

Modelling DNA sequence evolution with interacting particle systems

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1 Nucleotidic substitution processes

- The origins: Jukes and Cantor model
- Entering the field of interacting particle systems
- Model properties

2 Extension

- Adding 'cut-and-paste' mechanism
- Results
- How to use the dual process

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Stochastic nucleotidic substitution models

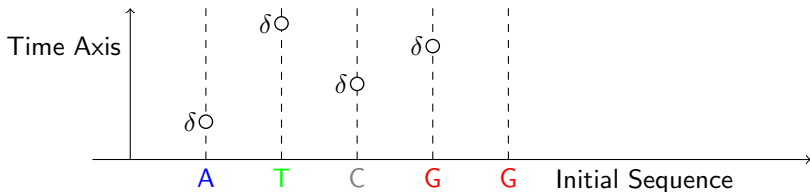
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- **Independent** evolution of the sites according to a **Markovian kernel**.

Example: Jukes and Cantor model (1969)

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- **Diagonal** entry $-q_{aa}$ is the substitution rate of nucleotide a , here $q_{aa} = -3\lambda$.

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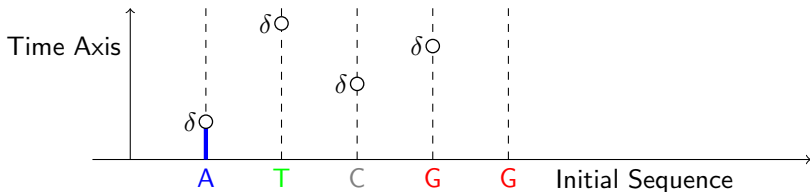
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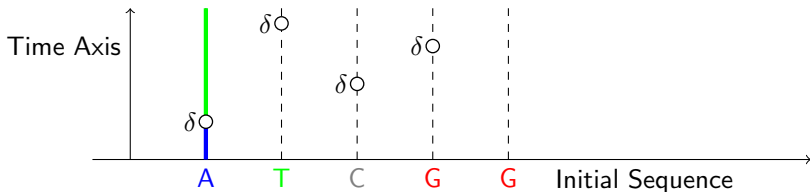
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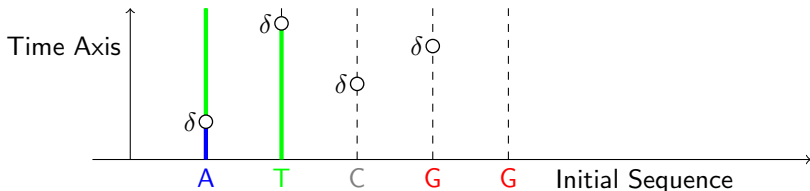
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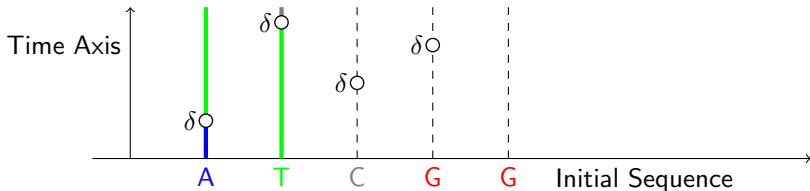
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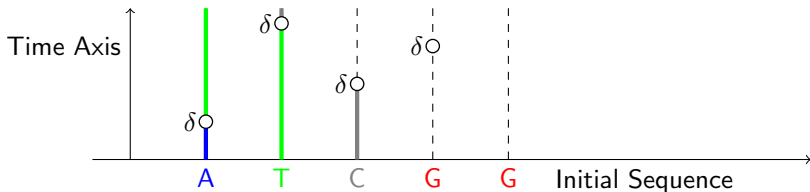
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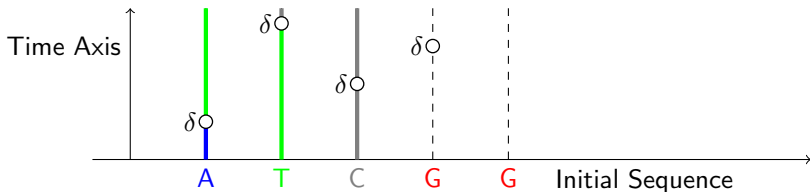
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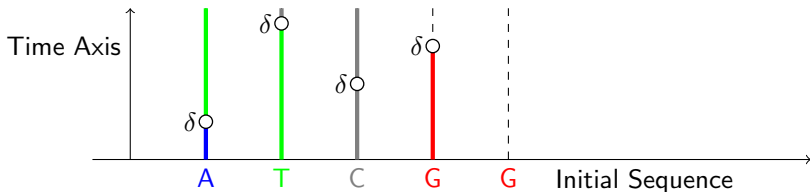
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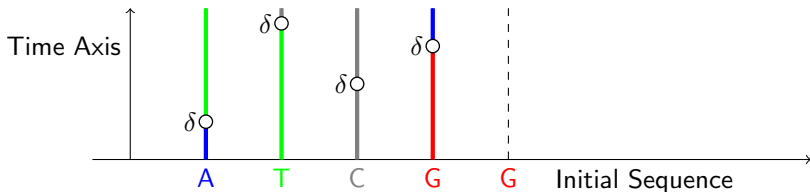
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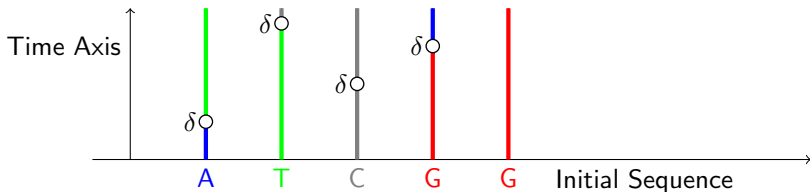
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Stochastic nucleotidic substitution models

