

Computational Biology

Lecturers:

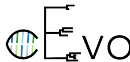
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Teaching Assistants:

Antoine Zwaans, Adrian Lison,
James Munday & Marcus Overwater

Computational Evolution
Department of Biosystems Science and Engineering

HS 2023



The Simulation Game

Studying evolution

Simulating evolution

Initializing the starting
sequence

Simulating the
substitutions

Pen and paper exercise

Algorithm

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How to study evolution?

CB

The easiest way to study something is by observation.

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The easiest way to study something is by observation.

► Wetlab

- Very realistic;
- Time-consuming and expensive;
- Impossible (sometimes).

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The easiest way to study something is by observation.

► Wetlab

- Very realistic;
- Time-consuming and expensive;
- Impossible (sometimes).

► Simulation

- A virtual experiment in which we mimic a (biological) process on a computer to study its properties
- Not necessarily realistic
- Allows us to:
 - * generate data with given assumptions;
 - * test predictive properties of models.

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The easiest way to study something is by observation.

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- Very realistic;
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- A virtual experiment in which we mimic a (biological) process on a computer to study its properties
- Not necessarily realistic
- Allows us to:
 - * generate data with given assumptions;
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Today we will simulate evolution!

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The tree of great apes

CB

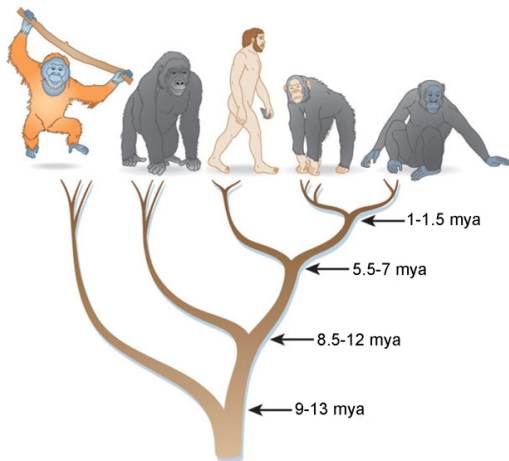


Figure adapted from [?]

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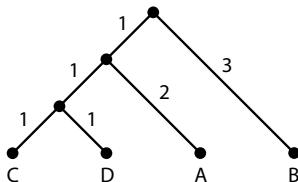
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- Format for tree representation
- To record a tree in Newick format:
 - Assign a label to each tip
 - Choose two tips that are a cherry (e.g. C and D)
 - Replace selected tips with a new tip of the form (tip1:branch1,tip2:branch2) (e.g. (C : 1, D : 1))
 - Branch length to the new tip is the branch length to the cherry
 - Repeat until the full tree is rewritten
- What is the Newick format for the rooted tree above?

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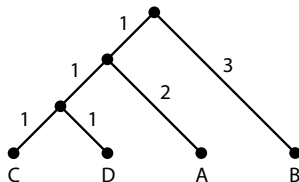
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- Format for tree representation
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 - Branch length to the new tip is the branch length to the cherry
 - Repeat until the full tree is rewritten
- What is the Newick format for the rooted tree above?
(((C : 1, D : 1) : 1, A : 2) : 1, B : 3);

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- Draw the tree given by the newick string:
(Bovine : 7, (Gibbon : 4, (Orangutan : 3, (Gorilla :
2, (Chimp : 2, Human : 1) : 1) : 0.5) : 2) : 5, Mouse : 12);

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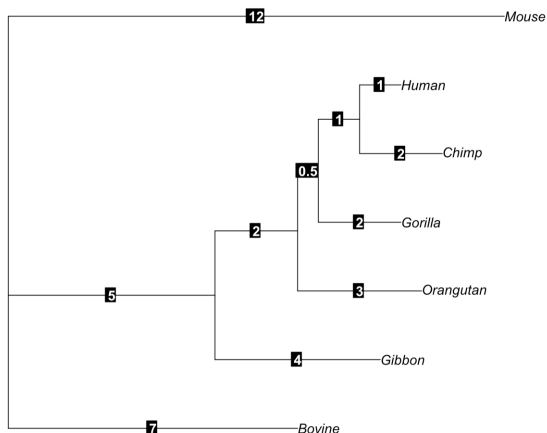
Algorithm

References

Storing trees: Newick format

CB

- Draw the tree given by the newick string:
(Bovine : 7, (Gibbon : 4, (Orangutan : 3, (Gorilla : 2, (Chimp : 2, Human : 1) : 0.5) : 2) : 5, Mouse : 12);



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Steps:

1. Initialization of the starting sequence:

- ▶ Sample a starting nucleotide for each position in the sequence

2. Iterative simulation of sequence evolution, along all branches of the tree

- ▶ Compute the transition probability matrix $P(t_b)$.
- ▶ Sample a new nucleotide for each position in the sequence.

