

# Making and using bathymetric maps in R with marmap

Eric Pante & Benoit Simon Bouhet

April 3, 2013

---

## Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>A quick tutorial</b>	<b>1</b>
2.1	Getting data into R . . . . .	1
2.2	Plotting bathymetric data . . . . .	2
2.3	Using bathymetric data for further analysis . . . . .	6
2.4	Using bathymetric data for least-cost path analysis . . . . .	11
2.5	Landscape Genetics . . . . .	14
2.6	3D plotting . . . . .	14
<b>3</b>	<b>Data import and export strategies in marmap</b>	<b>16</b>
3.1	Overview of the different import and export strategies available in marmap . . . . .	16
3.2	Getting bathymetric data from NOAA: read.bathy() . . . . .	17
3.3	Getting bathymetric data from NOAA: local SQL database . . . . .	18

---

## 1 Introduction

In this vignette we introduce `marmap`, a package designed for manipulating bathymetric data in R. `marmap` uses simple latitude-longitude-depth data in ascii format and takes advantage of the advanced plotting tools available in R to build publication-quality bathymetric maps. Functions to query data (bathymetry, sampling information...) directly by clicking on `marmap` maps are available. Bathymetric and topographic can also be used to constrain the calculation of realistic shortest path distances. Such information can be used in molecular ecology, for example, to evaluate genetic isolation by distance in a spatially-explicit framework.

## 2 A quick tutorial

In this section, we will produce a bathymetric maps of Papua New Guinea, Hawaii and the NW Atlantic.

### 2.1 Getting data into R

Launch R. Navigate to your work folder (for example, with `setwd()`). Then launch the `marmap` package. The simplest way to get bathymetric data into R for use with `marmap` is to use the `getNOAA.bathy()` function. It queries the ETOPO1 dataset (Armante and Eakins 2009) hosted on the NOAA server, based on coordinate a resolution given by the user. In one line, we can get the data into R and start plotting:

```
> library(marmap)
> getNOAA.bathy(lon1=140,lon2=155,lat1=-13,lat2=0, resolution=10) -> papoue
```

```
Querying NOAA database ...
This may take seconds to minutes, depending on grid size
Building bathy matrix ...
```

```
> summary(papoue)
```

```
Bathymetric data of class 'bathy', with 91 rows and 79 columns
Latitudinal range: -13 to 0
Longitudinal range: 140 to 155
Cell size: 10 minute(s)
```

```
Depth statistics:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-8775	-3121	-1551	-1642	-5	3539

```
First 5 columns and rows of the bathymetric matrix:
```

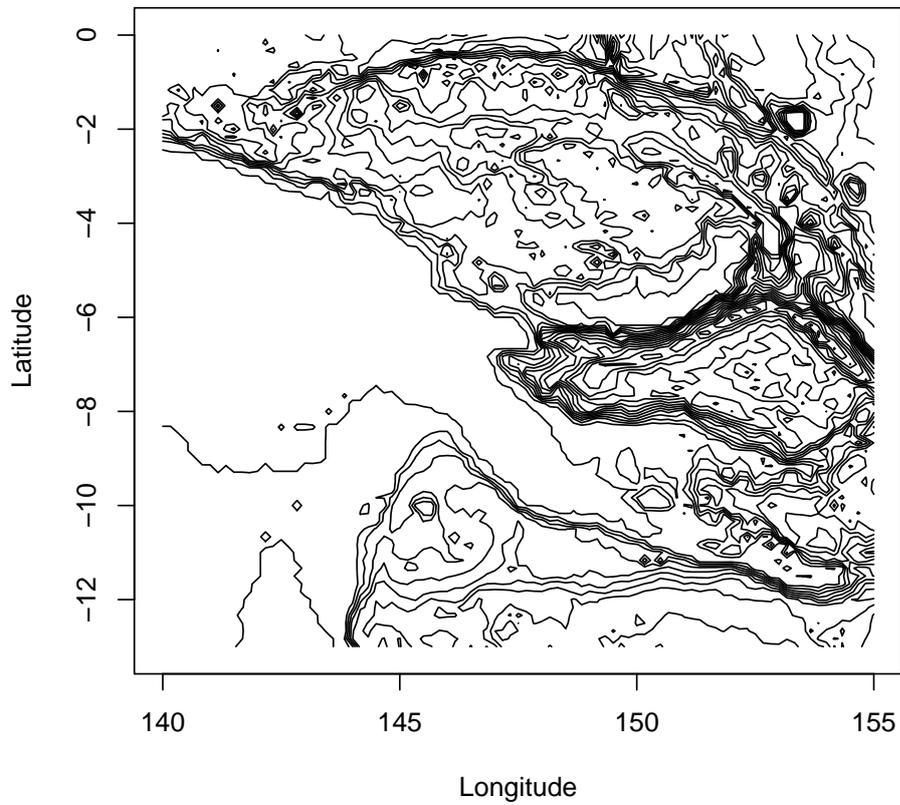
```
                -13 -12.83333333333334 -12.6666666666667 -12.5
140                -37                -37                -37  -37
140.166666666667 -37                -35                -36  -36
140.333333333334 -35                -33                -35  -35
140.5                -32                -33                -32  -32
140.666666666667 -30                -28                -28  -30
                -12.33333333333334
140                -38
140.166666666667 -35
140.333333333334 -33
140.5                -32
140.666666666667 -26
```

`summary.bathy()` helps you check the data ; because `bathy` is a class, and R an object-oriented language, you just have to use `summary()`. R will recognize that you are feeding `summary()` an object of class `bathy`. This is also true for `plot.bathy` and `plot()`.

## 2.2 Plotting bathymetric data

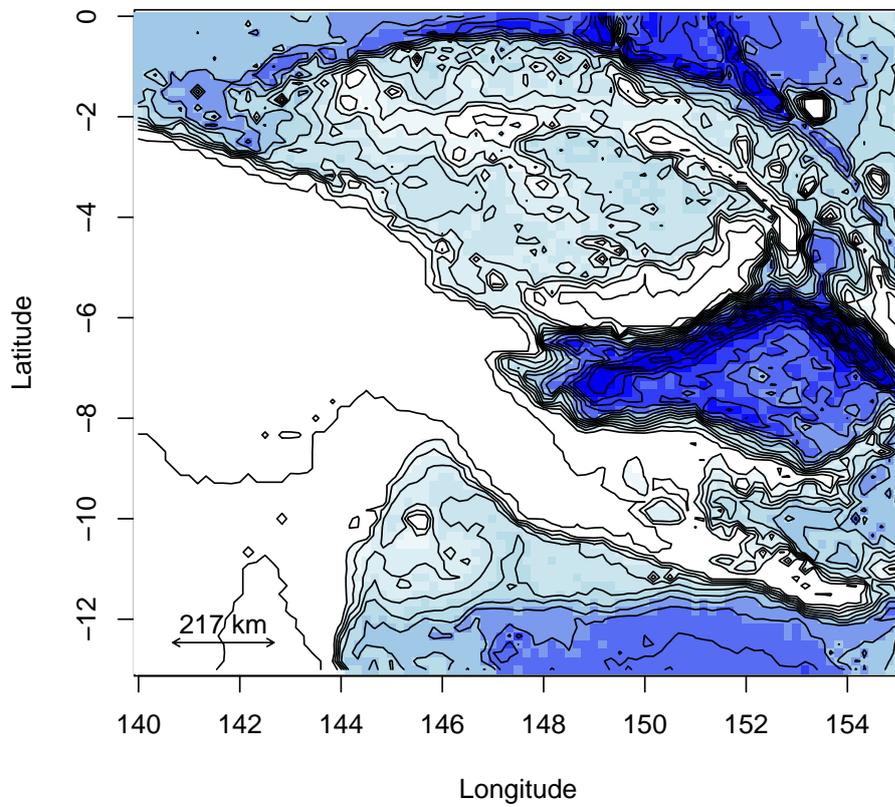
We can now use `plot.bathy()` (or `plot()`, because R will recognize the object is of class `bathy`) to map the data. You can see that the 10 minute resolution is a bit rough, but enough to demonstrate how `marmap` works (to increase the resolution, simply change the value for the `resolution` argument to a smaller value).