Consequences

- Convergence in distribution at any site
- Convergence in distribution of the whole sequence to the **product measure**.

Problems

- $(a_1 \dots a_\ell)_{\text{obs}} \neq (a_1)_{\text{obs}} \dots (a_\ell)_{\text{obs}}$.
- The substitution rate $\eta(x) \rightarrow a$ may **depend** on $\eta(x-1)$, $\eta(x)$ and $\eta(x+1)$.

Famous example : CpG dinucleotides

- Rate C \rightarrow T up to ten times larger when C is involved in a CpG (in fact C*_pG).

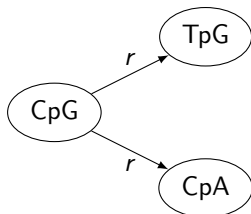
JC+CpG model

Bérard, Gouéré et Piau, *Mathematical Biosciences* (2008)

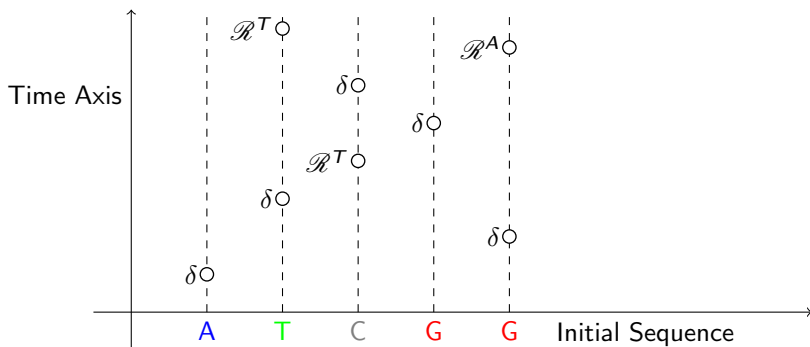
- A DNA sequence η is now **doubly infinite**, that is, an element of $\{A, T, C, G\}^{\mathbb{Z}}$.
- **Keep** Jukes and Cantor model

	A	T	C	G
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T	1	.	1	1
C	1	1	.	1
G	1	1	1	.

- **Superimpose** "double" substitution mechanism

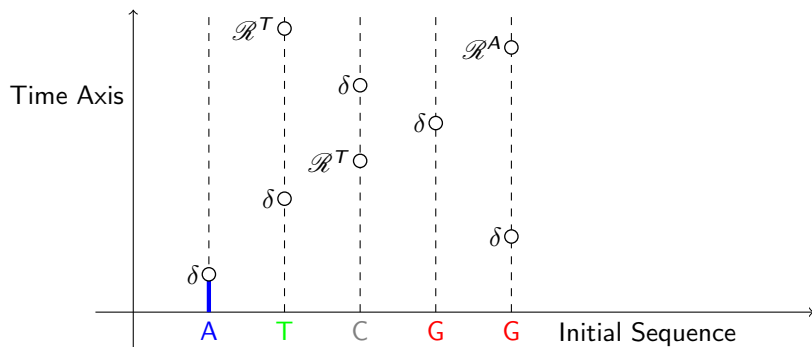


Construction with marked Poisson point processes



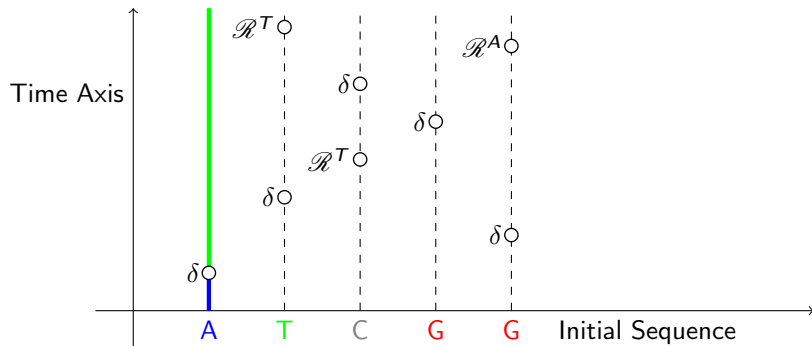
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δ	1	\dots with probability $1/4$.
R^a	r	\dots if $\eta(x, x+1) = CG$ and $a = T$ or if $\eta(x-1, x) = CG$ and $a = A$.

