test assignR@20190813 (mailto:assignR@20190813)

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Install assignR package from Github

```
#devtools::install_github("SPATIAL-Lab/assignR", force=T)
```

Load library

```
library(assignR)
```

```
## Loading required package: raster
```

```
## Loading required package: sp
```

```
## Loading required package: ggplot2
```

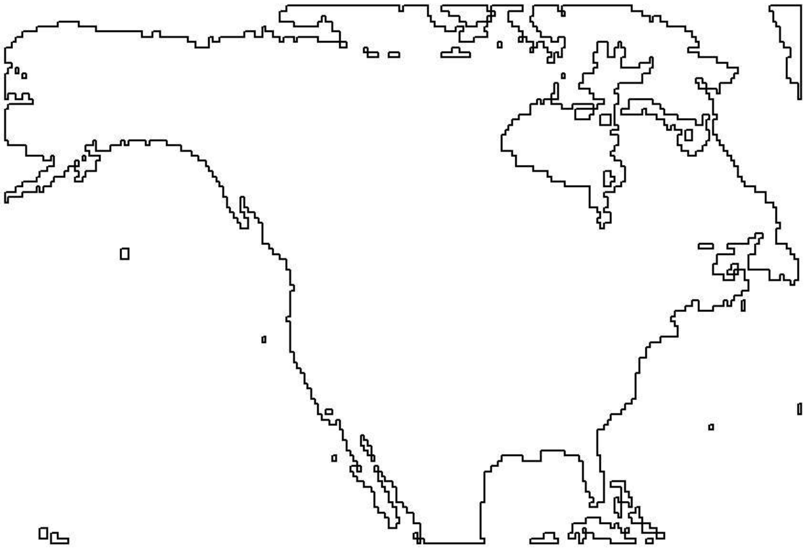
```
## Registered S3 method overwritten by 'dplyr':
##   method               from  
##   as.data.frame.tbl_df tibble
```

```
## Loading required package: rgdal
```

```
## rgdal: version: 1.4-4, (SVN revision 833)
##  Geospatial Data Abstraction Library extensions to R successfully loaded
##  Loaded GDAL runtime: GDAL 2.2.3, released 2017/11/20
##  Path to GDAL shared files: C:/Users/chao/Documents/R/win-library/3.6/rgdal/gdal
##  GDAL binary built with GEOS: TRUE 
##  Loaded PROJ.4 runtime: Rel. 4.9.3, 15 August 2016, [PJ_VERSION: 493]
##  Path to PROJ.4 shared files: C:/Users/chao/Documents/R/win-library/3.6/rgdal/proj
##  Linking to sp version: 1.3-1
```

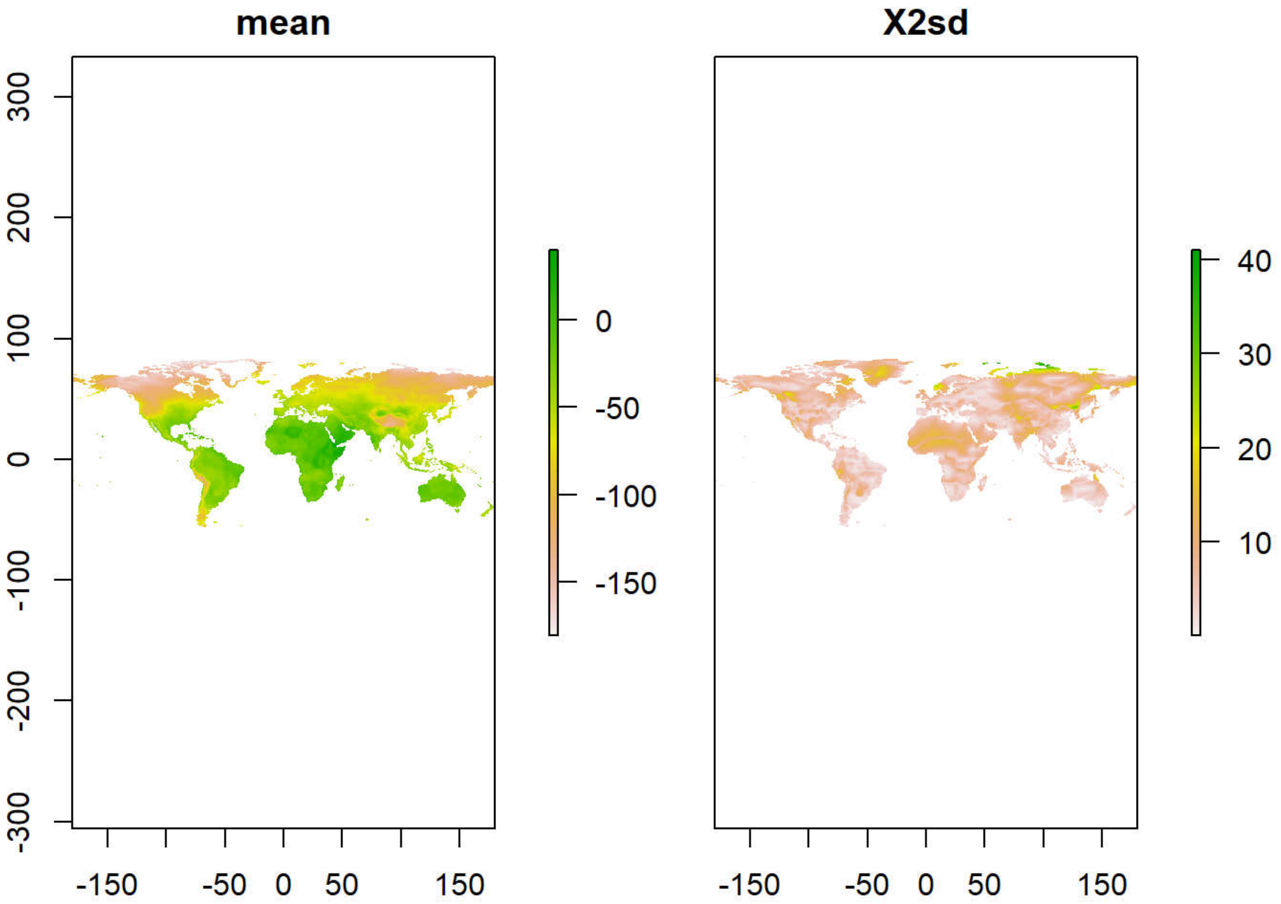
Load North America mask

```
data("naMap")
plot(naMap)
```



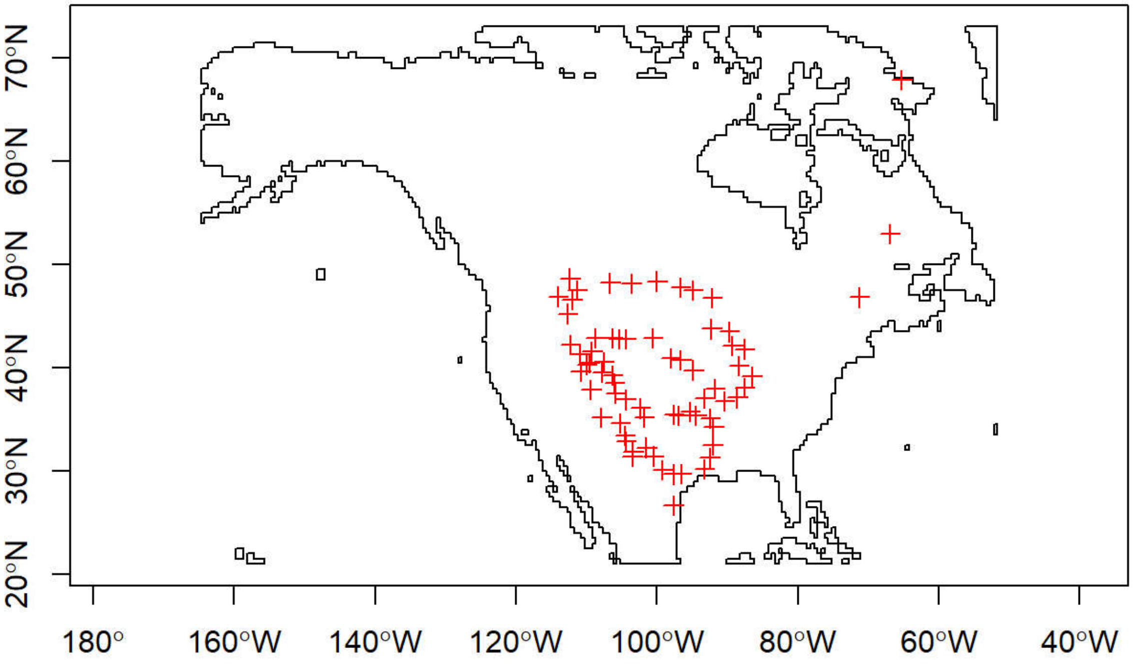
Load world precipitation hydrogen isoscape

```
data("d2h_world")
plot(d2h_world)
```



