

0. Given a gene-by-array expression profile matrix, $M_{g \times p}$, with g genes and p arrays. The following process can be applied for either gene or array grouping and sorting.
1. Compute the gene-by-gene proximity (e.g., correlation, Euclidean distance, etc.) matrix $R_{g \times g}$, (Figure 3a).
2. Select an HCT linkage type (e.g., single, complete, average, centroid, etc.) and construct the hierarchical clustering tree, HCT , for $R_{g \times g}$ with g terminal nodes, T_i ($i=1, \dots, g$), and $g-1$ intermediate nodes, N_j ($j=1, \dots, g-1$). We further define N_j^T ($j=1, \dots, g-1$) the set of terminal nodes spanned by intermediate node N_j , (Figure 3b).
3. Apply the converging sequence of iteratively formed correlation matrices [1] to $R_{g \times g}$ and obtain the rank-two ellipse seriation, $R2E$, for $R_{g \times g}$. Define relative positions ($1, \dots, g$) of the g terminal nodes, T_i ($i=1, \dots, g$), in $R2E$ as O_i ($i=1, \dots, g$) and define N_j^O ($j=1, \dots, g-1$) the set of relative positions of terminal nodes spanned by intermediate node N_j , (Figures 3c and 3b).
4. Use $R2E$ as an external reference to guide the flipping mechanism of HCT to obtain the final flipped tree, HCT_R2E . For an intermediate node N_j with two sub-nodes N_{j1} and N_{j2} , assign N_{jk} as the upper sub-node of N_j if $\text{mean}(N_{jk}^O) = \min(\text{mean}(N_{j1}^O), \text{mean}(N_{j2}^O))$, (Figure 3d).
5. Sort $M_{g \times p}$ according to the relative terminal node positions of HCT_R2E , (Figure 3d).