Computational & Systems Biology

Double description method

$$K = \begin{bmatrix} \equiv & \vec{D} & + \\ \equiv & \vec{D} & + \\ \equiv & \vec{D} & + \end{bmatrix} \longrightarrow H^{+} \text{ defined as positive entries}$$

For metabolism, steady state assumt assop assumption
is Reasonable

→ Rank
→ Kernel matrix
→ Gaussian β elimination
→ --- (last algorithm)

$\longrightarrow k_1 \longrightarrow A \overset{\nwarrow}{\longrightarrow} k_2 \longrightarrow$

$\overset{k_1}{\longrightarrow} A \overset{k_2}{\longrightarrow}$

$\dfrac{k_1}{k_2}$ → dependent on degradation.