Load hydrogen isotope for human hair in North America

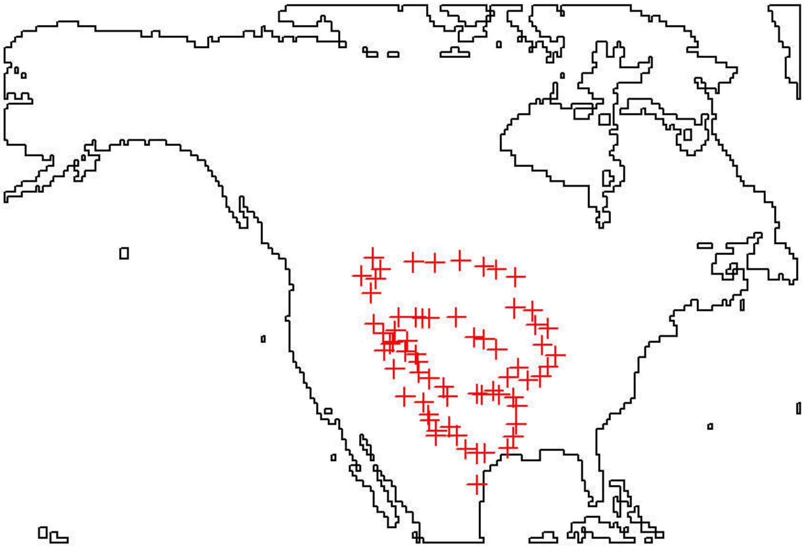
```
d = subOrigData(taxon = c("Homo sapiens"), mask = naMap)
```



```
## 233 data points are found
```

Exclude some outliers. This step is optional, which depends on your data quality

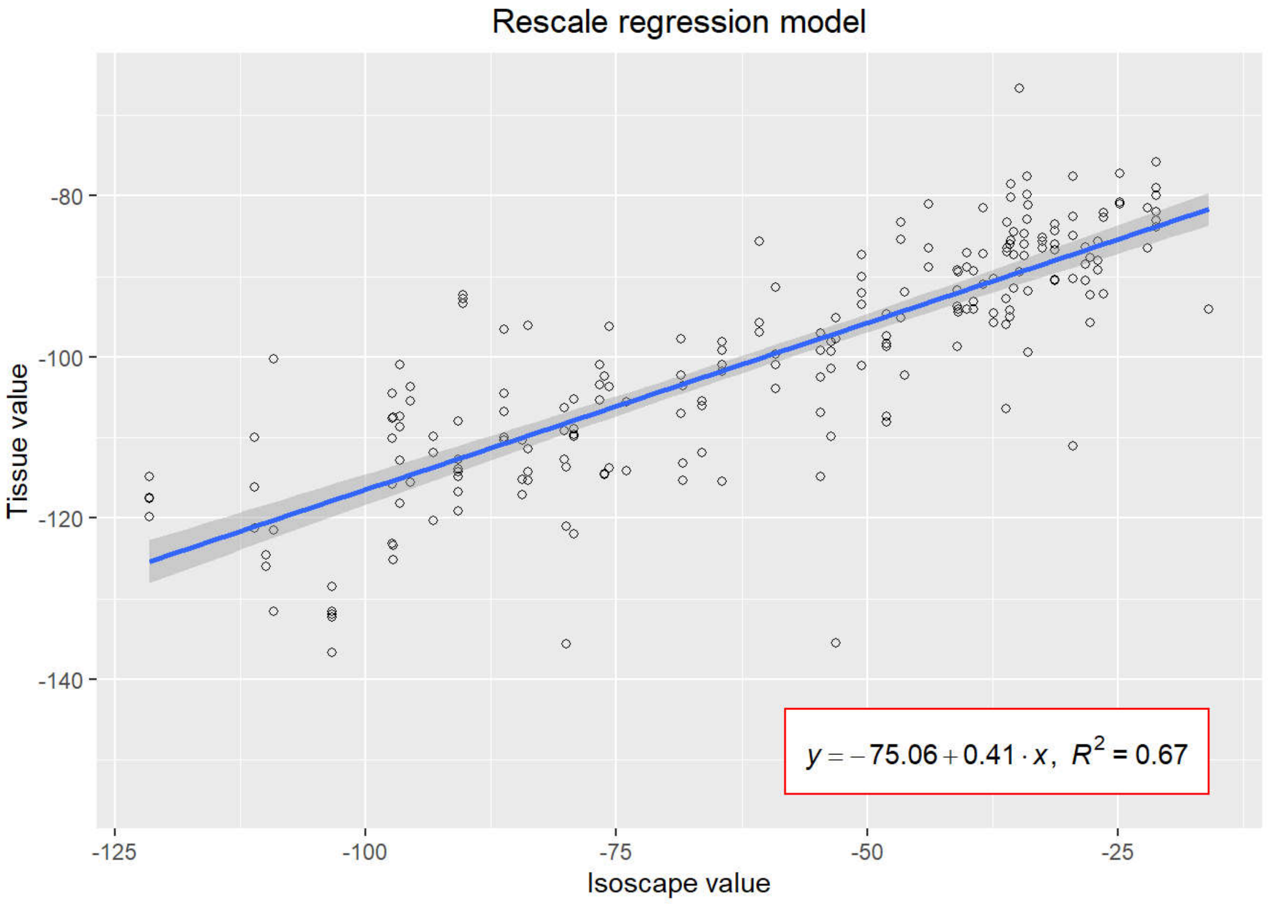
```
dd = d[d$coords.x1<(-80),]

plot(naMap)
plot(dd, add=T, col=2)
```

