Electronic Supplementary Material (ESI) for Molecular BioSystems.

Supplementary Figures to

Steady state statistical correlations predict bistability in reaction motifs

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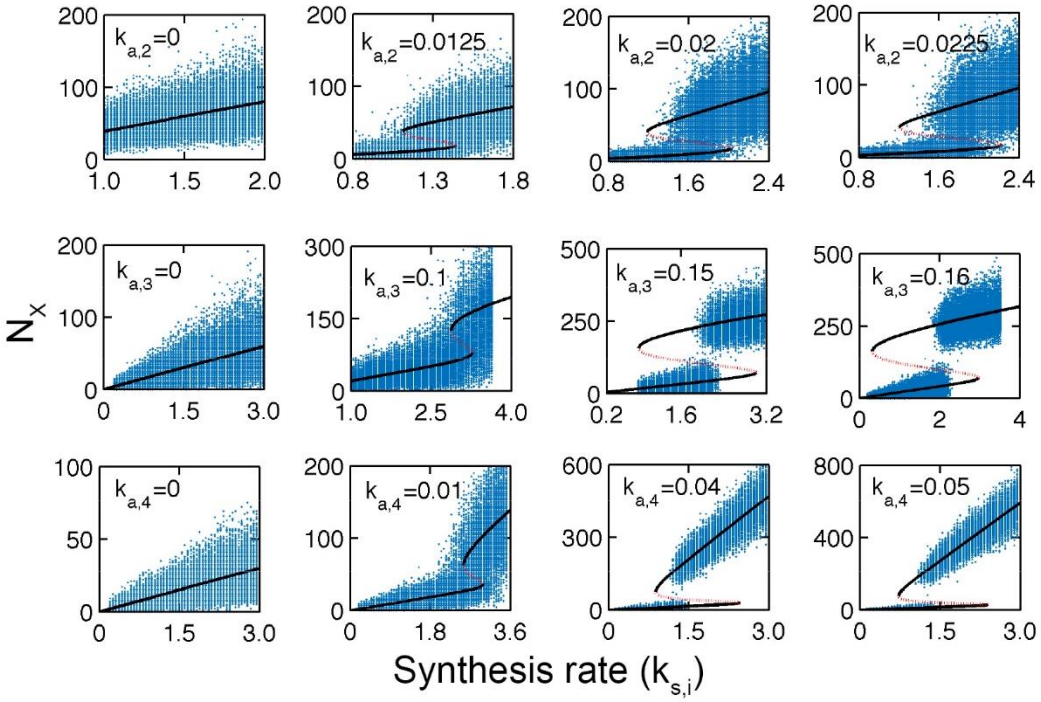
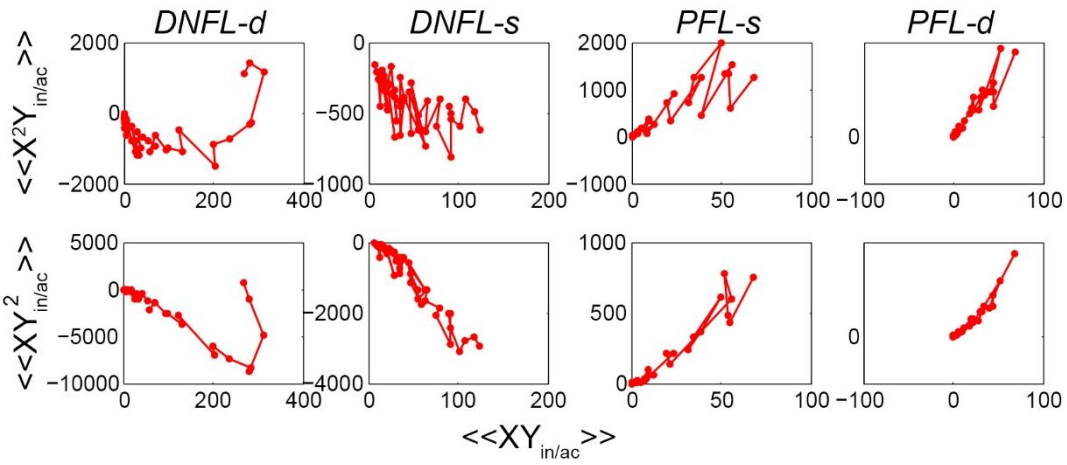
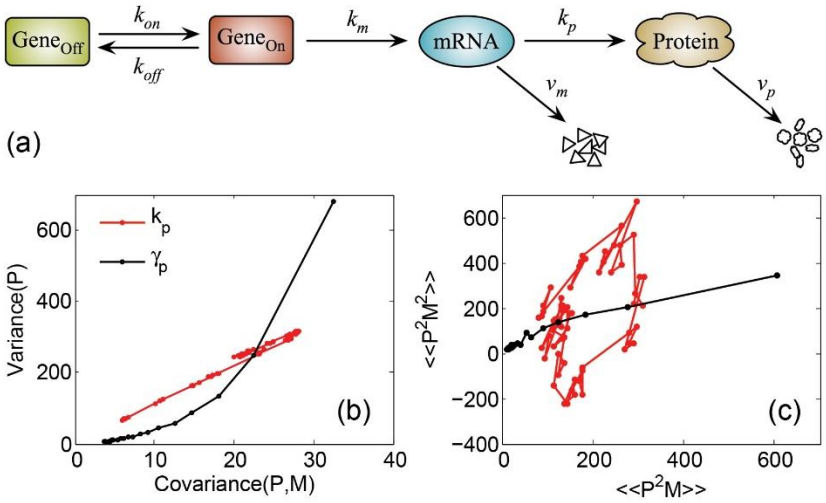


