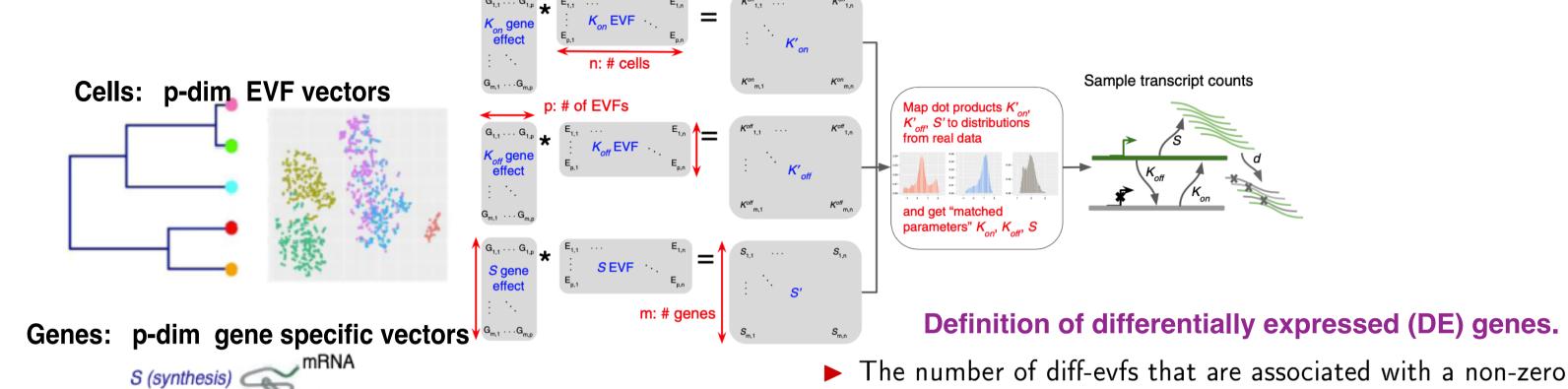
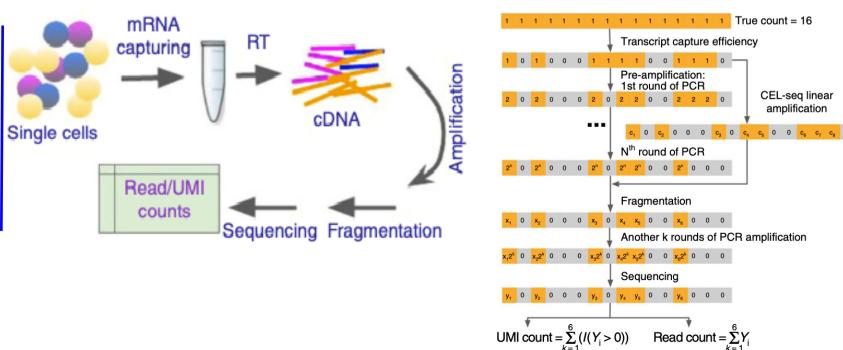
## Generating True Counts based on two-state kinetic model



- ► The number of diff-evfs that are associated with a non-zero gene effect value based on the kinetic parameters (should larger than zero)
- ▶ Theoretical log2 fold change analysis is based on the kinetic parameters (should larger than  $0.6 \sim 1$ ).

## **Simulating PCR and Sequencing platform**



d (degradation)

 $\kappa_{On}$ 

K<sub>Off</sub>

On