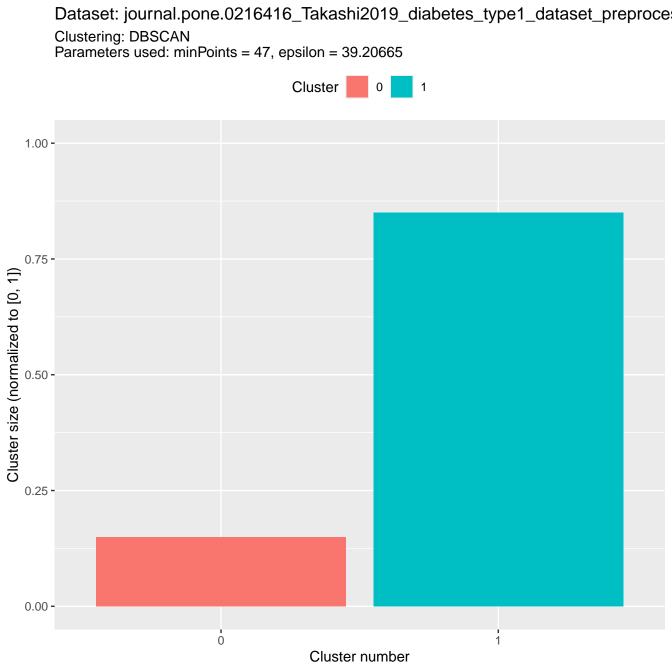
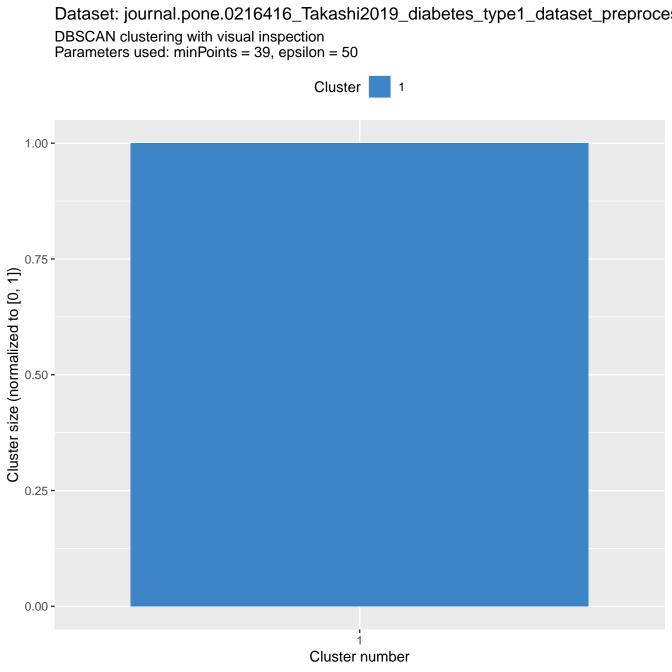
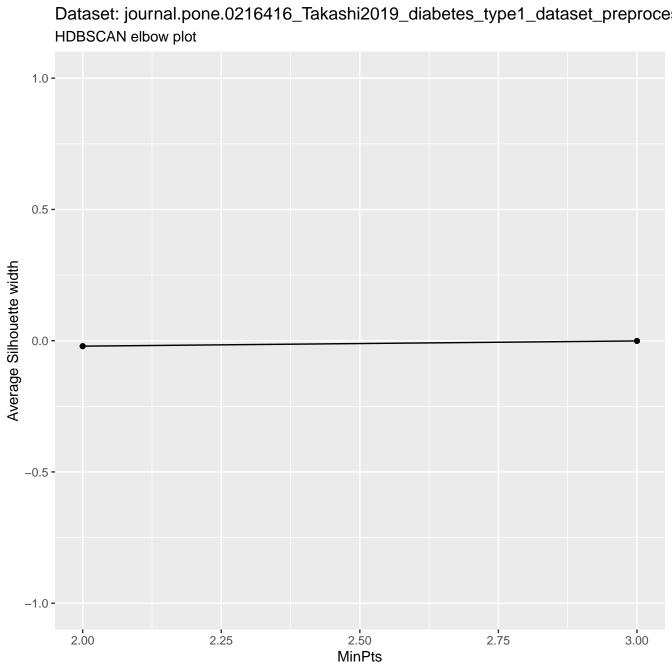


Dataset: journal.pone.0216416\_Takashi2019\_diabetes\_type1\_dataset\_preproce DBSCAN elbow plot 1.0 minPoints **→** 21 **→** 41 22 -- 42 23 - 43 24 - 44 0.5 -25 -- 45 26 Average Silhouette width 27 -- 47 28 -- 48 29 -- 49 0.0 -30 -- 50 31 -- 51 32 -- 52 33 - 53 34 -- 54 35 -- 55 -0.5 **-**36 --56 37 - 57 38 58 39 **--** 59 40 -1.0 **-**40 30 50 **Epsilon** 







Dataset: journal.pone.0216416\_Takashi2019\_diabetes\_type1\_dataset\_preproce Clustering: HDBSCAN Parameters used: minPoints = 3 Cluster 3 1.00 -0.75 -Cluster size (normalized to [0, 1]) 0.50 -0.25 -0.00 -0 3 2 Cluster number

Dataset: journal.pone.0216416\_Takashi2019\_diabetes\_type1\_dataset Hyperparameter combinations ranked by its average Silhouette score minPoints = 48epsilon = 39.46252minPoints = 47epsilon = 39.20665 minPoints = 40epsilon = 38.07322minPoints = 39 epsilon = 39.51018 minPoints = 39epsilon = 37.99056minPoints = 38epsilon = 39.40318 minPoints = 38epsilon = 37.88767 method minPoints = 37epsilon = 39.25402 **DBSCAN** minPoints = 37epsilon = 37.74425minPoints = 36epsilon = 37.72093minPoints = 32epsilon = 37.3467 minPoints = 23epsilon = 35.96295 minPoints = 22epsilon = 35.54263minPoints = 21epsilon = 35.10972 minPoints = 21epsilon = 33.80936-0.50.5 -1.00.0 1.0 Silhouette score

