

RNA-interference and Register Machines



Masahiro HAMANO

PRESTO, JST (Japan Science and Technology Agency)

MecBic 2012 Newcastle upon Tyne

Table of Contents

- RNA interference (RNAi)
- Naive Interpretation of RNAi in Minsky Register Machine
- RNAi as Chemical Reactions (Chemical Ground Form)
- Recursive RNAi and Probabilistic Termination
- Chemical Ground Form with Delayed Inputs

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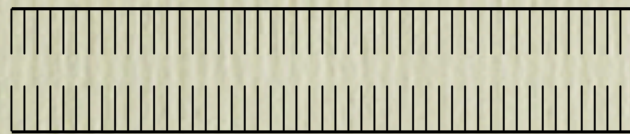
RNA interference

- RNAi (also known as RNA silencing) is a mechanism in which short interfering RNA's (siRNA's) (21~26 nt's) directly control gene expression.
- RNAi consists of three fundamental biochemical processes:

Step 1 RNAi

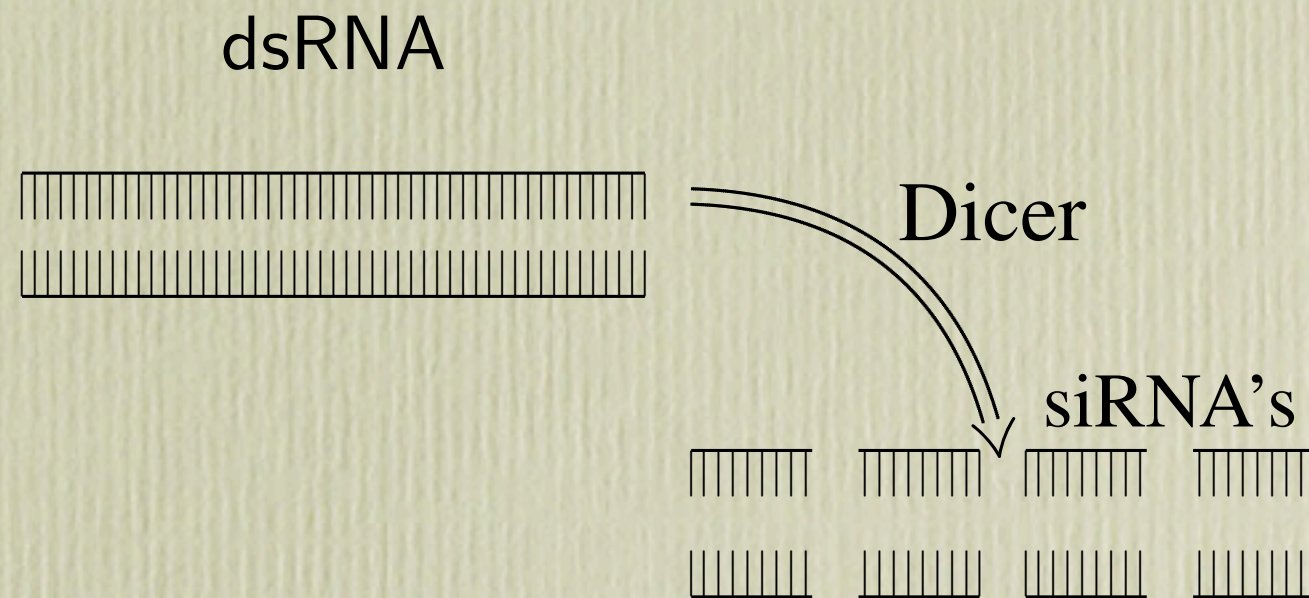
Formation of double stranded RNA (dsRNA)

