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| **S1 Algorithm. Pseudo code of DEclust.** |
|  **Input**: $G=\{g\_{1}, g\_{2}, …, g\_{n}\}$ (set of genes to be clustered). |
|  **Output**: *N* (Hierarchical tree written in Newick tree format). |
|  **Procedure**:  Assign one gene to each cluster. Calculate the distance *D* according to equation (3) for all pairs of clusters. |
|  **while** there is more than one cluster **do** Search for a pair of clusters with the minimum distance. **If** Any pairs of clusters have the same distance **then** Compare conventional distance of expression levels. **end if** Merge the clusters. Store the clusters and the distance *D* in Newick format to *N*. Calculate the distance *D* using the equation (3) between a new cluster and other clusters. **end while** **return** *N* |