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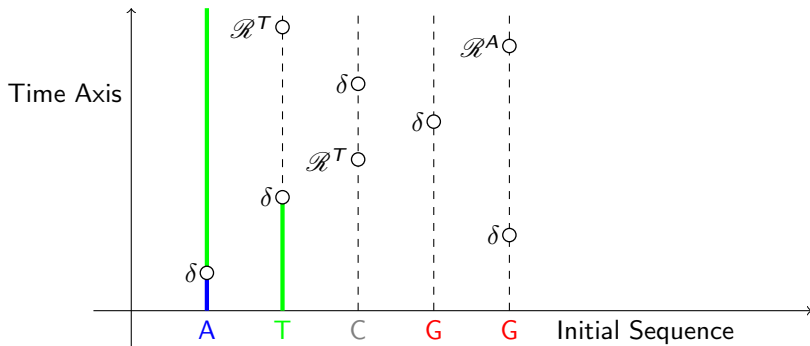
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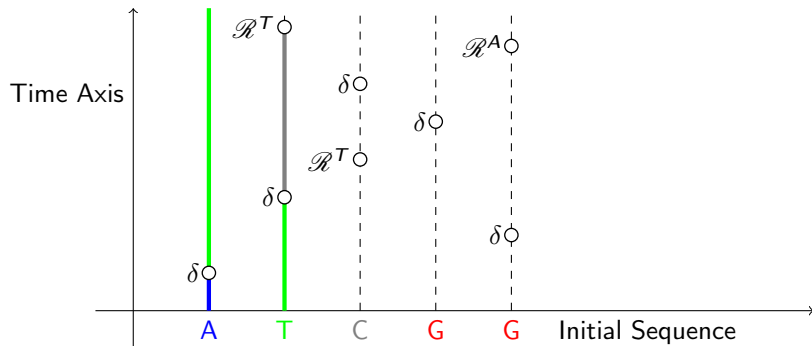
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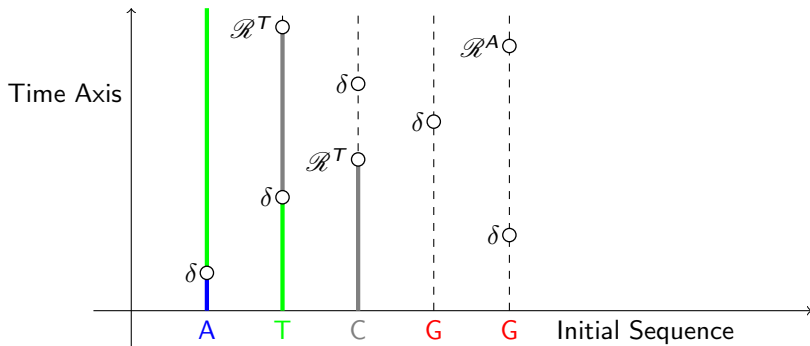
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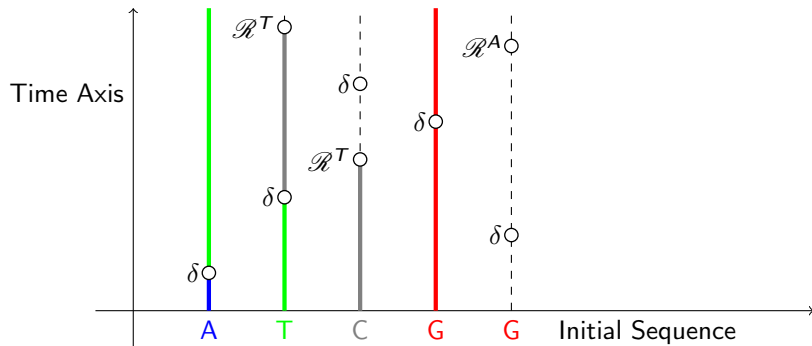
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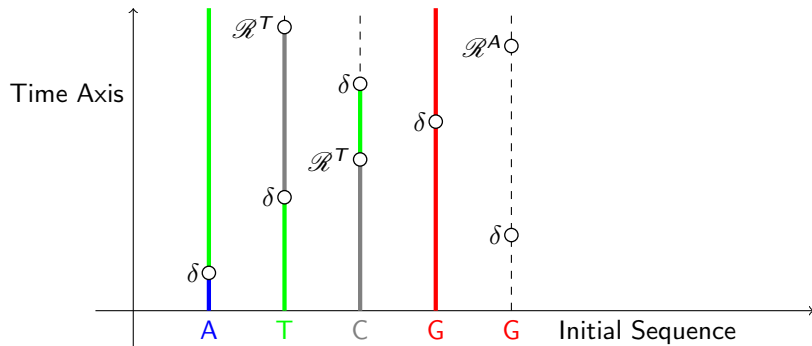
