# Computational Biology

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Computational Evolution
Department of Biosystems Science and Engineering

HS 2019



Tree reconstribution

Tree reconstruction

Distance matrices
Hamming distance
JC69 distance

UPGMA algorithm

In reality we observe the sequences at present and the tree is unknown.

Tree reconstribution

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Distance matrices

Hamming distance JC69 distance K80 distance

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In reality we observe the sequences at present and the tree is unknown.

How do we build a tree from an alignment?

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This time we will use UPGMA

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In reality we observe the sequences at present and the tree is unknown.

How do we build a tree from an alignment?

This time we will use UPGMA:

1. Build the initial distance matrix;

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In reality we observe the sequences at present and the tree is unknown.

How do we build a tree from an alignment?

This time we will use UPGMA:

- 1. Build the initial distance matrix;
- 2. Repeat until all sequences are clustered:

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In reality we observe the sequences at present and the tree is unknown.

How do we build a tree from an alignment?

This time we will use UPGMA:

- 1. Build the initial distance matrix;
- 2. Repeat until all sequences are clustered:
  - 2.1 Cluster two closest nodes;

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In reality we observe the sequences at present and the tree is unknown.

How do we build a tree from an alignment?

This time we will use UPGMA:

- 1. Build the initial distance matrix;
- 2. Repeat until all sequences are clustered:
  - 2.1 Cluster two closest nodes;
  - 2.2 Recalculate the distances to the new merged node.

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# Hamming distance

Hamming distance: number of segregating sites.

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# Hamming distance

Hamming distance: number of segregating sites.

Orangutan CTGCTACTGAAACCAGACTA
Gorilla CTGCTGTTTAGAAAAAACTA

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# Hamming distance

Hamming distance: number of segregating sites.

Orangutan CTGCTACTGAAACCAGACTA
Gorilla CTGCTGTTTAGAAAAAACTA

 $\hat{d}_{\text{hamming}} = 7$ 

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Orangutan (O)

CTGCTACTGAAACCAGACTA Gorilla (G) CTGCTGTTTAGAAAAACTA

Chimpanzee (C) CTGCTGTTTAGTAAGAACCA

Human (H) CTGCTGTTTAGTAAGAACTA Tree reconstribution

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Orangutan (O) CTGCTACTGAAACCAGACTA
Gorilla (G) CTGCTGTTTAGAAAAAACTA
Chimpanzee (C) CTGCTGTTTAGTAAGAACCA
Human (H) CTGCTGTTTAGTAAGAACTA

	0	G	C	Н
0				
G				
С				
Н				

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Orangutan (O) CTGCTACTGAAACCAGACTA
Gorilla (G) CTGCTGTTTAGAAAAAACTA
Chimpanzee (C) CTGCTGTTTAGTAAGAACCA
Human (H) CTGCTGTTTAGTAAGAACTA

	0	G	C	Н
0		7	10	9
G			3	2
С				1
Н				

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Orangutan (O) CTGCTACTGAAACCAGACTA
Gorilla (G) CTGCTGTTTAGAAAAAACTA
Chimpanzee (C) CTGCTGTTTAGTAAGAACCA
Human (H) CTGCTGTTTAGTAAGAACTA

	0	G	C	Н
0	-	7	10	9
G	7	-	3	2
С	10	3	-	1
Н	9	2	1	1

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Exercise Solution

JC69 distance:  $\hat{d} = -\frac{3}{4}\log(1-\frac{4}{3}\hat{p})$ 

JC69 distance:  $\hat{\mathbf{d}} = -\frac{3}{4}\log(1 - \frac{4}{3}\hat{\mathbf{p}})$ 

Orangutan CTGCTACTGAAACCAGACTA
Gorilla CTGCTGTTTAGAAAAAACTA

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JC69 distance: 
$$\hat{\mathbf{d}} = -\frac{3}{4}\log(1 - \frac{4}{3}\hat{\mathbf{p}})$$

Orangutan CTGCTACTGAAACCAGACTA
Gorilla CTGCTGTTTAGAAAAAACTA

$$\hat{p} = \frac{7}{20} = 0.35$$

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JC69 distance:  $\hat{\mathbf{d}} = -\frac{3}{4}\log(1 - \frac{4}{3}\hat{\mathbf{p}})$ 