```
> plot(papoue)
```



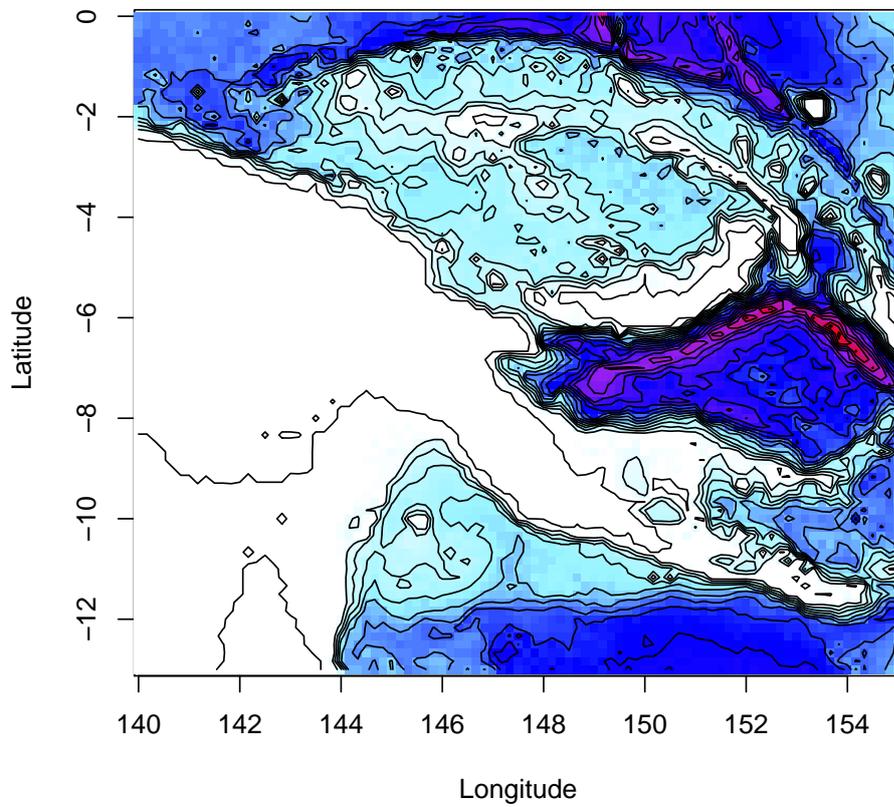
We can now use some of the options of `plot.bathy()` to make the map more informative. First, we can plot a heat map, using the built in color palette. We can also add a scale in kilometers.

```
> plot(papoue, image=T)
> scaleBathy(papoue, deg=2, x="bottomleft", inset=5)
```



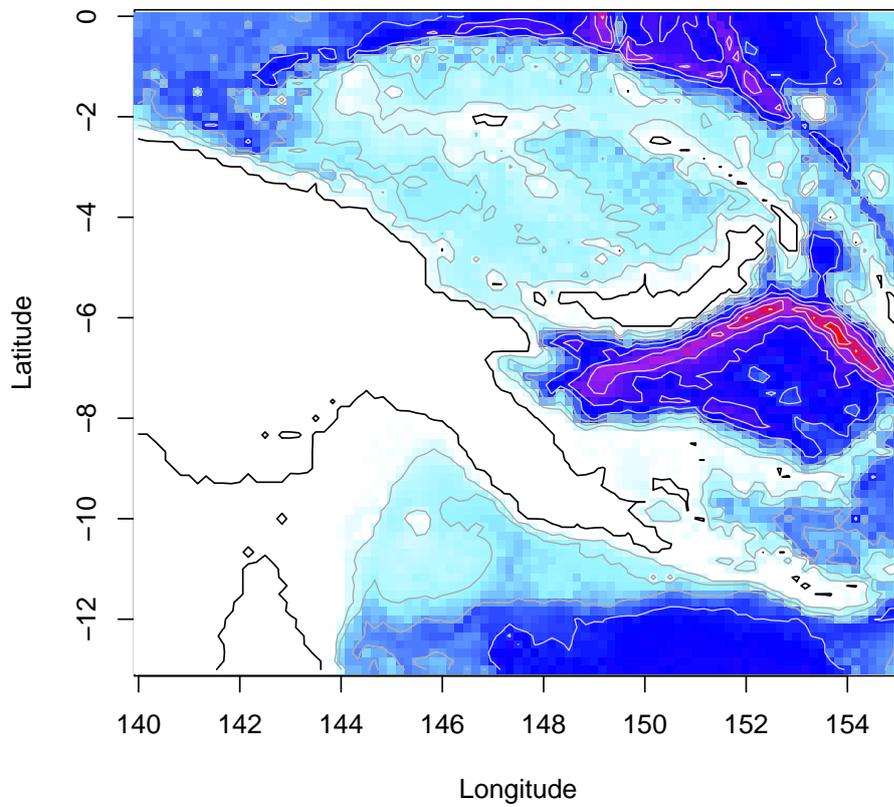
The `bpal` options allows you to use a custom color palette, which can be easily prepared with the R function `colorRampPalette()`. We store the color ramp in the object called `blues`, and when we call it in `plot.bathy()`, we specify how many colors need to be used in the palette (here 100).

```
> colorRampPalette(c("red", "purple", "blue", "cadetblue1", "white")) -> blues
> plot(papoue, image=T, bpal=blues(100))
```



For maps using the `image` option of `plot.bathy()`, you will see that the PDF rendering of your map is slightly different from the way it looks in R: the small space between cells becomes visible. This is probably due to the way your system handles PDFs. A simple way around this phenomenon is to export the map in a raster (rather than vector) format. You can use the `tiff()`, `jpeg()`, `bmp()` or `png()` functions available in R. This map looks a little crowded ; let's dim the isobaths (dark grey color and lighter line width), and strengthen the coastline (black color and thicker line width). The deepest isobaths will be hard to see on a dark blue background ; we can therefore choose to plot these in light grey to improve contrast. The option `drawlabel` controls whether isobath labels (e.g. "-3000") are plotted or not.