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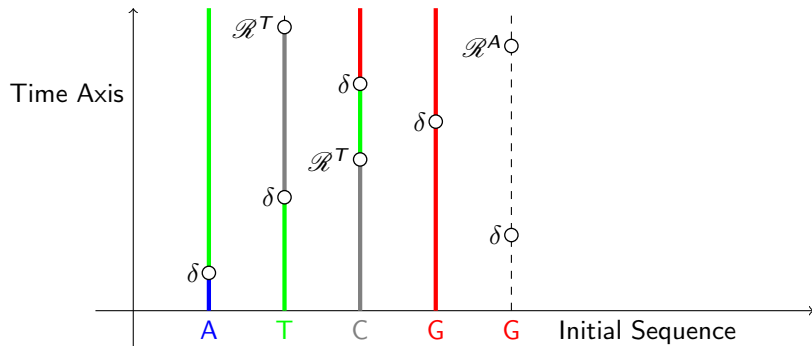
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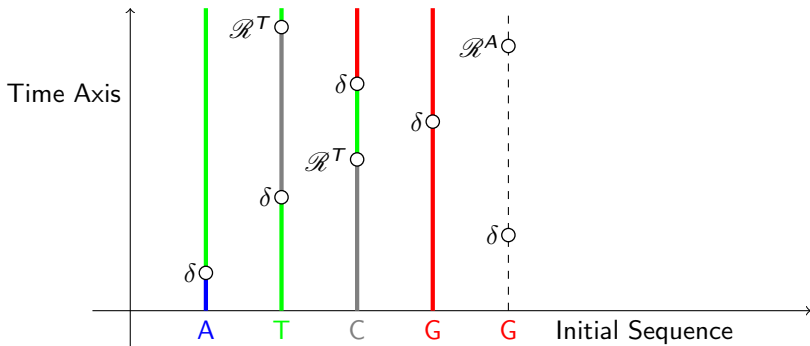
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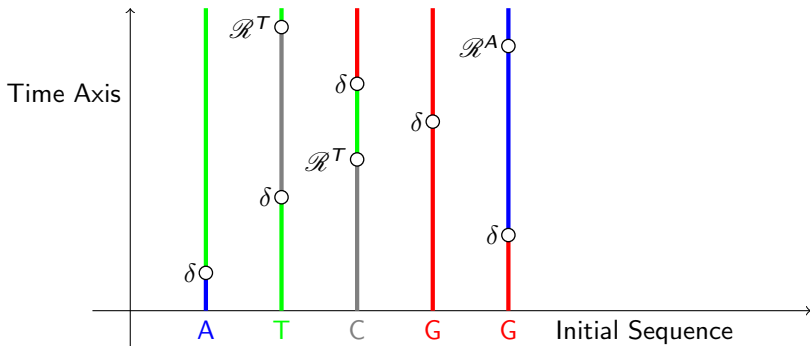
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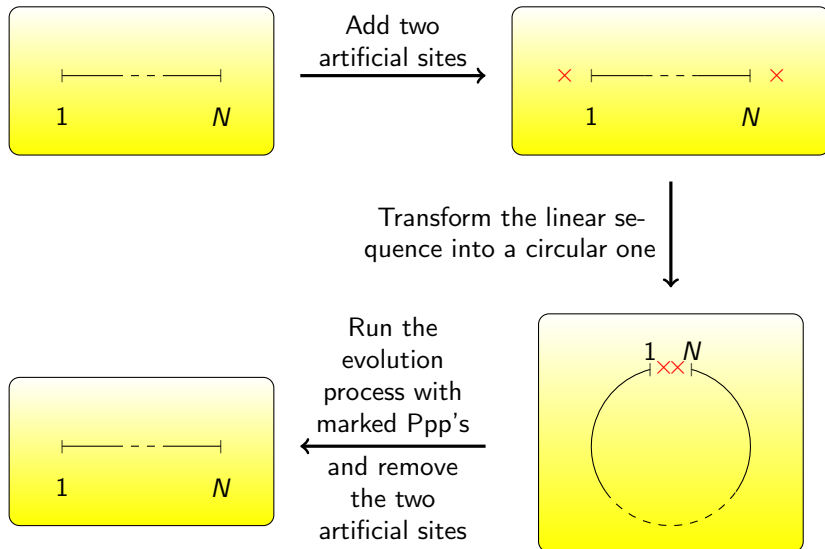
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Properties

