

Table S1. Feature vector component of each circRNA-disease pair.

First type of feature for circRNA/disease (F_1)	$F_{1.num.nei}$	The number of $c(i)/d(j)$'s neighbors
	$F_{1.sim.ave}$	The average similarity score of circRNA $c(i)$ and disease $d(j)$
	$F_{1.dis.num}$	The distribution number of similarity scores of $c(i)$ and $d(j)$ in each distribution interval
Second type of feature for circRNA/disease (F_2)	$F_{2.num.nei}$	The neighbor's number of $c(i)$ and $d(j)$ based on the unweighted circRNA/disease similarity network
	$F_{2.K.sim}$	The top 10 similarity scores of $c(i)$ and $d(j)$
	$F_{2.ave.featl}$	The average first type feature of $c(i)$ and $d(j)$ by the top 10 neighbors
	$F_{2.W.ave.featl}$	The average of the first type features among the top 10 neighbors weighted by its corresponding similarity values
	$F_{2.bc}, F_{2.cc}, F_{2.ec}$	Betweenness centrality, closeness centrality and eigenvector centrality of each $c(i)$ and $d(j)$ node
Third type of feature of circRNA (F_3)	$F_{3.GC.Cont}$	The content of GC base in nucleic acid sequence
	$F_{3.Base.K-mer}$	The sequence assembly K-mer algorithms is used to count the number of matching base combination patterns
Forth type of feature of circRNA-disease association pair (F_4)	$F_{4.svd}$	Latent vector of $c(i)$ and $d(j)$ based on SVD algorithm
	$F_{4.c.d.num}$	The number of circRNA $c(i)$'s neighbors
	$F_{4.d.c.num}$	The number of disease $d(j)$'s neighbors
	$F_{4.c.d.bc}, F_{4.c.d.cc}, F_{4.c.d.ec}$	The betweenness centrality, closeness centrality and eigenvector centrality of node in circRNA-disease associations network