```
> plot(papoue, image=T, bpal=blues(100),
+      deep=c(-9000,-3000,0), shallow=c(-3000,-10, 0), step=c(1000, 1000, 0),
+      col=c("lightgrey","darkgrey","black"), lwd=c(0.8,0.8,1), lty=c(1,1,1),
+      drawlabel=c(F,F,F))
```



### 2.3 Using bathymetric data for further analysis

We can use the `get.transect()` and `plotProfile()` functions to extract and plot a depth cross section from the `papoue` dataset. `get.transect()` will use the coordinates you input to calculate the coordinates and depths along your transect, and calculate the great circle distance separating each point along the transect from the point of origin (in kilometers).

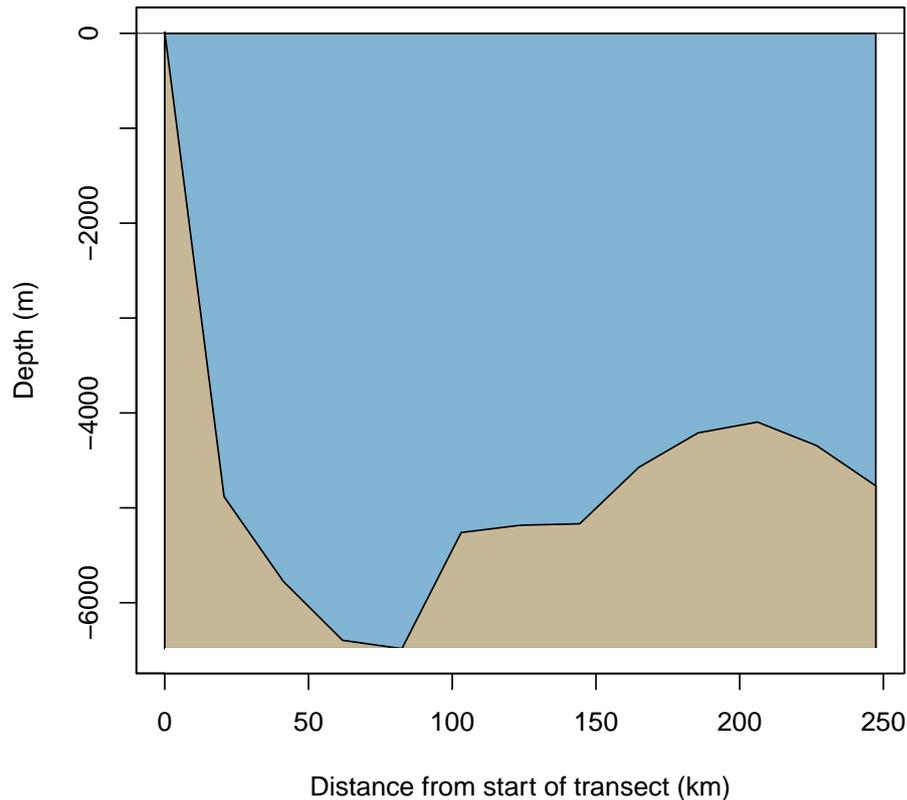
```
> get.transect(papoue, 151, -6, 153, -7, distance=T)
```

	lon	lat	dist.km	depth
1	151.0000	-6.000000	0.00000	14
2	151.1667	-6.083333	20.62793	-4882
3	151.3333	-6.166667	41.25331	-5775
4	151.5000	-6.250000	61.87610	-6396
5	151.6667	-6.333333	82.49627	-6484
6	151.8333	-6.416667	103.11378	-5260
7	152.0000	-6.500000	123.72859	-5183
8	152.1667	-6.583333	144.34067	-5168
9	152.3333	-6.666667	164.94999	-4572
10	152.5000	-6.750000	185.55650	-4210
11	152.6667	-6.833333	206.16018	-4096
12	152.8333	-6.916667	226.76098	-4344
13	153.0000	-7.000000	247.35888	-4768

We can plot that information on a map and make a cross section plot with `plotProfile()`. Again, the very low resolution of the dataset produces an analysis with little information. You can get transect

information and make a cross-section plot by directly clicking on the map, using the locator option of `get.transect()`.

```
> get.transect(papoue, 151, -6, 153, -7, distance=T) -> transect
> plotProfile(transect)
```



We can also use `get.sample()` and `get.depth()` to retrieve depth information and sample information by clicking on the map (see help pages). The output will look like this (pound symbols are followed by comments):

```
> # click once on the map:
> get.depth(papoue)
[1] -1655

> # click twice on the map to delimit an area:
> get.depth(papoue)
Bathymetric data of class 'bathy', with 17 rows and 14 columns
Latitudinal range: -5.833333 to -3.666667
Longitudinal range: 146.833333 to 149.5
Cell size: 10 minute(s)

Depth statistics:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-2222  -1827   -1538   -1301   -1109     770

First 5 columns and rows of the bathymetric matrix:
```

```

-3.666667 -3.833333 -4 -4.166667 -4.333333
146.833333 -1929 -1924 -2097 -1976 -1891
147 -1922 -2037 -1986 -1985 -1850
147.166667 -1930 -1822 -1905 -1939 -1894
147.333333 -1807 -1690 -1909 -1973 -1970
147.5 -1390 -1598 -1672 -2050 -1973

```

`get.sample()` is used in combination with a table containing sampling information. Let's make a fake table of sampling data, print it in a file, then, for the sake of the example, import it in R as a csv file, and use it for plotting and use with `get.sample()`:

```

> x = c(142.1390,142.9593,144.0466,145.9141,
+       145.9372,146.0115,145.9141,146.8589,
+       146.6651,147.1772,147.2856,152.7475,
+       152.5025,152.7816,152.9010,153.2314)
> y = c(-2.972065,-3.209449,-3.391399,-4.675720,
+       -4.914153,-5.130116,-5.329641,-2.587792,
+       -2.897221,-3.250368,-2.720080,-6.005769,
+       -6.211152,-6.326915,-5.990206,-6.023344)
> paste("station",1:16, sep="") -> station
> data.frame(x, y, station) -> sampling
> write.table(sampling, "sampling.csv", sep="," , quote=F, row.names=F)

```

We have now created a small example file that we can use for further analysis. Let's load these data, and plot them on a map:

```

> read.csv("sampling.csv", header=TRUE) -> samp
> head(samp) # a little preview of the first 6 of the 16 lines of the dataset.

```