dsRNA



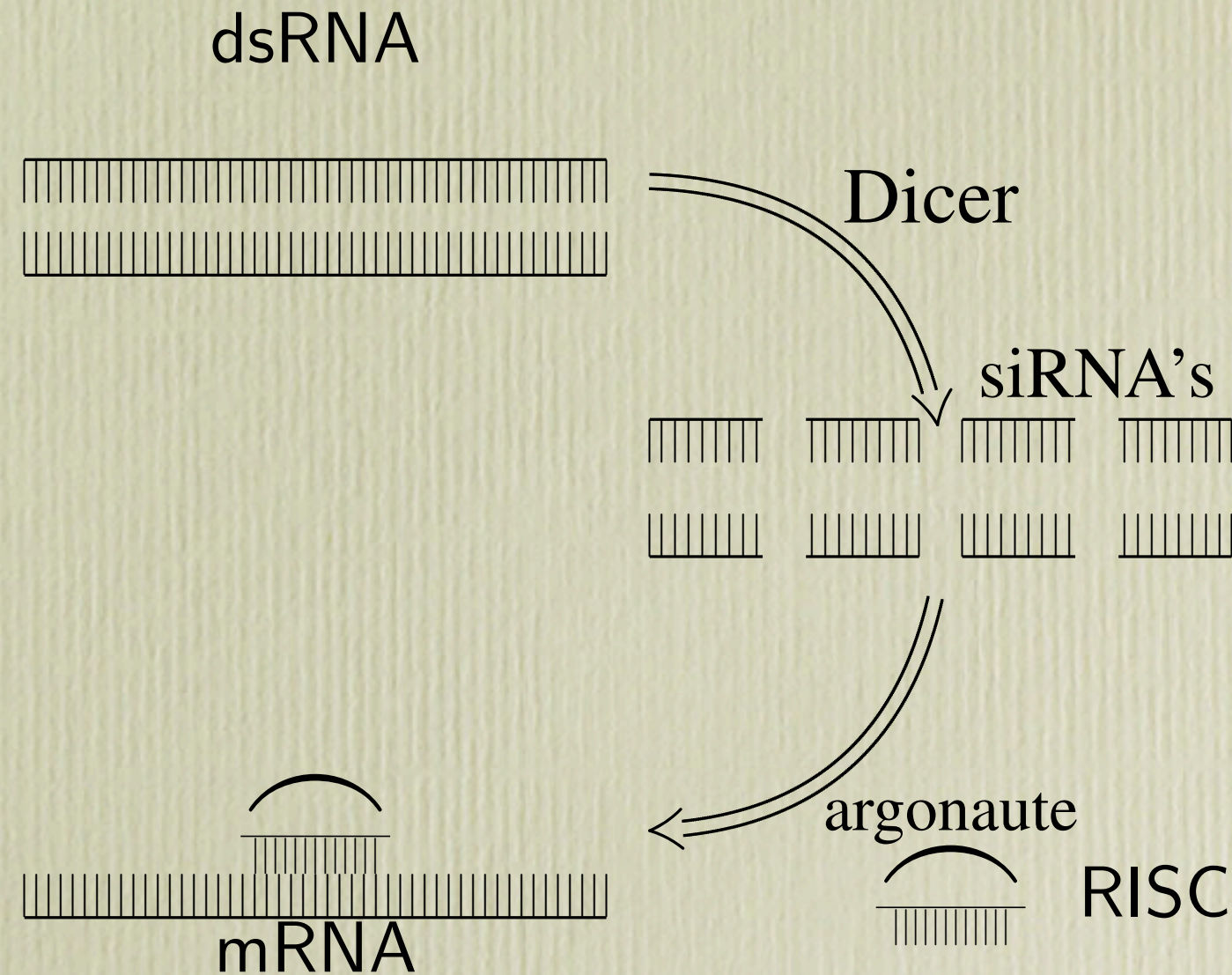
Step 2 RNAi

Dicer enzyme cleaves dsRNA into siRNA's:

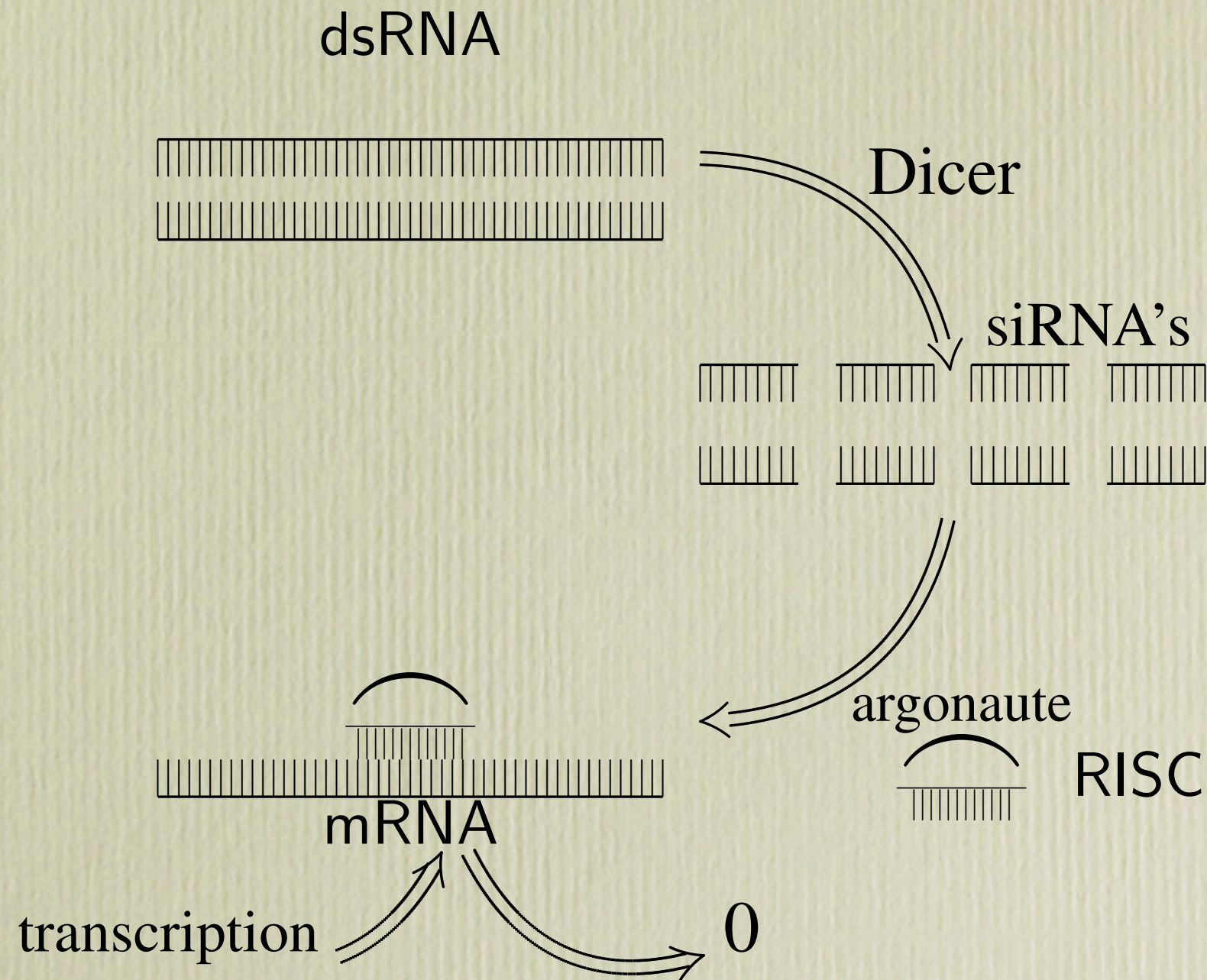


Step 3 RNAi

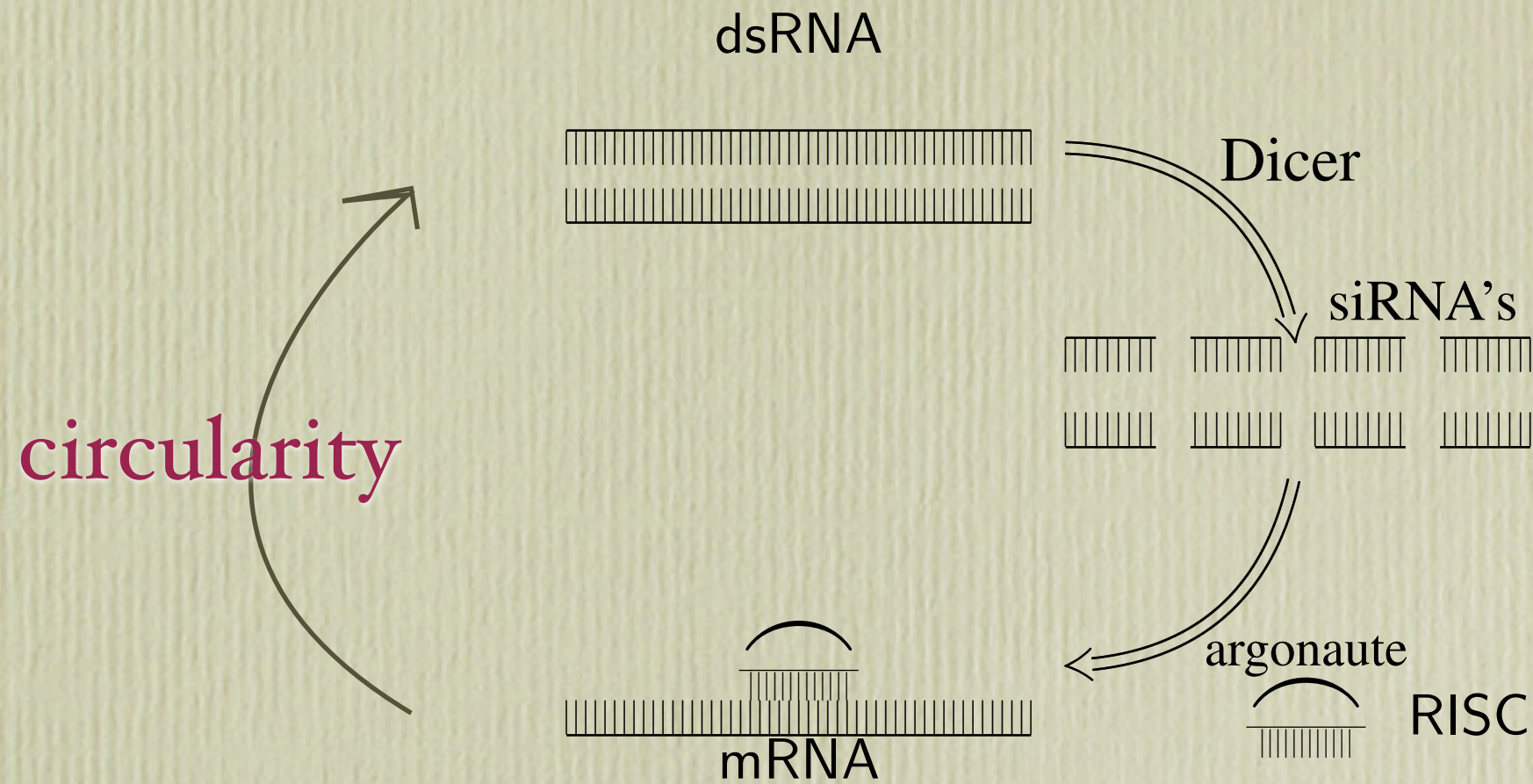
Incorporation of siRNA into RNA-induced silencing complex (RISC), targeting a long single-stranded mRNA by complementarity.



Finally, RISC degrades mRNA.

