heterotrophy	0.063	0.064	0.076 [6]
Mixotrophy	0.043	0.056	0.059 [6]

Table 4: Properties of the GSM model for *Synechocystis* (iJG706), for the previous *Synechocystis* models (iJN678, iSyn811 and iSyn669) shown for comparison

Organism	Model	Genes	Reactions	Metabolites
<i>Synechocystis</i> (This work)	iJG706	706	2172	1619
<i>Synechocystis</i>	iJN678	678	863	795
<i>Synechocystis</i>	iSyn811 [8]	811	956	911
<i>Synechocystis</i>	iSyn669 [9]	669	882	790

Conclusion

- The reconstruction process did not reveal any genomic evidence of enzymes associated with methane metabolism
- Both models were validated regarding spontaneous growth, growth rates in different conditions, auxotrophies and uptake/secretion values
- The models are subject to change as new approaches are employed towards fine-tuning
- Next steps will involve the incorporation of possible methane-utilizing pathways in the models

References

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