`geoGraph`: implementing geographic graphs for large-scale spatial modelling

Thibaut Jombart, François Balloux, Andrea Manica

July 1, 2010

Contents

1 Introduction

This document describes the `geoGraph` package for the R software. `geoGraph` aims at implementing graph approaches for geographic data. In `geoGraph`, a given geographic area is modelled by a fine regular grid, where each vertice has a set of spatial coordinates and a set of attributes, which can be for instance habitat descriptors, or the presence/abundance of a given species. 'Travelling' within the geographic area can then be easily modelled as moving between connected vertices. The cost of moving from one vertex to another can be defined according to attribute values, which allows for instance to define *friction routes* based on habitat.

geoGraph harnesses the full power of graph algorithms implemented in R by the graph and RBGL (R Boost Graph Library) packages. In particular, RBGL is an interface between R and the comprehensive *Boost Graph Library* in C++, which provides fast and efficient implementations of a wide range of graph algorithms. Once we have defined frictions for an entire geographic area, we can easily, for instance, find the least costs path from one location to another, or find the most parsimonious way of connecting a set of locations.

Interfacing spatial data and graphs can be a complicated task. The purpose of geoGraph is to provide tools to achieve and simplify this 'preliminary' step. This is achieved by defining new classes of objects which are essentially geo-referenced graphs with node attributes (gGraph objects), and interfaced spatial data (gData objects). In this vignette, we show how to install geoGraph, construct and handle gGraph/gData objects, and illustrate some basic features of graph algorithms.

2 First steps

2.1 Installing the package

What is tricky here is that a vignette is basically available once the package is installed. Assuming you got this document before installing the package, here are some clues about installing geoGraph.

First of all, geoGraph depends on several other packages, including, graph and RBGL, both on Bioconductor (http://www.bioconductor.org/). These dependencies are mandatory, that is, you actually need to have these packages installed before using geoGraph. Also, it is better to make sure you are using the latest versions of these packages. graph and RBGL are no longer released on CRAN, although some outdated versions still persist there. To make sure you are using the right package versions, use the command installDep.geoGraph() while connected on the internet. Do NOT use install.packages, or related functionalities from the interactive menus. In all cases, the latest version of geoGraph can be found from https://r-forge.r-project.org/projects/geograph/.

When loading the package, dependencies are also loaded:

```
> library(geoGraph)
```

```
        Note: polygon geometry computations in maptools
         depend on the package gpclib, which has a
         restricted licence. It is disabled by default;
         to enable gpclib, type gpclibPermit()

Checking rgeos availability as gpclib substitute:
```

```
FALSE

        ========================
        geoGraph 1.0-0 is loaded
        ========================
```

```
> search()
```

```
 [1] ".GlobalEnv"        "package:geoGraph"  "package:fields"
 [4] "package:spam"      "package:maptools"  "package:lattice"
 [7] "package:foreign"   "package:sp"        "package:RBGL"
[10] "package:graph"     "package:datasets"  "package:adegenet"
[13] "package:ade4"      "package:MASS"      "package:utils"
[16] "package:stats"     "package:graphics"  "package:grDevices"
[19] "package:methods"   "Autoloads"         "package:base"
```

The package is now ready to use.

2.2 Data representation

Data representation refers to the way a given type of data is handled by a computer program. Two types of objects are used in geoGraph: gGraph, and gData objects. Both objects are defined as formal (S4) classes and often have methods for similar generic function (*e.g.*, getNodes is defined for both objects). Essentially, gGraph objects contain underlying layers of informations, including a spatial grid and possibly node attributes, and covering the area of interest. gData are sets of locations – like sampled sites, for instance – which have been interfaced to a gGraph object, to allow further manipulations such as finding paths on the grid between pairs of locations.

2.2.1 gGraph objects

The definition of the formal class gGraph can be obtained using:

```
> getClass("gGraph")
```

```
Class "gGraph" [package "geoGraph"]

Slots:

Name:      coords nodes.attr       meta      graph
Class:     matrix data.frame       list   graphNEL
```

and a new empty object can be obtained using the constructor:

```
> new("gGraph")
```

```
=== gGraph object ===

@coords: spatial coordinates of 0 nodes
     lon lat

@nodes.attr: 0 nodes attributes
data frame with 0 columns and 0 rows

@meta: list of meta information with 0 items

@graph:
A graphNEL graph with undirected edges
Number of Nodes = 0
Number of Edges = 0
```

The documentation `?gGraph` explains the basics about the object's content. In a nutshell, these objects are spatial grids with nodes and segments connecting neighbouring nodes, and additional informations on the nodes or on the graph itself. `coords` is a matrix of longitudes and latitudes of the nodes. `nodes.attr` is a data.frame storing attributes of the nodes, such as habitat descriptors; each row corresponds to a node of the grid, while each column corresponds to a variable. `meta` is a list containing miscellanous informations about the graph itself. There is no contraint applying to the components of the list, but some typical components such as `$costs` or `$colors` will be recognised by certain functions. For instance, you can specify plotting rules for representing a given node attribute by a given color by defining a component `$colors`. Similarly, you can associate costs to a given node attribute by defining a component `$costs`. An example of this can be found in already existing `gGraph` objects. For instance, `worldgraph.10k` is a graph of the world with approximately 10,000 nodes, and only on-land connectivity (*i.e.* no travelling on the seas).

```
> data(worldgraph.10k)
> worldgraph.10k


=== gGraph object ===

@coords: spatial coordinates of 10242 nodes
        lon       lat
1 -180.0000  90.00000
2  144.0000 -90.00000
3  -33.7806  27.18924
...

@nodes.attr: 1 nodes attributes
  habitat
1     sea
2     sea
3     sea
...

@meta: list of meta information with 2 items
[1] "$colors" "$costs"

@graph:
A graphNEL graph with undirected edges
Number of Nodes = 10242
Number of Edges = 6954


> worldgraph.10k@meta


$colors
           habitat       color
1              sea        blue
2             land       green
3         mountain       brown
4       landbridge light green
5 oceanic crossing  light blue
6  deselected land   lightgray

$costs
           habitat cost
1              sea  100
2             land    1
3         mountain   10
4       landbridge    5
5 oceanic crossing   20
6  deselected land  100
```

Lastly, the graph component is a graphNEL object, which is the standard class for graphs in the graph and RBGL packages. This object contains all information on the connections between nodes, and the weights (costs) of these connections.

Four main gGraph are provided with geoGraph: rawgraph.10k, rawgraph.40k, worldgraph.10k, and worldgraph.40k. These datasets are available using the command data. The grid used in these datasets are the best geometric approximation of a regular grid for the surface of a sphere. One advantage of working with these grids is that we do not have to use a projection for geographic coordinates, which is a usual issue in regular GIS.

The difference between rawgraphs and worldgraphs is that the first are entirely connected, while in the second connections occur only on land. Numbers '10k' and '40k' indicate that the grids consist of roughly 10,000 and 40,000 nodes. For illustrative purposes, we will often use the 10k grids, since they are less heavy to handle. For most large-scale applications, the 40k versions should provide sufficient resolution. New gGraph can be constructed using the constructor (new(...)), but this topic is not documented in this vignette.

2.2.2 gData objects

gData are essentially sets of locations that are interfaced with a gGraph object. During this operation, each location is assigned to the closest node on the grid of the gGraph, then allowing for travelling between locations using the grid. Then, it is for instance possible to find the shortest path between two locations through various types of habitats.