```

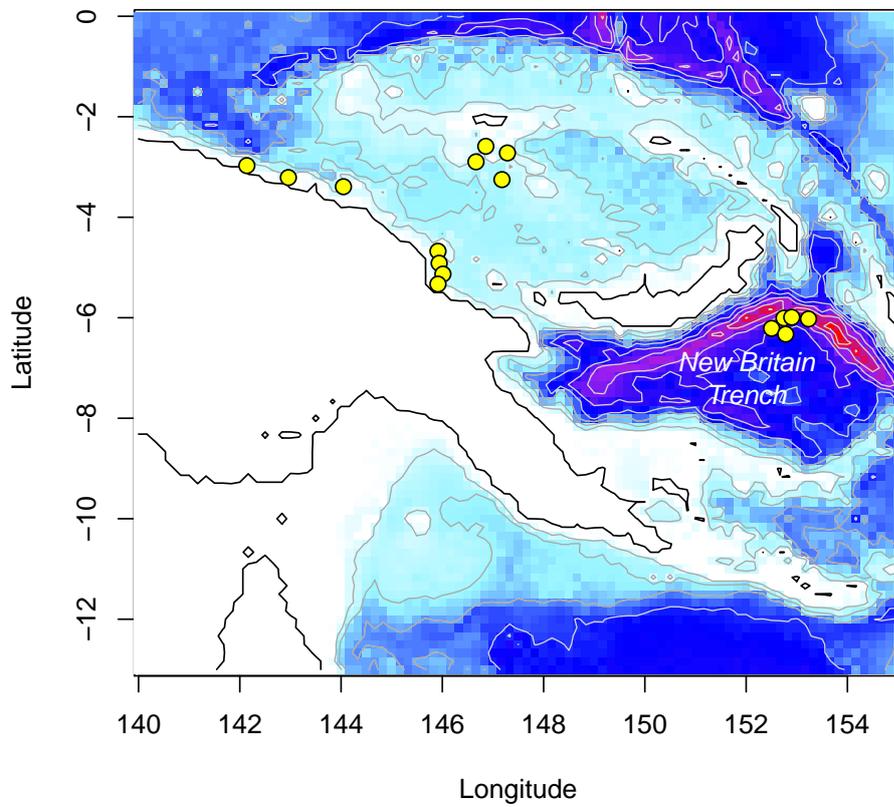
      x      y station
1 142.1390 -2.972065 station1
2 142.9593 -3.209449 station2
3 144.0466 -3.391399 station3
4 145.9141 -4.675720 station4
5 145.9372 -4.914153 station5
6 146.0115 -5.130116 station6

```

```

> plot(papoue, image=T, bpal=blues(100),
+      deep=c(-9000,-3000,0), shallow=c(-3000,-10, 0), step=c(1000, 1000, 0),
+      col=c("lightgrey","darkgrey","black"), lwd=c(0.8,0.8,1), lty=c(1,1,1),
+      drawlabel=c(F,F,F))
> # add points from the sampling.csv, and add text to the plot:
> points(samp$x, samp$y, pch=21,col="black", bg="yellow", cex=1.3)
> text(152,-7.2, "New Britain\nTrench", col="white",font=3)

```



By clicking on the map, we can select the area in the New Britain Trench, to get information on the sampling stations of that area. `get.sample()` will detect that there are samples in the area selected, and return the locations relative for these samples.

```
> # click twice on the map to delimit an area:
> get.sample(papoue, samp, col.lon=1, col.lat=2)
      x      y station
12 152.7475 -6.005769 station12
13 152.5025 -6.211152 station13
14 152.7816 -6.326915 station14
15 152.9010 -5.990206 station15
16 153.2314 -6.023344 station16
```

We can use the depth data when plotting points:

```
> # make a table of fake sampling information, with fake depth
> samp.depth = sample(seq(-3000,-1000, by=50), size=16)
> data.frame(samp$x, samp$y, samp.depth) -> sp
> names(sp) <- c("lon", "lat", "depth")
> head(sp)

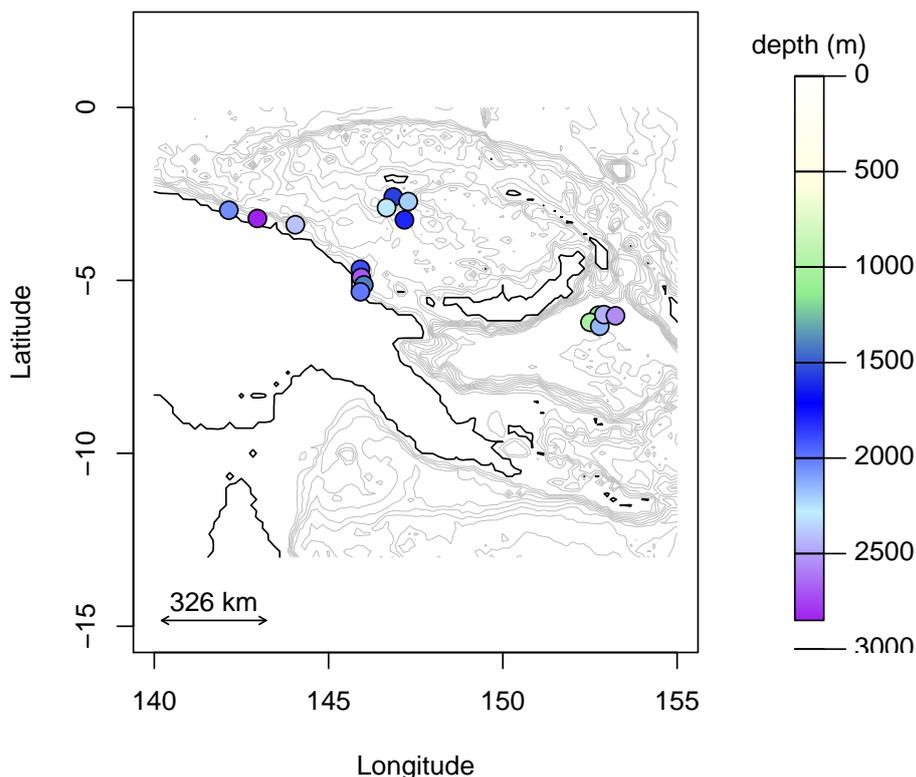
      lon      lat depth
1 142.1390 -2.972065 -2050
2 142.9593 -3.209449 -2850
3 144.0466 -3.391399 -2400
4 145.9141 -4.675720 -1900
```

