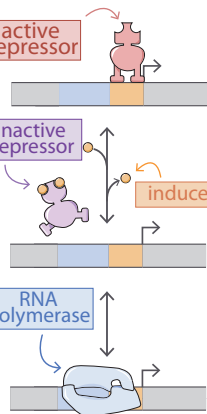
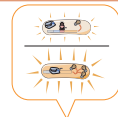


THE SIMPLE REPRESSION ARCHITECTURE



A PREDICTIVE THEORY OF ALLOSTERIC INDUCTION

fold-change in gene expression



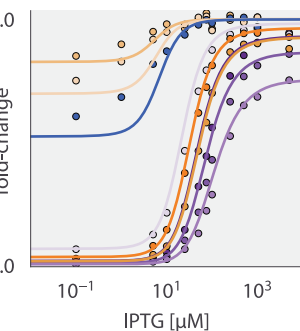
fold-change =

$$\text{fold-change} = \left(1 + \frac{\left(1 + \frac{C}{K_A}\right)^2}{\left(1 + \frac{C}{K_A}\right)^2 + e^{-\beta \Delta \epsilon_{AI}} \left(1 + \frac{C}{K_I}\right)^2} \frac{R}{N_{NS}} e^{-\beta \Delta \epsilon_{RA}} \right)^{-1}$$

The equation is accompanied by several diagrams and labels:

- inducer concentration:** A box containing orange circles representing inducer molecules.
- repressor copy number:** A box containing red and purple shapes representing repressor molecules.
- active repressor inducer dissociation constant:** A diagram showing a repressor bound to an inducer, with a double-headed arrow indicating the dissociation constant.
- active-inactive state energy difference:** A diagram showing a repressor bound to DNA, with a vertical arrow indicating the energy difference between the active and inactive states.
- inactive repressor inducer dissociation constant:** A diagram showing a repressor bound to an inducer, with a double-headed arrow indicating the dissociation constant.
- DNA binding energy:** A diagram showing a repressor bound to DNA, with a vertical arrow indicating the binding energy.

PHENOTYPIC DATA COLLAPSE



$$\text{fold-change} = \frac{1}{1 + e^{-\beta F}}$$

