
Algorithm 1: Metabolic Optimization

Data: Genome Scale Model \mathbf{S} , Flux Constraints \mathcal{C} , Objective Weights \mathcal{W} , Cell Type τ , Biomass \mathcal{B}

Result: Optimum \mathbf{z} , Cellular Fluxes \mathbf{v}

$$R_{obj} = \sum \mathcal{W}^T \cdot \mathbf{v}$$

$\mathbf{v}_{exp} = \text{Get Export}(\tau)$

$\mathbf{v}_{fix} = \text{Get Fixation Reaction}(\tau)$

$\mathbf{S}_{cat} = \text{Generate Catabolic Model}(\mathbf{S})$

$\mathbf{z}, \mathbf{v} = \text{Anabolize}(\mathbf{S}, \mathcal{C}, \mathcal{B}, \mathcal{B}_T, R_{obj}, \mathcal{O})$

if *Anabolism successful* **then**

return \mathbf{z}, \mathbf{v}

else

$\mathbf{z}, \mathbf{v} = \text{Primary Produce}(\mathbf{S}, \mathcal{C}, \mathcal{B}, \mathcal{B}_T, \mathbf{v}_{exp}, \mathbf{v}_{fix}, R_{obj})$

if *Primary Production successful* **then**

return \mathbf{z}, \mathbf{v}

else

$\mathbf{z}, \mathbf{v} = \text{Catabolize}(\mathbf{S}_{cat}, \mathcal{C}, \mathcal{B}, R_{obj})$

if *Catabolism successful* **then**

return \mathbf{z}, \mathbf{v}

else

 Die

return $\{\}$