```

5 145.9372 -4.914153 -2700
6 146.0115 -5.130116 -1400

> # plot map
> par(mai=c(1,1,1,1.5))
> plot(papoue, deep=c(-4500,0), shallow=c(-50,0), step=c(500,0),
+      lwd=c(0.3,1), lty=c(1,1), col=c("grey","black"), drawlabels=c(F,F))
> scaleBathy(papoue, deg=3, x="bottomleft", inset=5)
> # set color palette
> mx = max(-sp$depth, na.rm=TRUE) -> mx
> colorRampPalette(c("white","lightyellow","lightgreen","blue","lightblue1","purple")) -> ramp
> blues <- ramp(mx)
> # plot points and color depth scale
> points(sp[,1:2], col="black", bg=blues[-sp$depth], pch=21,cex=1.5)
> require(shape)
> colorlegend(zlim=c(mx,0), col=rev(blues), main="depth (m)",posx=c(0.85,0.88))

```



The function `get.area()` can be used to calculate the projected surface area (the projecting surface being the ocean surface). For example, in the case of the Hawaiian Archipelago, we can calculate the surface area of the bathyal (1,000 to 4,000 m) and abyssal regions (4,000 to about 6,000 m).

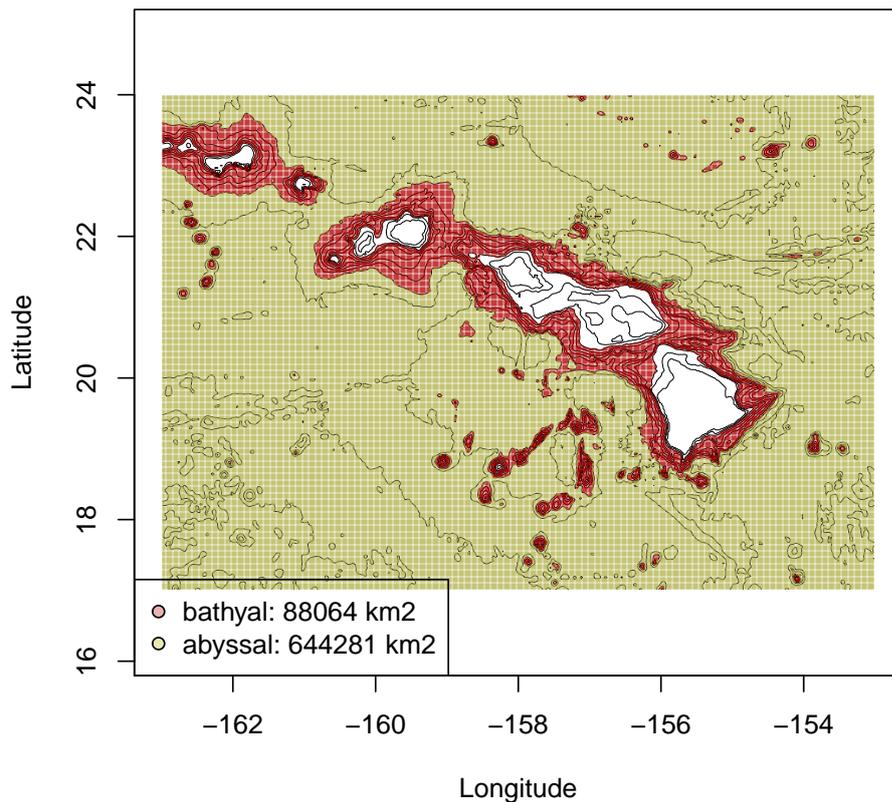
```

> data(hawaii)
> get.area(hawaii, level.inf=-4000, level.sup=-1000) -> bathyal
> get.area(hawaii, level.inf=min(hawaii), level.sup=-4000) -> abyssal
> round(bathyal$Square.Km, 0) -> ba
> round(abyssal$Square.Km, 0) -> ab

```

The function `get.area()` returns a surface area un square kilometers (`$$Square.Km`), and a matrix of zeros and ones delimiting the area of interest. The `$Lon`, `$Lat` and `$Area` objects can be used to display these areas:

```
> plot(hawaii, lwd=0.2)
> image(bathyal$Lon, bathyal$Lat, bathyal$Area, col=c(rgb(0,0,0,0), rgb(.7,0,0,.3)), add=T)
> image(abyssal$Lon, abyssal$Lat, abyssal$Area, col=c(rgb(0,0,0,0), rgb(.7,.7,0.3,.3)), add=T)
> legend(x="bottomleft", legend=c(paste("bathyal:", ba, "km2"), paste("abyssal:", ab, "km2")),
+       col="black", pch=21, pt.bg=c(rgb(.7,0,0,.3), rgb(.7,.7,0,.3)) )
```



## 2.4 Using bathymetric data for least-cost path analysis

`marmap` contains functions to facilitate least-cost path analysis that are based on the `raster` and `gdistance` packages (van Etten 2012a, 2012b). `gdistance` calculates routes in a heterogeneous landscape, taking obstacles into account. These obstacles can be defined in `marmap` based on bathymetric data. We will use the Hawaiian islands as our playground for this section.

```
> data(hawaii, hawaii.sites)
> sites <- hawaii.sites[-c(1,4),]
> rownames(sites) <- 1:4
```

We first compute a transition to be used by `lc.dist` to compute least cost distances between locations. The transition object generated by `trans.mat` contains the probability of transition from one cell of a bathymetric grid to adjacent cells, and depends on user defined parameters. `trans.mat` is especially useful when least cost distances need to be calculated between several locations at sea. The default

values for `min.depth` and `max.depth` ensure that the path computed by `dist.geo` will be the shortest path possible at sea avoiding land masses. The path can be constrained to a given depth range by setting manually `min.depth` and `max.depth`. For instance, it is possible to limit the possible paths to the continental shelf by setting `max.depth=-200`. Inaccuracies of the bathymetric data can occasionally result in paths crossing land masses. Setting `min.depth` to low negative values (e.g. -10 meters) can limit this problem.

`trans1` is a transition object contained only by land masses. `trans2` is a transition object that makes travel impossible in waters shallower than 200 meters depth. This step takes a little time.

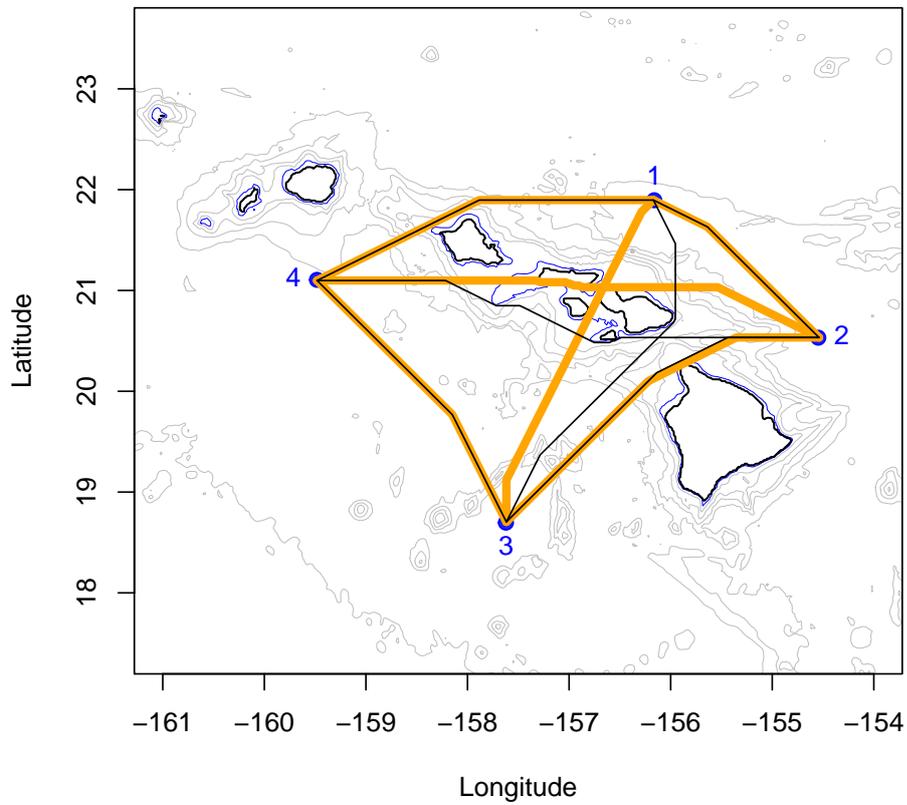
```
> trans1 <- trans.mat(hawaii)
> trans2 <- trans.mat(hawaii,min.depth=-200)
```

We can now use these transition objects to calculate least cost distances for `trans1` and `trans2`. The output of `lc.dist` is a list of geographic positions corresponding to the least-cost path.