Like for gGraph, the content of the formal class gData can be obtained using:

```
> getClass("gData")
```

```
Class "gData" [package "geoGraph"]

Slots:

Name:       coords    nodes.id        data gGraph.name
Class:      matrix   character         ANY   character
```

and a new empty object can be obtained using the constructor:

```
> new("gData")
```

```
=== gData object ===

@coords: spatial coordinates of 0 nodes
     lon lat

@nodes.id: nodes identifiers
character(0)

@data: data
NULL

Associated gGraph:
```

As before, the description of the content of these objects can be found in the documentation (?gData). coords is a matrix of xy (longitude/latitude) coordinates in which each row is a location. nodes.id is vector of characters giving the name of the vertices matching the locations; this is defined automatically when creating a new gData, or using the function closestNode. data is a slot storing data associated to the locations; it can be any type of object, but a data.frame should cover most requirements for storing data. Note that this object should be subsettable (i.e. the [operator should be defined), so that data can be subsetted when subsetting the gData object. Lastly, the slot gGraph.name contains the name of the gGraph object to which the gData has been interfaced.

Contrary to gGraph objects, gData objects will frequently be constructed by the user. In the next sections, we illustrate how we can build and use gData objects from a set of locations.

3 Using geoGraph

An overview of the material implemented in the package is summarized the package's manpage, accessible via:

```
> `?`(geoGraph)
```

The html version of this manpage may be preferred to browse more easily the content of geoGraph; it is accessible by typing:

```
> help("geoGraph", package = "geoGraph", html = TRUE)
```

To revert help back to text mode, simply type:

```
> options(htmlhelp = FALSE)
```

In the following, we go through various tasks that can be achieve using geoGraph.

3.1 Importing geographic data

Geographic data consist of a set of locations, possibly accompanied by additional information. For instance, one may want to study the migrations amongst a set of biological populations with known geographic coordinates. In geoGraph, geographic data are stored in gData objects. These objects match locations to the closest nodes on a grid (a gGraph object), and store additional data if needed.

As a toy example, let us consider four locations: Bordeaux (France), London (UK), Malaga (Spain), and Zagreb (Croatia). Since we will be working with a crude grid (10,000 nodes), locations need not be exact. We enter the longitudes and latitudes (in this order, that is, xy coordinates) of these cities in decimal degrees, as well as approximate population sizes:

```
> Bordeaux <- c(-1, 45)
> London <- c(0, 51)
> Malaga <- c(-4, 37)
> Zagreb <- c(16, 46)
> cities.dat <- rbind.data.frame(Bordeaux, London, Malaga, Zagreb)
> colnames(cities.dat) <- c("lon", "lat")
> cities.dat$pop <- c(1e+06, 1.3e+07, 5e+05, 1200000)
> row.names(cities.dat) <- c("Bordeaux", "London", "Malaga", "Zagreb")
> cities.dat
```

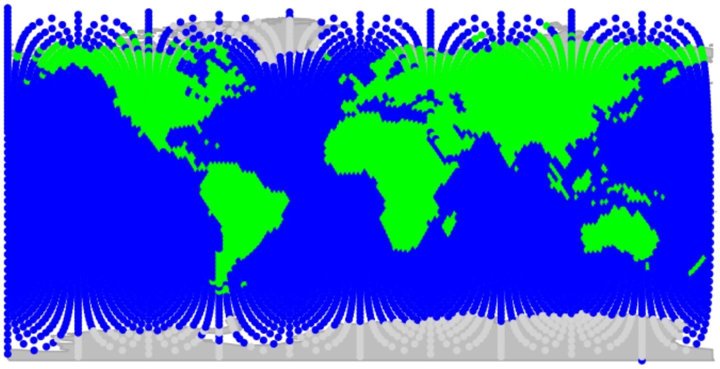
```
         lon lat     pop
Bordeaux  -1  45 1.0e+06
London     0  51 1.3e+07
Malaga    -4  37 5.0e+05
Zagreb    16  46 1.2e+06
```

We load a `gGraph` object which contains the grid that will support the data:

```
> data(worldgraph.10k)
> worldgraph.10k
```

```
=== gGraph object ===

@coords: spatial coordinates of 10242 nodes
        lon       lat
1 -180.0000  90.00000
2  144.0000 -90.00000
3  -33.7806  27.18924
...

@nodes.attr: 1 nodes attributes
  habitat
1     sea
2     sea
3     sea
...

@meta: list of meta information with 2 items
[1] "$colors" "$costs"

@graph:
A graphNEL graph with undirected edges
Number of Nodes = 10242
Number of Edges = 6954
```

```
> plot(worldgraph.10k)
```

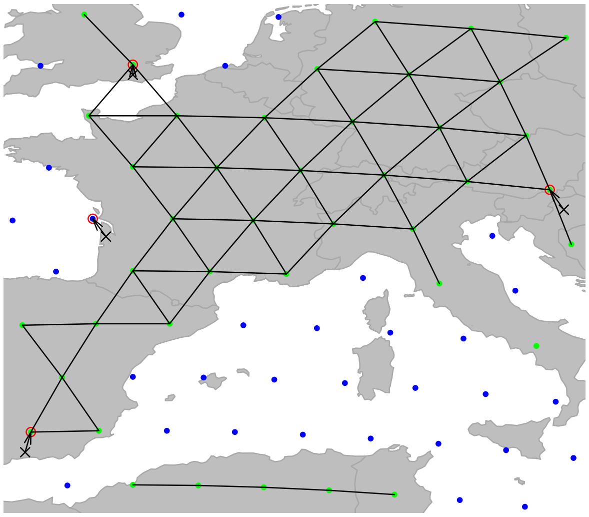


(we could use `worldgraph.40k` for a better resolution). In this figure, each node is represented with a color depending on the habitat type, either 'sea' (blue) or 'land' (green). We are going to interface the cities data with this grid; to do so, we create a `gData` object using `new` (see `?gData` object):

```
> cities <- new("gData", coords = cities.dat[, 1:2], data = cities.dat[,
+     3, drop = FALSE], gGraph.name = "worldgraph.10k")
> cities
```

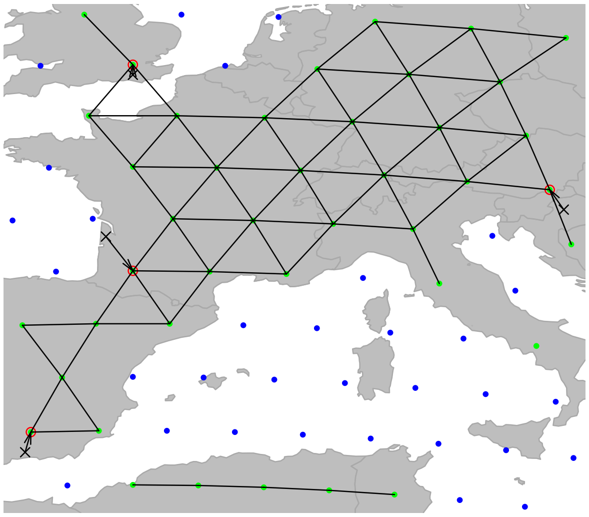
```
=== gData object ===

@coords: spatial coordinates of 4 nodes
  lon lat
1  -1  45
2   0  51
3  -4  37
...

@nodes.id: nodes identifiers
     1      2      3
"5774" "6413" "4815"
...

@data: 4 data
             pop
Bordeaux 1.0e+06
London   1.3e+07
Malaga   5.0e+05
...

Associated gGraph: worldgraph.10k
```

```
> plot(cities, type = "both", reset = TRUE)
> plotEdges(worldgraph.10k)
```



