**Pulse-chase anaysis strategy**

The general steps of the analysis are as follows:

1. Use the relative fraction of RNA that is 4sU labeled (denoted *θ*) after the pulse and after the chase to estimate the degradation rate constant in each of the two experimental conditions for each of the chase times.
2. Perform a number of transformations using the delta approximation to estimate means and variances of the transformed random variables
   1. Transforming from logit(*θ*) (what bakR will estimate in each sample) to log(*k*deg)
3. Perform differential kinetic analysis as in vanilla bakR

Key realization is that during a 4sU pulse (assuming population of cells are at steady-state and thus the total concentration of RNA is the ratio of *k*syn to *k*deg):

Once the chase begins, the amount of 4sU labeled RNA degrades exponentially, making the fraction new during a chase:

Therefore, if we estimate and with bakR, we can estimate , since:

L2FC()s and their associated uncertainties can be estimated using the logit(*θ*) estimates and uncertainties provided by bakR when the NSS parameter in bakRFit() is set to TRUE, as well as statistical theory regarding means and variances of functions of random variables. I employed a strategy called the delta approximation, which is nicely derived and described on [this Stack Exchange post](https://stats.stackexchange.com/questions/5782/variance-of-a-function-of-one-random-variable)