Step 2: Collapse joined taxa into new group and make collapsed

new distance table 27 identical to UPGMA

$$d(B,DE) = \frac{1}{2} \left( 1.9 + 1.6 \right) = \frac{3.5}{2} = 1.75$$

REPEAT ...

BC smallest . ..

only 3-groups => use 3-point formula

$$7 = \frac{1}{2} \left( d(3,C) + d(8,DE) - d(c,DE) \right)$$

$$= \frac{1}{2} \left[ 1.14 (.75 + 1.3) = \frac{1.55}{2} = .775 \right]$$

$$y = d(B,C) - .775 = 1.1 - .775 =$$

$$Z = d(C,DE) - .325 = .975$$

LAST STEP: Combine again using average

FITCH - MARGOLIASH:

\* not used in practice, but a means to one NJ = neighbor joining

Same distance table used for UPGMA.

Step 1: Choose closest 2 taxa tojon

A,B

Different!

 $= \{C, D, E\}$ Collapse all other remains taxa into group &

and form temporary distance table for A,B, G

CDE

d(A, CDE) = d(A,E) + d(A,D) + d(A,C)

= ,5+.6+,7 = 1.8

 $d(B,CDE) = \frac{1.1+1.9+1.6}{3} = \frac{4.6}{3} = 1.8$ 

Use 3-point formula to fit chosen taxa (A,B)

to tree

A & Z COE

Reset to 3000!

Tors away temporary take

Step 2: Join AB into group for rest of analysis, Create new current distance table from original table just as in UPGMA.

REPEAT ...

Notice: Fitch-Margoliash

- i) constructs a non-ultrametric (also unnoted) tree which
- 2) has the same topology as the unrooted version of the UPBMA tree since both methods use the same collapsed distance takes to choose which 2 taxa to join in the next step.

The 'problem's with gitch-Margoliash is evident in metric trees like the following: a

metric tree with y>>x
y>2x sufficient

Both UPGMA, FM will choose to join bic first, since they are closest leading to by the wrong tree.

These algorithms make a mistake in the very first step.

Defn: Two leaves of a tree are NEIGHBORS or form a CHERRY of the graph-theoretical distance between them is 2.

Eg. b,c are neighbors, a,d form a cherry.

To remedy the potential downfall of FM described above, notice (assuming d(b,c)+d(a,d)>d(b,d)+d(a,c)=d(a,b)+d(c,d) distances >0)

$$T_i: d(a,b) + d(c,d) < d(a,c) + d(b,d) = d(a,d) + d(b,c)$$

$$T_{a}$$
:  $d(a,c) + d(b,d) < d(a,b) + d(c,d) = d(a,d) + d(b,c)$ 

$$T_3$$
:  $d(a,d) + d(b,c) < d(c,b) + d(c,d) = d(c,c) + d(b,a)$ 

POINT: There inequalities and equalities, shoose the tree in which (a,b) are neighbors.

Theorem: If T is a metric quartet tree with X = {a,b,c,d}

and all pairwise distances are positive, then

(a,b) and (c,d) are neighbors

if, and only if,

d(a,b)+ d(c,d) < d(a,c)+ d(b,d) = d(a,d)+d(b,c).

How to use this to reconstruct trees?

Defn: Let  $S: X \times X$  be a dissimilarity map on X. Then S satisfies the A-Point Condition if for all  $x_1y_1z_1w \in X$   $S(x,y) + S(z,w) \leq \max \left\{ S(x,z) + S(y,w), S(x,w) + S(y,z) \right\}$  l.e. 2 are equal and at least as big as the third.

Note:

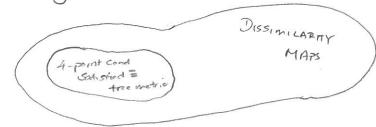
- \* used & and not just & This allows non-binary trees.
- + the taxa names x, y, Z, w are not no ressarily distinct

Theorem: If (T, w) is a metric tree with positive edge weights, then Hs tree metric is a dissimilarity map satisfying The 4-point condition

Remarkably, the converse is true

Theorem: If |x| = 3 and of is a dissimilarity map with of (x,y) +0 for xxy and & satisfies the 4-point condition, then

there is a unique X-tree with positive edge weights whose tra metric agrees with of



Proof (parts there of).

n=3: follows from 3- point formules

n=4: Case 1: (Strict inequality) Suppose X = { a, b, c, d} with

d(@,6)+d(c,d) < d(a,c)+d(b,d)=d(c,d)+d(b,c)

Then the topology is a x d with xxo.

Use the 3-point formulas to find the distances to terminal branches

Selve for x via

Case Z: Equality: d(a,b) +d(c,d) = d(a,c) + d(b,d) = d(a,d)+ d(b,c)