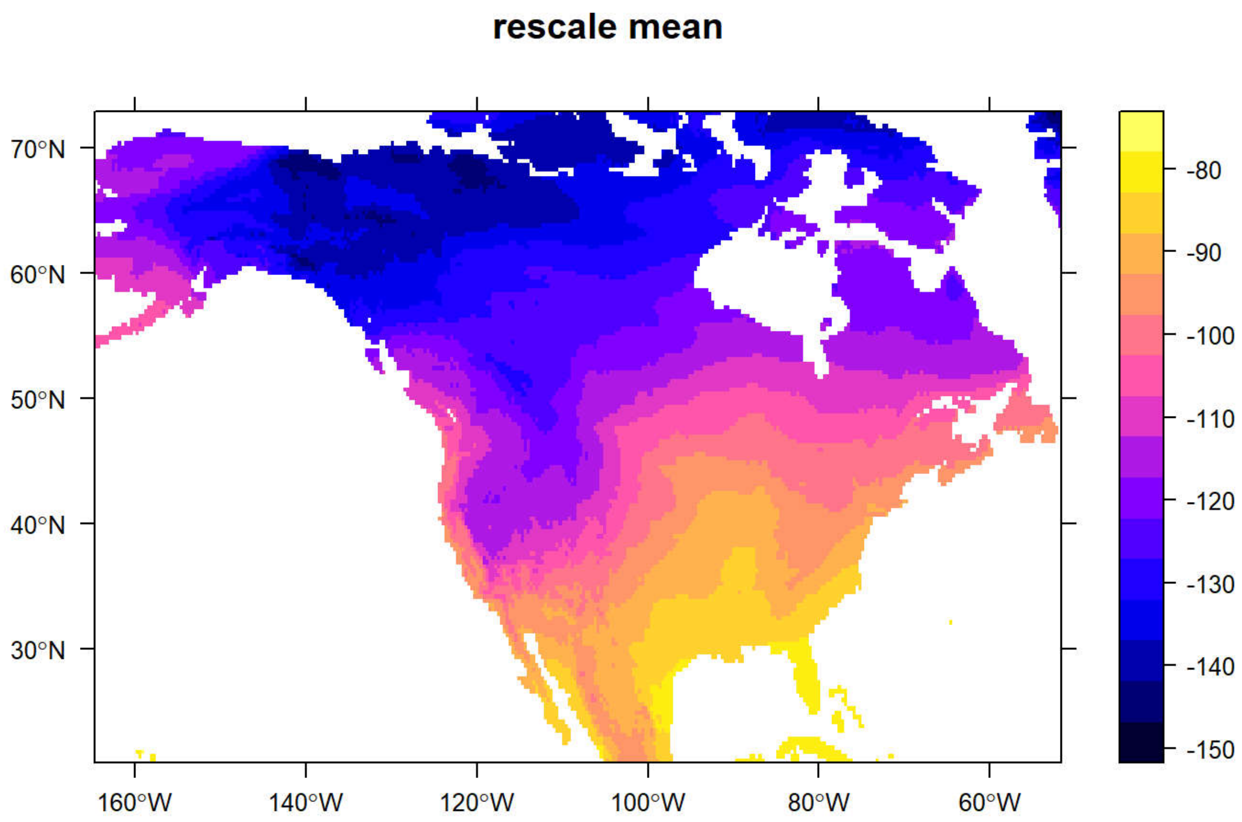


Rescale from environmental isoscape to tissue isoscape

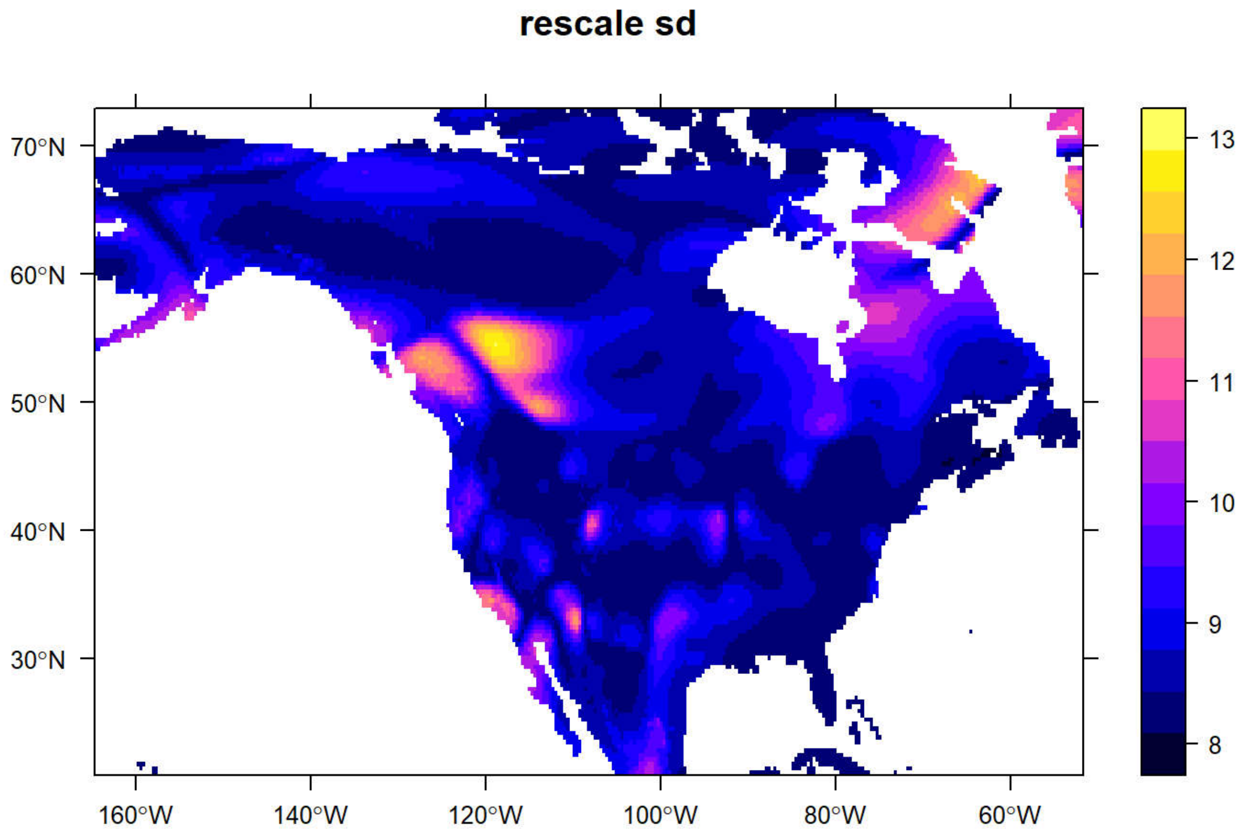
```
r = calRaster(known = dd, isoscape = d2h_world, mask = naMap)
```

```
##
##
## ----------------------------------------------------------------------------------
## rescale function uses linear regression model, the summary of this model is:
## ----------------------------------------------------------------------------------
##
## Call:
## lm(formula = tissue.iso   isoscape.iso[, 1])
##
## Residuals:
##     Min      1   Median      3      Max
## -38.407  -4.035   0.233   4.419  22.834
##
## Coefficients:
##                    Estimate Std. Error t value Pr(  t )
## (Intercept)       -75.06067    1.32160  -56.80   <2e-16
## isoscape.iso[, 1]   0.41389    0.01996   20.74   <2e-16
## ---
## Signif. codes:  0 '   ' 0.001 '  ' 0.01 ' ' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.078 on 213 degrees of freedom
## Multiple R-squared:  0.6687, Adjusted R-squared:  0.6672
##  -statistic:   430 on 1 and 213 D ,  p-value: < 2.2e-16
```


Rescale regression model
Tissue value
-80
-100
-120
-140
Isoscape value
-125
-100
-75
-50
-25
$y = -75.06 + 0.41 \cdot x,\ R^2 = 0.67$



```
##  arning in dir.create("output"): 'output' already exists
```



Four unknown origin examples

```
id = letters[1:6]
d2H = seq(-160, -80, by=80/5)
un = data.frame(id,d2H)
```

