The initial matrix and species (as provided):

First, the smallest interspecies distance is found, in this case it occurs between the first row and second column (corresponding to species 'a' and 'b'). These two species are now combined into a new species 'a,b'. The value assigned to each interspecies distance for this species 'a,b' is a weighted average calculated with

$$d('s_a, s_b', 's_i') = \frac{|'s_a'| \cdot d('s_a', 's_i') + |'s_b'| \cdot d('s_b', 's_i')}{|'s_a'| + |'s_b'|}$$

Where $'s_i'$ represents species the current species, $'s_a'$ and $'s_0'$ represents the respectively chosen species and $|'s_n'|$ is the number of sub-species the species contains (on the first iteration this is always 1).

These species can now be added to the phylogenetic tree with species 'a,b' being the root with children 'a' and 'b' each with edge weightings being half of their interspecies distance of 15.0 (7.5).

Calculating these and inserting them to the end of the matrix yields the following.

The next smallest distance is between the new species 'a,b' and 'e', note here that |a,b'|=2.

This now makes 'e,a,b' the root of the tree with children 'e' and 'a,b', the edge weightings are now set such that adding up the weights by following any single path down from the root yields the same total (in this case 12.0).

Combining these species produces the following matrix.

The smallest distance is now between 'c' and 'd' at 30.0, adding these to the tree now creates a separate tree (which will become a sub-tree) with 'c,d' being the root and 'c' and 'd' as children each with weightings half of the distance between them (15.0), this now yields the following matrix.

'e,a,b' and 'c,d' are now chosen to become 'e,a,b,c,d', this now combines the separate trees into one and produces the following matrix.

Combining these last two species to create the final root node 'f,e,a,b,c,d' produces the following matrix.

As there is only one species left, the algorithm is complete, producing the following final tree.