This figure illustrates the matching of original locations (black crosses) to nodes of the grid (red circles). As we can see, an issue occured for Bordeaux, which has been assigned to a node in the sea (in blue). Locations can be re-assigned to nodes with restrictions for some node attribute values using `closestNode`; for instance, here we constrain matching nodes to have an `habitat` value (defined as node attribute in `worldgraph.10k`) equalling `land` (green points):

```
> cities <- closestNode(cities, attr.name = "habitat", attr.value = "land")
> plot(cities, type = "both", reset = TRUE)
> plotEdges(worldgraph.10k)
```



Now, all cities have been assigned to a 'land' node of the grid (again, better accuracy will be gained on 40k or finer grids - we use 10k for illustrative purposes only). Content of `cities` can be accessed via various accessors (see `?gData`). For instance, we can retrieve original locations, assigned nodes, and stored data using:

```
> getCoords(cities)
```

```
     lon lat
5775  -1  45
6413   0  51
4815  -4  37
7699  16  46
```

```
> getNodes(cities)
```

```
  5775   6413   4815   7699
"5775" "6413" "4815" "7699"
```

```
> getData(cities)
```

```
             pop
Bordeaux 1.0e+06
London   1.3e+07
Malaga   5.0e+05
Zagreb   1.2e+06
```

We can also get the coordinates of the matching nodes (*i.e.*, red circle on previous figure) using:

```
> getCoords(cities, original = FALSE)
```

```
               lon      lat
5775  1.001791e-05 43.73025
6413  1.001791e-05 51.37555
4815 -3.787658e+00 37.74879
7699  1.547808e+01 46.73633
```

More interestingly, we can now retrieve all the geographic information contained in the underlying grid (*i.e.*, gGraph object) as node attributes:

```
> getNodesAttr(cities)
```

```
     habitat
5775    land
6413    land
4815    land
7699    land
```

In this example, the information stored in worldgraph.10k is rather crude: habitat only distinguishes the land from the sea. However, more complex habitat information could be incorporated, for instance from GIS shapefiles (see dedicated section below).

3.2 Visualizing data

An essential aspect of spatial analysis lies in visualizing the data. In geoGraph, the spatial grids (gGraph) and spatial data (gData) can be plotted and browsed using a variety of functions.

3.2.1 Plotting gGraph objects

Displaying a gGraph object is done through plot and points functions. The first opens a new plotting region, while the second draws in the current plotting region; functions have otherwise similar arguments (see ?plot.gGraph).

By default, plotting a gGraph displays the grid of nodes overlaying a shapefile (by default, the landmasses). Edges can be plotted at the same time (argument edges), or added afterwards using plotEdges. If the gGraph object possesses an adequately formed @meta$colors component, the colors of the nodes are chosen according to the node attributes and the color scheme specified in @meta$colors. Alternatively, the color of the nodes can be specified via the col argument in plot/points.

Here is an example using worldgraph.10k:

```
> data(worldgraph.10k)
> worldgraph.10k@meta$colors
```

```
           habitat       color
1              sea        blue
2             land       green
3         mountain       brown
4       landbridge light green
5 oceanic crossing  light blue
6  deselected land   lightgray
```

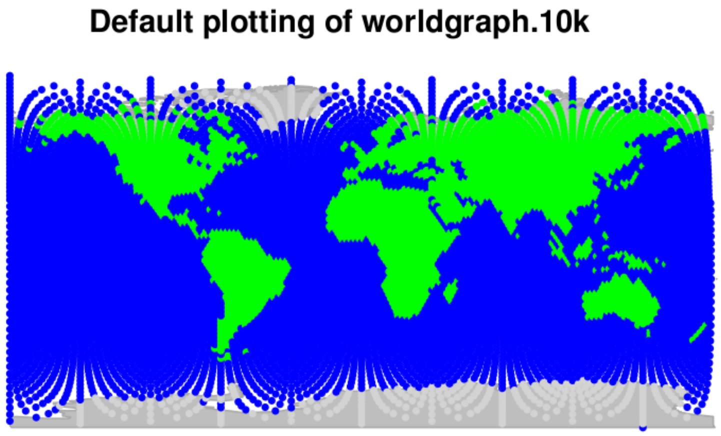
```
> head(getNodesAttr(worldgraph.10k))
```

```
  habitat
1     sea
2     sea
3     sea
4     sea
5     sea
6     sea
```

```
> table(getNodesAttr(worldgraph.10k))
```

```
deselected land            land             sea
            290            2632            7320
```

```
> plot(worldgraph.10k, reset = TRUE)
> title("Default plotting of worldgraph.10k")
```



It may be worth noting that plotting `gGraph` objects involves plotting a fairly large number of points and edges. On some graphical devices, the resulting plotting can be slow. For instance, one may want to disable *cairo* under linux: this graphical device yields better graphics than *Xlib*, but at the expense of increase computational time. To switch to *Xlib*, type:

```
> X11.options(type = "Xlib")
```

and to revert to *cairo*, type:

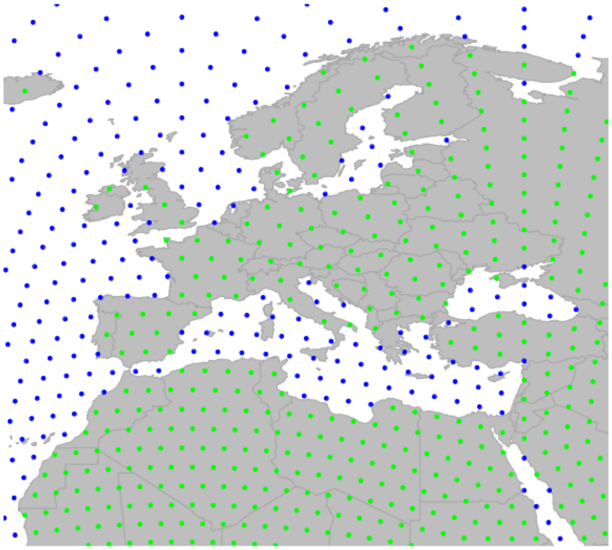
```
> X11.options(type = "cairo")
```

3.2.2 Zooming in and out, sliding, etc.

In practice, it is often useful to be able to peer at specific regions, and more generally to navigate inside the graphical representation of the data. For this, we can use the interactive functions `geo.zoomin`, `geo.zoomout`, `geo.slide`, `geo.back`, `geo.bookmark`, and `geo.goto`. The zoom and slide functions require to left-click on the graphics to zoom in, zoom out, or slide to adjacent areas; in all cases, a right click ends the function. Also note that `geo.zoomin` can accept an argument specifying a rectangular region, which will be adapted by the function to fit best a square area with similar position and centre, and zoom to this area (see `?geo.zoomin`). `geo.bookmark` and `geo.goto` respectively set and go to a bookmark, *i.e.* a tagged area. This is most useful when one has to switch between distant areas repeatedly.