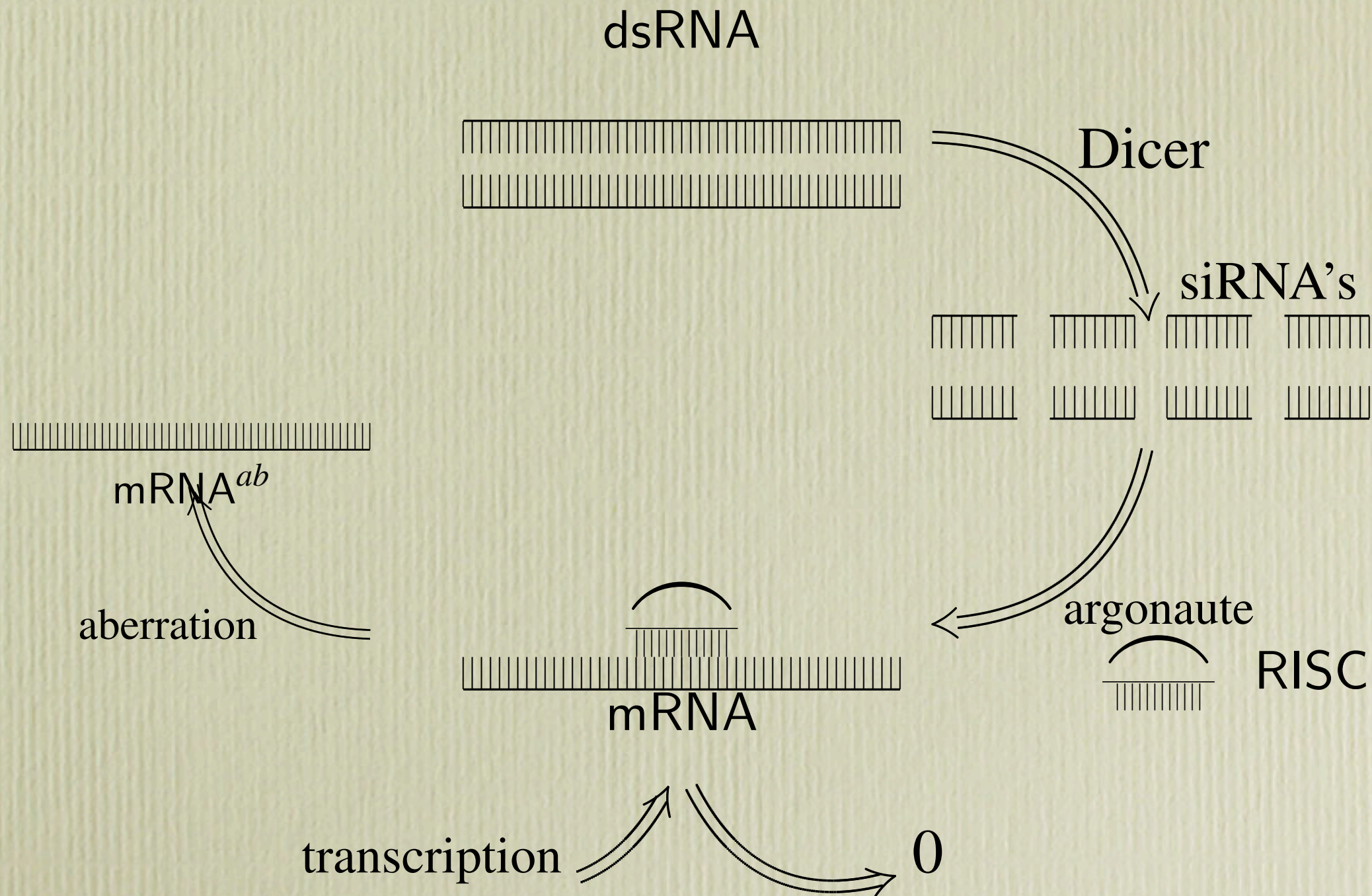


Moreover RNAi has a **circularity** to synthesize dsRNA

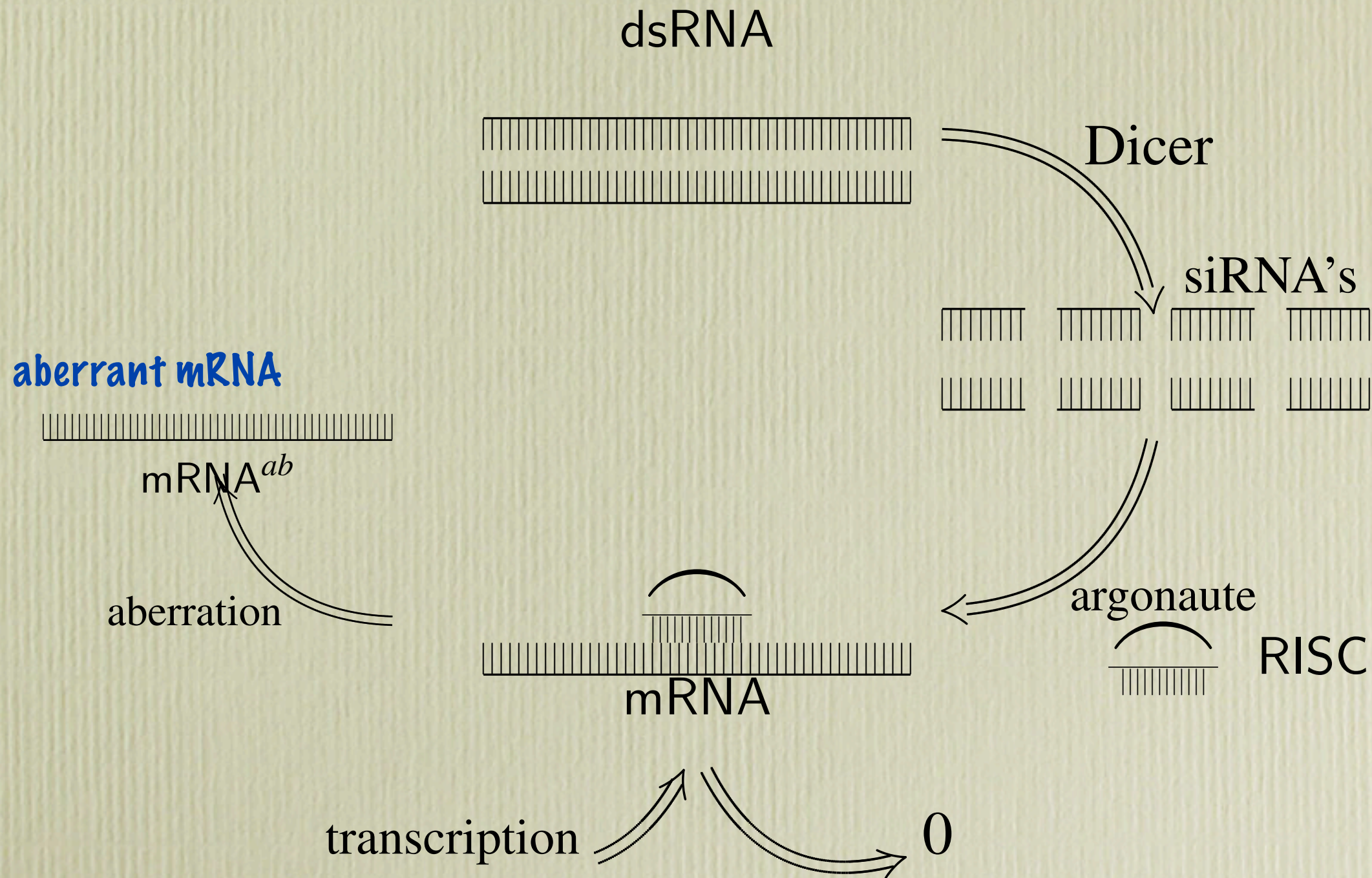


This is realized by
polymerization
of **aberrant mRNA** caused by RISC degradation

That is, RISC degrades mRNA **or** makes it **aberrated**.

