

Figure 5 – figure supplement 1

ECHODOTS algorithm

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Compute the Spearman distance  $\mathbf{D}$  across all the essential genes ----- (1)
For each  $\mathbf{d}$  in 30:200
  For each  $\mathbf{i}$  in 1:200
    Set  $\mathbf{i}$  as the initial seed
    Run t-SNE with  $\mathbf{D}$  as density matrix and get 2D coordinates ----- (2)
    Compute the range of the data points in t-SNE map  $\mathbf{L}(\mathbf{i})$ 
    Compute the neighborhood threshold  $\varepsilon(\mathbf{i}) = \mathbf{L}(\mathbf{i})/\mathbf{d}$  ----- (3)
    Run DBSCAN with  $\varepsilon(\mathbf{i})$  to find clusters for the essential genes  $\mathbf{C}(\mathbf{d},\mathbf{i})$  ----- (4)
  Find consistent clusters  $\mathbf{CC}(\mathbf{d})$  among  $\mathbf{C}(\mathbf{d},\mathbf{i})$ ,  $\mathbf{i} = \{1, \dots, 200\}$  ----- (5)
Find the lower bound  $\mathbf{d}_0$  such that  $\mathbf{d} \geq \mathbf{d}_0$  ----- (6)
Pick three  $\mathbf{d}$  and corresponding cluster sets  $\mathbf{CC}(\mathbf{d})$  ----- (7)
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