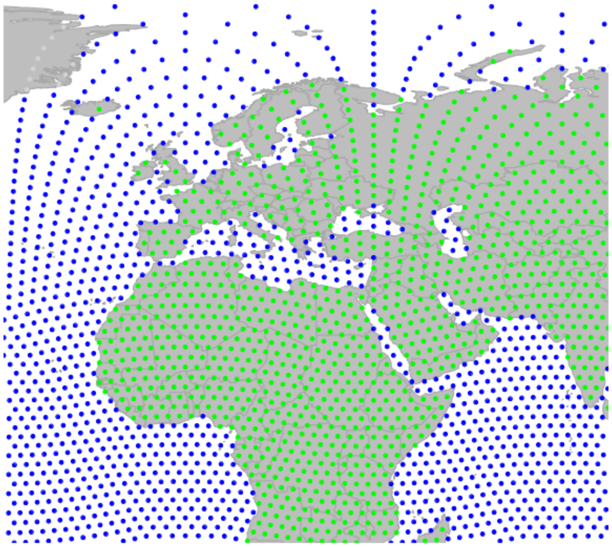
Here are some examples based on the previous plotting of `worldgraph.10k`:Zooming in:

```
> geo.zoomin()
```



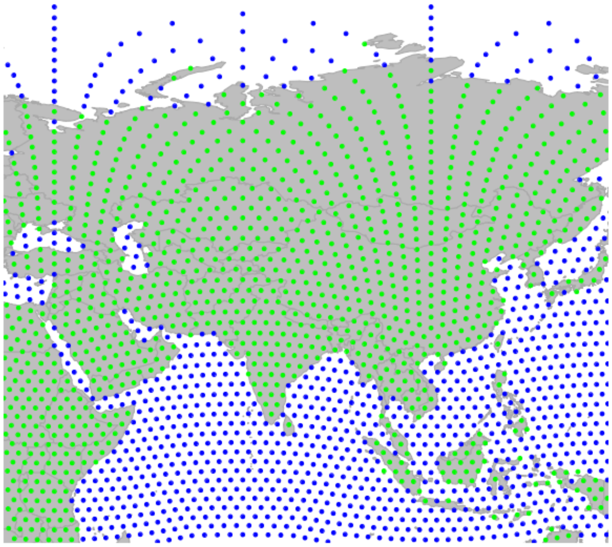
Zooming out:

```
> geo.zoomout()
```



Sliding to the east:

```
> geo.slide()
```



One important thing which makes plotting gGraph objects different from most other plotting in R is that geoGraph keeps the changes made to the plotting area in memory. This allows to undo one or several moves using geo.back. Moreover, even if the graphical device is killed, plotting again a gGraph will use the old parameters by default. To disable this behavior, set the argument reset=TRUE when calling upon plot. Technically, this 'plotting memory' is implemented by storing plotting information in an environment defined as the hidden variable .geoGraphEnv:

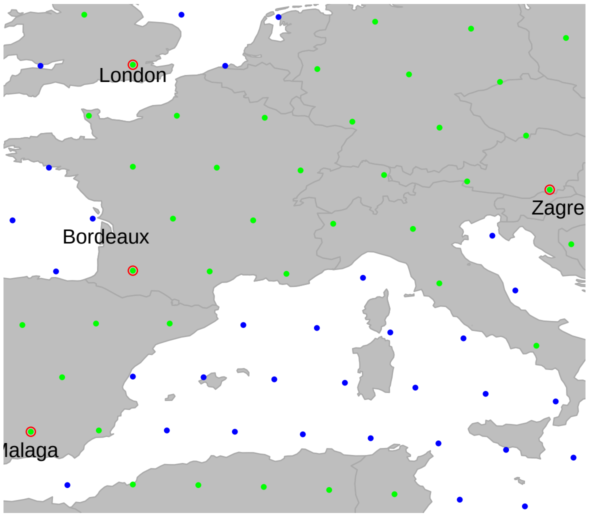
```
> .geoGraphEnv

<environment: 0x551e0d8>

> ls(env = .geoGraphEnv)

[1] "bookmarks"       "last.plot"       "last.plot.param" "last.points"
[5] "psize"           "sticky.points"   "usr"             "zoom.log"

> get("last.plot", .geoGraphEnv)

plot(worldgraph.10k, reset = TRUE)
```

It is recommended not to modify these objects directly, unless you really know what you are doing. In any case, plotting a gGraph object with argument reset=TRUE will remove previous plotting history and undo possible wrong manipulations.

3.2.3 Plotting gData objects

gData objects are by default plotted overlaying the corresponding gGraph. For instance, using the cities example from above:

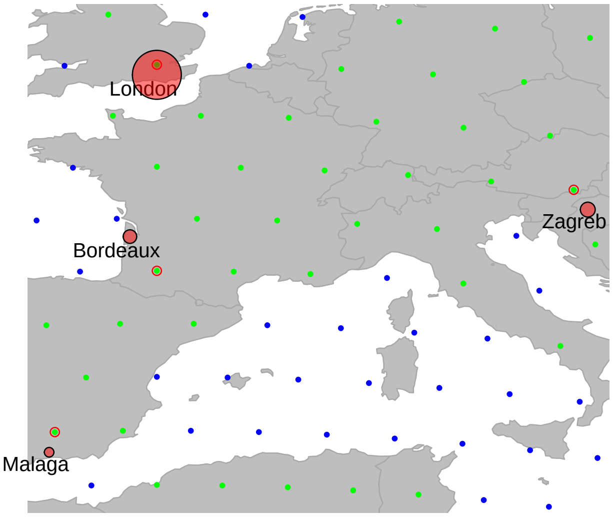
```
> plot(cities, reset = TRUE)
> text(getCoords(cities), rownames(getData(cities)))
```



Note the argument reset=TRUE, which tells the plotting function to adapt the plotting area to the geographic extent of the dataset.

To plot additional information, it can be useful to extract the spatial coordinates from the data. This is achieved by getCoords. This method takes an extra argument original, which is TRUE if original spatial coordinates are seeked, or FALSE for coordinates of the nodes on the grid. We can use this to represent, for instance, the population sizes for the different cities:

```
> plot(cities, reset = TRUE)
> par(xpd = TRUE)
> text(getCoords(cities) + -0.5, rownames(getData(cities)))
> symbols(getCoords(cities)[, 1], getCoords(cities)[, 2], circ = sqrt(unlist(getData(cities))),
+     inch = 0.2, bg = transp("red"), add = TRUE)
```



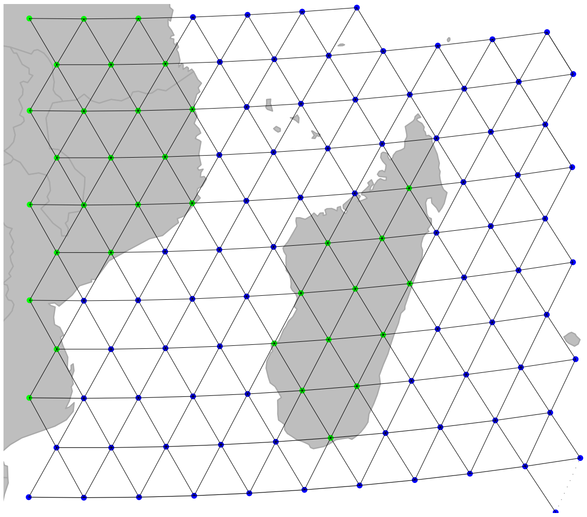
3.3 Editing gGraphs

Editing graphs is an essential task in geoGraph. While available gGraph objects provide a basis to work with (see ?worldgraph.10k), one may want to adapt a graph to a specific case. For instance, connectivity should be defined according to biological knowledge of the organism under study. gGraph can be modified in different ways: by changing the connectivity, the costs of edges, or the attribute values.