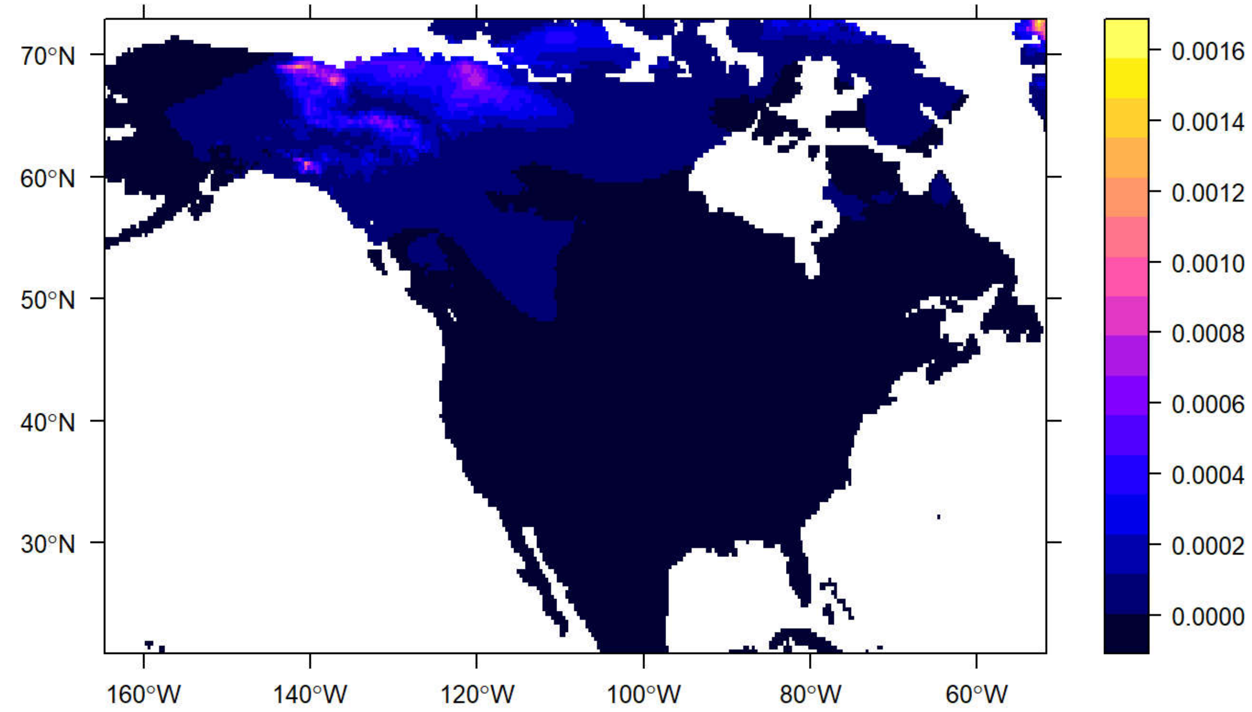
Assignment for unknown origin examples

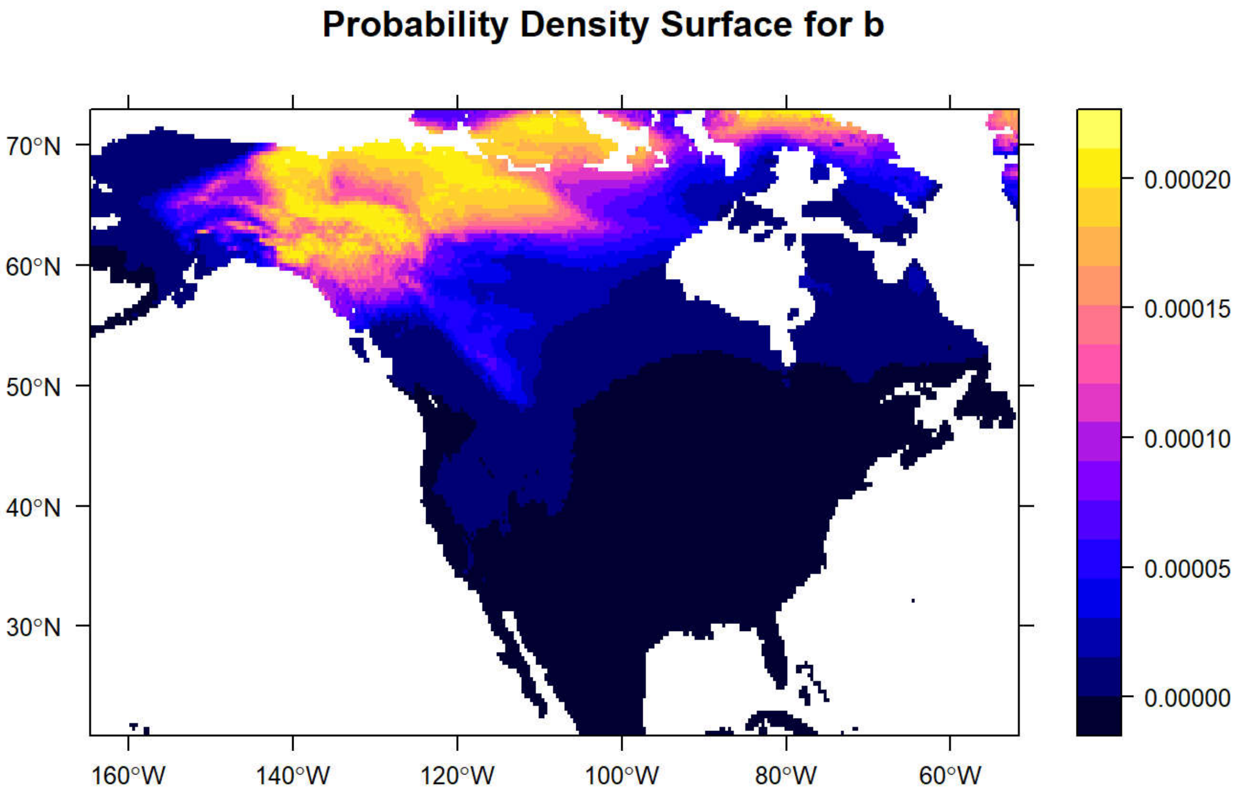
```
asn = pdRaster(r,unknown=un,mask=naMap)
```

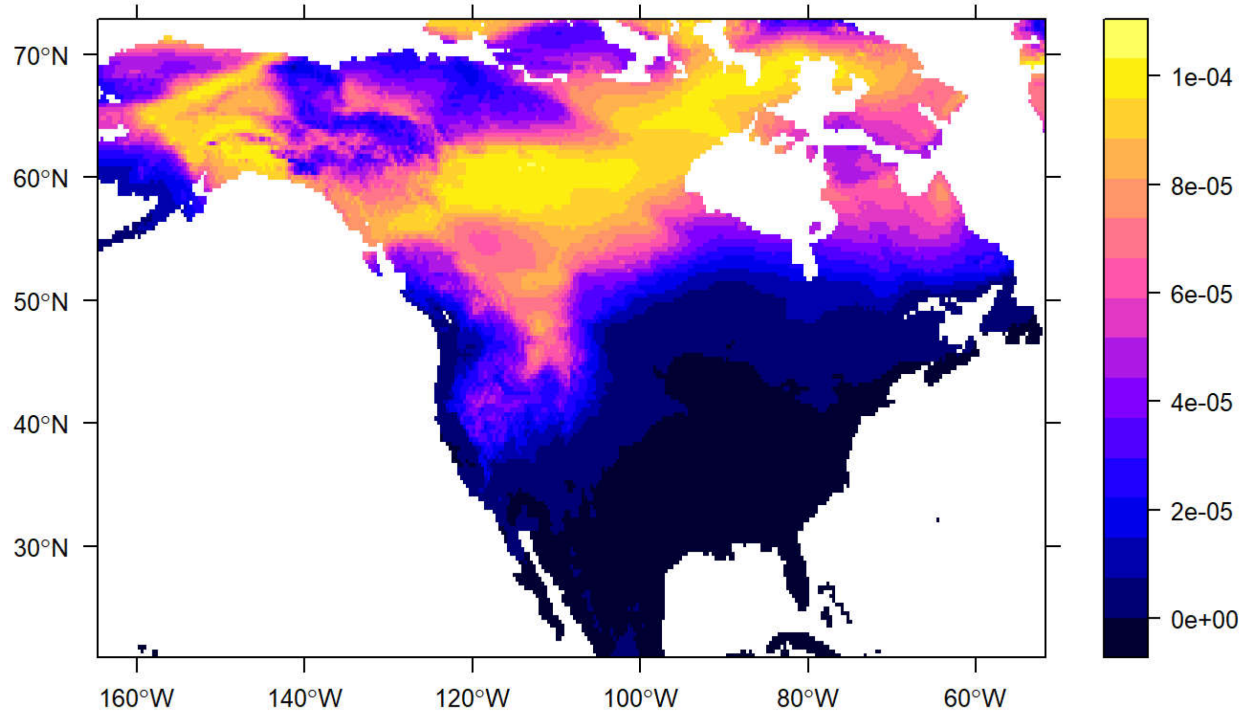
```
##  arning in dir.create("output"): 'output' already exists
```

```
##  arning in dir.create("output/pdRaster_Gtif"): 'output pdRaster_Gtif'
## already exists
```