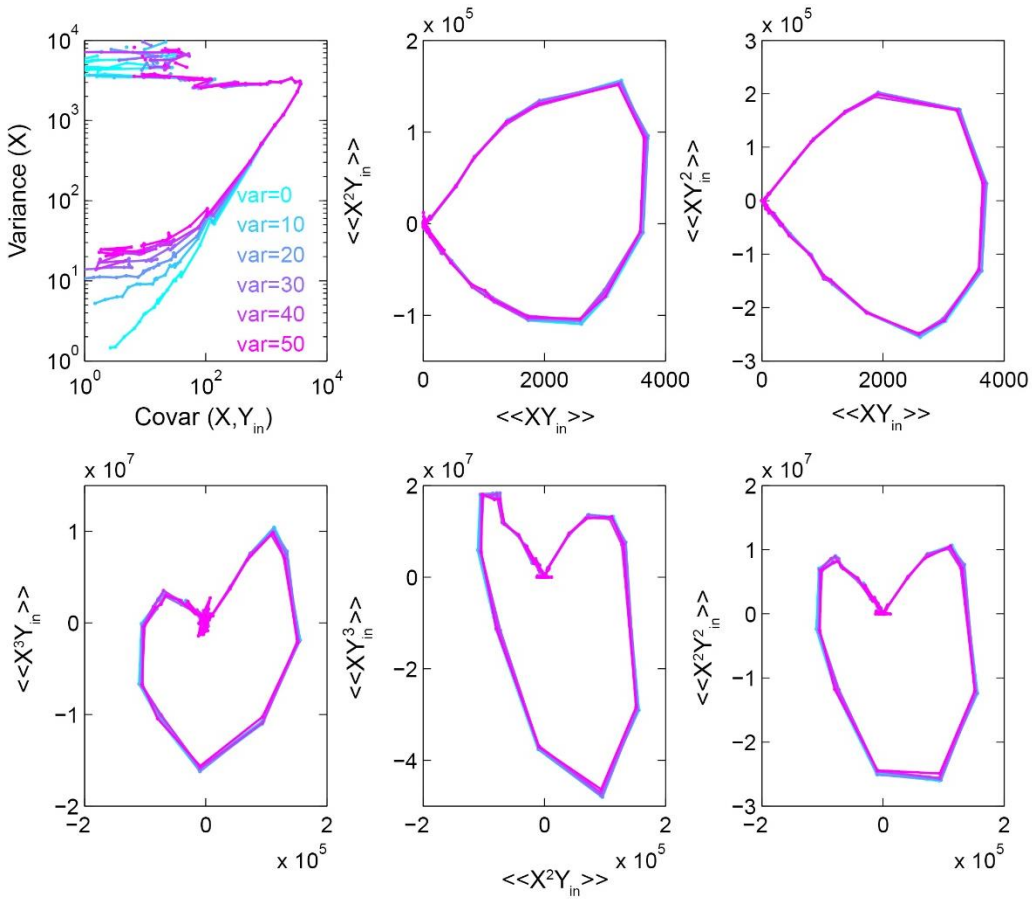
Supplementary Figure 1: Bimodality of steady state distributions, stochastic analogue of deterministic bifurcation diagram. The steady state distributions of X are plotted for a range of values of the synthesis rate ($k_{s,i}$) from stochastic simulations for the models with indicated strengths of positive feedback. Top row: *DNFL-s*, middle row: *PFL-s* and bottom row: *PFL-d*. The corresponding deterministic bifurcation diagrams are overlaid on top of the distribution.