Orangutan CTGCTACTGAAACCAGACTA
Gorilla CTGCTGTTTAGAAAAAACTA

$$\hat{p} = \frac{7}{20} = 0.35$$

$$\hat{d} = -\frac{3}{4}\log(1 - \frac{4}{3}0.35)$$

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JC69 distance: 
$$\hat{\mathbf{d}} = -\frac{3}{4}\log(1 - \frac{4}{3}\hat{\mathbf{p}})$$

Orangutan CTGCTACTGAAACCAGACTA
Gorilla CTGCTGTTTAGAAAAAACTA

$$\hat{p} = \frac{7}{20} = 0.35$$

$$\hat{d} = -\frac{3}{4}\log(1 - \frac{4}{3}0.35) \approx 0.4715$$

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K80 distance: 
$$\hat{\mathbf{d}} = -\frac{1}{2}\log(1-2S-V) - \frac{1}{4}\log(1-2V)$$

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K80 distance: 
$$\hat{\mathbf{d}} = -\tfrac{1}{2}\log(1-2S-V) - \tfrac{1}{4}\log(1-2V)$$
 Orangutan CTGCTACTGAAACCAGACTA GOrilla CTGCTGTTTAGAAAAAACTA

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K80 distance: 
$$\hat{\mathbf{d}} = -\frac{1}{2}\log(1-2S-V) - \frac{1}{4}\log(1-2V)$$
  
Orangutan CTGCTACTGAAACCAGACTA  
Gorilla CTGCTGTTTAGAAAAAACTA

Transition proportion (T 
$$\leftrightarrow$$
 C, A  $\leftrightarrow$  G)  $S = \frac{4}{20} = 0.2$ 

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K80 distance: 
$$\hat{\mathbf{d}} = -\frac{1}{2}\log(1-2S-V) - \frac{1}{4}\log(1-2V)$$
  
Orangutan CTGCTACTGAAACCAGACTA  
Gorilla CTGCTGTTTAGAAAAAACTA

Transition proportion (T 
$$\leftrightarrow$$
 C, A  $\leftrightarrow$  G) S =  $\frac{4}{20}$  = 0.2  
Transversion proportion (T  $\leftrightarrow$  G, A  $\leftrightarrow$  C, A  $\leftrightarrow$  T, C  $\leftrightarrow$  G) V =  $\frac{3}{20}$  = 0.15

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K80 distance: 
$$\hat{\mathbf{d}} = -\frac{1}{2}\log(1-2S-V) - \frac{1}{4}\log(1-2V)$$
  
Orangutan CTGCTACTGAAACCAGACTA  
Gorilla CTGCTGTTTAGAAAAAACTA

Transition proportion (T 
$$\leftrightarrow$$
 C, A  $\leftrightarrow$  G)  $S = \frac{4}{20} = 0.2$   
Transversion proportion (T  $\leftrightarrow$  G, A  $\leftrightarrow$  C, A  $\leftrightarrow$  T, C  $\leftrightarrow$  G)  $V = \frac{3}{20} = 0.15$ 

$$\hat{\mathbf{d}} = -\frac{1}{2} log(1 - 2 \cdot 0.2 - 0.15) - \frac{1}{4} \cdot log(1 - 2 \cdot 0.15)$$

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K80 distance: 
$$\hat{\mathbf{d}} = -\frac{1}{2}\log(1-2S-V) - \frac{1}{4}\log(1-2V)$$
  
Orangutan CTGCTACTGAAACCAGACTA  
Gorilla CTGCTGTTTAGAAAAACTA

Transition proportion (T 
$$\leftrightarrow$$
 C, A  $\leftrightarrow$  G)  $S = \frac{4}{20} = 0.2$   
Transversion proportion (T  $\leftrightarrow$  G, A  $\leftrightarrow$  C, A  $\leftrightarrow$  T, C  $\leftrightarrow$  G)  $V = \frac{3}{20} = 0.15$ 

$$\hat{\mathbf{d}} = -\frac{1}{2} log(1 - 2 \cdot 0.2 - 0.15) - \frac{1}{4} \cdot log(1 - 2 \cdot 0.15) \approx 0.4884$$

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Tree reconstruction

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# Distance matrix comparison

Hamming:

	0	G	С	Н
0		7	10	9
G			3	2
С				1
Н				

JC69:

	0	G	С	Н
О		0.4715	0.8240	0.6872
G			0.1674	0.1073
С				0.0517
Н				

K80:

	0	G	С	Н
0		0.4884	0.9324	0.7297
G			0.1702	0.1076
С				0.0527
Н				

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UPGMA algorithm

Data: Distance matrix D

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UPGMA algorithm

**Data:** Distance matrix D

**Result:** Ultrametric phylogenetic tree

Tree reconstribution

Tree reconstruction

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UPGMA algorithm

Data: Distance matrix D

**Result:** Ultrametric phylogenetic tree

for  $\mathfrak{i} \leftarrow 1$  to N do

$$n_i \leftarrow 1;$$
 $s_i \leftarrow \mathsf{node}(i)$ 

end

Tree reconstribution

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end

```
Data: Distance matrix D
Result: Ultrametric phylogenetic tree
for i \leftarrow 1 to N do
    n_i \leftarrow 1:
    s_i \leftarrow \mathsf{node}(i)
end
while size(D) > (1, 1) do
     Choose s_i, s_i such that min(D) = d[s_i, s_i];
    n_{i,i} \leftarrow n_i + n_i;
    s_{i,i} \leftarrow \{s_i, s_i\};
    branch(s_{i,i}, s_i) \leftarrow d[s_i, s_i]/2 - distance\_to\_tip(s_i);
    branch(s_{i,i}, s_i) \leftarrow d[s_i, s_i]/2 - distance\_to\_tip(s_i);
    for all m \neq i and m \neq j do
         d[s_m, s_{i,j}] \leftarrow \frac{n_i d[s_i, s_m] + n_j d[s_j, s_m]}{n_i + n_j};
    end
     Delete node s_i from D:
     Delete node s_i from D;
```

Tree reconstribution

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UPGMA algorithm

### Step 1

```
\label{eq:while} \begin{aligned} & \text{while} \ \mathsf{size}(D) > (1,1) \ \text{do} \\ & | \ \mathsf{Choose} \ s_i, \ s_j \ \mathsf{such \ that} \ \mathsf{min}(D) = d[s_i, s_j]; \\ & \dots \end{aligned}
```

	0	G	С	Н
0	-	7	10	9
G	7	-	3	2
С	10	3	-	1
Н	9	2	1	-

Tree reconstribution

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### Step 1

```
\label{eq:while} \begin{split} & \text{while } \mathsf{size}(D) > (1,1) \text{ do} \\ & \middle| \quad \mathsf{Choose } s_i, \ s_j \ \mathsf{such that } \min(D) = d[s_i, s_j]; \\ & \middle| \quad \ldots \\ & \mathsf{end} \end{split}
```

	0	G	С	Н
0	-	7	10	9
G	7	-	3	2
С	10	3	-	1
Н	9	2	1	-

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Exercise
Solution

### Step 1

```
\label{eq:while} \begin{aligned} & \text{while} \ \mathsf{size}(D) > (1,1) \ \text{do} \\ & | \ \mathsf{Choose} \ s_i, \ s_j \ \mathsf{such \ that} \ \mathsf{min}(D) = d[s_i, s_j]; \\ & \dots \end{aligned}
```

	0	G	С	Н
0	-	7	10	9
G	7	-	3	2
С	10	3	-	1
Н	9	2	1	-

⇒ Merge Human and Chimp.

## Step 2

```
\label{eq:while_size} \begin{array}{c} \textbf{while} \ \mathsf{size}(D) > (1,1) \ \textbf{do} \\ & \dots \\ & n_{i,j} \leftarrow n_i + n_j; \\ & s_{i,j} \leftarrow \{s_i, s_j\}; \\ & \mathsf{branch}(s_{i,j}, s_i) \leftarrow d[s_i, s_j]/2 - \mathsf{distance\_to\_tip}(s_i); \\ & \mathsf{branch}(s_{i,j}, s_j) \leftarrow d[s_i, s_j]/2 - \mathsf{distance\_to\_tip}(s_j); \\ & \dots \\ & \mathsf{end} \end{array}
```

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UPGMA algorithm

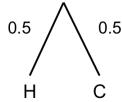
## Step 2

while 
$$size(D) > (1, 1)$$
 do

```
\begin{array}{c} \dots \\ n_{i,j} \leftarrow n_i + n_j; \\ s_{i,j} \leftarrow \{s_i, s_j\}; \\ \text{branch}(s_{i,j}, s_i) \leftarrow d[s_i, s_j]/2 - \text{distance\_to\_tip}(s_i); \\ \text{branch}(s_{i,j}, s_j) \leftarrow d[s_i, s_j]/2 - \text{distance\_to\_tip}(s_j); \\ \dots \end{array}
```