Step 1: Initialization of the starting sequence

CB

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1a. Sample a starting nucleotide n

Step 1: Initialization of the starting sequence

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1a. Sample a starting nucleotide n

From the vector of equilibrium frequencies of nucleotides

	T	C	A	G
Π	0.22	0.26	0.33	0.19

Step 1: Initialization of the starting sequence

CB

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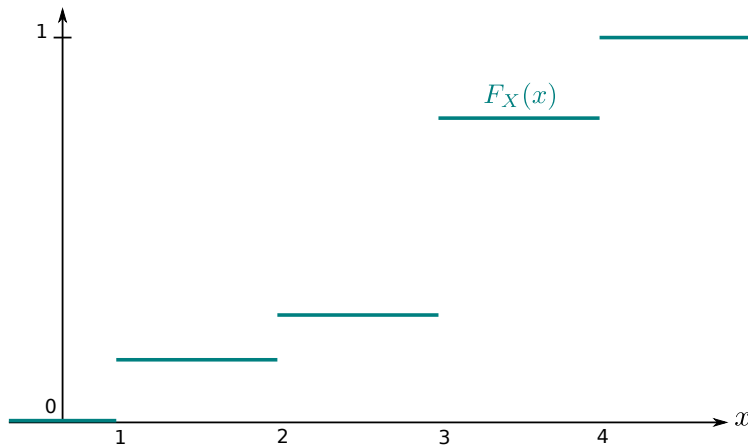
	T	C	A	G
Π	0.22	0.26	0.33	0.19

Knowing Π , how do we sample a nucleotide?

Inverse transform method

CB

- Sample u from $U(0, 1)$;



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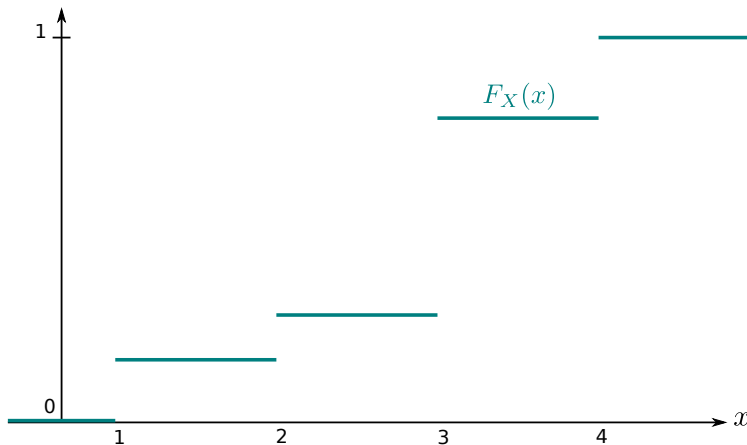
Algorithm

References

Inverse transform method

CB

- ▶ Sample u from $U(0, 1)$;
- ▶ Transform u into a sample from the desired distribution using the **CDF** == **C**umulative **D**istribution **F**unction $F_X(x) = P(X \leq x)$.



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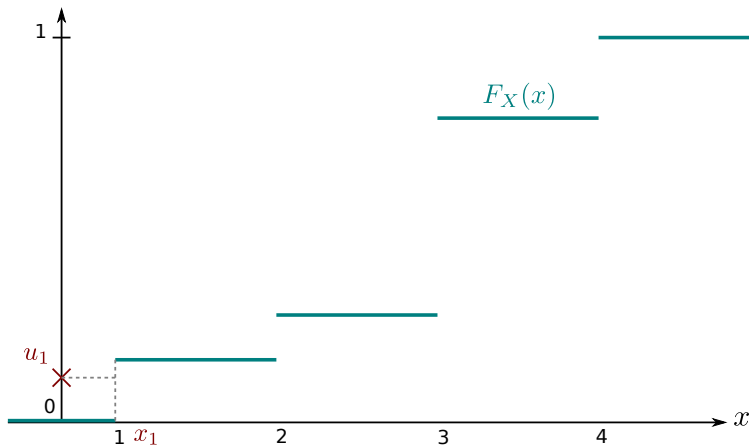
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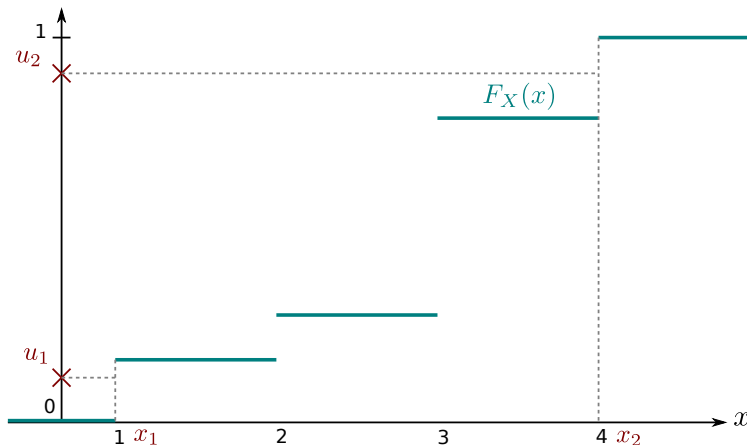
Pen and paper exercise