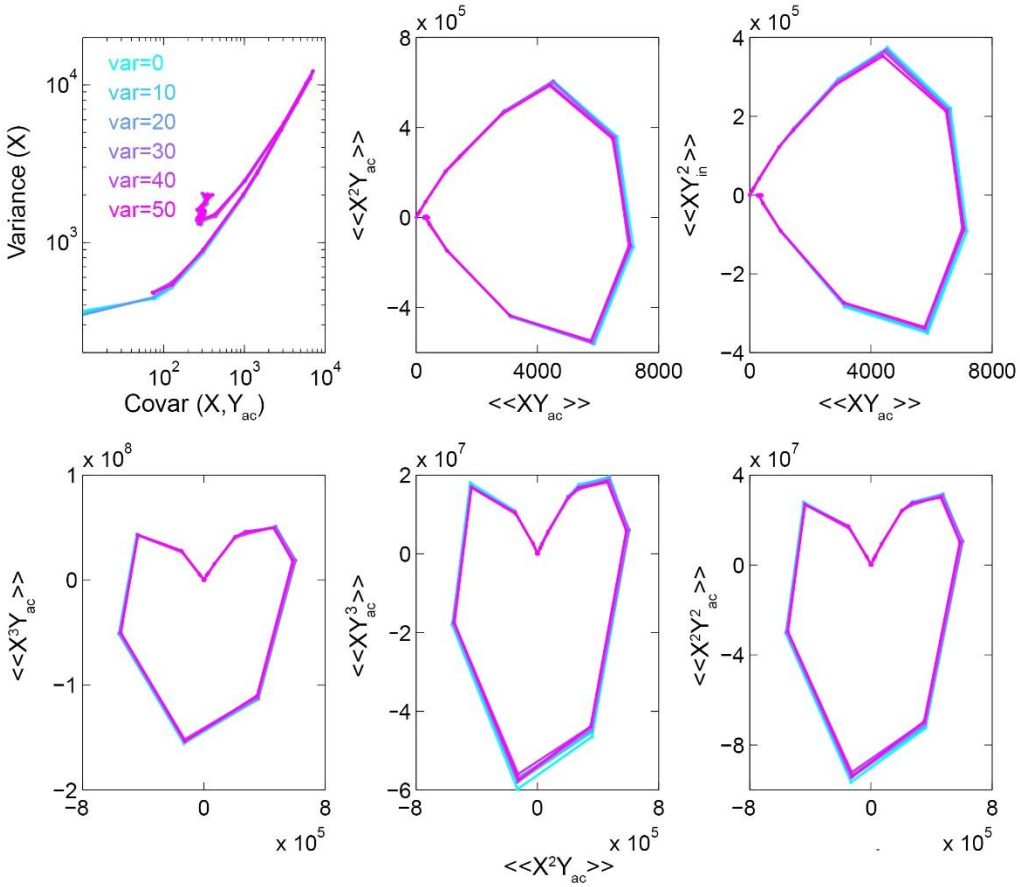
Supplementary Figure 2: 3rd order vs 2nd order cumulants for four different models without intrinsic bistability.



Supplementary Figure 3: a) Schematic diagram of gene expression model. The rate constant of each elementary reaction is mentioned in the diagram. b) Variance of protein (P) is correlated with the covariance between protein and mRNA (M) for varied range of translation rate constant (k_p) or degradation rate constant (γ_p). While the translational rate is varied the variance-covariance shows is cusp-shaped structure (red line) falsely indicating bistability. However, when degradation rate constant of protein is varied the cusp-shape disappears confirming monostability. (d) Similar conclusion are made based on plot of 4th order cross-cumulant with 3rd order cross-cumulant.



Supplementary Figure 4: Various statistical analysis of *DNFL-d* model with added Gaussian noise (zero mean). The strengths of the added noise are indicated inside the plot. The positive feedback strength is chosen to be $k_{a,1} = 0.01$.



Supplementary Figure 5: Various statistical analysis of *PFL-s* model with added Gaussian noise (zero mean). The strengths of the added noise are indicated inside the plot. The positive feedback strength is chosen to be $k_{a,3} = 0.16$.