end

	0	G	C	Н
0	-	7	10	9
G	7	-	3	2
С	10	3	-	1
Н	9	2	1	-



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```
\label{eq:while_size} \begin{split} \text{while } \mathsf{size}(D) &> (1,1) \text{ do} \\ & \qquad \qquad . \dots \text{for } \mathit{all} \ \mathsf{m} \neq \mathsf{i} \ \mathit{and} \ \mathsf{m} \neq \mathsf{j} \ \mathsf{do} \\ & \qquad \qquad \mid \ \ d[s_{\mathfrak{m}}, s_{\mathfrak{i}, \mathsf{j}}] \leftarrow \frac{n_{\mathfrak{i}} \, d[s_{\mathfrak{i}}, s_{\mathfrak{m}}] + n_{\mathfrak{j}} \, d[s_{\mathfrak{j}}, s_{\mathfrak{m}}]}{n_{\mathfrak{i}} + n_{\mathfrak{j}}}; \\ & \quad \text{end} \\ & \quad \mathsf{Delete} \ \mathsf{node} \ s_{\mathfrak{i}} \ \mathsf{from} \ \mathsf{D}; \\ & \quad \mathsf{Delete} \ \mathsf{node} \ s_{\mathfrak{j}} \ \mathsf{from} \ \mathsf{D}; \\ & \quad \mathsf{end} \\ \end{split}
```

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UPGMA algorithm

$$\textbf{while} \ \mathsf{size}(D) > (1,1) \ \textbf{do}$$

$$\begin{split} \dots & \text{for all } m \neq i \text{ and } m \neq j \text{ do} \\ & \middle| d[s_m, s_{i,j}] \leftarrow \frac{n_i d[s_i, s_m] + n_j d[s_j, s_m]}{n_i + n_j}; \end{split}$$

### end

Delete node  $s_i$  from D;

Delete node  $s_j$  from D;

#### end

$$d[O, H.C] = \frac{1 \cdot 10 + 1 \cdot 9}{1 + 1} = 9.5$$

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UPGMA algorithm

while 
$$size(D) > (1, 1)$$
 do

$$\begin{split} \dots & \text{for all } m \neq i \text{ and } m \neq j \text{ do} \\ & \middle| \quad d[s_m, s_{i,j}] \leftarrow \frac{n_i d[s_i, s_m] + n_j d[s_j, s_m]}{n_i + n_j}; \end{split}$$

### end

Delete node  $s_i$  from D; Delete node  $s_i$  from D;

#### end

$$\begin{array}{l} \text{d[O, H.C]} = \frac{1 \cdot 10 + 1 \cdot 9}{1 + 1} = 9.5 \\ \text{d[G, H.C]} = \frac{1 \cdot 3 + 1 \cdot 2}{1 + 1} = 2.5 \end{array}$$

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UPGMA algorithm

while 
$$size(D) > (1, 1)$$
 do

$$\label{eq:constraints} \begin{array}{l} \dots \text{for all } \mathfrak{m} \neq \mathfrak{i} \text{ and } \mathfrak{m} \neq \mathfrak{j} \text{ do} \\ \mid \ d[s_{\mathfrak{m}}, s_{\mathfrak{i}, \mathfrak{j}}] \leftarrow \frac{\mathfrak{n}_{\mathfrak{i}} d[s_{\mathfrak{i}}, s_{\mathfrak{m}}] + \mathfrak{n}_{\mathfrak{j}} d[s_{\mathfrak{j}}, s_{\mathfrak{m}}]}{\mathfrak{n}_{\mathfrak{i}} + \mathfrak{n}_{\mathfrak{j}}}; \end{array}$$

#### end

Delete node  $s_i$  from D;

Delete node  $s_j$  from D;

#### end

$$\begin{array}{l} \text{d[O, H.C]} = \frac{1 \cdot 10 + 1 \cdot 9}{1 + 1} = 9.5 \\ \text{d[G, H.C]} = \frac{1 \cdot 3 + 1 \cdot 2}{1 + 1} = 2.5 \end{array}$$

	O	G	C	H	H.C
0	-	7	10	9	9.5
G	7	-	3	2	2.5
С	10	3	-	1	0
Н	9	2	1	-	0
H.C	9.5	2.5	0	0	-

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while 
$$size(D) > (1, 1)$$
 do