```
> out1 <- lc.dist(trans1,sites,res="path")
|=====| 100%
> out2 <- lc.dist(trans2,sites,res="path")
|=====| 100%
```

We use the `lapply` function to extract information from these lists and plot lines. Thick orange lines correspond to least-cost paths only constrained by landmasses Thin black lines are paths constrained by the 200 m isobath. We store the result of `lapply` in a dummy variable to avoid printing of unnecessary information. The coastline is in black, the 200 m isobath is in blue, and isobaths between 5000 and 200 m depth are in grey. Our sampling points are in blue.

```
> plot(hawaii, xlim=c(-161,-154), ylim=c(18,23),
+      deep=c(-5000,-200,0), shallow=c(-200,0,0),
+      col=c("grey","blue", "black"), step=c(1000,200, 1),
+      lty=c(1,1,1), lwd=c(0.6,0.6,1.2), draw=c(F,F,F))
> points(sites,pch=21,col="blue",bg=col2alpha("blue",.9),cex=1.2)
> text(sites[,1],sites[,2],lab=rownames(sites),pos=c(3,4,1,2),col="blue")
> lapply(out1,lines,col="orange",lwd=5,lty=1) -> dummy
> lapply(out2,lines,col="black",lwd=1,lty=1) -> dummy
```



The option `res` of `lc.dist` controls whether path coordinates or distances between points (in kilometers) are outputted. Let's see how these different scenarios (no constraint: great-circle distance, `dist0` ; avoid landmasses: `dist1` ; avoid areas shallower than 200 m: `dist2`) effect distances between sampling points:

```
> library(fossil)
> dist0 <- round(earth.dist(sites), 0)
> dist1 <- lc.dist(trans1,sites,res="dist")
> dist2 <- lc.dist(trans2,sites,res="dist")
> dist0
      1  2  3
2 226
3 387 381
4 355 517 331

> dist1
      1  2  3
2 230
3 391 401
4 365 529 334

> dist2
      1  2  3
2 230
```

```
3 423 403
4 365 533 334
```

Note: You can check out the help file for `lc.dist` to see how we can combine these functions with cross-section calculations and plotting.

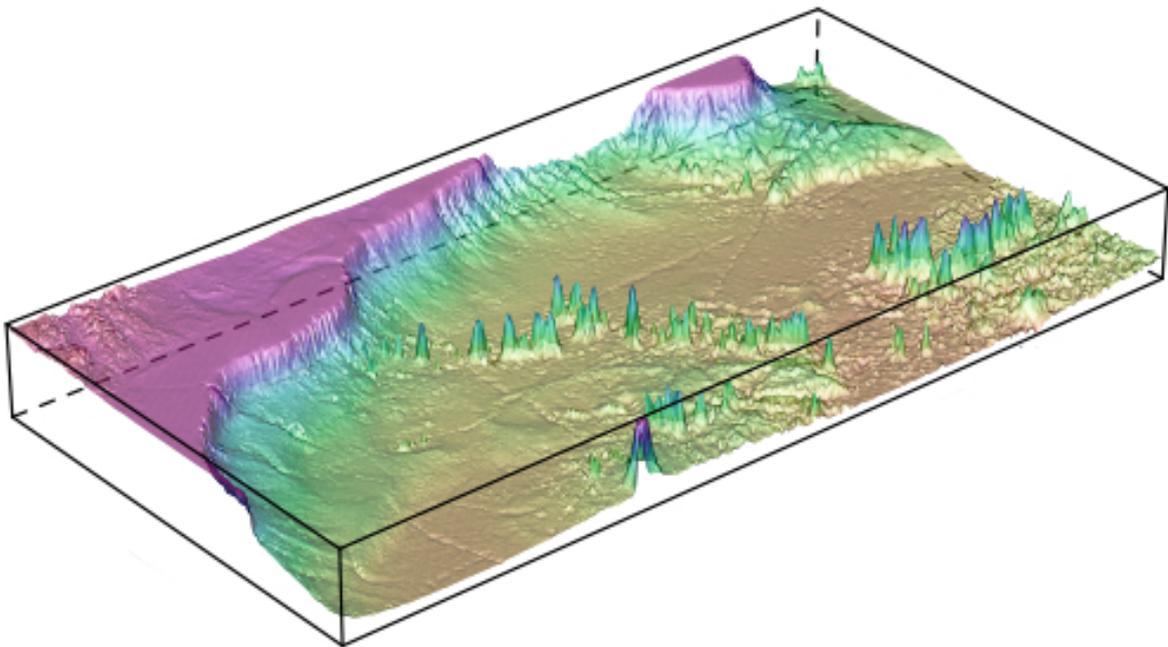
## 2.5 Landscape Genetics

The distance objects created in the section above are formatted as matrices that can be used in R or exported to be used in GenePop (Rousset 2008), TESS (Durand et al 2009), or other software. As an example, these distances can be used to perform a Mantel test, as implemented in the package `ade4` (`mantel.rtest()` function ; Chessel and Dufour 2004, Dray et al 2007, Dray and Dufour 2007). The matrices produced in `marmap` are ready for use with `ade4`. For export and use in external programs, the function `write.matrix()` of the `MASS` package (Venables and Ripley 2002) will be helpful.

## 2.6 3D plotting

R contains tools to plot data in three dimensions. We can use the function `wireframe()` of the package `lattice` to make a 3D representation of the NW Atlantic and its seamount chains. `wireframe()` is not part of `marmap`, and was therefore not meant to work with objects of class `bathy`. We need to use the function `unclass()` to make our data available to `wireframe()`. Make sure to adjust the `aspect` option of `wireframe()`, to minimize vertical exaggeration and biased latitude / longitude aspect ratio.

