

Additional Material: Overview of functions included in the WGCNA package

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Category	Function name	Short description
Rudimentary data cleaning	checkSets	Check whether given multi-set expression data have valid format
	fixDataStructure	Put single-set data into a form useful for multi-set calculations
	goodGenes	Filter out genes with too many missing entries
	goodGenesMS	Filter out genes with too many missing entries across multiple sets
	goodSamples	Filter out samples with too many missing entries
	goodSamplesGenes	Iterative filtering of samples and genes with too many missing entries
	goodSamplesGenesMS	Iterative filtering of samples and genes with too many missing entries across multiple data sets
	goodSamplesMS	Filter out samples with too many missing entries across multiple data sets
Network construction	keepCommonProbes	Keep probes that are shared among given data sets
	adjacency	Calculate adjacency from similarity
	bicor	biweight midcorrelation
	cor	faster calculation of correlations
	corFast	faster calculation of correlations
	checkAdjMat	Check whether a matrix satisfies conditions on an adjacency matrix
	TOMsimilarity	Calculate topological overlap
	TOMsimilarityFromExpr	Calculate topological overlap directly from expression data
	TOMdist	Calculate dissimilarity based on topological overlap
	GTOMdist	Calculate dissimilarity based on generalized topological overlap
	sigmoidAdjacencyFunction	Alternative soft-thresholding adjacency function
signumAdjacencyFunction	Adjacency function to construct an unweighted network	

Module detection		<p>cutreeStatic moduleNumber cutreeStaticColor</p> <p>blockwiseModules blockwiseConsensusModules closestNeighborConnectivity</p> <p>closestNeighborConnectivityMS</p> <p>consensusProjectiveKMeans</p> <p>dynamicMergeCut mergeCloseModules</p>	<p>Constant-height branch cut Constant-height branch cut Constant-height branch cut using color labels for returned modules</p> <p>Automatic module detection Automatic consensus module detection Connectivity to a fixed number of nearest neighbors</p> <p>Connectivity to a fixed number of nearest neighbors in several sets</p> <p>Consensus projective K-means clustering of expression data</p> <p>Threshold for module merging Merge close modules in gene expression data</p>
Module summary		<p>addTraitToMEs</p> <p>alignExpr</p> <p>moduleEigengenes multiSetMEs</p> <p>orderMEs</p>	<p>Add a trait to an existing collection of module eigengenes</p> <p>Align the expression of a module with a given vector</p> <p>Calculate module eigengenes Calculate module eigengenes across multiple data sets</p> <p>Put close eigengenes next to each other</p>
Gene selection		<p>signedKME</p> <p>networkScreening</p> <p>networkScreeningGS automaticNetworkScreening automaticNetworkScreeningGS corPredictionSuccess relativeCorPredictionSuccess</p>	<p>Module eigengene-based intramodular connectivity</p> <p>Gene screening based on gene-trait correlation and network information</p> <p>Gene screening with external gene significance Automatic selection of genes relating to a trait Automatic selection of genes relating to a trait</p>
Differential Analysis	Network	<p>correlationPreservation preservationNetworkConnectivity</p>	<p>Preservation of eigengene correlations Network preservation calculations</p>
Network topological characteristics		<p>clusterCoef hubGeneSignificance intramodularConnectivity nearestNeighborConnectivity</p> <p>nearestNeighborConnectivityMS</p> <p>networkConcepts</p> <p>pickHardThreshold</p>	<p>Clustering coefficient calculation Hub gene significance of module hub genes Intramodular connectivity Connectivity to a constant number of nearest neighbors</p> <p>Connectivity to a constant number of nearest neighbors across multiple data sets</p> <p>Calculation of various network concepts (topological properties, network indices)</p> <p>Evaluate scale free indices in unweighted networks</p>

	pickSoftThreshold	Evaluate scale free indices in weighted networks
	softConnectivity	Connectivity in an unweighted network
Data simulation	createEigengeneNetwork	Simulate an eigengene network from a causal model
	simulateDatExpr	Simulate expression data with a modular structure
	simulateDatExpr5Modules	Simulate expression data in 5 modules
Visualization	addGrid	Add grid lines to an existing plot
	addGuideLines	Add vertical guide lines to an existing dendrogram plot
	displayColors	Show colors used to label modules
	greenBlackRed	Green-black-red color sequence
	greenWhiteRed	Green-white-red color sequence
	labeledBarplot	Barplot with text or color labels
	labeledHeatmap	Produce a labeled heatmap plot
	labels2colors	Convert numerical labels to colors
	matchLabels	Relabel modules to best approximate a reference
	plotClusterTreeSamples	Cluster microarray samples and plot the tree together with color-coded sample trait
	plotColorUnderTree	Plot color rows under a dendrogram
	plotDendroAndColors	Plot a hierarchical clustering dendrogram and corresponding color labels
	plotEigengeneNetworks	Summary plot of consensus eigengene networks across several data sets
	plotMEpairs	Summary pair plot of module eigengenes and sample trait
	plotModuleSignificance	Barplot of mean gene significance across modules
	plotNetworkHeatmap	Network heatmap plot
	TOMplot	Plot network heatmap with hierarchical clustering dendrograms and module assignment
	scaleFreePlot	Visual evaluation of scale free topology
Data export to other software	exportNetworkToCytoscape	Export network data in format readable by Cytoscape
	exportNetworkToVisANT	Export network data in format readable by VisANT
Miscellaneous	collectGarbage	Iterative garbage collection
	colQuantileC	Fast column-wise quantile of a matrix
	corPvalueFisher	Fisher's asymptotic p-value for correlation
	corPvalueStudent	Student asymptotic p-value for correlation
	initProgInd	Inline display of progress
	moduleColor.getMEprefix	Get the prefix used to label module eigengenes
	nPresent	Number of present data entries
	normalizeLabels	Transform numerical labels into normal order
	numbers2colors	Color representation for a numeric variable

overlapTable

Overlap counts and Fisher exact tests for two sets of module labels