3.3.1 Changing the global connectivity of a gGraph

There are two main ways of changing the connectivity of a gGraph, which match two different objectives. The first approach is to perform global and systematic changes of the connectivity of the graph. Typically, one will want to remove all connections over a given type of landscape, which is uncrossable by the organism under study. Let's assume we are interested in saltwater fishes. To model fish dispersal, we have to define a graph which connects only nodes overlaying the sea. We load the gGraph object rawgraph.10k, and zoom in to a smaller area (Madagascar) to illustrate changes in connectivity:

```
> data(rawgraph.10k)
> geo.zoomin(c(35, 54, -26, -10))
> plotEdges(rawgraph.10k)
```



We shall set a bookmark for this area, in case we would want to get back to this place later on:

```
> geo.bookmark("madagascar")
```

```
Bookmark ' madagascar  'saved.
```

What we now want to do is remove all but sea-sea connections. To do so, the easiest approach is to i) define costs for the edges based on habitat, with land being given large costs and ii) remove all edges with large costs.

Costs of a given node attribute (here, 'habitat') are indicated in the `@meta$costs` slot:

```
> rawgraph.10k@meta$costs
```

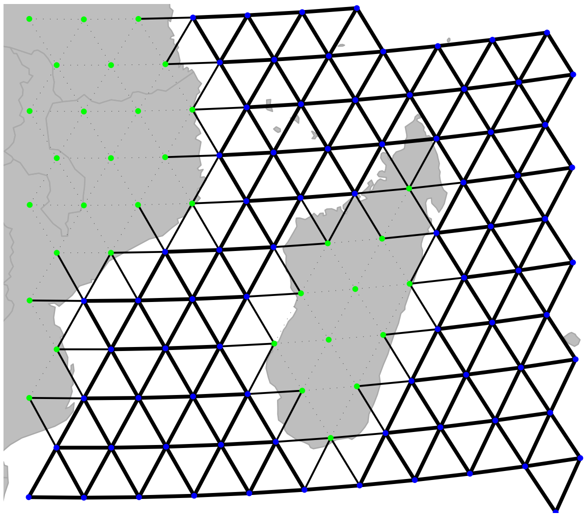
```
           habitat cost
1              sea  100
2             land    1
3         mountain   10
4       landbridge    5
5 oceanic crossing   20
6  deselected land  100
```

```
> newGraph <- rawgraph.10k
> newGraph@meta$costs[2:6, 2] <- 100
> newGraph@meta$costs[1, 2] <- 1
> newGraph@meta$costs
```

```
           habitat cost
1              sea    1
2             land  100
3         mountain  100
4       landbridge  100
5 oceanic crossing  100
6  deselected land  100
```

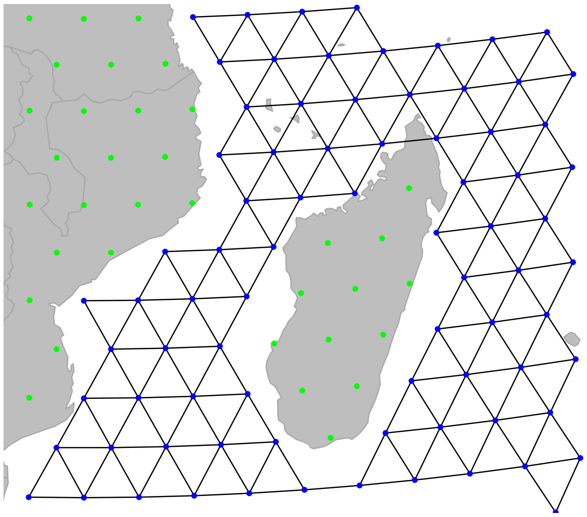
We have just changed the costs associated to habitat type, but this change is not yet effective on edges between nodes. We use `setCosts` to set the cost of an edge to the average of the costs of its nodes:

```
> newGraph <- setCosts(newGraph, attr.name = "habitat")
> plot(newGraph, edge = TRUE)
```



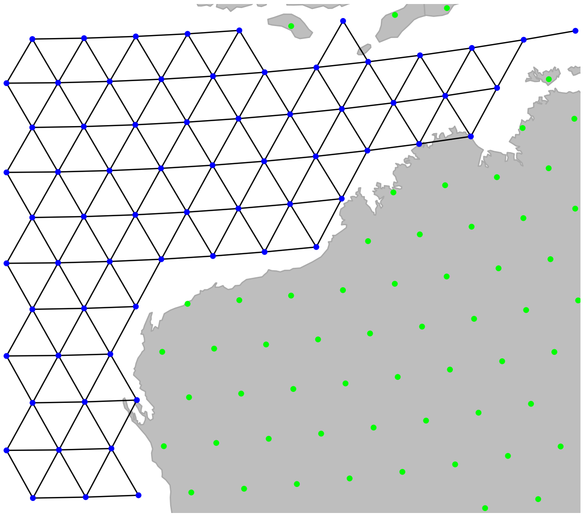
On this new graph, we represent the edges with a width inversely proportional to the associated cost; that is, bold lines for easy travelling and light edges/dotted lines for more costly mouvement. This is not enough yet, since travelling on land is still possible. However, we can tell `geoGraph` to remove all edges associated to too strong a cost, as defined by a given threshold (using `dropDeadEdges`). Here, only sea-sea connections shall be retained, that is, edges with cost 1.

```
> newGraph <- dropDeadEdges(newGraph, thres = 1.1)
> plot(newGraph, edge = TRUE)
```



Here we are: `newGraph` only contains connections in the sea. Note that, although we restrained the plotting area to Madagascar, this change is effective everywhere. For instance, travelling to the nort-west Australian coasts:

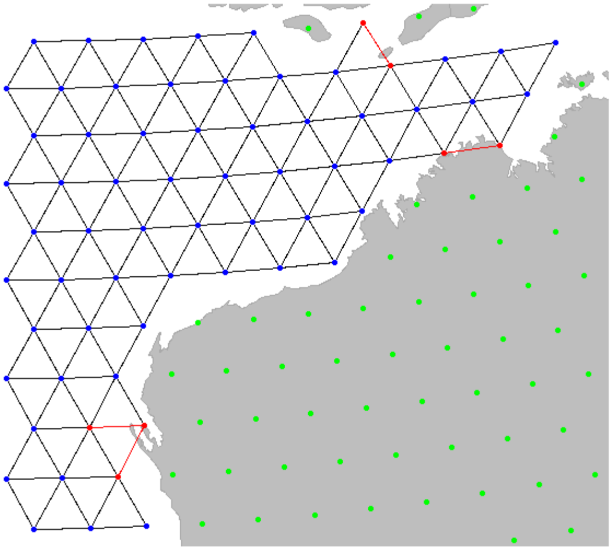
```
> geo.zoomin(c(110, 130, -27, -12))
> geo.bookmark("australia")


Bookmark ' australia  'saved.
```



3.3.2 Changing local properties of a gGraph

A second approach to changing a gGraph is to refine the graph by hand, adding or removing locally some connections, or altering the attributes of some nodes. This can be necessary to connect components such as islands to the main landmasses, or to correct erroneous data. Adding and removing edges from the grid of a gGraph can be achieved by geo.add.edges and geo.remove.edges, respectively. These functions are interactive, and require the user to select individual nodes or a rectangular area in which edges are added or removed. See ?geo.add.edges for more information on these functions. For instance, we can remove a few odd connections in the previous graph, near the Australian coasts (note that we have to save the changes using <-):

```
> geo.goto("autralia")
> newGraph <- geo.remove.edges(newGraph)
```



When adding connections within an area or in an entire graph, node addition is based on another `gGraph`, *i.e.* only connections existing in another `gGraph` serving as reference can be added to the current `gGraph`. For graphs based on 10k or 40k grids, the raw graphs provided in `geoGraph` should be used, (`rawgraph.10k`, `rawgraph.40k`), since they are fully connected.