Algorithm

References

Inverse transform method

- ▶ Sample u from $U(0, 1)$;
- ▶ Transform u into a sample from the desired distribution using the **CDF** == **Cumulative Distribution Function**
 $F_X(x) = P(X \leq x)$.



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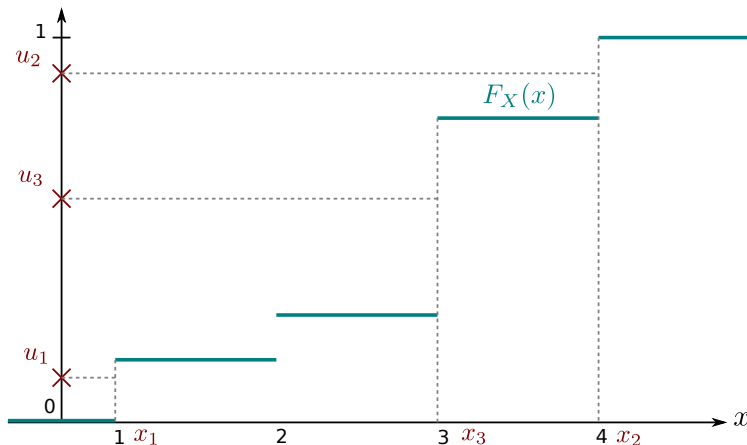
Pen and paper exercise

Algorithm

References

Inverse transform method

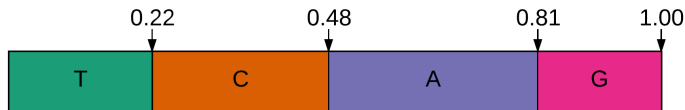
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- ▶ Transform u into a sample from the desired distribution using the **CDF** == **C**umulative **D**istribution **F**unction
 $F_X(x) = P(X \leq x)$.



Sampling discrete random variables

CB

	T	C	A	G
Π	0.22	0.26	0.33	0.19
CDF	0.22	0.48	0.81	1.00



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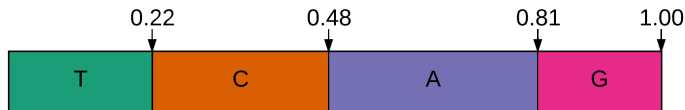
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Sampling discrete random variables

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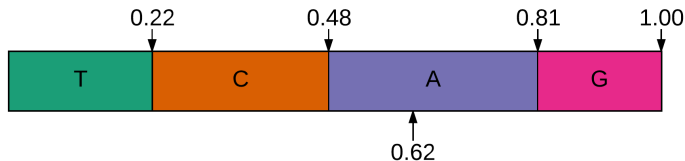
Algorithm

References

Sampling discrete random variables

CB

	T	C	A	G
Π	0.22	0.26	0.33	0.19
CDF	0.22	0.48	0.81	1.00



Sample u from $U(0, 1)$.

E.g. $u = 0.62$.

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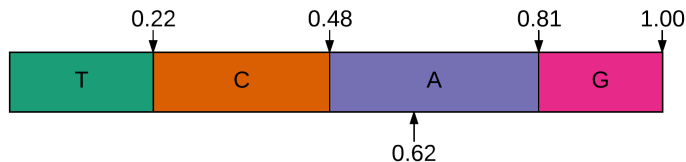
Algorithm

References

Sampling discrete random variables

CB

	T	C	A	G
Π	0.22	0.26	0.33	0.19
CDF	0.22	0.48	0.81	1.00



Sample u from $U(0, 1)$.

E.g. $u = 0.62$.

Select nucleotide **A**.

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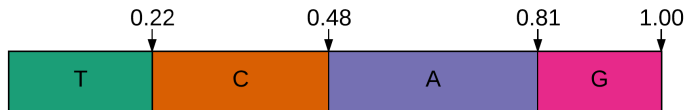
Algorithm

References

Sampling discrete random variables

CB

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Π	0.22	0.26	0.33	0.19
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Sample u from $U(0, 1)$.

