

a. For S use code Hw#3 with \$V

$$\$V = \begin{cases} \text{Balance.E.JL for balanced } \underline{S} \\ \text{out Balance.JL for unbalanced } \underline{S} \end{cases}$$

b. Not balanced originally added in a

"H<sub>2</sub>O → " - export rxn

"ATP ⇌ ADP" - Exchange rxn or coupled rxn need to provide energy for other rxns.

This check is performed in the same code for a.

and the matrix that is the Q when balanced elementally is called ebs,

c. optimal value is contained in opt-value, produced by code Hw #3 FBA.jl, used balanced S here, Also used given assumptions in Pset#3,

- For V-boundaries they were calculated as

if only → ⇒  $0 \leq V_{\#} \leq \underbrace{k_{cat}}_{\text{given}} E \left( \underbrace{\frac{a}{k_m + a}}_{\substack{\text{substrate/metabolite} \\ \text{calculated in excel file} \\ \text{nChem bio 2027-53410} \\ \text{and matched}}} \right)$

The usual definition of  $k_m$

if ⇌ ⇒  $-k_{cat} E \left( \frac{a}{k_m + a} \right) \leq V_{\#} \leq k_{cat} E \left( \frac{a}{k_m + a} \right)$

if not an exchange flux else it is;

$$0 \leq V_{\#} \leq 10 \frac{\text{mmol}}{\text{gDW} \cdot \text{hr}} \quad \text{if } \rightarrow$$

or

$$-10 \frac{\text{mmol}}{\text{gDW} \cdot \text{hr}} \leq V_{\#} \leq 10 \frac{\text{mmol}}{\text{gDW} \cdot \text{hr}} \quad \text{if } \rightleftharpoons$$