Probability Density Surface for a

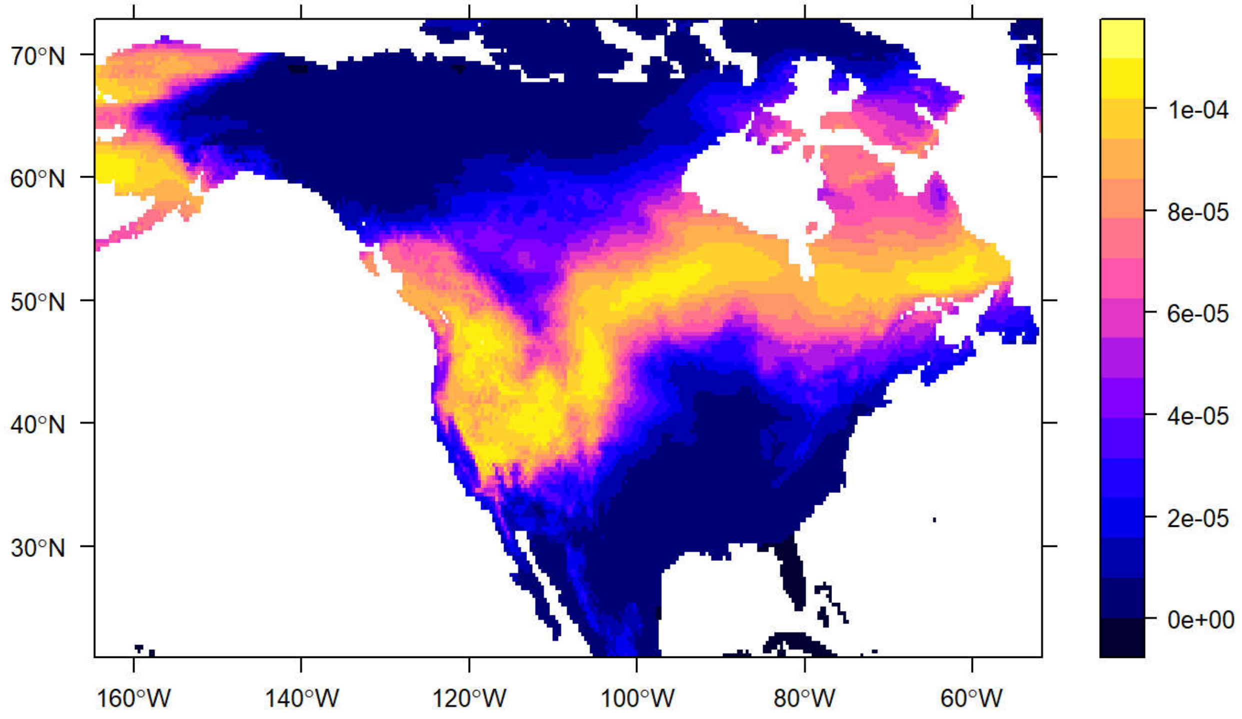


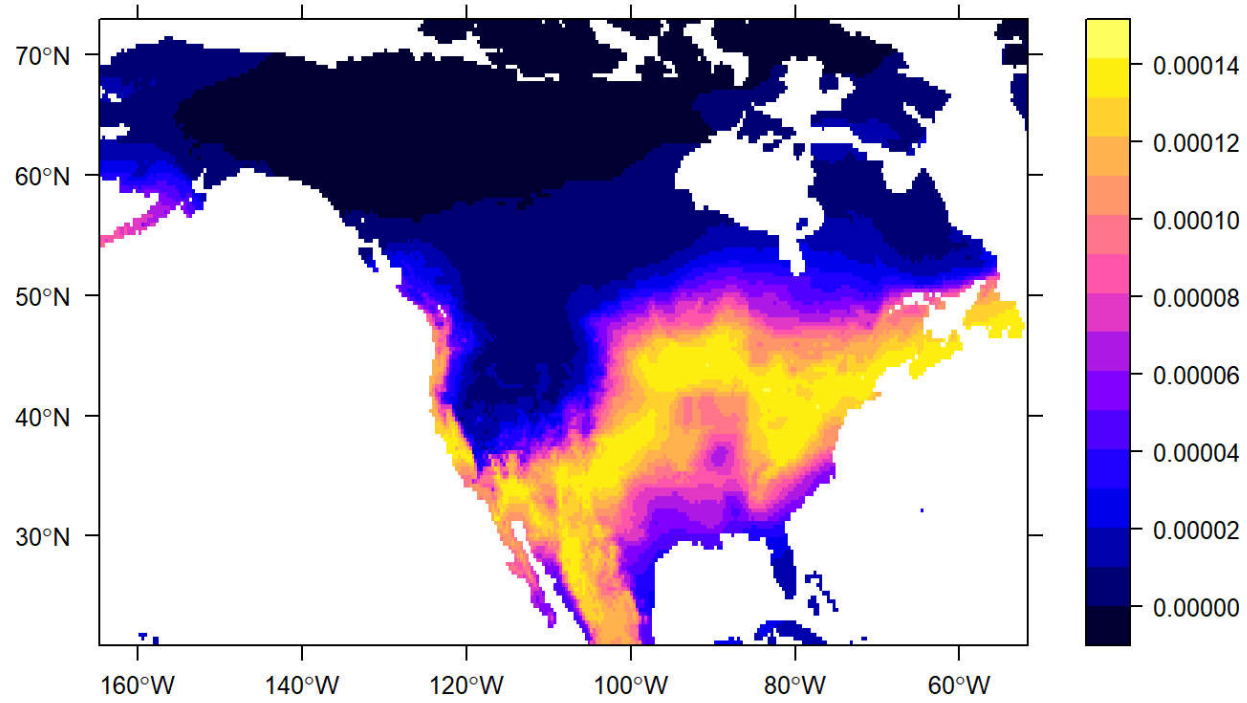

Probability Density Surface for b
70°N
60°N
50°N
40°N
30°N
160°W
140°W
120°W
100°W
80°W
60°W
0.00020
0.00015
0.00010
0.00005
0.00000

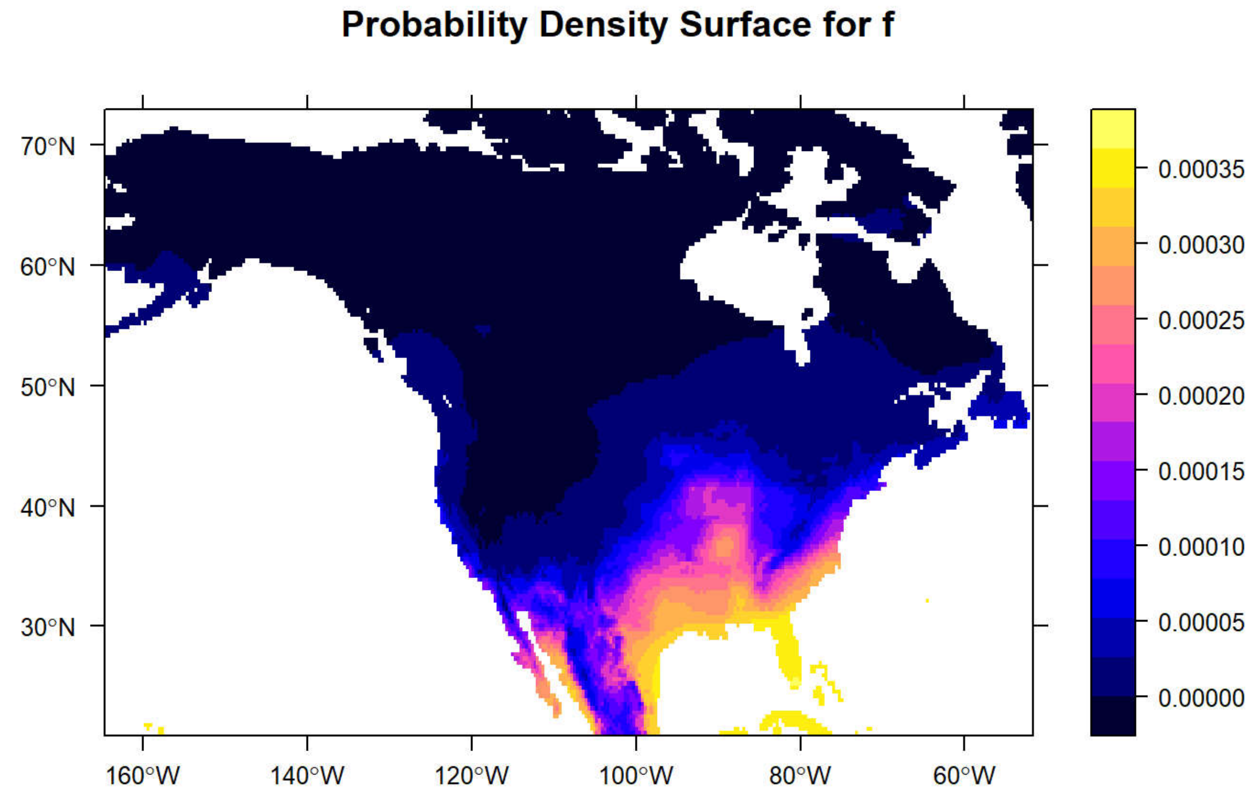


Probability Density Surface for c

Probability Density Surface for d




Probability Density Surface for e



Create SpatialPolygons with two polygons

```
p1 <- c(-100,60,-100,65,-110,65,-110,60,-100,60)
p1 <- matrix(p1, 5,2, byrow = T)
p1 <- Polygon(p1)
p1 <- Polygons(list(p1), "p1")
p2 <- c(-100,40,-100,45,-110,45,-110,40,-100,40)
p2 <- matrix(p2, 5,2, byrow = T)
p2 <- Polygon(p2)
p2 <- Polygons(list(p2), "p2")
p12 <- SpatialPolygons(list(p1,p2),1:2)
plot(p12)
```