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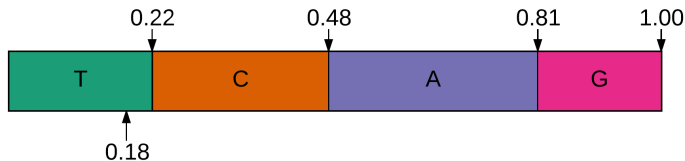
Algorithm

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Sampling discrete random variables

CB

	T	C	A	G
Π	0.22	0.26	0.33	0.19
CDF	0.22	0.48	0.81	1.00



Sample u from $U(0, 1)$.

E.g. $u = 0.18$.

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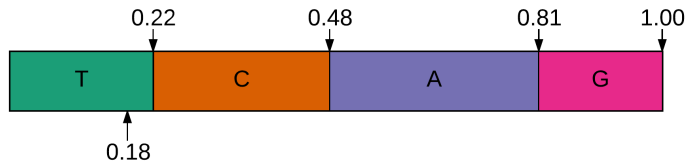
Algorithm

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	T	C	A	G
Π	0.22	0.26	0.33	0.19
CDF	0.22	0.48	0.81	1.00



Sample u from $U(0, 1)$.

E.g. $u = 0.18$.

Select nucleotide **T**.

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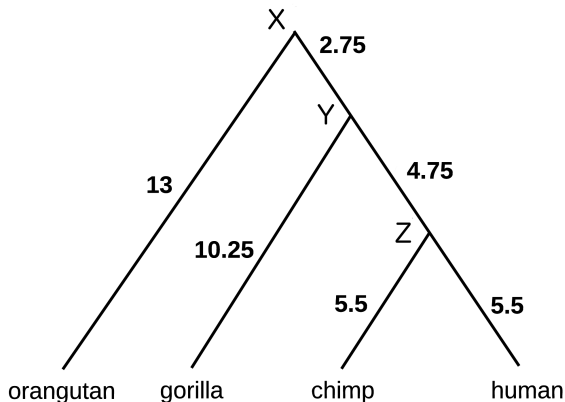
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Step 1: Initializing the starting sequence

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1b. Place n on the root node;



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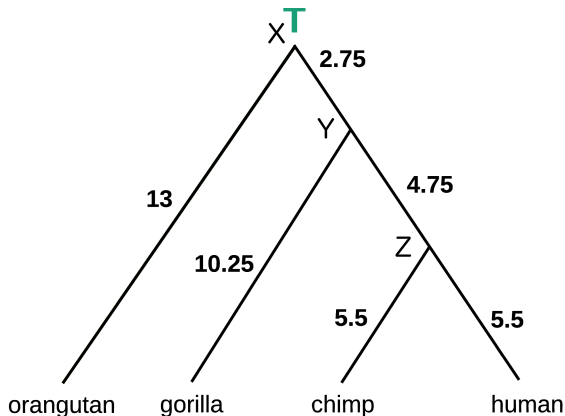
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References

Step 1: Initializing the starting sequence

CB

1b. Place n on the root node;



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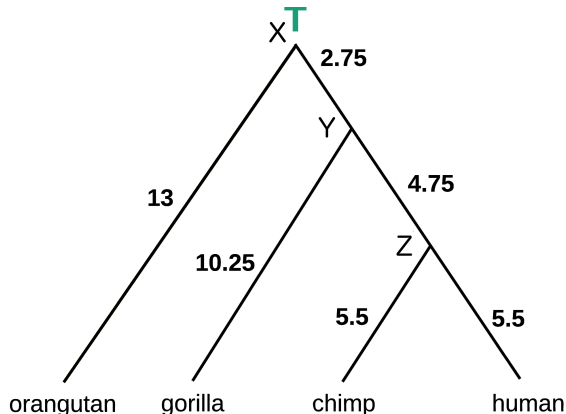
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Step 2a: Choose the next branch for simulation

CB

Get a branch b with a nucleotide at the start;
 $t_b = \text{length}(b)$;
 n = nucleotide at start of branch b ;



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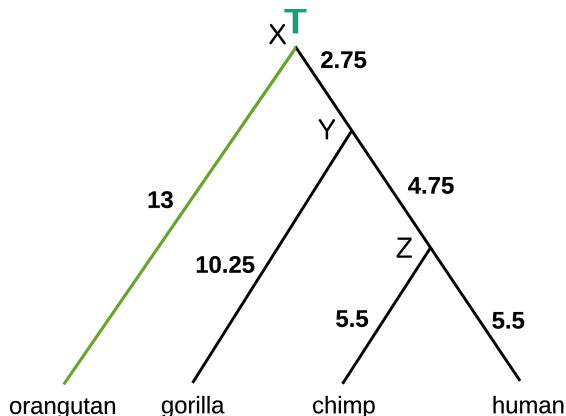
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Step 2a: Choose the next branch for simulation