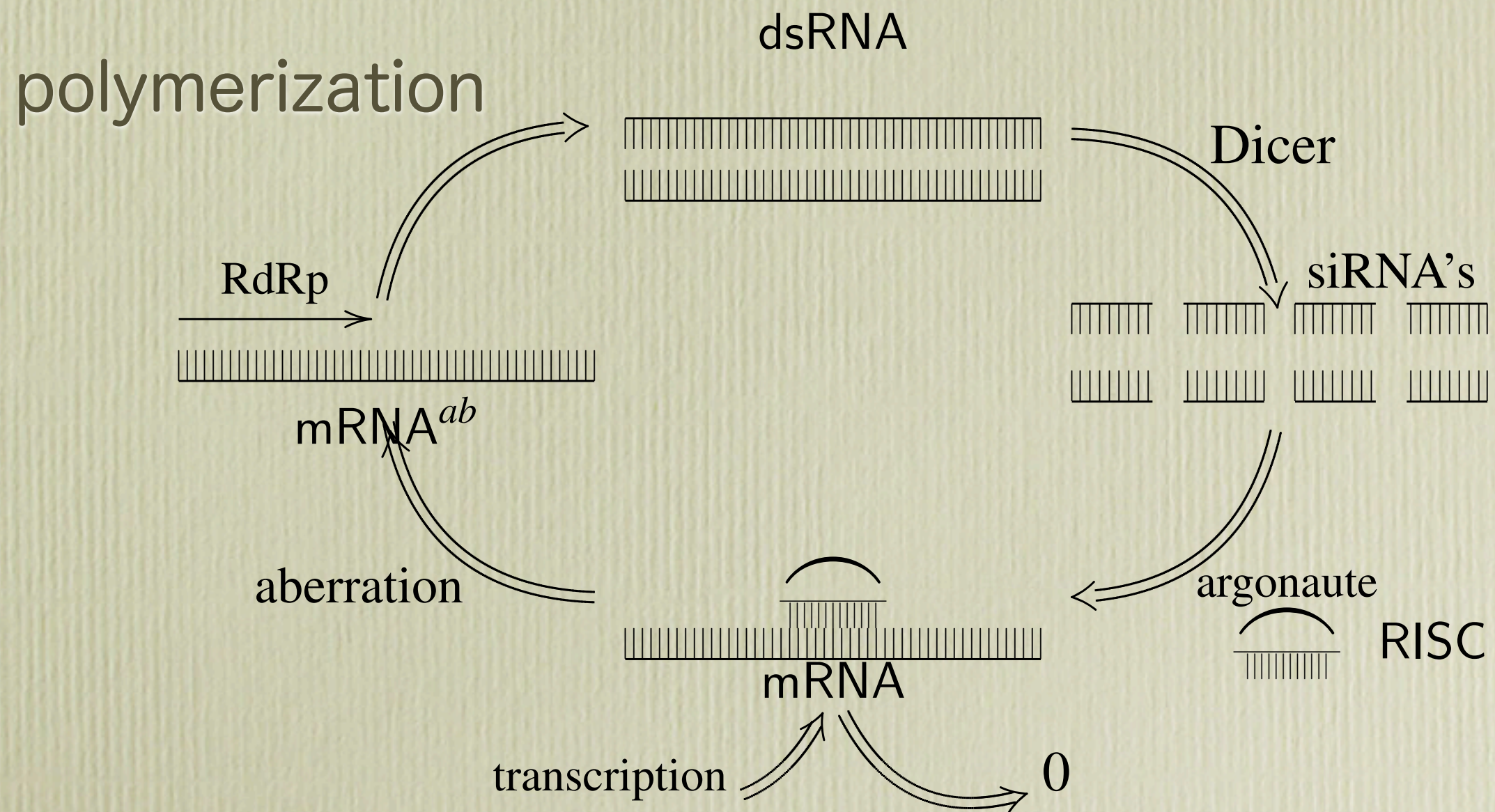


That is, RISC degrades mRNA **or** makes it **aberrated**.



Circularity of RNAi

by polymerization to duplicate dsRNA



Starting Point of Our Wotk

Given that

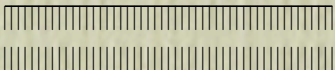
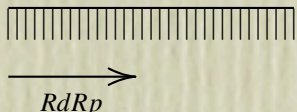
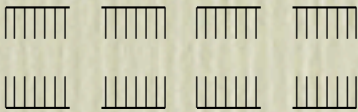
- Each Step of RNAi is digital
- Their combination maintains the circularity,

RNAi resembles a kind of (digital)
computation !



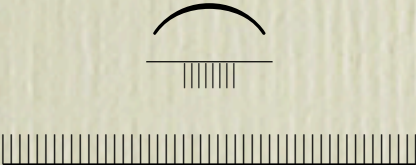
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A Naive Interpretation of RNAi in Register Machine

register	values	increment/decrement
r_1	<div>$\overbrace{\text{dsRNA} \mid \cdots \mid \text{dsRNA}}^{m_1}$ dsRNA </div>	<div>$\text{Inc}(r_1) := RdRp$ </div> <div>$\text{Dec}(r_1) := Dicer$ </div>

(a) register r_1

register	values	increment/decrement
r_2	<div>$\overbrace{\text{mRNA} \mid \cdots \mid \text{mRNA}}^{m_2}$ mRNA </div>	<div>$\text{Inc}(r_2) := \text{transcription}$ </div> <div>$\text{Dec}(r_2) := \text{RISC}$ </div>

(b) register r_2

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Chemical Ground Form (Cardelli 2008)

(a minimal stochastic process calculus describing chemical reactions)

- Interaction Prefix $\tau_{(r)} \dot{?} a_{(r)} \dot{!} a_{(r)}$
- Parallel Composition $|$ and choice \oplus

