Transfer learning: Degradation Factor Concentration

Equation for degradation of $mRNA_i$ with degradation factor DF_j:

$$mRNA_i + DF_j \xrightarrow{r_{ij}} \emptyset_i + DF_j$$

with reaction rate $r_{ij} = K_{ij} \cdot DF_j \cdot mRNA_i$, where

- K_{ij} ~ binding probability of $mRNA_i$ and DF_j
- DF_j ~ concentration of DF_j
- $mRNA_i$ ~ concentration of $mRNA_i$.

The half-life of an $mRNA_i$ is determined by all the r_{ij}'s in combination:

$$mRNA_i + DF_1 \xrightarrow{r_{i1}} \emptyset_i + DF_1$$

$$\vdots \qquad\qquad\qquad \vdots$$

$$mRNA_i + DF_n \xrightarrow{r_{in}} \emptyset_i + DF_n$$

Now, let $\varphi_{ij} := K_{ij} \cdot DF_j$ and consider $r_{ij} = \varphi_{ij} \cdot mRNA_i$.
Then $\varphi_i := \sum_j \varphi_{ij}$ leads to the simplification

$$mRNA_i \xrightarrow{\varphi_i} \emptyset_i\,,$$

where $\frac{1}{\varphi_i}$ ~ Half-life of $mRNA_i$.

We can try to model this simplification in order to learn a metric of concentration of the different DF_j's across different tissues:

$$\varphi_{ij} = K_{ij} \cdot DF_j$$

- φ_{ij} ↑ proportional to experimentally obtained half-life: $HL_i \sim \frac{1}{\varphi_i}$ with $\varphi_i = \sum_j \varphi_{ij}$
- K_{ij} ↑ obtained from previous models
- DF_j ↑ learned parameters

$$\underbrace{\begin{bmatrix} K_{i1} \\ \vdots \\ K_{in} \end{bmatrix}}_{K_i} \odot \underbrace{\begin{bmatrix} DF_1 \\ \vdots \\ DF_n \end{bmatrix}}_{DF} = \underbrace{\begin{bmatrix} \varphi_{i1} \\ \vdots \\ \varphi_{in} \end{bmatrix}}_{\vec{\varphi_i}} \rightarrow (+) \rightarrow \varphi_i$$

for each tissue-type and each $mRNA_i$.

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