Create data.frame with two points

```
pp1 <- c(-100,45)
pp2 <- c(-100,60)
pp12 <- as.data.frame(rbind(pp1,pp2))
```

Caculate odds ratio for the two polygons created above

```
oddsRatio(asn, p12)
```

```
## $ P1/P2_odds_ratio
##            a            b            c            d            e 
## 4.088128e 03 2.344395e 02 6.480108e 00 9.690121e-02 6.121049e-04 
##            f 
## 1.919561e-06 
## 
## $ ratio of numbers of cells in two polygons
## [1] 1
```

Caculate odds ratio for the two points created above

```
oddsRatio(asn, pp12)
```

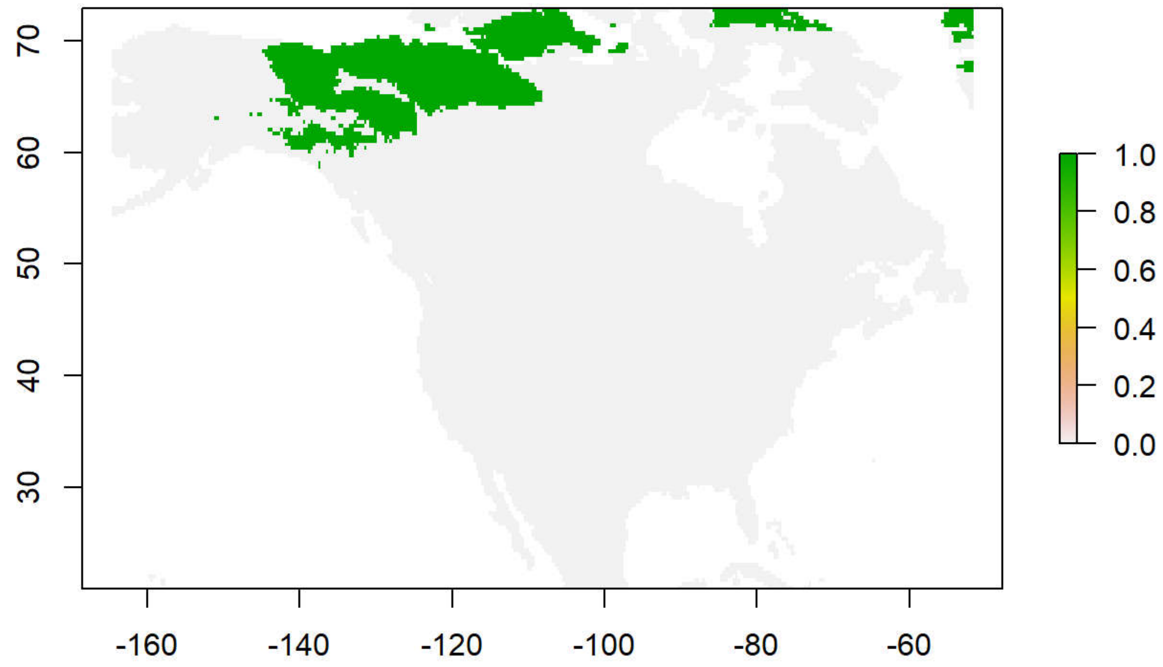
```
## $ P1/P2_odds_ratio
##            a            b            c            d            e 
## 1.146839e-08 8.417012e-06 4.205954e-03 1.431251e 00 3.316179e 02 
##            f 
## 5.230446e 04 
## 
## $ odds of a pixel to the odds of the max/min pixel
##   ratioToMax.a ratioToMax.b ratioToMax.c ratioToMax.d ratioToMax.e
## 1 1.626156e-11 2.111854e-06  0.002773832   0.02499529  1.166192978
## 2 1.080405e-02 2.359802e-01  0.257425866   0.13306854  0.003307999
##   ratioToMax.f ratioToMin.a ratioToMin.b ratioToMin.c ratioToMin.d
## 1 1.241220e-01 6.034369e 10     313.3168 1.113673e 04 9.275299e 19
## 2 9.263921e-07 1.793020e 12    1439.8675 3.025310e 11 2.208380e 13
##   ratioToMin.e ratioToMin.f
## 1 1.730175e 08     498340.6
## 2 2.018424e 01    1088710.9
```

Binary reclassification

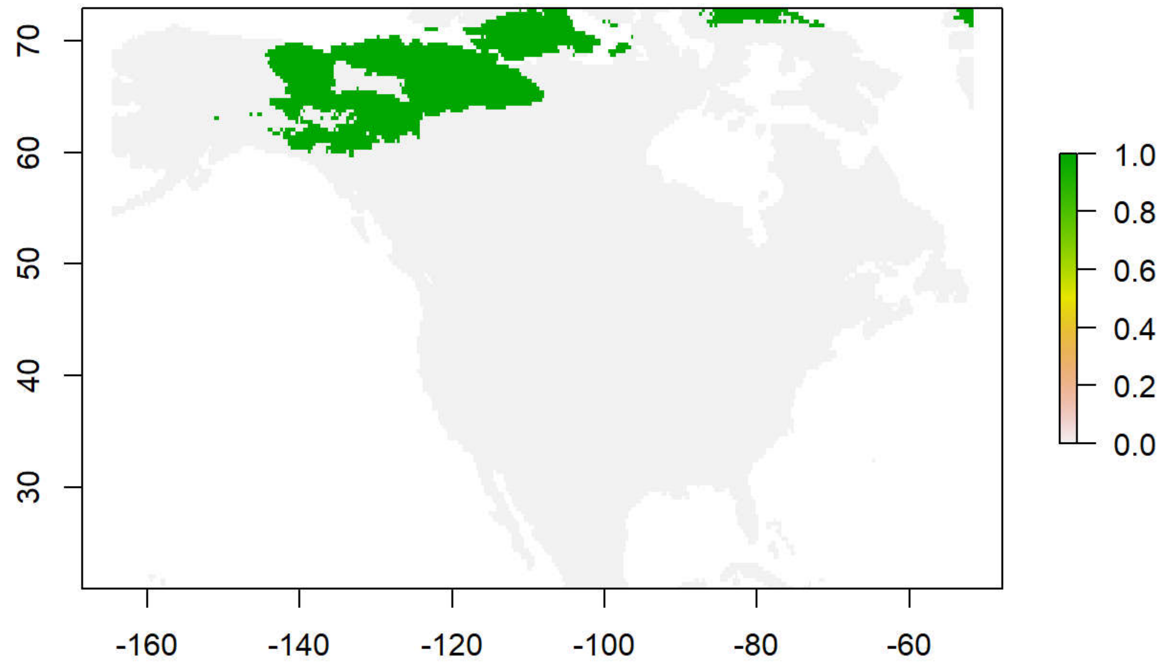
Top 10 of probability surface (defined by area)