Molecule-decay

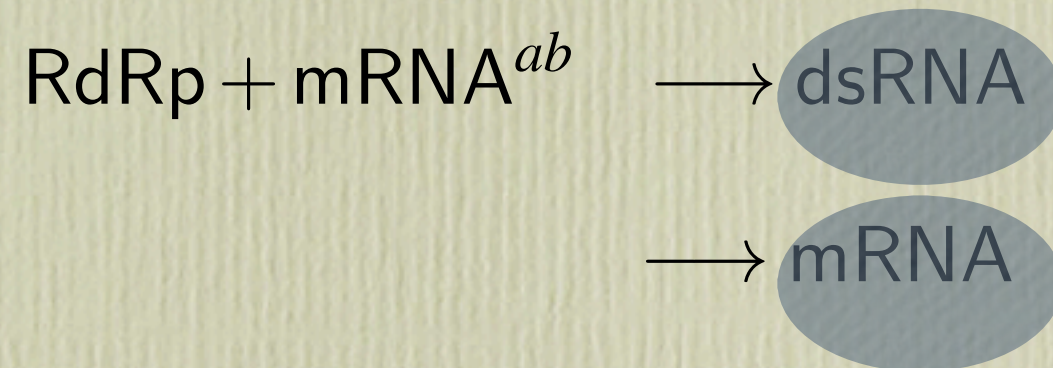
$$\dots \oplus \tau_{(r)}.Q \oplus \dots \longrightarrow Q$$

Molecules-collision

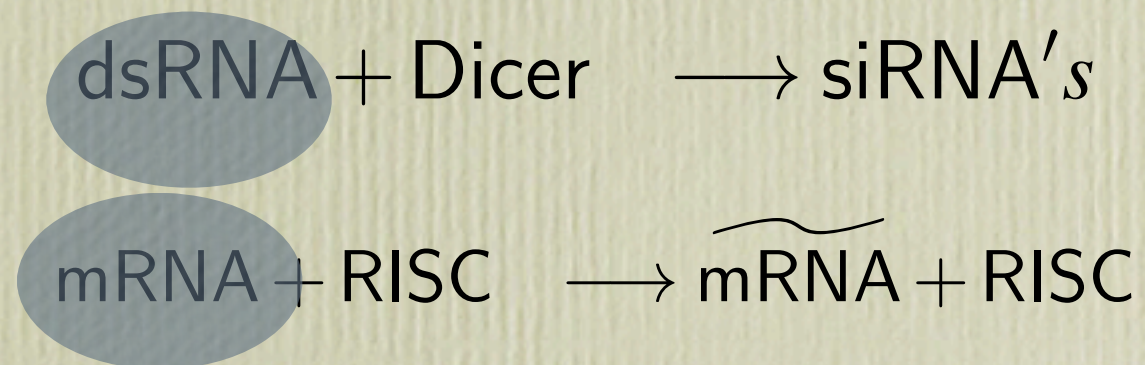
$$\dots \oplus ?a_{(r)}.Q \oplus \dots \mid \dots \oplus !a_{(r)}.R \oplus \dots \longrightarrow Q \mid R$$

RNAi as Chemical Reactions

- Increment



- Decrement



RNAi in CGF

- Registers $r_1 = \prod_{l_1} \text{dsRNA}$ $r_2 = \prod_{l_2} \text{mRNA}$

$$\text{dsRNA} := ?a_1.(\text{siRNA} \mid \dots \mid \text{siRNA})$$

$$\text{mRNA} := ?a_2.(\tau.0 \oplus \tau.\text{mRNA}^{ab})$$

- Increment $I_i = \text{Inc}(r_j)$

$$I_i = \text{RdRp} \mid \tau.I_{i+1}$$

j=1

$$I_i = \text{mRNA} \mid \tau.I_{i+1}$$

j=2

- Decrement $I_i = \text{DecJump}(r_j, s)$

$$I_i = !a_1.(0 \mid I_{i+1}) \oplus \tau.I_s \quad \text{with Dicer} = !a_1.(0 \mid I_{i+1})$$

j=1

$$I_i = !a_2.(\text{RISC} \mid I_{i+1}) \oplus \tau.I_s \quad \text{with RISC} = !a_2.(\text{RISC} \mid I_{i+1})$$

j=2

Decrement Instruction I_i makes an error !

$$I_i = \text{DecJump}(r_j, s)$$

wrongly jumps to I_s even if the register $r_j \neq 0$.

$$I_i = \underbrace{!a_j}_{\text{decrement}} \cdot (0 \mid I_{i+1}) \oplus \underbrace{\tau}_{\text{jump}} \cdot I_s \quad \text{Register} = \prod ?a_j \dots$$

Due to the absence of zero-test against the registers,
which is related to Turing Incompleteness of CGF.

Zavattaro-Cardelli (2008) Soloveichik-Winfrey, et al. (2008)

Question:

How to probabilistically **moderate** the error jumps of RNAi in CGF ?

