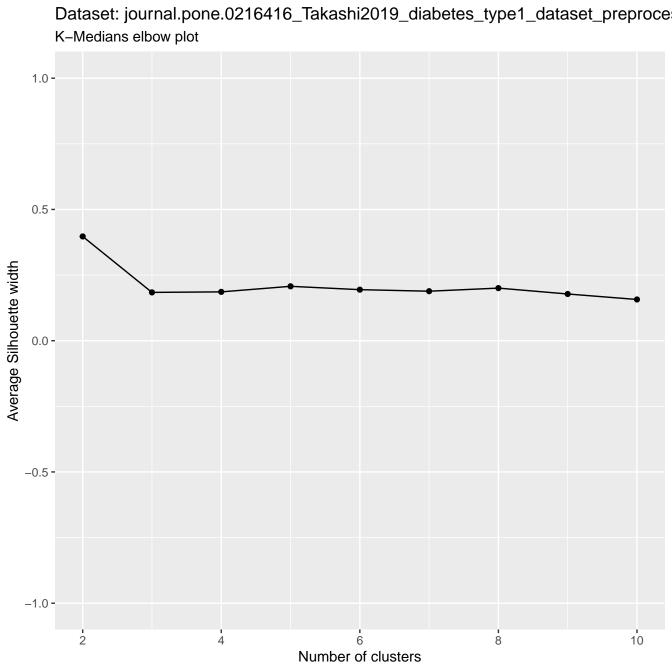
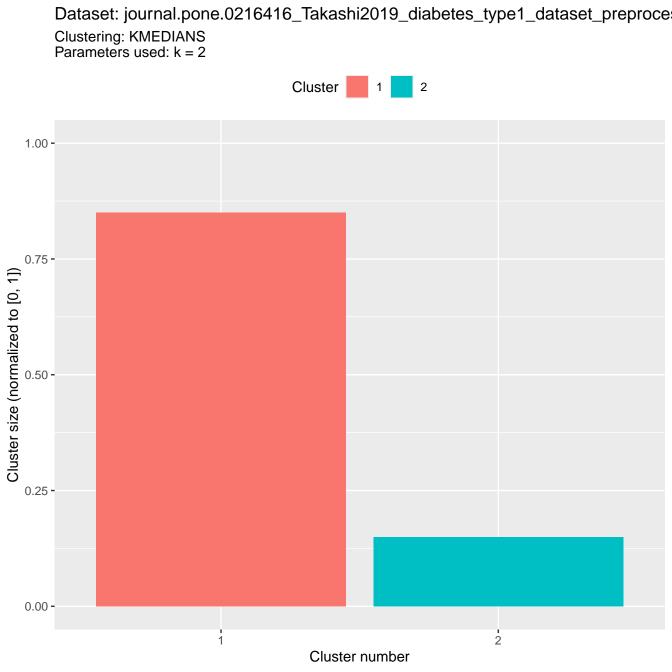
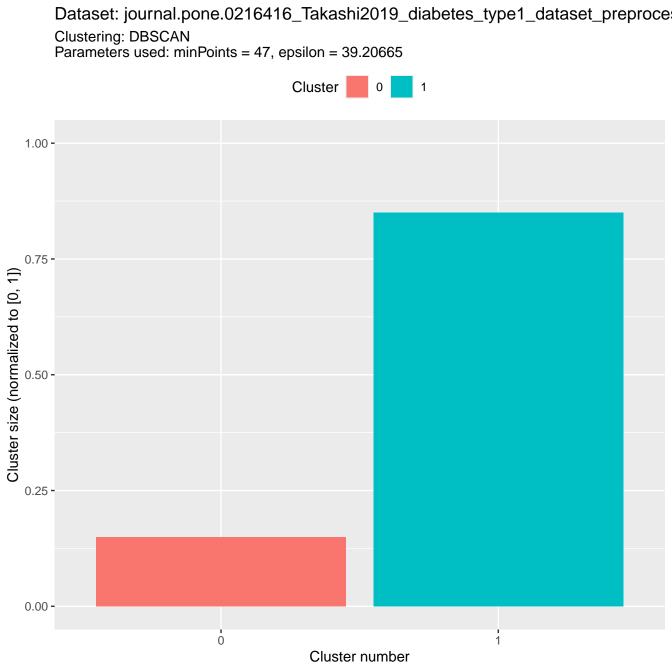


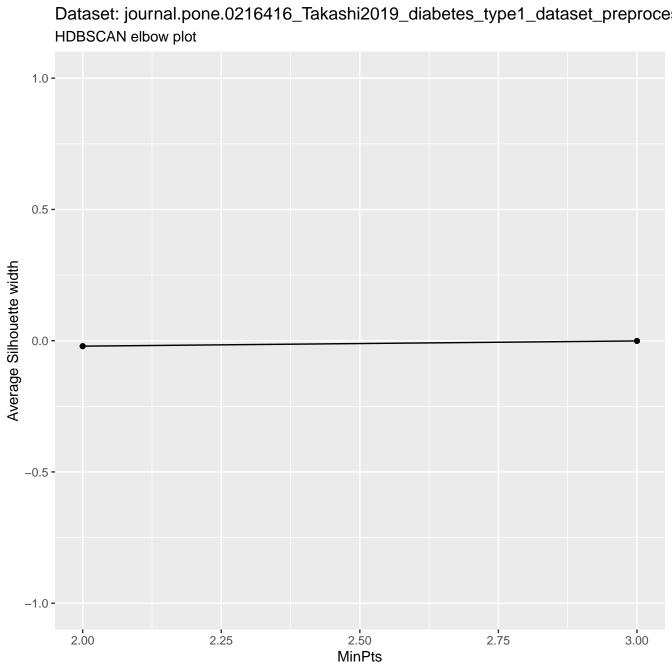
Dataset: journal.pone.0216416_Takashi2019_diabetes_type1_dataset_preproce Clustering: KMEANS Parameters used: k = 5, method = binary Cluster 3 5 1.00 -0.75 -Cluster size (normalized to [0, 1]) 0.50 -0.25 -0.00 -2 5 Cluster number





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

Hyperparameter combinations ranked by its average Silhouette score minPoints = 480.38742 epsilon = 39.46252minPoints = 470.38742 epsilon = 39.20665 minPoints = 37 0.38579 epsilon = 39.25402minPoints = 370.38579 epsilon = 37.74425 minPoints = 360.38579 epsilon = 37.72093minPoints = 320.38579 epsilon = 37.3467 minPoints = 23method 0.38579 epsilon = 35.96295**DBSCAN** minPoints = 220.38579 epsilon = 35.54263 **KMEANS** minPoints = 21**KMEDIANS** 0.38579 epsilon = 35.10972 minPoints = 210.38579 epsilon = 33.80936 k = 50.97015 method = binary k = 40.95522 method = binary k = 30.66827 method = binary k = 20.73637 method = binary k = 2 -0.39709 -0.50.0 0.5 1.0 -1.0

Silhouette score

Dataset: journal.pone.0216416_Takashi2019_diabetes_type1_dataset

