Kinetic Modeling Equation for LIRA

Abbreviations

Abbreviation	Description
k _{di21}	miR21 diffusion rate constant
k _{di92}	miR92a diffusion rate constant
k _{de_aeB}	aeBlue degradation rate constant
k _{de21}	miR21 degradation rate constant
k _{de92}	miR92a degradation rate constant
k _{de_OLS}	Open LIRA Switch degradation rate constant
k _{de_CLS}	Close LIRA Switch degradation rate constant
k _{tr}	Trancription Rate Constant
k _{tl}	Translation Rate Constant
k _{21_CLS}	miR21-CLS Complex Formation Constant
k _{92_CLS}	miR92a-CLS Complex Formation Constant
k _{OLS192}	OLS1-miR92 Complex Formation Constant or OLSc Formation
k _{OLS221}	OLS2-miR21 Complex Formation Constant or OLSc Formation
miR21 ₀	miR21 extracellular
miR92 ₀	miR92a extracellular
miR21₁	miR21 intracellular
miR92₁	miR92a intracellular
Gene	Gene Coding for LIRA and Reporter
CLS	Close LIRA Switch
OLS	Open LIRA Switch
OLS ₁	Open LIRA Switch formed by CLS-miR21 complex formation

OLS ₂	Open LIRA Switch formed by CLS-miR92 complex formation
OLS _c	Open LIRA Switch formed by CLS-miR21-miR92a complex formation
aeB₁	aeBlue chromprotein translated from OLS₁
aeB ₂	aeBlue chromprotein translated from OLS ₂
aeB _c	aeBlue chromprotein translated from OLS _c
aeB _t	aeBlue chromprotein total = aeB ₁ + aeB ₂ + aeB _c
Ø	Degradated substance

Chemical Equation for two miRNAs

$$egin{aligned} [miR21_0]
ightarrow^{k_{di21}} & [miR21_1]
ightarrow^{k_{de21}} & \emptyset \ & [miR92_0]
ightarrow^{k_{di92}} & [miR92_1]
ightarrow^{k_{de92}} & \emptyset \ & [Gene]
ightarrow^{k_{tr}} & [CLS]
ightarrow^{k_{de_CLS}} & \emptyset \ & [CLS] + [miR21_1]
ightarrow^{k_{21_CLS}} & [OLS_1]
ightarrow^{k_{de_OLS_1}} & \emptyset \ & [OLS_1] + [miR92_1]
ightarrow^{k_{OLS_192}} & [OLS_c]
ightarrow^{k_{de_OLS_2}} & \emptyset \ & [CLS] + [miR92_1]
ightarrow^{k_{92_CLS}} & [OLS_2]
ightarrow^{k_{de_OLS_2}} & \emptyset \ & [OLS_2] + [miR21_1]
ightarrow^{k_{OLS_221}} & [OLS_c]
ightarrow^{k_{de_OLS_c}} & \emptyset \ & [OLS_1]
ightarrow^{k_{tl}} & [aeB_1]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_2]
ightarrow^{k_{tl}} & [aeB_2]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{de_aeB}} & \emptyset \ & [OLS_c]
ightarrow^{k_{tl}} & [aeB_c]
ightarrow^{k_{t$$

ODE for two miRNAs

$$rac{d[miR21_0]}{dt}=-k_{di21}[miR21_0]$$

$$rac{d[miR92_0]}{dt}=-k_{di92}[miR92_0]$$

$$\frac{d[miR21_1]}{dt} = k_{di21}[miR21_0] - k_{de21}[miR21_1] - k_{21_CLS}[CLS][miR21_1] - k_{OLS_221}[OLS_2][miR21_1]$$

$$\frac{d[miR92_1]}{dt} = k_{di92}[miR92_0] - k_{de92}[miR92_1] - k_{92_CLS}[CLS][miR92_1] - k_{OLS_192}[OLS_1][miR92_1]$$

$$rac{d[CLS]}{dt} = k_{tr} - k_{de_CLS}[CLS] - k_{21_CLS}[CLS][miR21_1] - k_{92_CLS}[CLS][miR92_1]$$

$$\frac{d[OLS_1]}{dt} = k_{21_CLS}[CLS][miR21_1] - k_{OLS_192}[OLS_1][miR92_1] - k_{de_OLS_1}[OLS_1]$$

$$rac{d[OLS_2]}{dt} = k_{92_CLS}[CLS][miR92_1] - k_{OLS_221}[OLS_2][miR21_1] - k_{de_OLS_2}[OLS_2]$$

$$rac{d[OLS_c]}{dt} = k_{OLS_192}[OLS_1][miR92_1] + k_{OLS_221}[OLS_2][miR21_1] - k_{de_OLS_c}[OLS_c]$$

$$rac{d[aeB_1]}{dt} = k_{tl}[OLS_1] - k_{de_aeB}[aeB_1]$$

$$rac{d[aeB_2]}{dt} = k_{tl}[OLS_2] - k_{de_aeB}[aeB_2]$$

$$rac{d[aeB_c]}{dt} = k_{tl}[OLS_c] - k_{de_aeB}[aeB_c]$$

$$rac{d[aeB_t]}{dt} = rac{d[aeB_1]}{dt} + rac{d[aeB_2]}{dt} + rac{d[aeB_c]}{dt}$$