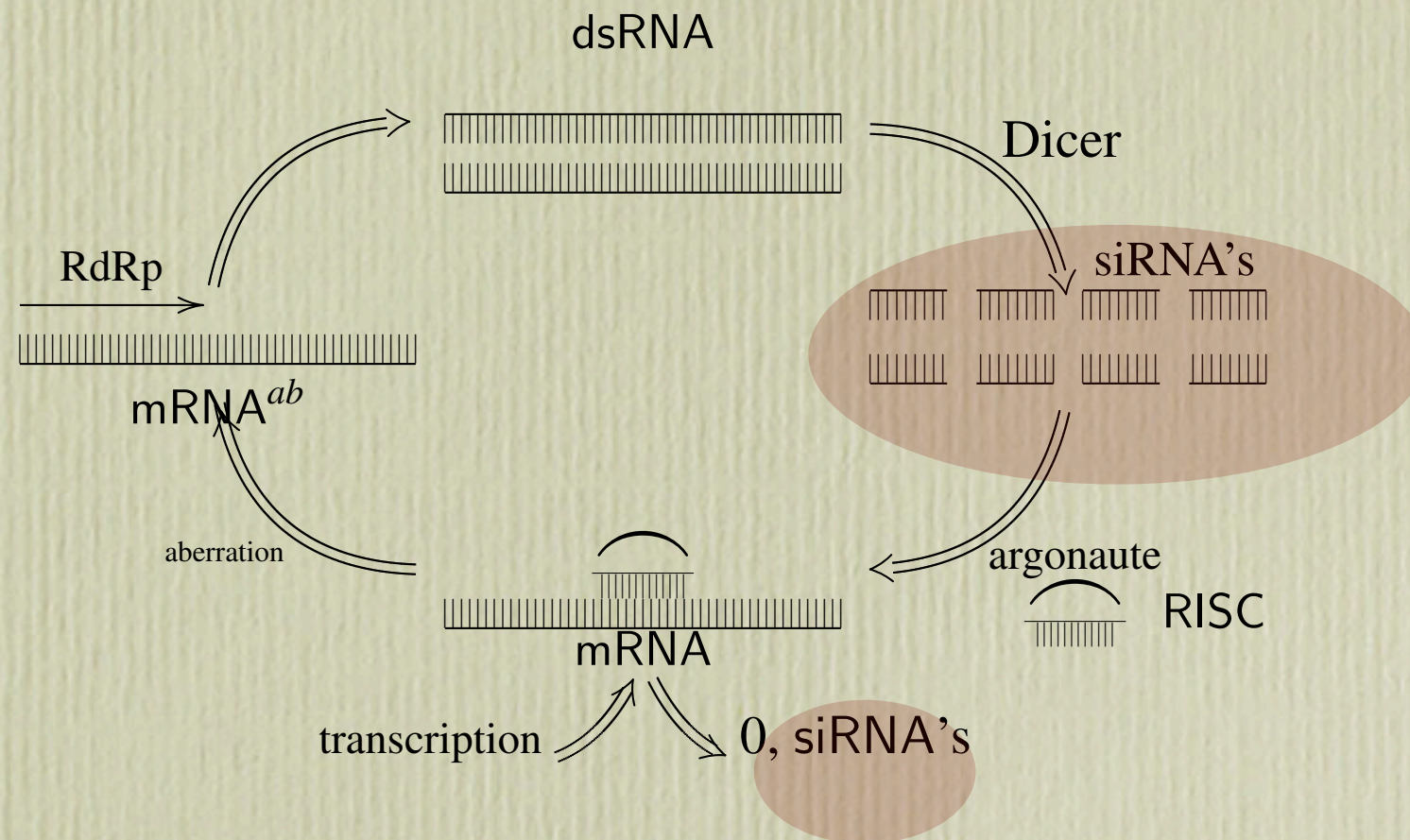
We propose:

- Theoretical idea of **Inhibitors** for the decrement instructions (motivated by Zavattaro-Cardelli 2008)
- The inhibitors are realized by a biological extension of **Recursive RNAi** !

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For recursive RNAi,

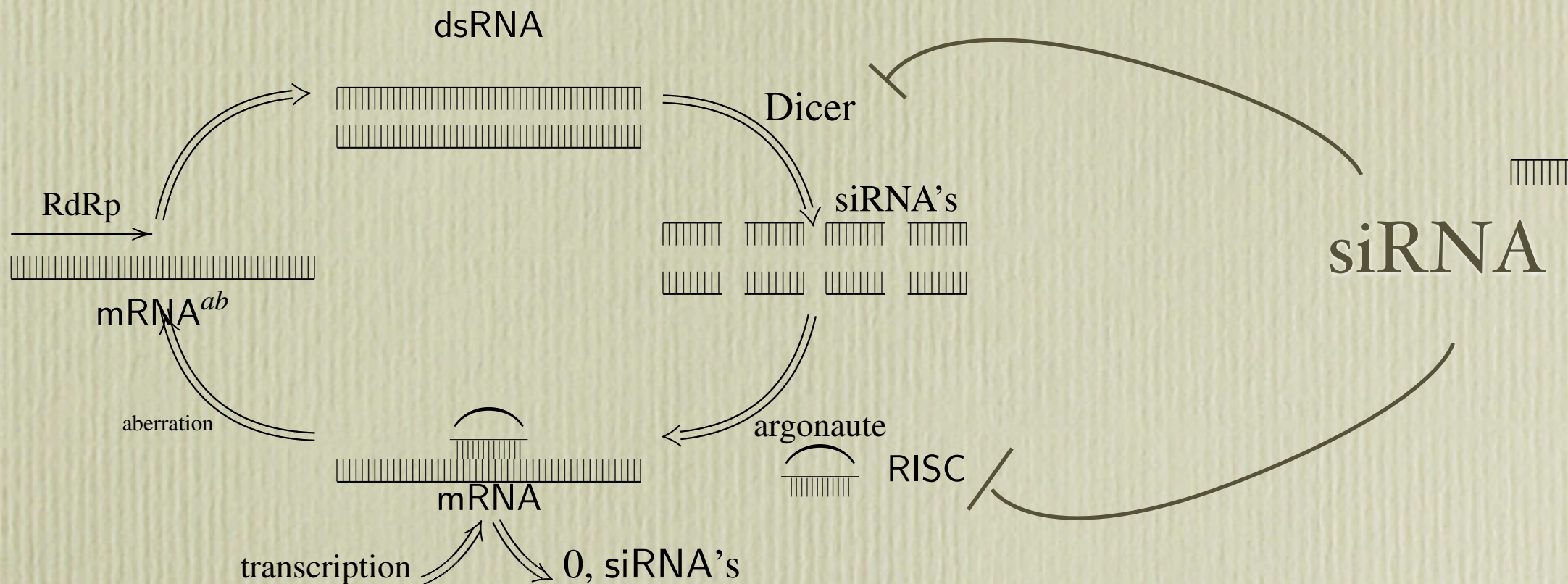


siRNAs floating/growing during the interference are to be taken into account !