$$\label{eq:continuity} \begin{array}{l} \dots \text{for all } \mathfrak{m} \neq \mathfrak{i} \text{ and } \mathfrak{m} \neq \mathfrak{j} \text{ do} \\ \mid \ d[s_{\mathfrak{m}}, s_{\mathfrak{i}, \mathfrak{j}}] \leftarrow \frac{\mathfrak{n}_{\mathfrak{i}} d[s_{\mathfrak{i}}, s_{\mathfrak{m}}] + \mathfrak{n}_{\mathfrak{j}} d[s_{\mathfrak{j}}, s_{\mathfrak{m}}]}{\mathfrak{n}_{\mathfrak{i}} + \mathfrak{n}_{\mathfrak{j}}}; \end{array}$$

#### end

Delete node  $s_i$  from D;

Delete node  $s_j$  from D;

#### end

$$\begin{array}{l} \text{d[O, H.C]} = \frac{1 \cdot 10 + 1 \cdot 9}{1 + 1} = 9.5 \\ \text{d[G, H.C]} = \frac{1 \cdot 3 + 1 \cdot 2}{1 + 1} = 2.5 \end{array}$$

	O	G	C	H	H.C
0	-	7	10	9	9.5
G	7	-	3	2	2.5
С	10	3	-	1	0
Н	9	2	1	-	0
H.C	9.5	2.5	0	0	-

	0	G	H.C
0	-	7	9.5
G	7	-	2.5
H.C	9.5	2.5	1

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	0	G	H.C
0	-	7	9.5
G	7	-	2.5
H.C	9.5	2.5	-

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	0	G	H.C
0	-	7	9.5
G	7	-	2.5
H.C	9.5	2.5	-

Tree reconstribution

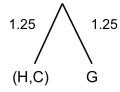
Tree reconstruction

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	Ο	G	H.C
0	-	7	9.5
G	7	-	2.5
H.C	9.5	2.5	-



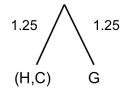
Tree reconstribution

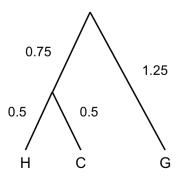
Tree reconstruction

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#### UPGMA algorithm

	0	G	H.C
0	1	7	9.5
G	7	-	2.5
H.C	9.5	2.5	-





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#### UPGMA algorithm

$$d[O, H.C.G] = \frac{1.7+2.9.5}{1+2} = 8.67$$

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UPGMA algorithm

$$d[O, H.C.G] = \frac{1.7 + 2.9.5}{1+2} = 8.67$$

	0	G	H.C	H.C.G
0	-	7	9.5	8.67
G	7	-	2.5	0
H.C	9.5	2.5	-	0
H.C.G	8.67	0	0	-

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UPGMA algorithm

$$d[O, H.C.G] = \frac{1.7+2.9.5}{1+2} = 8.67$$

	0	G	H.C	H.C.G
0	-	7	9.5	8.67
G	7	-	2.5	0
H.C	9.5	2.5	-	0
H.C.G	8.67	0	0	-

	0	H.C.G
0	-	8.67
H.C.G	8.67	-

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UPGMA algorithm

$$d[O, H.C.G] = \frac{1.7+2.9.5}{1+2} = 8.67$$

	0	G	H.C	H.C.G
0	-	7	9.5	8.67
G	7	-	2.5	0
H.C	9.5	2.5	-	0
H.C.G	8.67	0	0	-

	0	H.C.G
0	-	8.67
H.C.G	8.67	-

	0	H.C.G
0	-	8.67
H.C.G	8.67	_

	0	H.C.G
0	-	8.67
H.C.G	8.67	_

Tree reconstribution

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Distance matrices Hamming distance JC69 distance

K80 distance UPGMA algorithm

$$d[O, H.C.G] = \frac{1.7 + 2.9.5}{1 + 2} = 8.67$$

		0	G	H.C	H.C.G
	0	-	7	9.5	8.67
	G	7	-	2.5	0
	H.C	9.5	2.5	-	0
Г	H.C.G	8.67	0	0	-

	Ο	H.C.G
0	-	8.67
H.C.G	8.67	-

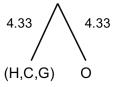
Tree reconstribution

Tree reconstruction

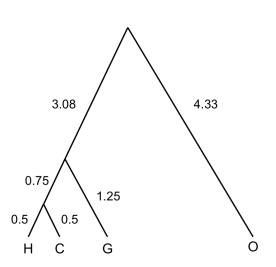
Distance matrices
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UPGMA algorithm

	Ο	H.C.G
0	-	8.67
H.C.G	8.67	-



### Final tree



Tree reconstribution

Tree reconstruction

Distance matrices
Hamming distance
JC69 distance
K80 distance

#### UPGMA algorithm

### Pen and paper exercise

end