Bérard, Guéré et Piau, *Mathematical Biosciences* (2008)

- **There exists a unique Markov process** on $\mathcal{A}^{\mathbb{Z}}$ with the transition rates defined before.
- The process is **ergodic**, its unique invariant probability measure π on $\mathcal{A}^{\mathbb{Z}}$ is **translation invariant** and **ergodic** with respect to the translations on \mathbb{Z} .
- Any collections $(\eta_x)_{x \in I}$ and $(\eta_y)_{y \in J}$ are **independent** as soon as $\text{dist}(I, J) \geq 3$.

Simulate the evolution of a finite DNA sequence



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Substitution processes

- Only one coordinate changes in each transition.
- The transition mechanism is specified by a non-negative function c defined on $\mathbb{Z} \times \mathcal{A} \times X$, with \mathcal{A} a finite alphabet and $X = \mathcal{A}^{\mathbb{Z}}$.
- We assume that, for any fixed site x and target a , the function $c(x, a, \cdot)$ depends on $\eta \in X$ only through a finite set $S_x^a \subset \mathbb{Z}$ depending on x and a .

Sufficient conditions for its existence

$$K = \sup\{c(x, a, \eta) : x \in \mathbb{Z}, a \in \mathcal{A}, \eta \in X\} < \infty \quad (1)$$

$$\text{and } s = \sup\{|S_x^a| : x \in \mathbb{Z}, a \in \mathcal{A}\} < \infty. \quad (2)$$

Example: JC+CpG

$$S_x^A = \{x-1, x\} \quad \text{and} \quad c(x, A, \eta) = \begin{cases} 1+r & \text{if } \eta(x-1, x) = CG, \\ 1 & \text{else,} \end{cases}$$

$$S_x^T = \{x, x+1\} \quad \text{and} \quad c(x, T, \eta) = \begin{cases} 1+r & \text{if } \eta(x, x+1) = CG, \\ 1 & \text{else,} \end{cases}$$

$$S_x^C = \emptyset \quad \text{and} \quad c(x, C, \eta) = 1,$$

$$S_x^G = \emptyset \quad \text{and} \quad c(x, G, \eta) = 1.$$

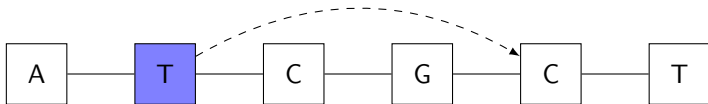
Example of single 'cut-and-paste'



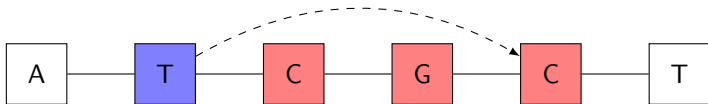
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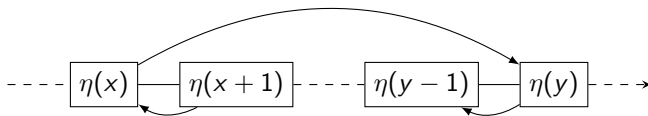


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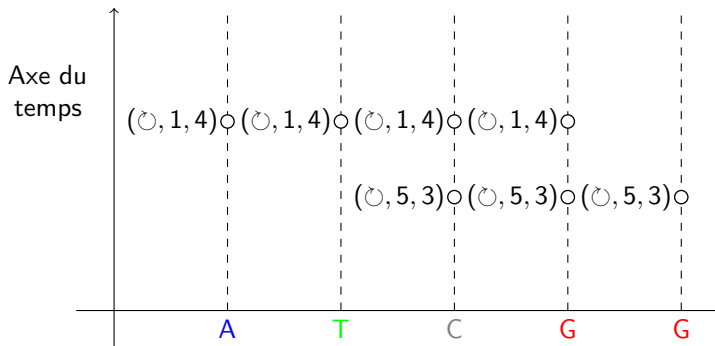
'Cut-and-paste' process

- The transition mechanisms are **circular permutations** of finitely many sites of \mathbb{Z} and are specified by a **transition probability matrix** p on $\mathbb{Z} \times \mathbb{Z}$ and a **cut rate per site** $\rho \geq 0$.
- The value $\rho \cdot p(x, y)$ represents the rate at which the coordinate $\eta(x)$ is transferred to site y . We assume that p is translation invariant on \mathbb{Z} .



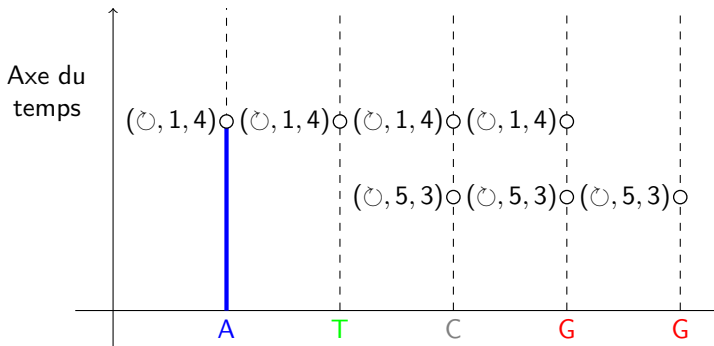
Sufficient condition for its existence: $\sum |x|p(0, x) < \infty$