Recursive RNAi (recRNAi)

Xie Z, Kasschau KD, Carrington JC, Negative feedback regulation of Dicer-like1 in Arabidopsis by microRNA-guided mRNA degradation. Curr Biol (2003)

feedback linkage in RNAi



siRNA inhibits (not only mRNA but also) Dicer and RISC.
I.e., siRNA inhibits the decrement instructions.

recRNAi in CGF with Fixed Points

$$I_i = \text{DecJump}(r_j, I_s)$$

$$\text{siRNA} = ?s.\text{siRNA}$$

$$I_i = \underbrace{!a_j.(0 \mid I_{i+1})}_{\text{Dicer cleaving dsRNA}} \oplus \underbrace{\tau.(!s.I_i \oplus \tau.I_s)}_{\text{Dicer being degraded by siRNA}}$$

Dicer cleaving dsRNA

Dicer being degraded by siRNA

$$(\ = \ \text{fix}_X.[a.(0 \mid I_{i+1}) \oplus \tau.(!s.X \oplus \tau.I_s)] \)$$

State with h-inhibitors of siRNAs

Given a state $(I_i, r_1 = l_1, r_2 = l_2)$ and a natural number h ,

$$\llbracket (I_i, r_1 = l_1, r_2 = l_2) \rrbracket_h := I_i \mid \prod_{l_1} \text{dsRNA} \mid \prod_{l_2} \text{mRNA} \mid \prod_h \text{siRNA}$$

recRNAi probabilistically computes

Given machine's one step computation

$$(I_i, r_1 = l_1, r_2 = l_2) \longmapsto (I_j, r_1 = l'_1, r_2 = l'_2)$$

- Inc is **precise**

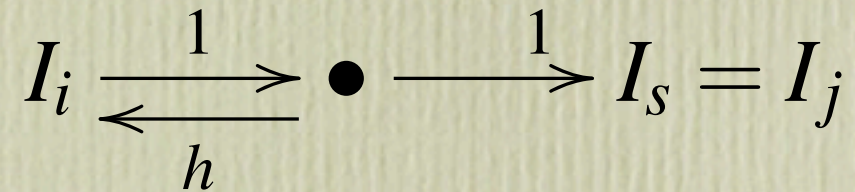
$\llbracket (I_i, r_1 = l_1, r_2 = l_2) \rrbracket_h$ is reachable to $\llbracket (I_j, r_1 = l'_1, r_2 = l'_2) \rrbracket_h$
with probability 1

- DecJump is **probabilistic** $> 1 - 1/h$

$\llbracket (I_i, r_1 = l_1, r_2 = l_2) \rrbracket_h$ is reachable to $\llbracket (I_j, r_1 = l'_1, r_2 = l'_2) \rrbracket_k$
for some $k \geq h+1$ with probability $> 1 - 1/h$

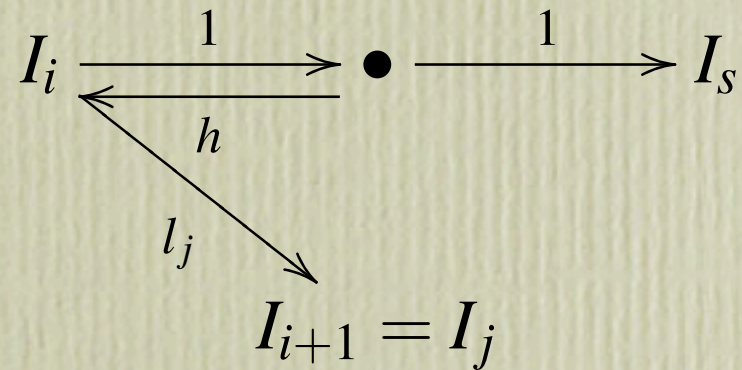
DecJump is probabilistic $> 1 - 1/h$

$$l_j = 0$$



$$\sum_{i=0}^{\infty} \left(\frac{h}{h+1}\right)^i \times \frac{1}{(h+1)} = 1$$

$$l_j \neq 0$$



$$\sum_{i=0}^{\infty} \left(\frac{1}{l_j+1} \times \frac{h}{h+1}\right)^i \times \frac{l_j}{l_j+1} > 1 - \frac{1}{h}$$

Probabilistic Termination

The following is equivalent

- Register Machine starting from $(I_j, r_1 = l_1, r_2 = l_2)$ terminates.
- RecRNAI starting from $\llbracket (I_j, r_1 = l_1, r_2 = l_2) \rrbracket_h$ probabilistically terminates with probability
$$> 1 - \sum_{k=h}^{\infty} \frac{1}{k}.$$

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Turing Complete Extensions of CGF

Cardelli-Zavattaro (2010)

BGF

(Biochemical GF)

association/dissociation
of agents

We propose

CGF

with delayed Inputs

CGF

Delayed Inputs

(for Π -calculus) van Breugel '97 , Merro-Sangiorgi '98

- Self Communication

$$!a. (?a. P \oplus M) \rightarrow P$$

- Guarding

$$?b. R \oplus N \mid !a. (?a. P \oplus M) \rightarrow ?b. R \oplus N \mid P$$

only if $b \neq a$.

Precise Encoding of RM into CGF with Delayed Inputs

By entangling channels,

- DecJump Instruction I_i

$$I_i = \text{DecJump}(r_j, s) = !a_j. (?a_j.I_s \oplus !b.I_{i+1})$$

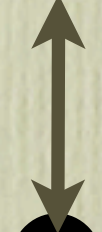
- Registers

$$r_j = \overbrace{?a_j.?b.0 \mid \cdots \mid ?a_j.?b.0}^{l_j}$$

Preciseness

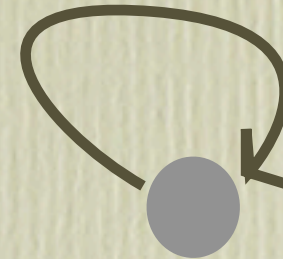
- Register hold $\neq 0$

DecJump



Register

- Register holds 0



$$?a_j. ?b.0 \mid !a_j. (?a_j.I_s \oplus !b.I_{i+1})$$

$$\longrightarrow ?b.0 \mid ?a_j.I_s \oplus !b.I_{i+1}$$

$$\longrightarrow 0 \mid I_{i+1}$$

$$!a_j. (?a_j.I_s \oplus ?b.I_{i+1})$$

$$\longrightarrow I_s$$

CGF with delayed input is
Turing complete.

Future Work

- Computational meaning of RNAi with another pathway of polymerization ?