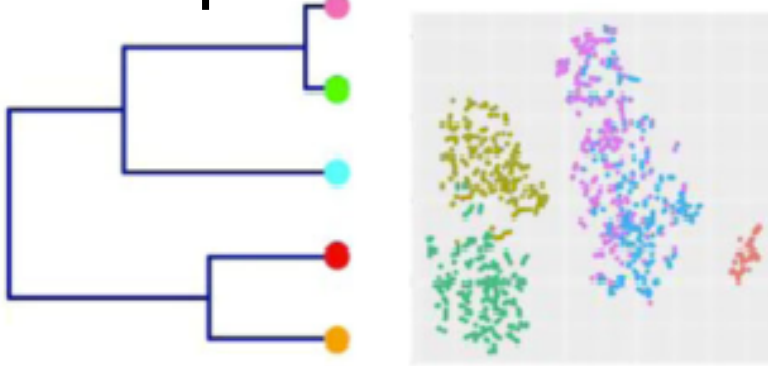
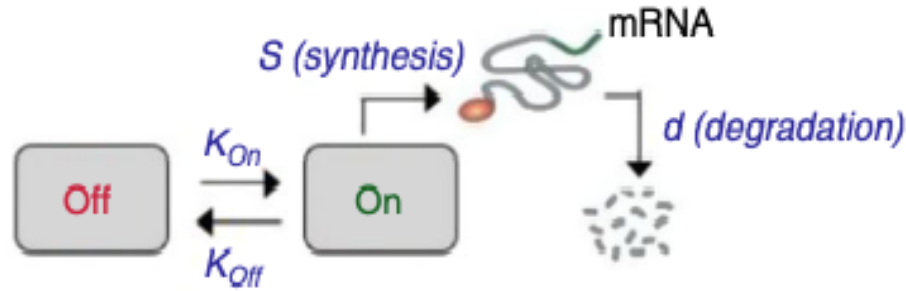


Generating True Counts based on two-state kinetic model

Cells: p-dim EVF vectors

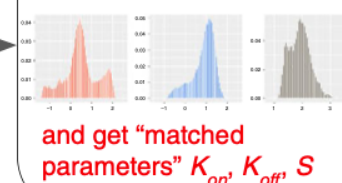


Genes: p-dim gene specific vectors



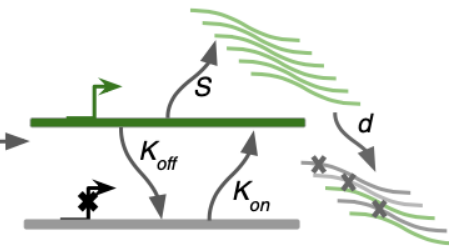
$$\begin{aligned}
 & \begin{matrix} G_{1,1} \dots G_{1,p} \\ \vdots \\ G_{m,1} \dots G_{m,p} \end{matrix} * \begin{matrix} E_{1,1} \dots E_{1,n} \\ \vdots \\ E_{p,1} \dots E_{p,n} \end{matrix} = \begin{matrix} K_{on,1,1} \dots K_{on,1,n} \\ \vdots \\ K_{on,m,1} \dots K_{on,m,n} \end{matrix} \\
 & \quad \quad \quad \text{K}_{on} \text{ gene effect} \quad \quad \quad \text{K}_{on} \text{ EVF} \quad \quad \quad \text{K}'_{on} \\
 & \quad \quad \quad \text{p: \# of EVFs} \\
 & \begin{matrix} G_{1,1} \dots G_{1,p} \\ \vdots \\ G_{m,1} \dots G_{m,p} \end{matrix} * \begin{matrix} E_{1,1} \dots E_{1,n} \\ \vdots \\ E_{p,1} \dots E_{p,n} \end{matrix} = \begin{matrix} K_{off,1,1} \dots K_{off,1,n} \\ \vdots \\ K_{off,m,1} \dots K_{off,m,n} \end{matrix} \\
 & \quad \quad \quad \text{K}_{off} \text{ gene effect} \quad \quad \quad \text{K}_{off} \text{ EVF} \quad \quad \quad \text{K}'_{off} \\
 & \begin{matrix} G_{1,1} \dots G_{1,p} \\ \vdots \\ G_{m,1} \dots G_{m,p} \end{matrix} * \begin{matrix} E_{1,1} \dots E_{1,n} \\ \vdots \\ E_{p,1} \dots E_{p,n} \end{matrix} = \begin{matrix} S_{1,1} \dots S_{1,n} \\ \vdots \\ S_{m,1} \dots S_{m,n} \end{matrix} \\
 & \quad \quad \quad \text{S gene effect} \quad \quad \quad \text{S EVF} \quad \quad \quad \text{S}' \\
 & \quad \quad \quad \text{m: \# of genes}
 \end{aligned}$$

Map dot products K'_{on} , K'_{off} , S' to distributions from real data



and get "matched parameters" K_{on} , K_{off} , S

Sample transcript counts



Simulating PCR and Sequencing platform