Construction with marked Poisson point processes



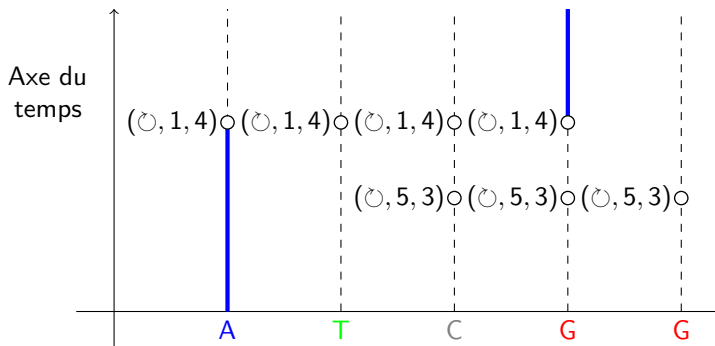
- Mark (\odot, x, y) distributed at rate $\rho \cdot p(x, y)$. If $x < y$, the contents of sites $x, x + 1, \dots, y$ are right circularly permuted. If $x > y$, the contents of sites $y, y + 1, \dots, x$ are left circularly permuted.

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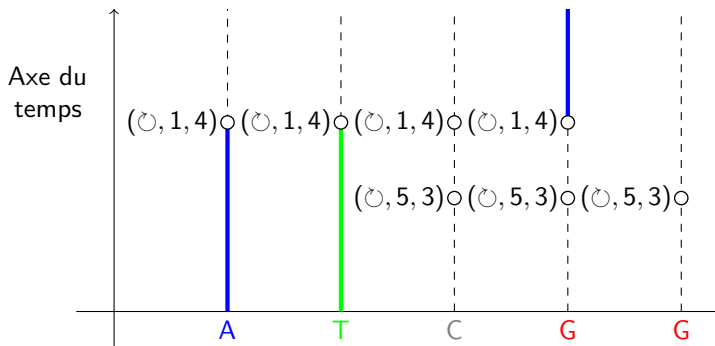
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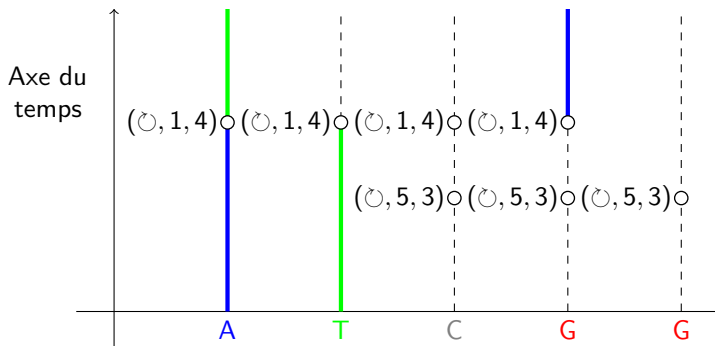
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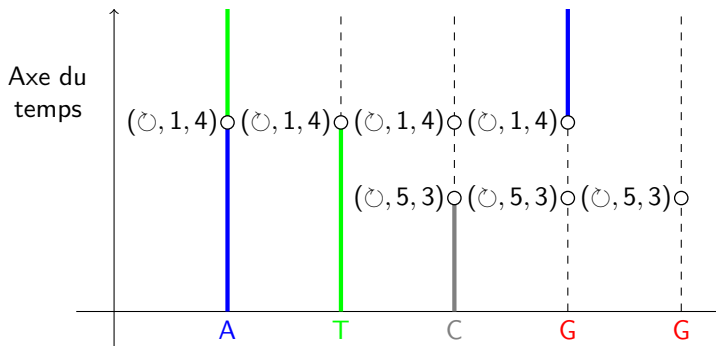
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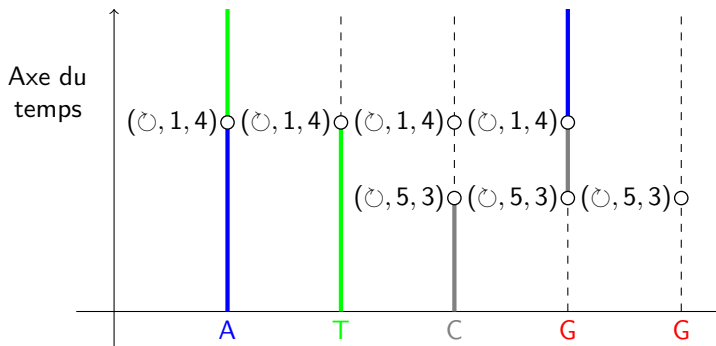
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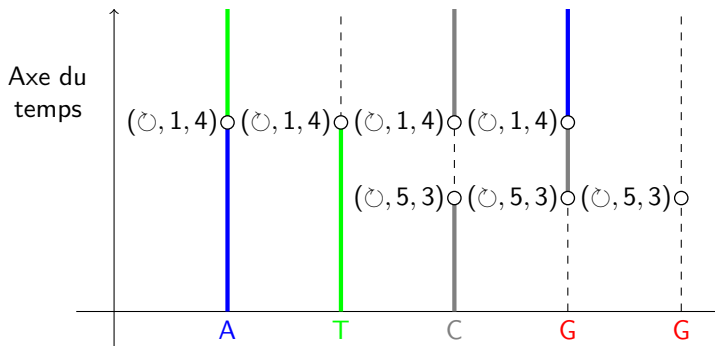