```
data(nw.atlantic)
atl <- as.bathy(nw.atlantic)
library(lattice)
wireframe(unclass(atl), shade=T, aspect=c(1/2, 0.1))
```



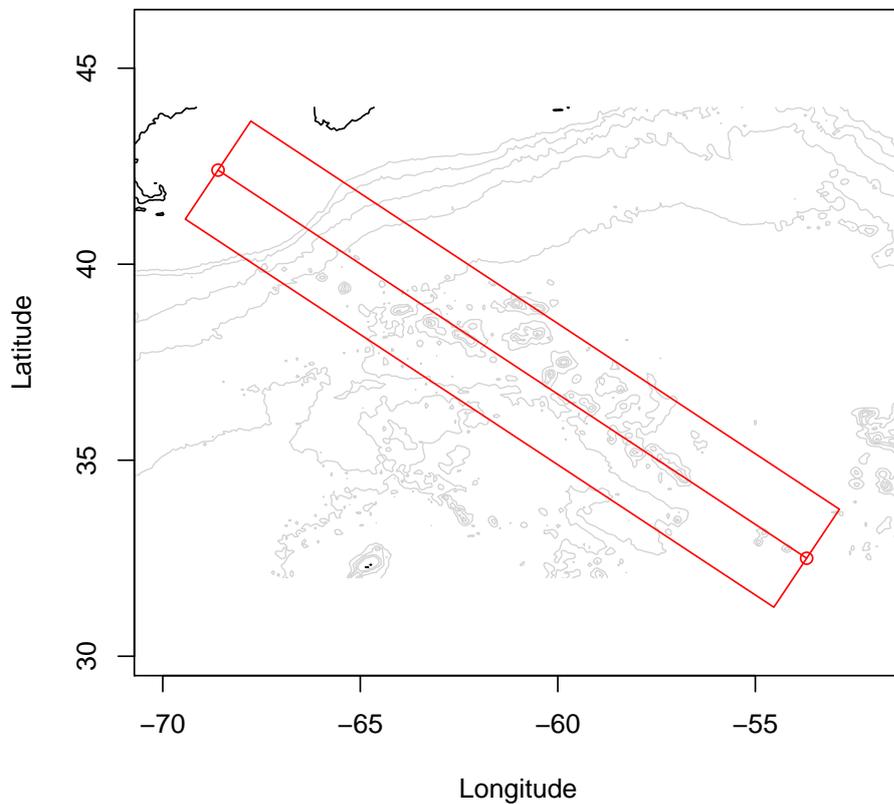
The `marmap` function `get.box()` can be coupled with the `lattice` function `wireframe` to produce 3D plots of belt transects of given width. Let's use the NW Atlantic data to investigate these functions, and look at the New England and Corner Rise seamount chains.

```
> data(nw.atlantic) ; atl <- as.bathy(nw.atlantic)
> plot(atl, xlim=c(-70,-52),
+       deep=c(-5000, 0), shallow=c(0,0), step=c(1000,0),
```

```

+       col=c("lightgrey","black"), lwd=c(0.8, 1), lty=c(1,1), draw=c(F,F))
> get.box(atl,
+         x1=-68.6, x2=-53.7, y1=42.4, y2=32.5,
+         width=3, col="red") -> out