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Step 2b-d: Sample the new nucleotide

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$$P(t_b) = e^{Qt_b};$$

Sample new nucleotide n_{new} from row n in $P(t_b)$;

Place n_{new} at the end of branch b ;

Step 2b-d: Sample the new nucleotide

CB

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References

$$P(t_b) = e^{Qt_b};$$

Sample new nucleotide n_{new} from row n in $P(t_b)$;

Place n_{new} at the end of branch b ;

To sample new nucleotide n_{new} we will need the substitution rate matrix Q , and transition probability matrix P .

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$\Pi = (\pi_T, \pi_C, \pi_A, \pi_G)$ - equilibrium frequencies.

α_1, α_2 - transition rates.

β - transversion rate.

$$Q_{\text{TN93}} = \begin{matrix} & \begin{matrix} T & C & A & G \end{matrix} \\ \begin{matrix} T \\ C \\ A \\ G \end{matrix} & \begin{pmatrix} \cdot & \alpha_1 \pi_C & \beta \pi_A & \beta \pi_G \\ \alpha_1 \pi_T & \cdot & \beta \pi_A & \beta \pi_G \\ \beta \pi_T & \beta \pi_C & \cdot & \alpha_2 \pi_G \\ \beta \pi_T & \beta \pi_C & \alpha_2 \pi_A & \cdot \end{pmatrix} \end{matrix}$$

The diagonals are set such that each row sums up to zero, e.g.

$$q_{TT} = -(\alpha_1 \pi_C + \beta \pi_A + \beta \pi_G).$$

$$\Pi = (0.22, 0.26, 0.33, 0.19)$$

$$\alpha_1 = 44.229, \alpha_2 = 21.781$$

$$\beta = 1$$

$$Q_{\text{TN93}} = \begin{matrix} & \begin{matrix} \text{T} & \text{C} & \text{A} & \text{G} \end{matrix} \\ \begin{matrix} \text{T} \\ \text{C} \\ \text{A} \\ \text{G} \end{matrix} & \begin{pmatrix} -0.01957 & 0.01873 & 0.00054 & 0.00031 \\ 0.01584 & -0.01669 & 0.00054 & 0.00031 \\ 0.00036 & 0.00042 & -0.00752 & 0.00674 \\ 0.00036 & 0.00042 & 0.01170 & -0.01249 \end{pmatrix} \end{matrix}$$

Note: the matrix is scaled to 0.0135 substitutions per mya so that we get reasonable sequences.

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$\Pi = (\pi_T, \pi_C, \pi_A, \pi_G)$ - equilibrium frequencies.

α_1, α_2 - transition rates.

β - transversion rate.

t_b - branch length.

$$P(t_b) = e^{t_b Q_{TN93}(\alpha_1, \alpha_2, \beta, \Pi)}$$

$$\Pi = (0.22, 0.26, 0.33, 0.19)$$

$$\alpha_1 = 44.229, \alpha_2 = 21.781$$

$$\beta = 1$$

$$t_b = 13 \text{ mya}$$

$$P_{\text{TN93}}(13 \text{ mya}) = \begin{matrix} & \begin{matrix} \text{T} & \text{C} & \text{A} & \text{G} \end{matrix} \\ \begin{matrix} \text{T} \\ \text{C} \\ \text{A} \\ \text{G} \end{matrix} & \begin{pmatrix} 0.795 & 0.194 & 0.007 & 0.004 \\ 0.164 & 0.824 & 0.007 & 0.004 \\ 0.005 & 0.005 & 0.913 & 0.077 \\ 0.005 & 0.005 & 0.134 & 0.856 \end{pmatrix} \end{matrix}$$

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We start with nucleotide **T**, so we are interested in row T:

$$P_{\text{TN93}}(13 \text{ mya}) = \begin{matrix} & \text{T} & \text{C} & \text{A} & \text{G} \\ \begin{matrix} \text{T} \\ \text{C} \\ \text{A} \\ \text{G} \end{matrix} & \begin{pmatrix} 0.795 & 0.194 & 0.007 & 0.004 \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \end{pmatrix} \end{matrix}$$

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We start with nucleotide **T**, so we are interested in row T:

$$P_{TN93}(13 \text{ mya}) = \begin{matrix} & \begin{matrix} T & C & A & G \end{matrix} \\ \begin{matrix} T \\ C \\ A \\ G \end{matrix} & \begin{pmatrix} 0.795 & 0.194 & 0.007 & 0.004 \\ . & . & . & . \\ . & . & . & . \\ . & . & . & . \end{pmatrix} \end{matrix}$$

Sample new nucleotide n_{new} with the weights

$[p_{T \rightarrow T}, p_{T \rightarrow C}, p_{T \rightarrow A}, p_{T \rightarrow G}]$

Sample u from $\mathcal{U}(0, 1)$.