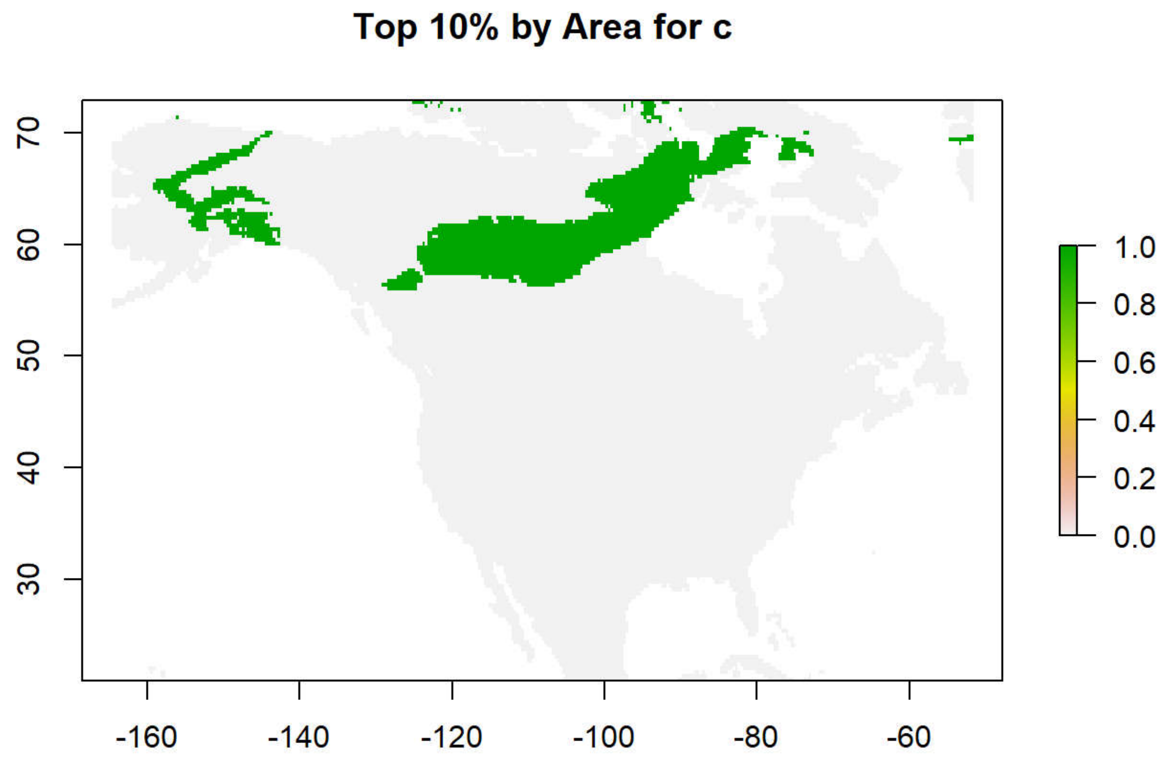
```
qtlRaster(asn, threshold = 0.1, thresholdType = 2)
```