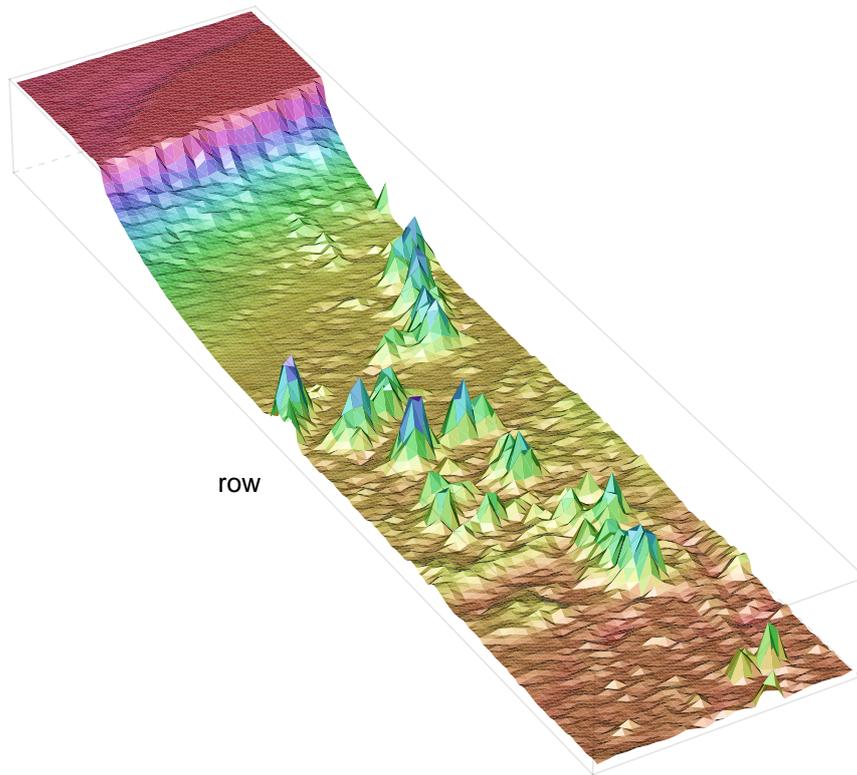
```



```

> library(lattice)
> wireframe(out, shade=T, zoom=1.1,
+          aspect=c(1/4, 0.1),
+          screen = list(z = -60, x = -55),
+          par.settings = list(axis.line = list(col = "transparent")),
+          par.box = c(col = rgb(0,0,0,0.1)))

```



### 3 Data import and export strategies in marmap

#### 3.1 Overview of the different import and export strategies available in marmap

`getNOAA.bathy()` is the easiest way to load data into R, but it depends on the NOAA download protocol, and one must have an internet connection. The way to use this function is demonstrated in the tutorial above. `read.bathy()` allows import of data into R, and this data can be located on a drive ; an internet connection is therefore not mandatory. This is a good way to import data that have been saved locally on your drive, and may be faster than re-downloading data from the NOAA server at the beginning of each R session. If the user is building maps routinely, we propose two functions to create a local database that can be accessed from within R. These functions are `setSQL()` and `subsetSQL()`.

Function	Job	Input	Output	Internet
<code>getNOAA.bathy()</code>	downloads data from NOAA server	coordinates of bounding box and resolution	data matrix of class <code>bathy</code>	yes
<code>read.bathy()</code>	imports data into R	name of external file with xyz data	data matrix of class <code>bathy</code>	no
<code>setSQL()</code>	creates a local SQL database of bathymetric data	name of external file with xyz data	an SQL database	no
<code>subsetSQL()</code>	queries a local SQL database	coordinates of bounding box and resolution	data matrix of class <code>bathy</code>	no
<code>as.xyz()</code>	converts a dataset of class <code>bathy</code> into an xyz table	dataset of class <code>bathy</code> (an R object)	an xyz table (an R object)	no
<code>as.bathy()</code>	converts an xyz table into an dataset of class <code>bathy</code>	an xyz table (an R object)	dataset of class <code>bathy</code> (an R object)	no

### 3.2 Getting bathymetric data from NOAA: `read.bathy()`

`read.bathy()` will read xyz data from any source. Here, we will get ETOPO1 data hosted on the NOAA GEODAS server (NOAA National Geophysical Data Center 2013). To get the data, use the following link:

[http://www.ngdc.noaa.gov/mgg/gdas/gd\\_designagrid.html](http://www.ngdc.noaa.gov/mgg/gdas/gd_designagrid.html)

To prepare data from NOAA, give a name to your custom grid, choose the database (ETOPO1 1-minute Global Relief), fill the custom grid form (upper latitude: 0, lower latitude: 13S, left longitude: 140E, right longitude: 155E) for a grid cell size of 10 minute, and choose "XYZ (lon,lat,depth)" as the "Output Grid Format", "No Header" as the "Output Grid Header", and either of the space, tab or comma as the column delimiter (either can be used, but "comma" is the default import format of `read.bathy()`). Choose "omit empty grid cells" to reduce memory usage. Submit your job, and retrieved your data. You will get a zipped folder, in which you will find (in a subfolder) a .xyz file with your data. Place it, for example, in your work folder.

The resolution of 10 minutes is a low resolution that will keep the size of the example file small, about 200 kb. Increasing the resolution to 1 minute would result in a file size of about 20 mb.

Launch R. Navigate to your work folder (for example, with `setwd()`). Then launch the `marmap` package, and load your xyz data (we will call it "png.xyz") with `read.bathy()`. This converts your data into an R object of class "bathy." `summary.bathy()` helps you check the data ; because `bathy` is a class, and R an object-oriented language, you just have to use `summary()`, because R will recognize that you are feeding `summary()` an object of class `bathy`. This is also true for `plot.bathy` and `plot()`.

```
> library(marmap)
> read.bathy('png.xyz', header=F, sep="\t") -> papoue
> summary(papoue)
```

```
Bathymetric data of class 'bathy', with 91 rows and 79 columns
Latitudinal range: -13 to 0
Longitudinal range: 140 to 155
Cell size: 10 minute(s)
```

Depth statistics:

```
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-8750  -3123   -1540   -1641     -4    3711
```

First 5 columns and rows of the bathymetric matrix:

```
      -13 -12.833333 -12.666667 -12.5 -12.333333
140      -36      -35      -35      -35      -35
140.166667 -35      -34      -34      -34      -33
140.333333 -33      -32      -32      -32      -31
140.5      -30      -30      -30      -29      -29
140.666667 -28      -28      -27      -27      -27
```

### 3.3 Getting bathymetric data from NOAA: local SQL database

`setSQL()` and `subsetSQL()` create and query a local SQL database for bathymetric data. These tools are made for routine use with no internet connection. The full ETOPO1 database, or a subset (for example), can be downloaded on your computer, and used to set an SQL database, which size will be approximately the same as your original xyz data (unzipped ETOPO1 is about 5 Go). The advantage of SQL, a language for querying large databases, are manifold. Its use will allow rapid upload of data into R, directly as bathy objects (and therefore directly useable for plotting and analysis) with a smaller footprint on your memory than if you tried to load a very large xyz file into R and then subset-ed it. Here is a simple example on how to set up and use an SQL database for marmap.

Use a local file with xyz data (we can re-use the `png.xyz` that we created above for use with `read.bathy()`), and submit it to `setSQL()`. Make sure that no file called `bathy_db` is present in your working directory. Also, make sure that the package `RSQLite` (James and Falcon 2012) is installed and properly working.

```
> setSQL(bathy="png.xyz", sep="\t")
```

```
[1] TRUE
```

This will create a file `bathy_db` in your directory, which size is about the size of (or larger than) your original data. If you want to create a database for frequent use, you just need to do this once. `subsetSQL()` will know where to get the data in future R sessions. If `setSQL()` worked properly, it will return `TRUE`. If there is a problem (e.g. database connection already open, database file already created ...) it will return `FALSE`. Let's query a subset of the `png` dataset, and check that it is indeed what we asked for with the `summary.bathy()` function:

```
> subsetSQL(min_lon=145,max_lon=150, min_lat=-2, max_lat=0) -> test
> summary(test)
```

```
Bathymetric data of class 'bathy', with 29 rows and 11 columns
Latitudinal range: -1.83 to -0.17
Longitudinal range: 145.17 to 149.83
Cell size: 10 minute(s)
```

```
Depth statistics:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-6650	-3282	-2076	-2594	-1543	72

```
First 5 columns and rows of the bathymetric matrix:
```

```
      -1.833333 -1.666667 -1.5 -1.333333 -1.166667
145.166667    -1001    -1348   -249    -1774    -2079
145.333333    -1137    -1579  -1938    -1794    -1957
145.5         -1069    -1833  -2007    -2097    -2166
145.666667    -1295    -2020  -2123    -2301    -2289
145.833333    -1728    -1912  -1981    -2183    -2350
```

Finally, if you are done with the SQL dataset, you can remove it with

```
> system("rm bathy_db")
```

## References

- [1] Amante C, Eakins BW (2009) Etopo1 1 arc-minute global relief model: Procedures, data sources and analysis. NOAA Technical Memorandum NESDIS NGDC-24 : 1-19.
- [2] Chessel D, Dufour A, Thioulouse J (2004) The ade4 package -I- One-table methods. R News 4: 5-10.
- [3] Dray S, Dufour A, Chessel D (2007) The ade4 package-II: Two-table and K-table methods. R News 7: 47-52.
- [4] Dray S, Dufour A (2007) The ade4 package: implementing the duality diagram for ecologists. Journal of Statistical Software 22: 1-20.
- [5] Durand E, Jay F, Gaggiotti O, François O (2009) Spatial inference of admixture proportions and secondary contact zones. Molecular Biology and Evolution 26: 1963-1973.
- [6] van Etten RJHJ (2012) raster: Geographic data analysis and modeling. URL <http://CRAN.R-project.org/package=raster>. R package version 2.0-41.
- [7] van Etten J (2012) gdistance: Distances and routes on geographical grids. URL <http://CRAN.R-project.org/package=gdistance>. R package version 1.1-4.

- [8] NOAA National Geophysical Data Center. GEODAS Grid Translator - Design a grid. URL [http://www.ngdc.noaa.gov/mgg/gdas/gd\\_designagrid.html](http://www.ngdc.noaa.gov/mgg/gdas/gd_designagrid.html).
- [9] James DA, Falcon S (2012) RSQlite: SQLite interface for R. URL <http://CRAN.R-project.org/package=RSQlite>. R package version 0.11.2.
- [10] Rousset F, (2008) GENEPOP'007: a complete re-implementation of the genepop software for Windows and Linux. *Molecular Ecology Resources* 8: 103-106.
- [11] Venables, W. N. and B. D. Ripley. 2002. *Modern Applied Statistics with S*. Fourth edition. Springer.