E.g. $u = 0.81$.

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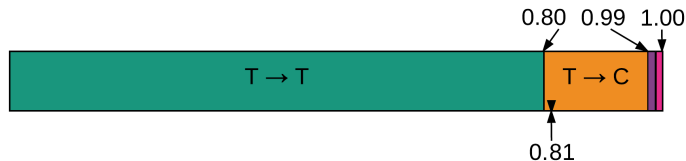
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Getting the substitution

CB

Sample u from $\mathcal{U}(0, 1)$.

E.g. $u = 0.81$.



Selected substitution is $T \rightarrow C$.

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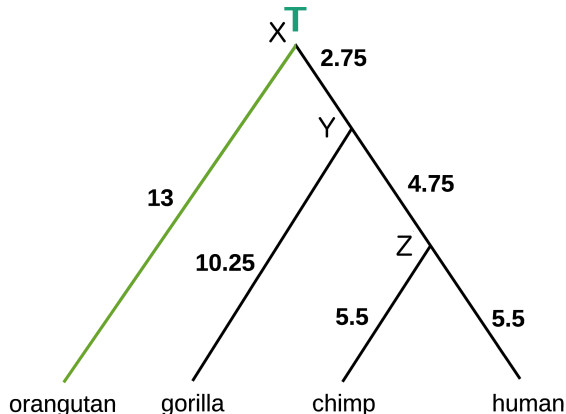
Step 2b-d: Sample the new nucleotide

CB

$$P(t_b) = e^{Q t_b};$$

Sample new nucleotide n_{new} from row n in $P(t_b)$;

Place n_{new} at the end of branch b ;



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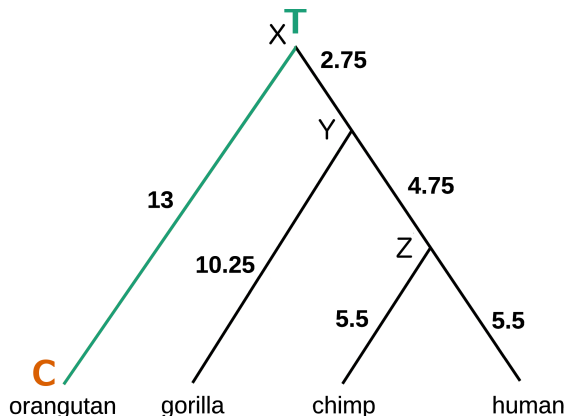
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while *not all branches are used* **do**

Get a branch \mathbf{b} with a nucleotide at the start;

$\mathbf{t_b} = \text{length}(\mathbf{b})$;

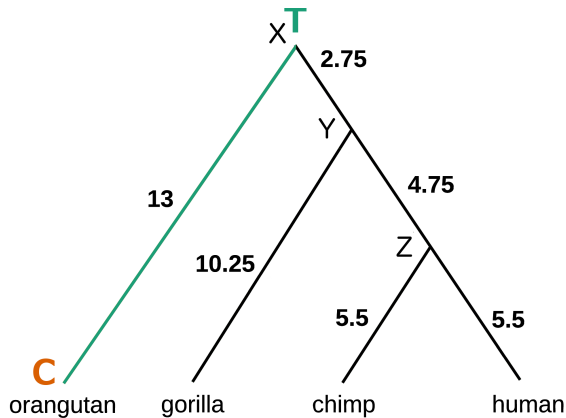
\mathbf{n} = nucleotide at start of branch \mathbf{b} ;

$P(\mathbf{t_b}) = e^{Q\mathbf{t_b}}$;

Sample new nucleotide $\mathbf{n_{new}}$ from row \mathbf{n} in $P(\mathbf{t_b})$;