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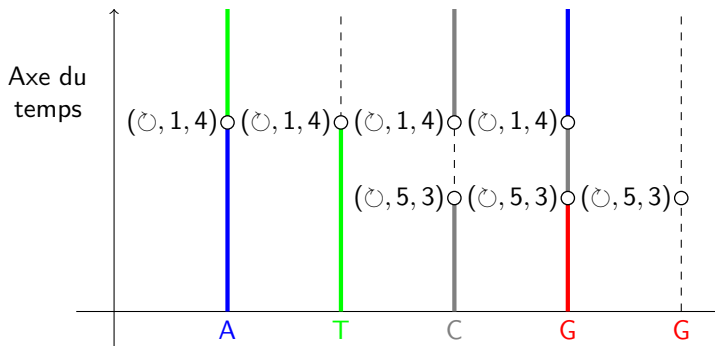
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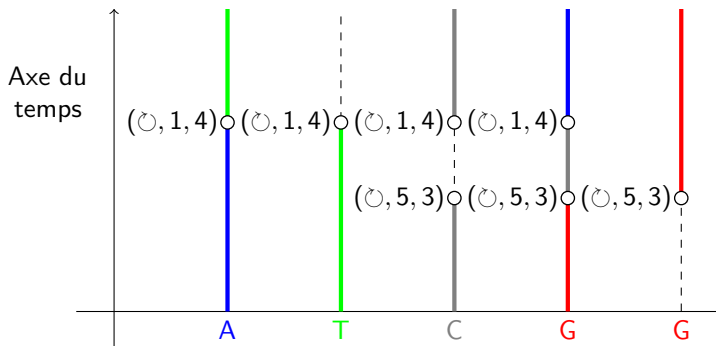
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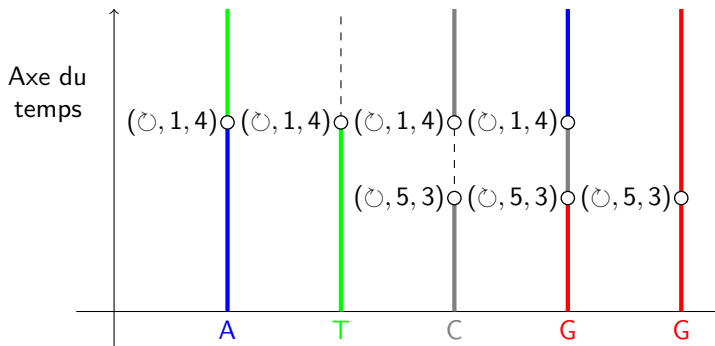
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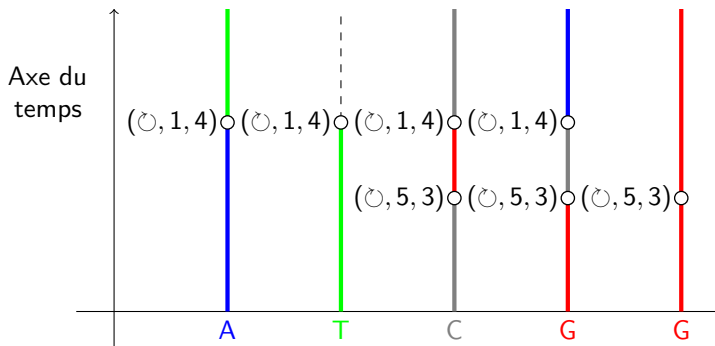
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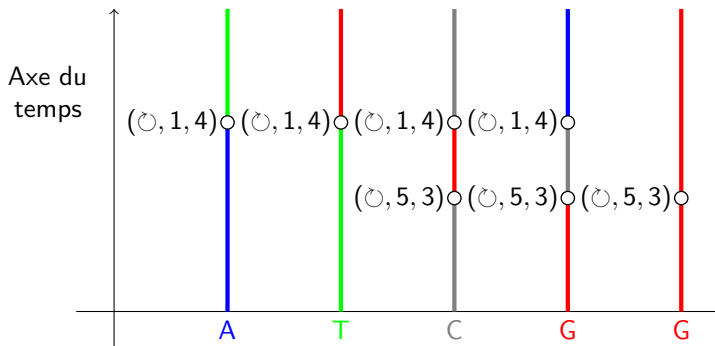
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Ergodicity for independent evolution models with 'cut-and-paste'

Theorem (Falconnet, Gantert and Saada)

Assume that the substitution rates are **independent** and are ruled by an irreducible Q -matrix. Then the process is **ergodic** and the invariant measure is the product measure on \mathbb{Z} .