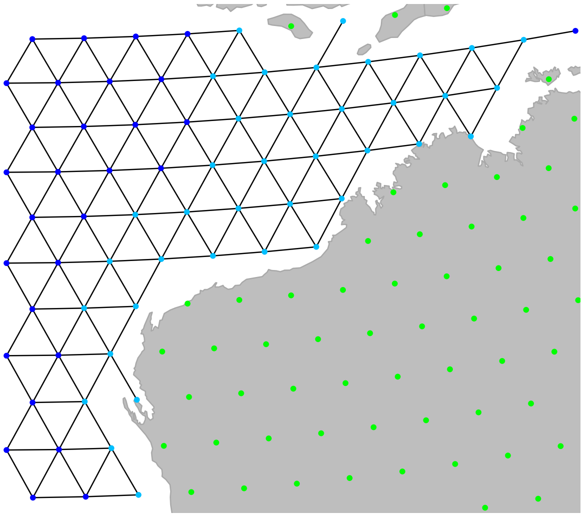
In addition to changing grid connectivity, we may also want to modify the attributes of specific nodes. This is again done interactively, using the function `geo.change.attr`. For instance, here, we define a new value `shalowwater` (plotted in light blue) for the attribute `habitat`, selecting affected nodes using the 'area' mode first, and refining the changes using the 'point' mode:

```
> plot(newGraph, edge = TRUE)
> temp <- geo.change.attr(newGraph, mode = "area", attr.name = "habitat",
+     attr.value = "shallowwater", newCol = "deepskyblue")
> temp <- geo.change.attr(temp, attr.name = "habitat", attr.value = "shallowwater",
+     newCol = "deepskyblue")
> newGraph <- temp
```

```
> newGraph@meta$colors
```

```
           habitat       color
1              sea        blue
2             land       green
3         mountain       brown
4       landbridge light green
5 oceanic crossing  light blue
6  deselected land   lightgray
7     shallowwater deepskyblue
```

```
> plot(newGraph, edge = TRUE)
```



Again, note that the changes made to the graph have to be save in an object (using `<-`) to be effective.

3.4 Extracting information from GIS shapefiles

An important feature of `geoGraph` is serving as an interface between *geographic information system* (GIS) layers and geographic data. As currently implemented, `geoGraph` can extract information from shapefiles with the Arc GIS (http://www.esri.com/software/arcgis/index.html) format, using the function `extractFromLayer`. Here, we illustrate this procedure using the shapefile `world-countries.shp` provided with the package. The GIS shapefile is first read in R using `readShapePoly` from the `maptools` package:

```
> world.countries <- readShapePoly(system.file("files/shapefiles/world-countries.shp",
+     package = "geoGraph"))
> class(world.countries)


[1] "SpatialPolygonsDataFrame"
attr(,"package")
[1] "sp"
```

```
> summary(world.countries)
```

```
Object of class SpatialPolygonsDataFrame
Coordinates:
         min       max
x -179.99917 181.79552
y  -89.90145  84.92937
Is projected: NA
proj4string : [NA]
Data attributes:
   WORCNTRY_I          ID                  NAME         ISO_2        ISO_NUM
 Min.   :  1.0   ABW    :  1   Afghanistan   :  1   AD     :  1   10     :  1
 1st Qu.: 60.5   AFG    :  1   Albania       :  1   AE     :  1   100    :  1
 Median :120.0   AGO    :  1   Algeria       :  1   AF     :  1   104    :  1
 Mean   :120.0   AIA    :  1   American Samoa:  1   AG     :  1   108    :  1
 3rd Qu.:179.5   ALB    :  1   Andorra       :  1   AI     :  1   112    :  1
 Max.   :239.0   AND    :  1   Angola        :  1   AL     :  1   116    :  1
                 (Other):233   (Other)       :233   (Other):233   (Other):233
      CAPITAL       POP_1994                 CONTINENT
 N/A      :  2   Min.   :0.000e+00   Africa       :59
 Victoria :  2   1st Qu.:1.384e+05   Antarctica   : 2
 Abidjan  :  1   Median :3.580e+06   Asia         :73
 Abu Dhabi:  1   Mean   :2.244e+07   Australia    : 2
 Accra    :  1   3rd Qu.:1.117e+07   Europe       :51
 (Other)  :209   Max.   :1.176e+09   North America:34
 NA's     : 23                       South America:18
```

The summary of `world.countries` shows the data (‘*attributes*’) stored in the layer. Let us assume that we are interested in retrieving continent and country information for the `worldgraph.10k` object. Note that `extractFromLayer` can extract information to other types of objects than `gGraph` (see `?extractFromLayer`)

```
> data(worldgraph.10k)
> summary(getNodesAttr(worldgraph.10k))
```

```
            habitat
 deselected land: 290
 land           :2632
 sea            :7320
```

```
> newGraph <- extractFromLayer(worldgraph.10k, layer = world.countries,
+     attr = c("CONTINENT", "NAME"))
> summary(getNodesAttr(newGraph))
```

```
            habitat             CONTINENT                     NAME
 deselected land: 290   Asia         : 957   Russian Federation: 339
 land           :2632   Africa       : 607   Antartica         : 241
 sea            :7320   North America: 430   United States     : 192
                        South America: 359   Canada            : 188
                        Antarctica   : 241   China             : 184
                        (Other)      : 325   (Other)           :1775
                        NA's         :7323   NA's              :7323
```

The new object `newGraph` is a `gGraph` which now includes, for each node of the grid, the corresponding continent and country retrieved from the GIS layer. We can use the newly acquired information for plotting `newGraph`, by defining new color rules:

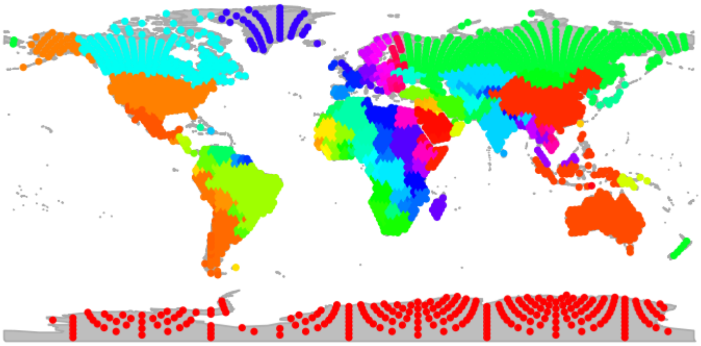
```
> temp <- unique(getNodesAttr(newGraph)$NAME)
> col <- c("transparent", rainbow(length(temp) - 1))
> colMat <- data.frame(NAME = temp, color = col)
> head(colMat)
```

```
          NAME       color
1         <NA> transparent
2    Antartica   #FF0000FF
3 Saudi Arabia   #FF0B00FF
4        Yemen   #FF1500FF
5      Somalia   #FF2000FF
6        China   #FF2B00FF
```

```
> tail(colMat)
```

```
          NAME     color
140     Latvia #FF0040FF
141    Belarus #FF0035FF
142    Eritrea #FF002AFF
143   Djibouti #FF0020FF
144 East Timor #FF0015FF
145     Jordan #FF000BFF
```

```
> plot(newGraph, col.rules = colMat, reset = TRUE)
```



This information could in turn be used to define costs for travelling on the grid. For instance, one could import habitat descriptors from a GIS, use these values to formulate a habitat model, and derive costs for dispersal on the grid.

