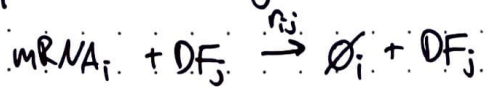


# Transfer learning: Degradation Factor Concentration

Equation for degradation of mRNA<sub>i</sub> with degradation factor DF<sub>j</sub>:



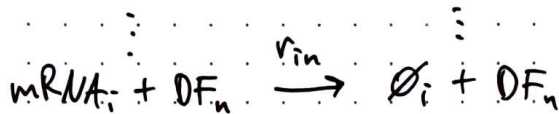
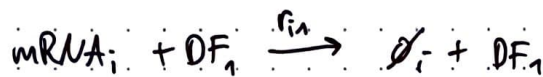
with reaction rate  $r_{ij} = k_{ij} \cdot \text{DF}_j \cdot \text{mRNA}_i$ , where

$k_{ij}$  ~ binding probability of mRNA<sub>i</sub> and DF<sub>j</sub>

$\text{DF}_j$  ~ concentration of DF<sub>j</sub>

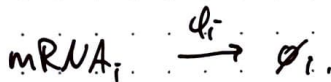
$\text{mRNA}_i$  ~ concentration of mRNA<sub>i</sub>

The half-life of an mRNA<sub>i</sub> is determined by all the  $r_{ij}$ 's in combination:



Now, let  $\varphi_{ij} = k_{ij} \cdot \text{DF}_j$  and consider  $r_{ij} = \varphi_{ij} \cdot \text{mRNA}_i$ .

Then  $\varphi_i = \sum_j \varphi_{ij}$  leads to the simplification

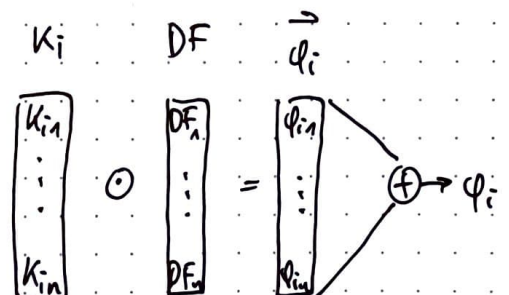


where  $\frac{1}{\varphi_i} \sim$  Half-life of mRNA<sub>i</sub>.

We can try to model this simplification in order to learn a metric of concentration of the different DF<sub>j</sub>'s across different tissues:

$$\varphi_{ij} = k_{ij} \cdot \text{DF}_j$$

$\nearrow$  proportional to experimentally obtained half-life:  
 $\uparrow$  obtained from previous models  
 $\uparrow$  learned parameters



for each tissue-type and each mRNA<sub>i</sub>.

$$HL_i \sim \frac{1}{\varphi_i}$$

$$\text{with } \varphi_i = \sum_j \varphi_{ij}$$