

Graphs in R

- Graph
- igraph-package
- GraphNEL
- KEGGgraph

Graph Package

- Is the base network manipulation library of R
- Later igraph library was made.
- Graph is still being developed ,for example graphNEL was added to it as a class later.
- igraph has most the common classes of graph in parallel
- For example:
 - In graph there is **addEdge(from, to, graph, weights)**
 - In igraph there is **add.edges(graph, edges, ..., attr=list())**
to add edges to existing graphs

Graph library examples

- `f <- c("a", "a", "b", "c", "d")`
- `t <- c("b", "c", "c", "d", "a")`
- `weight <- rep(1,length(f))`
- `df <- data.frame(from=f, to=t, weight=weight)`
- `g <- graphBAM(df)`
- `gd <- graphBAM(df, edgemode = "directed")`
- `nd <- nodes(g)`
- `w1 <- edgeWeights(g)`
- `w2 <- edgeWeights(g,"a")`
- `w3 <- edgeWeights(g,1)`
- `d1 <- edges(g)`
- `d2 <- edges(g,c("a", "b"))`
- `e1 <- edgeData(g)`
- `e2 <- edgeData(g, "a", "c", attr="weight")`
- `em <- edgeMatrix(g)`
- `id <- isDirected(g)`
- `sg <- subGraph(c("a","c","d"), g)`
- `ft <- extractFromTo(g)`
- `am <- as(g,"graphAM")`
- `nl <- as(g,"graphNEL")`
- `mt <- as(g,"matrix")`
- `k <- intersection(g,g)`
- `k <- union(g,g)`
- `g`
- `gd`

igraph

- igraph is a library for network analysis.
- The main goals of the igraph library is to provide a set of data types and functions for:
 - Pain-free implementation of graph algorithms
 - fast handling of large graphs, with millions of vertices and edges
 - allowing rapid prototyping via high level languages like R

Creating graphs in igraph

- There are many functions in igraph for creating graphs, both deterministic and stochastic
- Stochastic graph constructors are called 'games' in igraph
- To create small graphs with a given structure the `graph.formula` function is easiest
- To create graphs from field data, `graph.edgelist`, `graph.data.frame` and `graph.adjacency` are probably the best choices.

Example

- $g = \text{graph.formula}(A-B)$
- Or $g = \text{graph.formula}(A \text{-----} B)$
- In directed case:
 - $g2 = \text{graph.formula}(A \text{ -+ } B \text{ -+ } C)$
 - $g1 = \text{graph.formula}(b \text{-+} a, a \text{-+} c)$

Enges and vertex IDs in igraph

- Vertices and edges have numerical vertex ids in igraph.
- Vertex ids are always consecutive and they start with zero. I.e. for a graph with 'n' vertices the vertex ids are between '0' and 'n-1'.
- If some operation changes the number of vertices in the graphs, e.g. a subgraph is created via `subgraph`,
- then the vertices are renumbered to satisfy this criteria.
- The same is true for the edges as well, edge ids are always between zero and 'm-1' where 'm' is the total number of edges in the graph.

Attributes

- In igraph it is possible to assign attributes to the vertices or edges of a graph, or to the graph itself.
- igraph provides flexible constructs for selecting a set of vertices or edges based on their attribute values.
- see `get.vertex.attribute` and `iterators` for details

Attributes continue

- Some vertex/edge/graph attributes are treated specially. One of them is the 'name' attribute.
- This is used for printing the graph instead of the numerical ids, if it exists. Vertex names can also be used
- to specify a vector or set of vertices, in all igraph functions
E.g. degree has a 'v' argument that gives the vertices for which the degree is calculated. This argument can be given as character vector of vertex names as well
- Attribute values can be set to any R object, but note that storing the graph in some file formats might result the loss of complex attribute values. All attribute values are preserved if you use **save** and **load** to store/retrieve your graphs.

Visualization in igraph

- igraph provides three different ways for visualization. The first is the `plot.igraph` function.
- (Actually you don't need to write `plot.igraph`, `plot` is enough. This function uses base R graphic and can be used with any R device.
- The second function is `tkplot`, which uses a **Tk GUI** for basic interactive graph manipulation.
- (Tk is quite resource hungry, so don't try this for very large graphs.)
- The third way requires the `rgl` package and uses OpenGL. See the `rglplot` function for the details

example

- `pdf("16sep.pdf")`
- `plot(g3, layout=layout.kamada.kawai, vertex.color="green")`
- `library(plotrix)`
- `dev.off()`

File formats in igraphs

- igraph can handle various graph file formats, usually both for reading and writing. We suggest that
- you use the GraphML file format for your graphs, except if the graphs are too big. For big graphs a
- simpler format is recommended. See `read.graph` and `write.graph` for details

graphNEL

- It is a class that extends **graph** package
- This is a class of graphs that are represented in terms of nodes and an edge list.
- This is a suitable representation for a graph with a large number of nodes and relatively few edges

graphNEL

- The **edgeL** is a named list of the same length as the node vector. The names are the names of the nodes.
- Each element of **edgeL** is itself a list. Each element of this (sub)list is a vector (all must be the same length)
- and each element represents an edge to another node.
- The sublist named **edges** holds index values into the node vector.
- And each such entry represents an edge from the node which has the same name as the component of **edgeL** to the node with index provided.

graphNEL

- Another component that is often used is named weights. It represents edge weights.
- The user can specify any other edge attributes (such as types etc). They are responsible for any special handling that these might require.
- For an undirected instance all edges are reciprocated (there is an edge from A to B and from B to A).
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Conversion from graphNEL to igraph and back

- `igraph.from.graphNEL(graphNEL, name = TRUE, weight = TRUE, unlist.attrs = TRUE)`
- `igraph.to.graphNEL(graph)`

Example:

- `GNEL1 <- igraph.to.graphNEL(g1)`
- `GNEL2 <- igraph.to.graphNEL(g2)`

Mergin to graphnels:

- `G = mergeGraphs(list(GNEL1, GNEL2))`

KEGGgraph package

- Is an interface between **KEGG pathway** and **graph** object as well as a collection of tools to analyze, dissect and visualize these graphs
- **KEGGgraph** maintains the pathway topology and allows further analysis or dissection of pathway graphs

KEGGgraph Package cont

- This package is used in corporation to graph objects usually those in GraphNel class
- The package requires KGML (KEGG XML) files, which can be downloaded from KEGG
- FTP site (<ftp://ftp.genome.jp/pub/kegg/xml>) without license permission for academic
- reference:
http://watson.nci.nih.gov/bioc_mirror/packages/2.4/bioc/vignettes/KEGGgraph/inst/doc/KEGGgraph.pdf

KEGGgraph

- With this package we can :
- Read KGML file
 - > mapkKGML <-
system.file("extdata/hsa04010.xml",
 - +
 - package="KEGGgraph")
- Parse it : this will convert the pathway into graph
 - > mapkG <-
parseKGML2Graph(mapkKGML,expandGenes=TRUE)

KEGGgraph and GraphNEL in graph

We can merge them with graphNEL :

- `graphs <- list(mapk=mapkG, wnt=wntG)`
`merged <- mergeGraphs(graphs)`
`merged`

A graphNEL graph with directed edges

Number of Nodes = 386

Number of Edges = 1628