As soon as a GIS layer has been extracted to a `gGraph`, this information becomes also available for any `gData` interfaced with this object. For instance, we can re-use the `cities` example defined in a previous section, and interface it with `newGraph` to retrieve continent and country information for the cities of the dataset:

```
> cities.dat
```

```
         lon lat     pop
Bordeaux  -1  45 1.0e+06
London     0  51 1.3e+07
Malaga    -4  37 5.0e+05
Zagreb    16  46 1.2e+06
```

```
> cities <- new("gData", coords = cities.dat[, 1:2], data = cities.dat[,
+     3, drop = FALSE], gGraph.name = "newGraph")
> cities <- closestNode(cities, attr.name = "habitat", attr.value = "land")
> getData(cities)
```

```
             pop
Bordeaux 1.0e+06
London   1.3e+07
Malaga   5.0e+05
Zagreb   1.2e+06
```

```
> getNodesAttr(cities)
```

```
     habitat CONTINENT                 NAME
5775    land    Europe France, Metropolitan
6413    land    Europe       United Kingdom
4815    land    Europe                Spain
7699    land    Europe              Austria
```

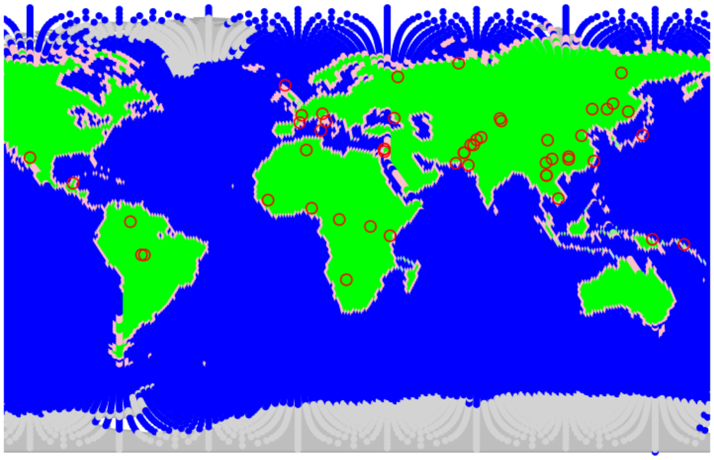
3.5 Finding least-cost paths

One of the most useful applications of geoGraph is the research of least-cost paths between couples of locations. This can be achieved using the functions dijkstraFrom and dijkstraBetween on a gData object which contains all the locations of interest. These functions return least-cost paths with the format gPath. dijkstraFrom compute the paths from a given node of the grid to all locations of the gData, while dijkstraBetween computes the paths between pairs of locations of the gData. Below, we detail the example of the documentation of these functions, which uses the famous dataset of native Human populations, HGDP:

```
> data(hgdp)
> data(worldgraph.40k)
> hgdp
```

```
=== gData object ===

@coords: spatial coordinates of 52 nodes
  lon lat
1  -3  59
2  39  44
3  40  61
...

@nodes.id: nodes identifiers
  28179   11012   22532
"26898" "11652" "22532"
...

@data: 52 data
  Population Region Label  n Latitude Longitude Genetic.Div
1   Orcadian EUROPE     1 15       59        -3   0.7258820
2     Adygei EUROPE     2 17       44        39   0.7297802
3    Russian EUROPE     3 25       61        40   0.7319749
...

Associated gGraph: worldgraph.40k
```

```
> plot(hgdp, reset = TRUE)
```



Populations of the dataset are shown by red circles, while the underlying grid (`worldgraph.40k`) is represented with colors depending on habitat (blue: sea; green: land; pink: coasts). Population genetics predicts that genetic diversity within populations should decay as populations are located further away from the geographic origin of the species. Here, we verify this relationship for a theoretical origin in Addis abeba, Ethiopia. We shall seek all paths through landmasses to the HGDP populations.

First, we check that all populations are connected on the grid using `isConnected`:

```
> isConnected(hgdp)
```

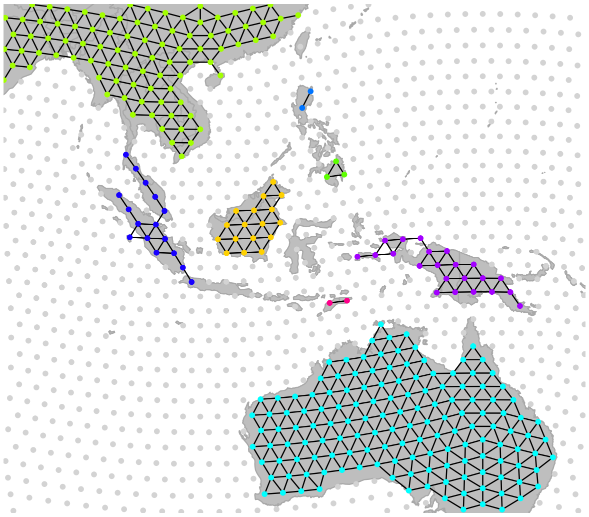
```
[1] TRUE
```

Note that in practice, we may often want to assess graphically the connectivity of the underlying grid, especially if not all locations of the `gData` are connected. This can be done using `connectivityPlot`, which has methods for both `gGraph` and `gData`, and represents different connected components using different colors. For instance, for `worldgraph.10k`:

```
> data(worldgraph.10k)
> connectivityPlot(worldgraph.10k, edges = TRUE, seed = 1)
```

```
> geo.zoomin(c(90, 150, 18, -25))
> title("Different connected components\n in worldgraph.10k")
```

Different connected components in worldgraph.10k



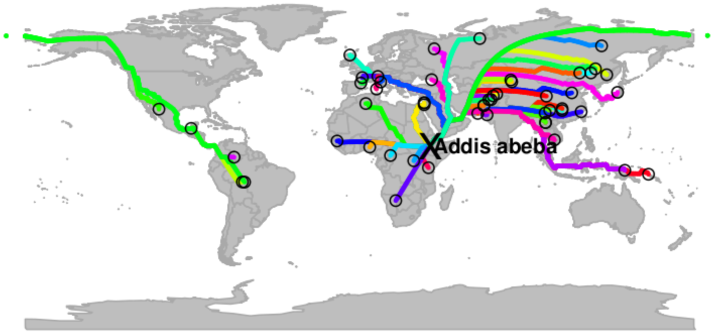
Since all locations in hgdp are connected, we can proceed further. We have to set the costs of edges in the gGraph grid. To do so, we can choose between i) strictly uniform costs (using dropCosts) ii) distance-based costs – roughly uniform – (using setDistCosts) or iii) attribute-driven costs (using setCosts).