Chemical Equation for one miRNA

To simulate 1 miRNA, we take it as miR21, because the parameter values we use in this simulation for both miR21 and miR92a are the same.

$$egin{aligned} [miR21_0]
ightarrow^{k_{di21}} & [miR21_1]
ightarrow^{k_{de21}} & \emptyset \ & [Gene]
ightarrow^{k_{tr}} & [CLS]
ightarrow^{k_{de_CLS}} & \emptyset \ & [CLS] + [miR21_1]
ightarrow^{k_{21_CLS}} & [OLS_1]
ightarrow^{k_{de_OLS_1}} & \emptyset \ & [OLS_1]
ightarrow^{k_{tl}} & [aeB_1]
ightarrow^{k_{de_aeB}} & \emptyset \end{aligned}$$

ODE for one miRNA

$$egin{aligned} rac{d[miR21_0]}{dt} &= -k_{di21}[miR21_0] \ rac{d[miR21_1]}{dt} &= k_{di21}[miR21_0] - k_{de21}[miR21_1] - k_{21_CLS}[CLS][miR21_1] \ rac{d[CLS]}{dt} &= k_{tr} - k_{de_CLS}[CLS] - k_{21_CLS}[CLS][miR21_1] \ rac{d[OLS_1]}{dt} &= k_{21_CLS}[CLS][miR21_1] - k_{de_OLS_1}[OLS_1] \ rac{d[aeB]}{dt} &= k_{tl}[OLS_1] - k_{de_aeB}[aeB_1] \end{aligned}$$

Modeling Parameters of LIRA

Symbol	Description	Value/Range	Unit	Reference(s)	Notes
k _{di21}	miR21 diffusion rate constant	1 x 10 ⁻²	s ⁻¹	(Levine <i>et al.,</i> 2007)	General miRNA rate diffusion with size ~20 nucleotide
k _{di92}	miR92a diffusion rate constant	1 x 10 ⁻²	s ⁻¹	(Levine <i>et al.</i> , 2007)	General miRNA rate diffusion with size ~20 nucleotide
k _{de_aeB}	aeBlue degradation rate constant	2.7 x 10 ⁻⁴	s ⁻¹	(Alon 2020)	General reporter degradation rate (1 hour)
k _{de21}	miR21 degradation rate constant	3 x 10 ⁻⁴	s ⁻¹	(Baabu et al., 2022)	General RNA degradation rate
k _{de92}	miR92a degradation rate constant	3 x 10 ⁻⁴	s ⁻¹	(Baabu et al., 2022)	General RNA degradation rate
k _{de_OLS}	Open LIRA Switch degradation rate constant	3 x 10 ⁻⁴	s ⁻¹	(Baabu <i>et al.</i> , 2022)	General RNA degradation rate
k _{de_CLS}	Close LIRA Switch degradation rate constant	3 x 10⁴	s ⁻¹	(Baabu et al., 2022)	General RNA degradation rate
k _{tr}	Trancription Rate Constant*	0.000779	M.s ⁻¹	(Stögbauer et al., 2012)	RNA Toehold and reporter transcription rate ~2.2 NtPs, this TU has around 1603 nucleotides
k _{tl}	Translation Rate Constant*	0.0344	S ⁻¹	Average translation rate -	Average translation rate in <i>E coli</i> ~8 amino acid per second

				Bacteria Escherichia coli - BNID 111689 (harvard.edu)	and aeBlue chromoprotein has 231 amino acids
k _{21_CLS}	miR21-CLS Complex Formation Constant	1 x 10⁵	M ⁻¹ .s ⁻¹	(Baabu et al., 2022)	miRNA-RNA toehold complex formation rate
k _{92_CLS}	miR92a-CLS Complex Formation Constant	1 x 10⁵	M ⁻¹ .s ⁻¹	(Baabu <i>et al.,</i> 2022)	miRNA-RNA toehold complex formation rate
k _{OLS192}	OLS1-miR92 Complex Formation Constant or OLSc Formation	1 x 10 ⁵	M ⁻¹ .s ⁻¹	(Baabu <i>et al.,</i> 2022)	miRNA-RNA toehold complex formation rate
k _{OLS221}	OLS2-miR21 Complex Formation Constant or OLSc Formation	1 x 10 ⁵	M ⁻¹ .s ⁻¹	(Baabu <i>et al.,</i> 2022)	miRNA-RNA toehold complex formation rate

*assumption: OLS₁, OLS₂, OLS_c have same degradation rate

Known that In E coli translation rate is 8 amino acids/second (<u>Average translation rate - Bacteria Escherichia coli - BNID 111689 (harvard.edu)</u>) and our aeBlue chromoprotein has 231 amino acids. So k_{tl} (**Translation Rate Constant**) = 1/average time for translation

Average time for translation = Number of amino acids × Time for addition of one amino acid

Time for addition of one amino acid = $\frac{1}{6}$ = 0.125 second per one amino acid

Average time for translation = 231×0.125

Translation Rate Constant = 1/231 × 0.125 = ~0.0344 / second

Trancription Rate Constant

molar_sec = 1603.62 nucleotide/sec / $(330 \text{ grams/mol} * 6.022 \text{ x } 10^{23} \text{ molecules/mol})$ molar_sec = 0.000779 molar/sec

References

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