

a) Method Characteristics					b) Evaluation Summary						
					Scores aggregation of all components						
Matrix Factorization / Matrix Completion		Algorithms	Networks	Language	Overall	Performance		Scalability		Usability	
HGIMC	HGBI, bounded matrix completion, Gaussian radial basis, ADMM		Bipartite network (drug-disease)	MATLAB	0.847		0.863		0.798	0.896	
ITRPCA	WKNN, TRPCA		Bipartite network (drug-disease)	MATLAB	0.824		0.863		0.742	0.868	
BNNR	nuclear norm regularization, ADMM		Bipartite network (drug-disease)	MATLAB	0.824		0.846		0.764	0.878	
VDA-GKSBMF	Gaussian kernel similarity bilinear matrix factorization, ADMM		Bipartite network (drug-disease)	MATLAB	0.82		0.851		0.781	0.805	
OMC	nuclear norm minimization, ADMM, KNN		Bipartite network (drug-disease)	MATLAB	0.817		0.853		0.782	0.779	
NMFDR	non-negative matrix factorization, Similarity Network Fusion		Bipartite network (drug-disease)	MATLAB	0.816		0.84		0.818	0.743	
MSBMF	bilinear matrix factorization, ADMM		Bipartite network (drug-disease)	MATLAB	0.81		0.814		0.794	0.827	
MLMC	Laplacian graph regularization, ADMM		Bipartite network (drug-disease)	MATLAB	0.8		0.876		0.702	0.767	
WRMF	similarity constrained weight regularization matrix factorization		Bipartite network (drug-disease)	MATLAB	0.795		0.836		0.809	0.641	
DRPADC	WKNKN, CKA-MKL		Bipartite network (drug-disease)	MATLAB	0.79		0.839		0.749	0.726	
GROBMC	Laplacian graph regularization, nuclear norm minimization, PPXA		Bipartite network (drug-disease)	MATLAB	0.783		0.748		0.814	0.823	
SCPMF	similarity constrained probabilistic matrix factorization		Bipartite network (drug-disease)	MATLAB	0.782		0.809		0.811	0.641	
DRRS	SVT, nuclear norm minimization		Bipartite network (drug-disease)	MATLAB	0.749		0.851		0.558	0.824	
DDAPRED	logistic matrix factorization, similar network fusion		Bipartite network (drug-disease)	Python	0.721		0.685		0.79	0.694	
DRIMC	logistic matrix factorization		Bipartite network (drug-disease)	R	0.575		0.416		0.724	0.753	
SCMFDD	similarity constrained matrix factorization		Bipartite network (drug-disease)	MATLAB	0.494		0.39		0.514	0.767	
Machine Learning											
deepDR	MDA, cVAE			Python	0.815		0.849		0.786	0.774	
DDA-SKF	similarity kernel fusion, Laplacian regularized least squares		Bipartite network (drug-disease)	MATLAB	0.813		0.856		0.775	0.763	
DDAGDL	geometric deep learning, XGBoost, autoencoder		Tripartite network (drug-disease-protein)	Python	0.705		0.715		0.666	0.753	
DRHGCN	graph convolutional network		Bipartite network (drug-disease)	Python	0.59		0.645		0.358	0.891	
HNRD	neighborhood information aggregation, Neural network		Bipartite network (drug-disease)	Python	0.583		0.641		0.414	0.745	
DRWBNCF	MLP, weighted bilinear aggregator		Bipartite network (drug-disease)	Python	0.539		0.483		0.522	0.737	
DRAGNN	GNN, attention, MLP		Bipartite network (drug-disease)	Python	0.518		0.466		0.481	0.749	
ANMF	autoencoder		Bipartite network (drug-disease)	Python	0.423		0.416		0.321	0.645	
LAGCN	graph convolutional network		Bipartite network (drug-disease)	Python	0.359		0.38		0.142	0.731	
Network Propagation											
iDrug	cross-network embedding, multiplicative update minimization		Tripartite network (drug-disease-target)	MATLAB	0.797		0.821		0.806	0.706	
MBiRW	bi-random walk		Bipartite network (drug-disease)	MATLAB	0.778		0.811		0.786	0.664	
HINGRL	Random walk, autoencoder		Tripartite network (drug-disease-protein)	Python	0.713		0.892		0.433	0.735	