Futa explains HCData file:

So if it’s a negative number, that represents which sample

So -134, -144 means that the 134th item and the 144th item in the order file are connected together the 134th and 144th before the whole input matrix got clustered

If the number is a positive number, let’s say 3, that means that the linkage created in the third line of the HCData file

so if your line is -141, 1 that means that the 141th sample in the file is connected with the first link .

A B Height

-191 -378 8.48743107154308

-93 -377 9.5789618642558

-381 -392 10.1994976699112

-320 -375 10.2286080989752

-1 -307 10.4212761904422

-268 -269 10.916431331169

-141 1 11.2297029011894

so in this chunk here, the 191th sample in the original order, and the 378th are linked at a height of 8.4 the 141th sample will connect with that linkage (the 191 and 378 linkage) since it connects with +1

1. GET HIGHEST CUT BAR POSITION: Subtract (number of cuts – 1) to get array element of divider bar that is the highest cut. All other bars will be below this bar (Exp: 399 rows and 5 cuts = bar at array position 395)
2. GET OTHER CUT BAR POSITIONS: Starting at top look at all rows above the highest cut bar position (exp: 395). For each of these rows, look at the right and left values. If either of them are less than the highest cut bar position in the array, they will be cut bars. Now you have a list of array bar positions that contain one entry for each cut.
3. GET LEFTMOST DATA POSITION FOR EACH CUT BAR: This will be the terminus of a given cut bar (e.g. Sample/Gene at bottom). Walk the first number (left) of the bar downward, using that number as the array row number to go to next, until you arrive at a negative number. The absolute value of this number is the sorted position of the sample/gene in the clustered matrix.
4. GET THE RIGHTMOST DATA POSITION FOR EACH CUT BAR: Same as 3, except using the right number.