Place $\mathbf{n_{new}}$ at the start of the daughter branches of
 \mathbf{b} ;

end



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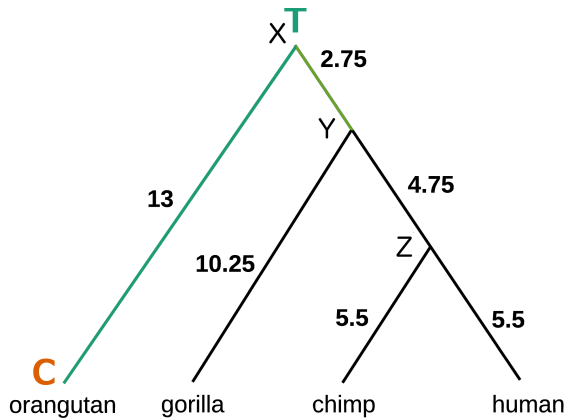
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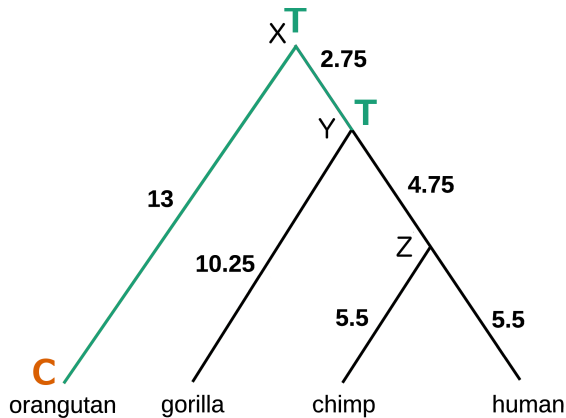
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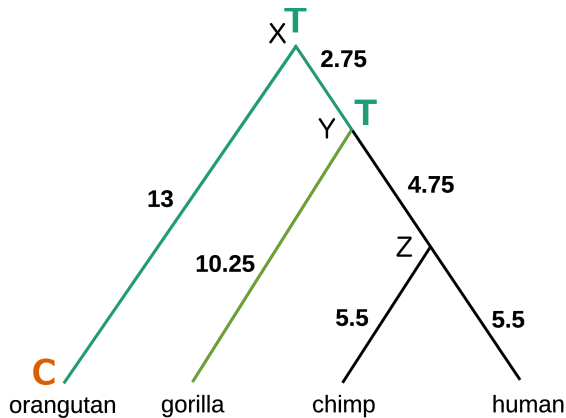
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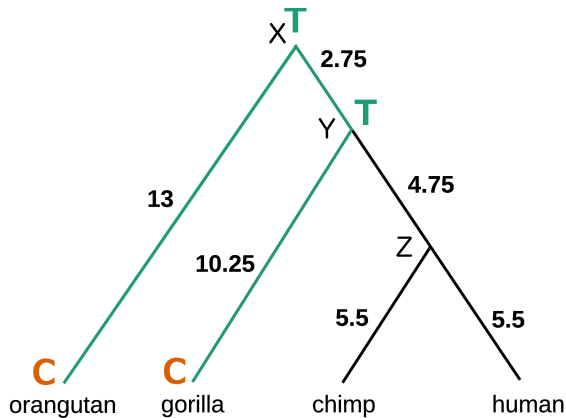
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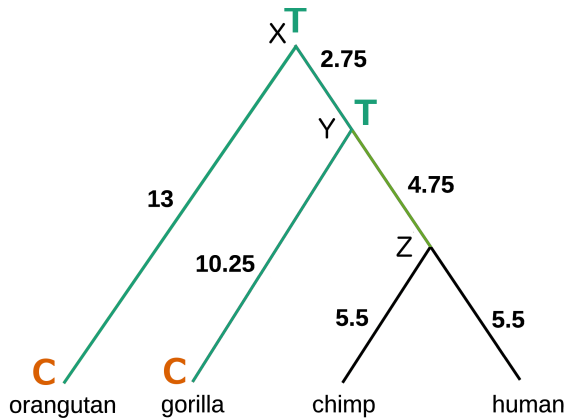
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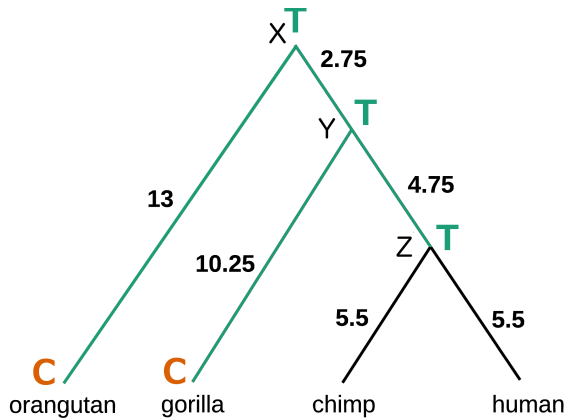
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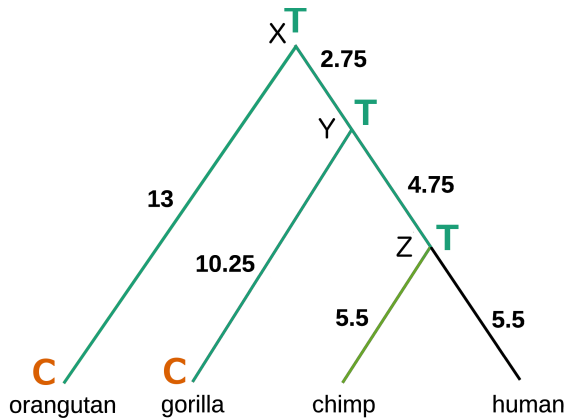
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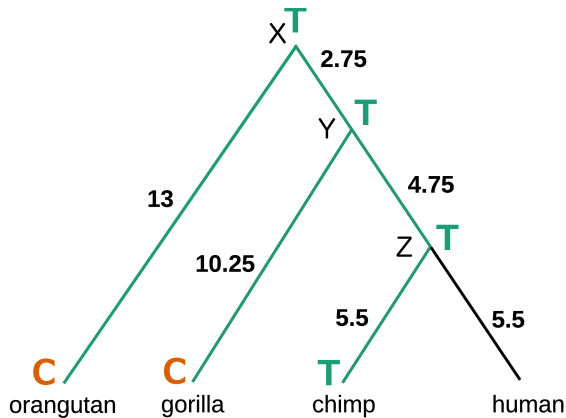
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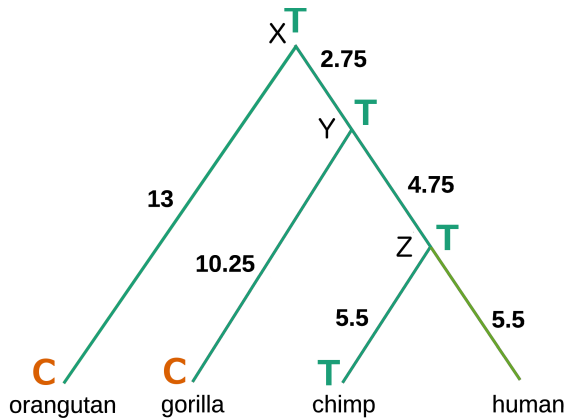
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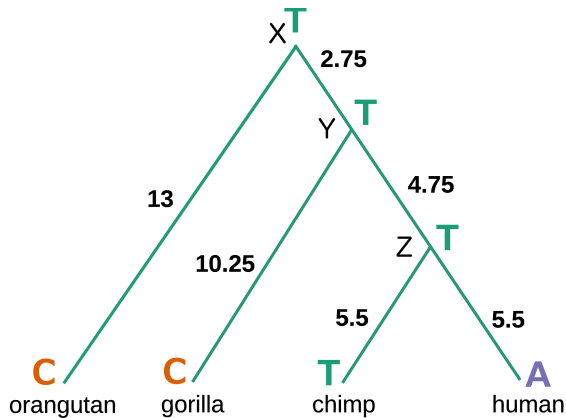