```
 \begin{split} &\text{for } i \leftarrow 1 \text{ to N do} \\ & \quad n_i \leftarrow 1; \\ & \quad s_i \leftarrow \mathsf{node}(i) \\ &\text{end} \\ &\text{while size}(D) > (1,1) \text{ do} \\ & \quad \mathsf{Choose } s_i, s_j \text{ such that } \mathsf{min}(D) = d[s_i, s_j]; \\ & \quad n_{i,j} \leftarrow n_i + n_j; \\ & \quad s_{i,j} \leftarrow \{s_i, s_j\}; \\ & \quad \mathsf{branch}(s_{i,j}, s_i) \leftarrow d[s_i, s_j]/2 - \mathsf{distance\_to\_tip}(s_i); \\ & \quad \mathsf{branch}(s_{i,j}, s_i) \leftarrow d[s_i, s_j]/2 - \mathsf{distance\_to\_tip}(s_j); \\ & \quad \mathsf{for } \mathit{all } \ m \neq i \ \mathit{and } \ m \neq j \ \mathsf{do} \\ & \quad \mid \quad d[s_m, s_{i,j}] \leftarrow \frac{n_i \ \mathit{d}[s_i, s_m] + n_j \ \mathit{d}[s_j, s_m]}{n_i + n_j}; \\ & \quad \mathsf{end} \\ & \quad \mathsf{Delete } \ \mathsf{node } s_i \ \mathsf{from } D; \\ & \quad \mathsf{Delete } \ \mathsf{node } s_j \ \mathsf{from } D; \\ & \quad \mathsf{Delete } \ \mathsf{node } s_j \ \mathsf{from } D; \\ & \quad \mathsf{Delete } \ \mathsf{node } s_j \ \mathsf{from } D; \\ \end{split}
```

	0	G	С	Н
О		0.4884	0.9324	0.7297
G			0.1702	0.1076
С				0.0527
Н				

Tree reconstribution

Tree reconstruction

Distance matrices

Hamming distance JC69 distance K80 distance

UPGMA algorithm

#### Exercise

Solutio

## Exercise solution: distances and branches (1)

	0	G	С	Н
0		0.4884	0.9324	0.7297
G			0.1702	0.1076
С				0.0527
Н				

branch[C.H, C] = 
$$\frac{0.0527}{2}$$
 = 0.02635  
branch[C.H, H] =  $\frac{0.0527}{2}$  = 0.02635  
d[C.H, O] =  $\frac{1\cdot0.9324+1\cdot0.7297}{1+1}$  = 0.83105  
d[C.H, G] =  $\frac{1\cdot0.1702+1\cdot0.1076}{1+1}$  = 0.1389

	0	G	C.H
0		0.4884	0.83105
G			0.1389
C.H			

Tree reconstribution

Distance matrices
Hamming distance
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UPGMA algorithm

## Exercise solution: distances and branches (2)

	0	G	C.H
0		0.4884	0.83105
G			0.1389
C.H			

$$\begin{aligned} & \text{branch}[\text{C.H.G, G}] = \frac{0.1389}{2} = 0.06945 \\ & \text{branch}[\text{C.H.G, C.H}] = \frac{0.1389}{2} - 0.02635 = 0.0431 \\ & \text{d}[\text{C.H.G, O}] = \frac{1 \cdot 0.4884 + 2 \cdot 0.83105}{1 + 2} = 0.71683 \end{aligned}$$

	0	C.H.G
0		0.71683
C.H.G		

Tree reconstribution

Distance matrices

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UPGMA algorithm

# Exercise solution: distances and branches (3)

	0	C.H.G
0		0.71683
C.H.G		

branch[C.H.G.O, C.H.G] = 
$$\frac{0.71683}{2} - 0.06945 = 0.288965$$
  
branch[C.H.G.O, O] =  $\frac{0.71683}{2} = 0.358415$ 

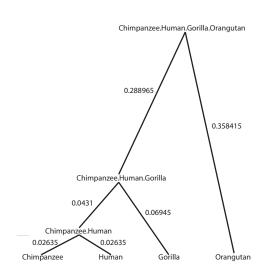
Tree reconstribution

Tree reconstruction

Distance matrices
Hamming distance
JC69 distance
K80 distance

UPGMA algorithm

### Exercise solution: tree



Tree reconstribution

Tree reconstruction

Distance matrices
Hamming distance
JC69 distance
K80 distance

UPGMA algorithm