We shall first illustrate the strictly uniform costs. After setting a gGraph with uniform costs, we use dijkstraFrom to find the shortest paths between Addis abeba and the populations of hgdp:

```
> myGraph <- dropCosts(worldgraph.40k)
> hgdp@gGraph.name <- "myGraph"
> addis <- cbind(38, 9)
> ori <- closestNode(myGraph, addis)
> paths <- dijkstraFrom(hgdp, ori)
```

The object paths contains the identified paths, which are stored as a list with class gPath (see ?gPath). Paths can be plotted easily:

```
> addis <- as.vector(addis)
> plot(newGraph, col = NA, reset = TRUE)
> plot(paths)
> points(addis[1], addis[2], pch = "x", cex = 2)
> text(addis[1] + 35, addis[2], "Addis abeba", cex = 0.8, font = 2)
> points(hgdp, col.node = "black")
```

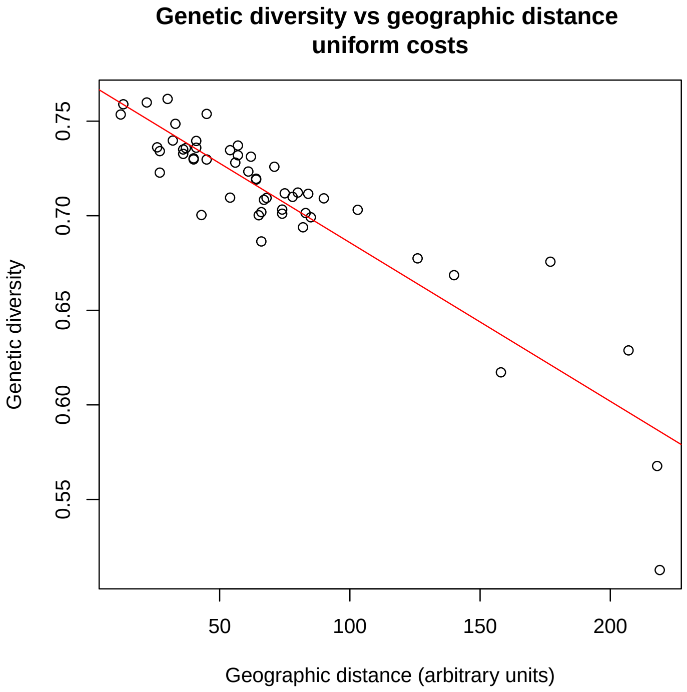


In this graph, each path is plotted with a different color, but several paths overlap in several places. We can extract the distances from the 'origin' using as.dist.gPath, and then examine the relationship between genetic diversity within populations (stored in hgdp) and the distance from the origin:

```
> div <- getData(hgdp)$Genetic.Div
> dgeo.unif <- as.dist.gPath(paths, res.type = "vector")
> plot(div ~ dgeo.unif, xlab = "Geographic distance (arbitrary units)",
+     ylab = "Genetic diversity")
> lm.unif <- lm(div ~ dgeo.unif)
> abline(lm.unif, col = "red")
> summary(lm.unif)
```

```
Call:
lm(formula = div ~ dgeo.unif)

Residuals:
       Min         1Q     Median         3Q        Max 
-0.0732681 -0.0066024  0.0007424  0.0101509  0.0544886 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  7.697e-01  4.575e-03  168.24   <2e-16
dgeo.unif   -8.389e-04  5.307e-05  -15.81   <2e-16

Residual standard error: 0.01851 on 50 degrees of freedom
Multiple R-squared: 0.8333,	Adjusted R-squared: 0.8299 
F-statistic: 249.9 on 1 and 50 DF,  p-value: < 2.2e-16
```

```
> title("Genetic diversity vs geographic distance \n uniform costs ")
```



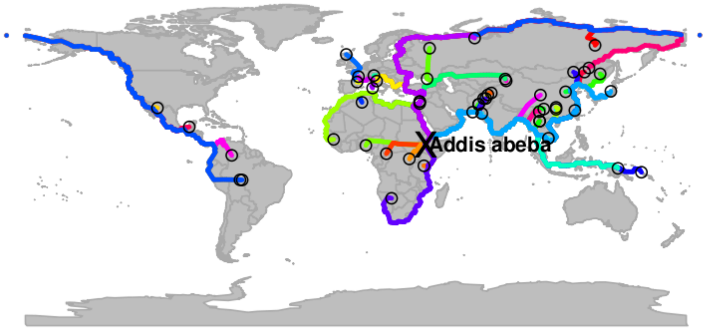
Alternatively, we can use costs based on habitat. As a toy example, we will consider that coasts are four times more favourable for dispersal than the rest of the landmasses. We define these new costs, and then compute and plot the corresponding shortest paths:

```
> myGraph@meta$costs[7, ] <- c("coast", 0.25)
> myGraph@meta$costs
```

```
           habitat cost
1              sea  100
2             land    1
3         mountain   10
4       landbridge    5
5 oceanic crossing   20
6  deselected land  100
7            coast 0.25
```

```
> myGraph <- setCosts(myGraph, attr.name = "habitat")
> paths.2 <- dijkstraFrom(hgdp, ori)
```

```
> plot(newGraph, col = NA, reset = TRUE)
> plot(paths.2)
> points(addis[1], addis[2], pch = "x", cex = 2)
> text(addis[1] + 35, addis[2], "Addis abeba", cex = 0.8, font = 2)
> points(hgdp, col.node = "black")
```

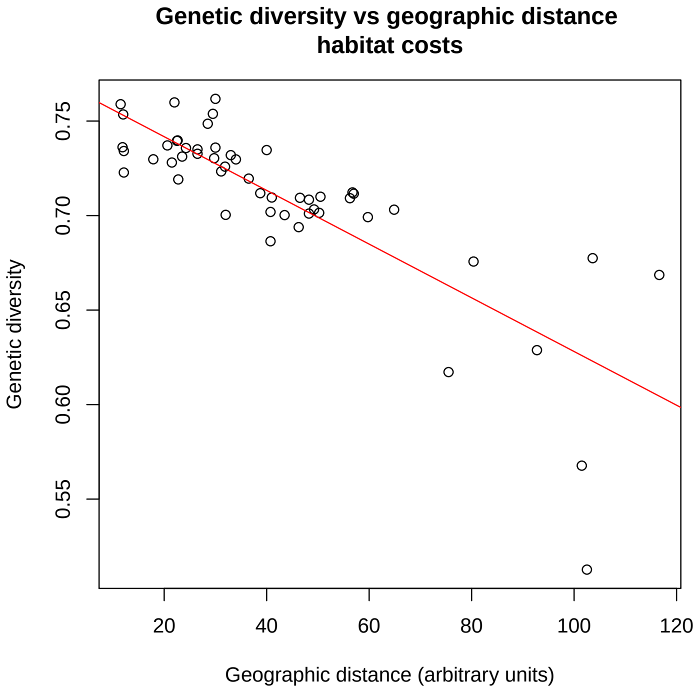


The new paths are slightly different from the previous ones. We can examine the new relationship with genetic distance:

```
> dgeo.hab <- as.dist.gPath(paths.2, res.type = "vector")
> plot(div ~ dgeo.hab, xlab = "Geographic distance (arbitrary units)",
+     ylab = "Genetic diversity")
> lm.hab <- lm(div ~ dgeo.hab)
> abline(lm.hab, col = "red")
> summary(lm.hab)
```

```
Call:
lm(formula = div ~ dgeo.hab)

Residuals:
      Min        1Q    Median        3Q       Max 
-0.111832 -0.009761  0.001327  0.012163  0.064126 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept)  0.770137   0.007174 107.358  < 2e-16
dgeo.hab    -0.001421   0.000145  -9.795 3.21e-13

Residual standard error: 0.02653 on 50 degrees of freedom
Multiple R-squared: 0.6574,	Adjusted R-squared: 0.6505 
F-statistic: 95.94 on 1 and 50 DF,  p-value: 3.214e-13 
```

```
> title("Genetic diversity vs geographic distance \n habitat costs ")
```



Of course, the distinction between coasts and inner landmasses is a somewhat poor description of habitat. In practice, complex habitat models can be used as simply.