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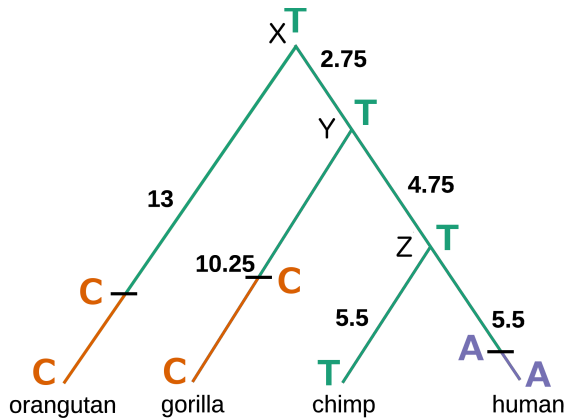
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1. Use a random number generator to “roll dice”
2. Evolve a character along the tree;

All of the characters together will produce an alignment.


```
N = number of sites in the alignment;
Q = substitution rate matrix;
for i = 1 to N do
    | Sample a nucleotide  $n$  from the initial distribution;
    | Add  $n$  to the sequence of the root node;
end
while not all branches are visited do
    | Get a branch  $b$  with a sequence at the start;
    |  $t_b = \text{length}(b)$ ;
    |  $P(t_b) = e^{Qt_b}$ ;
    | for i = 1 to N do
    | |  $n =$  nucleotide at position i at the start of branch  $b$ ;
    | | Sample new nucleotide  $n_{\text{new}}$  from row  $n$  in  $P(t_b)$ ;
    | | Place  $n_{\text{new}}$  at the end of sequences in the daughter
    | | branches of  $b$ ;
    | end
end
```

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