- Especially, for any usual substitution model (JC69, K80, T92, etc.) and any 'cut-and-paste' mechanism invariant by translation, the dynamic of the process is ergodic.

Ergodicity for substitution processes with 'cut-and-paste' mechanism

Theorem (Falconnet, Gantert and Saada)

Define

$$\begin{aligned} m &= \inf\{c(x, a, \eta) : x \in \mathbb{Z}, a \in \mathcal{A}, \eta \in X\}, \\ K &= \sup\{c(x, a, \eta) : x \in \mathbb{Z}, a \in \mathcal{A}, \eta \in X\}, \\ s &= \max_{x \in \mathbb{Z}, a \in \mathcal{A}} |S_x^a|. \end{aligned} \quad (3)$$

Assume that

$$m > 0 \quad \text{and} \quad (s - 1)(K - m) < |\mathcal{A}|m.$$

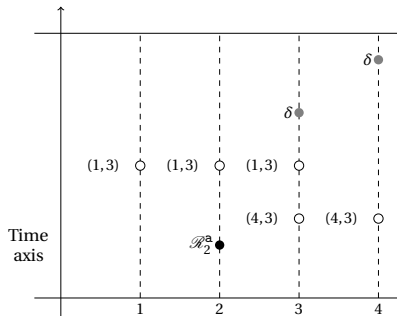
Then, for any $\rho \geq 0$, the superimposition of a substitution process and a 'cut-and-paste' mechanism is **exponentially ergodic**.

Especially, the JC+CpG+'cut-and-paste' model is ergodic as soon as

$$r < 4\lambda.$$

Method : construction of a generalized dual process. Inspired from Ferrari, **Annals of probability (1990)**.

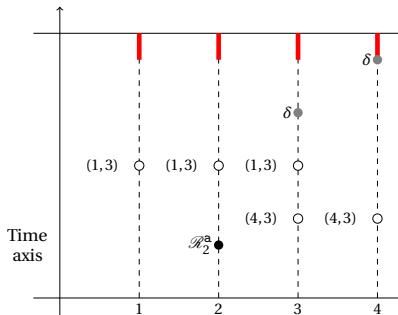
Introduction of a marked branching structure



When we go back in time and the dual process meets

- a δ -mark at site x , the branch **dies**;
- a \mathcal{R}^a -mark at site x , the branch dies and **is replaced** by 2 new branches.
- a (x, y) -mark, the involved branches are **circularly permuted**.

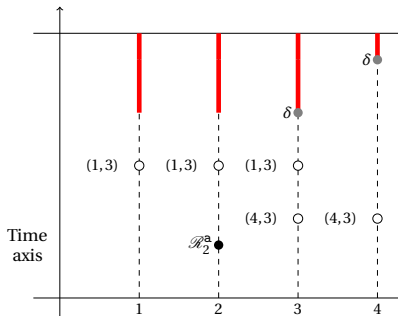
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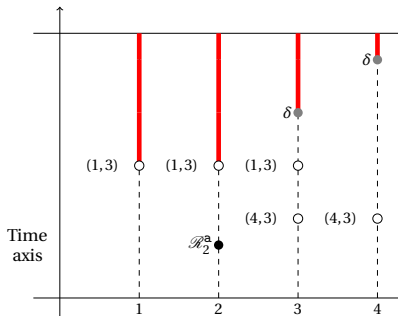
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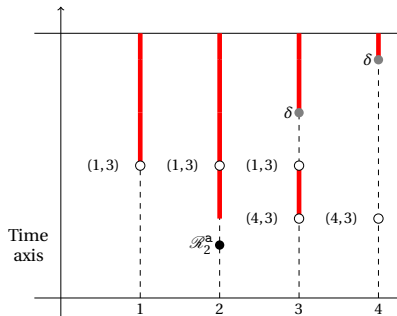
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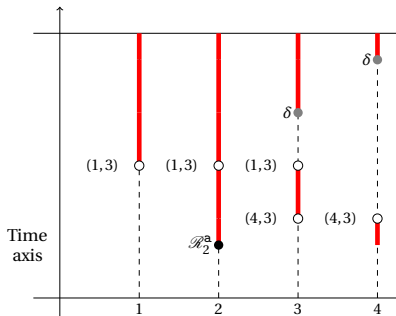
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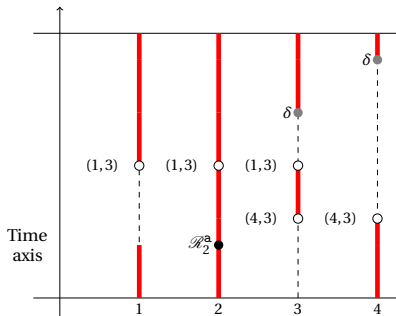
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Central idea

- When we go back in time and the dual process meets a δ -mark at site x , it is not necessary to go further to know the value of $\eta(x)$, because it is determined at that point by an independent random variable.
- Conditions are obtained by coupling with a dying branching process.

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