(a) Estimate flux distribution and enzyme contribution in a reference state (e.g. wildtype)

$$\text{Minimize} \quad \left\| \frac{{}^{13}C\ \text{MFA estimated flux} - \textbf{Flux (w)}}{{}^{13}C\ \text{MFA error}} \right\| + \frac{\left\| \textbf{Enzyme contribution } (W^{enz}) \right\|}{\text{Gene expression level}}$$

$$\text{s.t.} \quad \text{Measurement} - \text{Error} \le \textbf{External flux} \le \text{Measurement} + \text{Error}$$

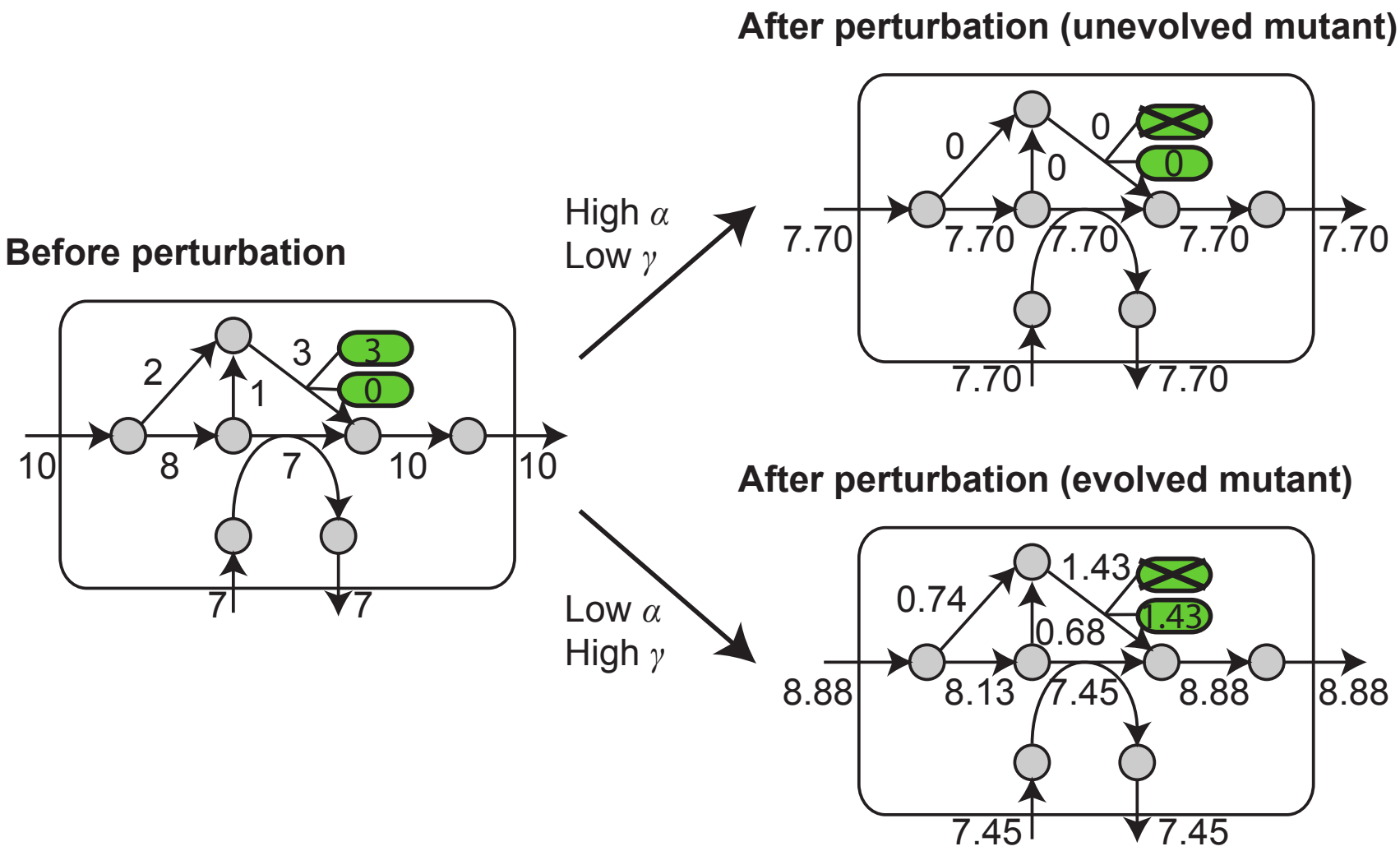
$$-\sum \textbf{Enzyme contribution} \le \textbf{Internal flux} \le \sum \textbf{Enzyme contribution}$$

$$\left(\text{e.g. } -(W^{TktA}_{TKT1} + W^{TktB}_{TKT1}) \le w_{TKT1} \le (W^{TktA}_{TKT1} + W^{TktB}_{TKT1}) \text{ for transketolase}\right)$$

(b) Predict metabolic flux distribution in a perturbed state (e.g. a knockout mutant)

$$\text{Minimize} \quad \left\| \begin{matrix} \textbf{Relative flux changes} \\ (w - v) / w \end{matrix} \right\| + \text{Penalty } (\alpha) * \sum \begin{matrix} \textbf{Enzyme contribution } (V^{enz}) \\ (\text{for enzymes with } W^{enz} = 0) \end{matrix}$$

$$\text{s.t.} \quad -\sum \textbf{Enzyme contribution} \le \textbf{Internal flux} \le \sum \textbf{Enzyme contribution}$$

$$\textbf{Enzyme contribution} \le \begin{pmatrix} \text{Increase} \\ \text{limit } (\gamma) \end{pmatrix} * \begin{pmatrix} \text{Reference enzyme} \\ \text{contribution} \end{pmatrix} \quad (\text{for } W^{enz} \neq 0)$$

(c)