Top 10% by Area for a

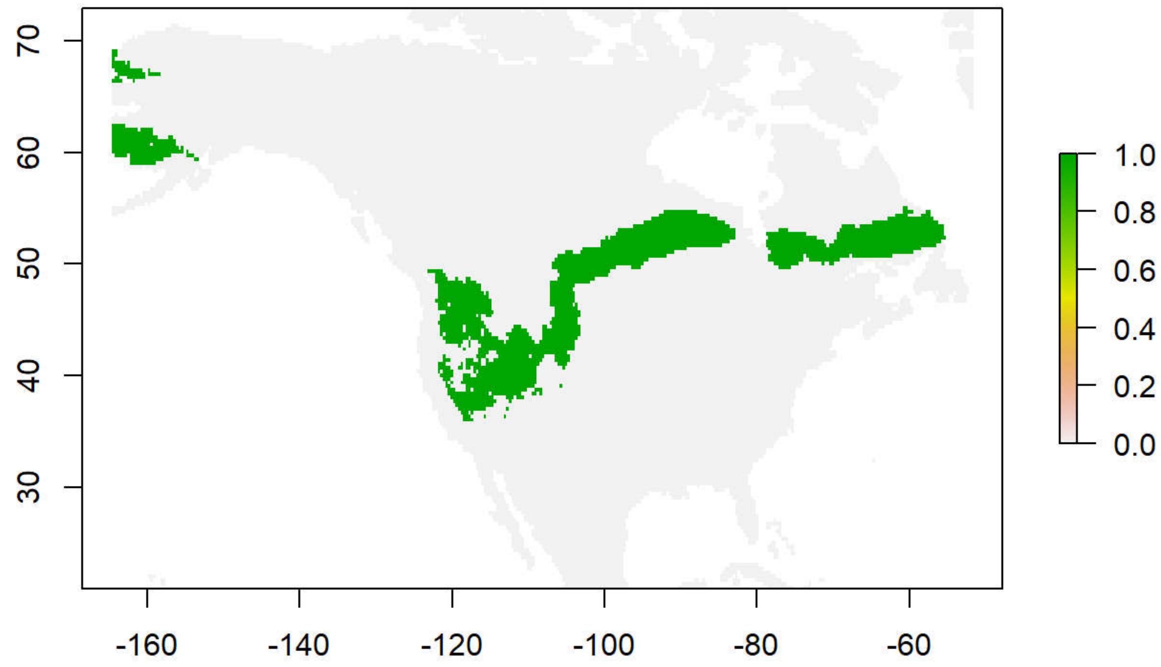


Top 10% by Area for b

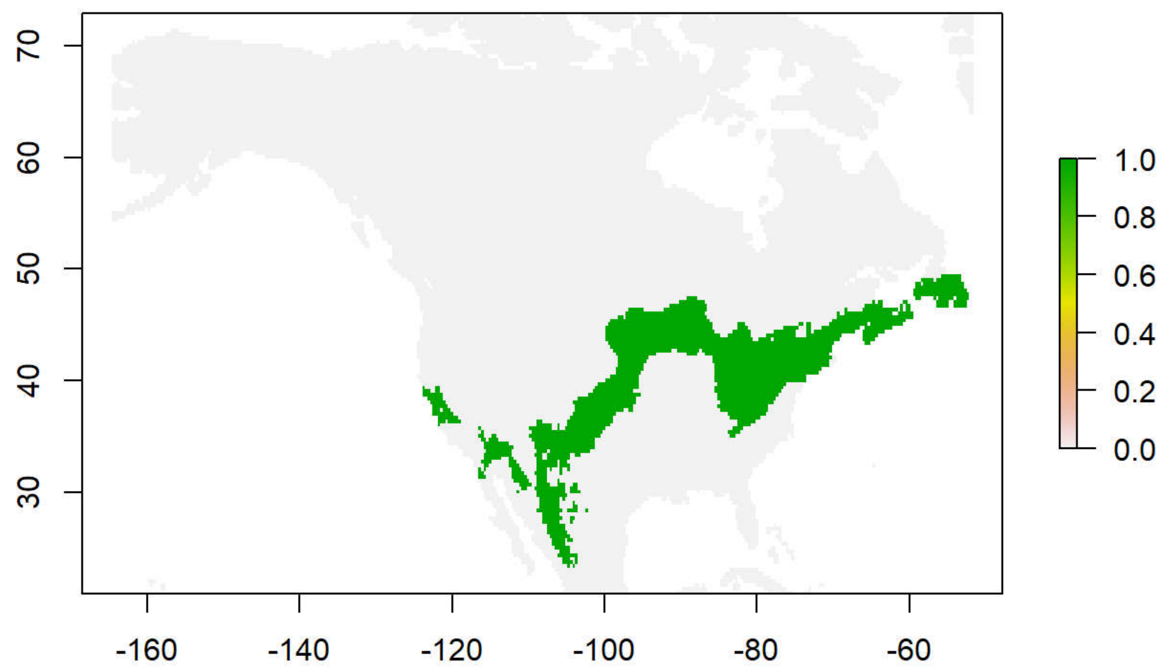


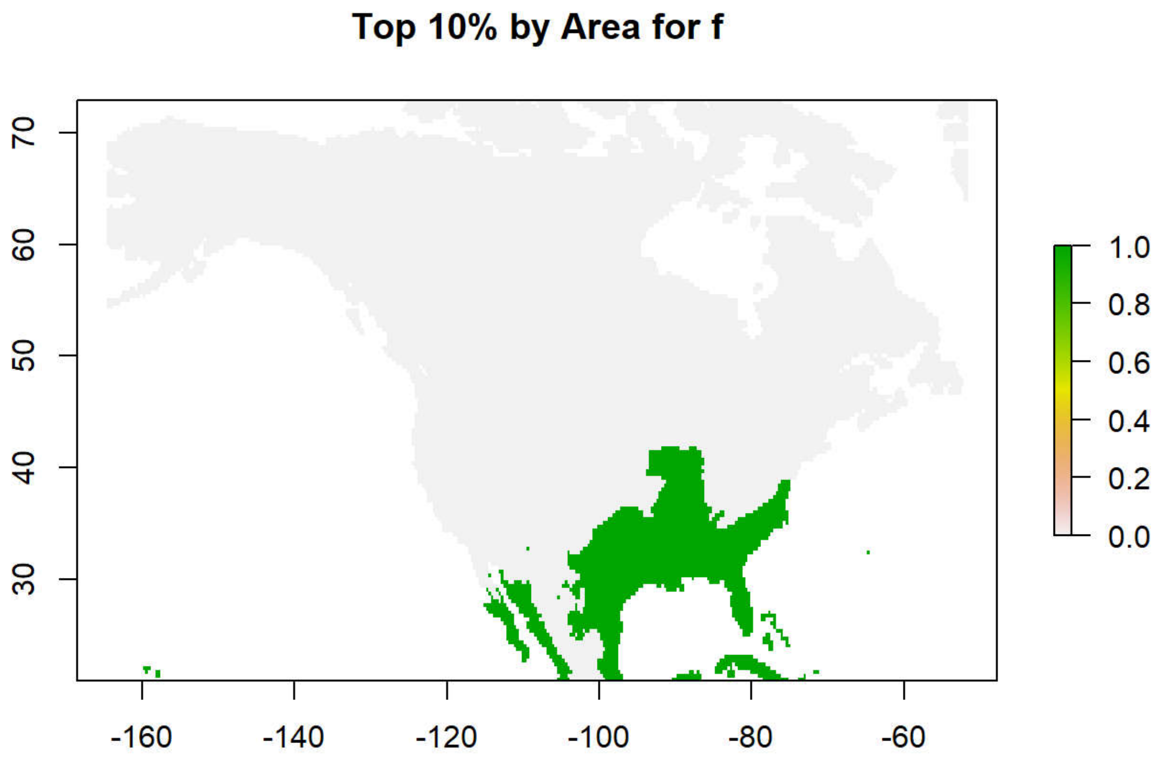

Top 10% by Area for c
70
60
50
40
30
-160
-140
-120
-100
-80
-60
1.0
0.8
0.6
0.4
0.2
0.0

Top 10% by Area for d



Top 10% by Area for e



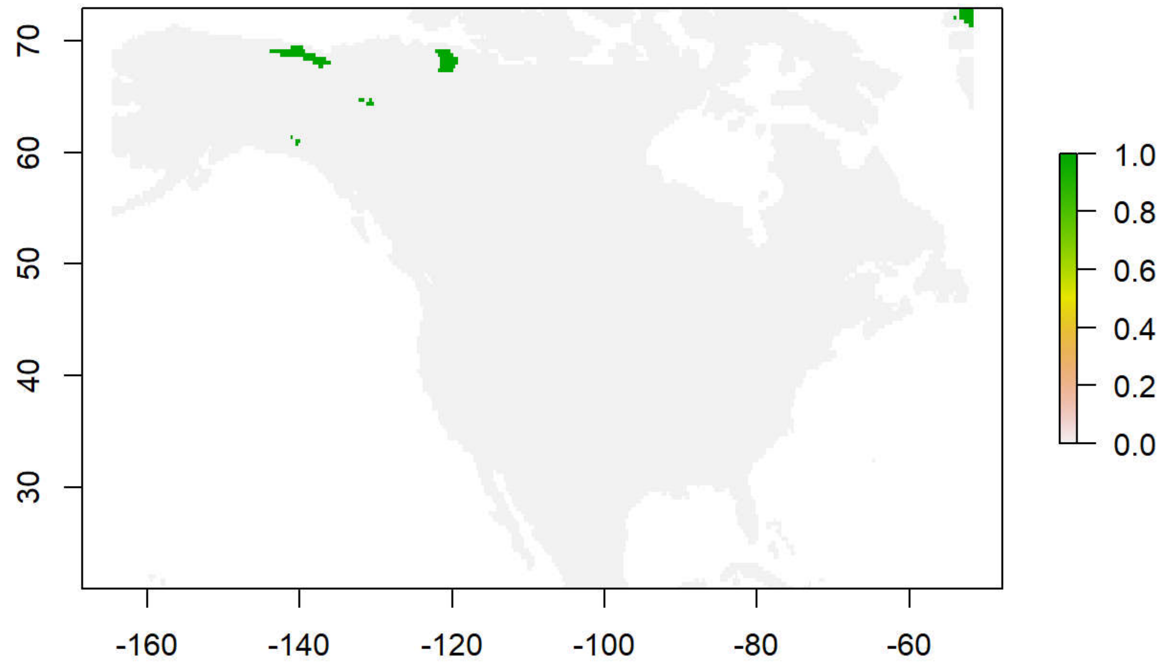


```
## class       : RasterStack
## dimensions : 156, 339, 52884, 6  (nrow, ncol, ncell, nlayers)
## resolution : 0.3333332, 0.3333332  (x, y)
## extent      : -164.6667, -51.66672, 20.91662, 72.9166  (xmin, xmax, ymin, ymax)
## crs         :  proj=longlat  datum= GS84  no_defs  ellps= GS84  towgs84=0,0,0
## names       : a, b, c, d, e, f
## min values : 0, 0, 0, 0, 0, 0
## max values : 1, 1, 1, 1, 1, 1
```

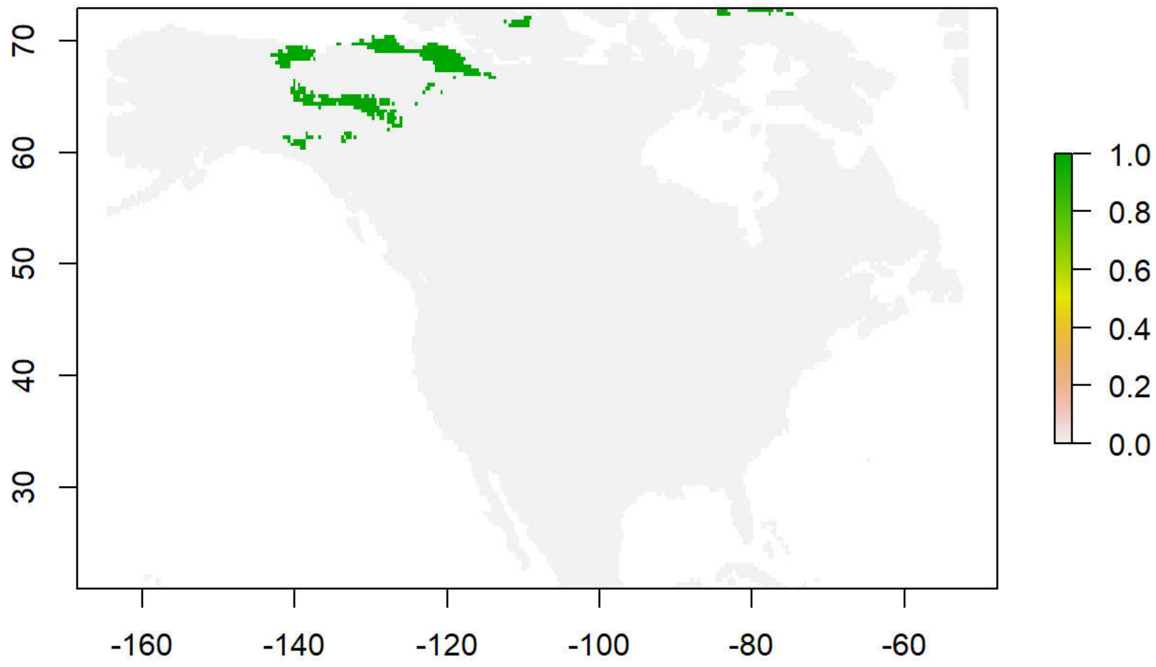
Top 10 of probability surface (defined by cumulative probability)

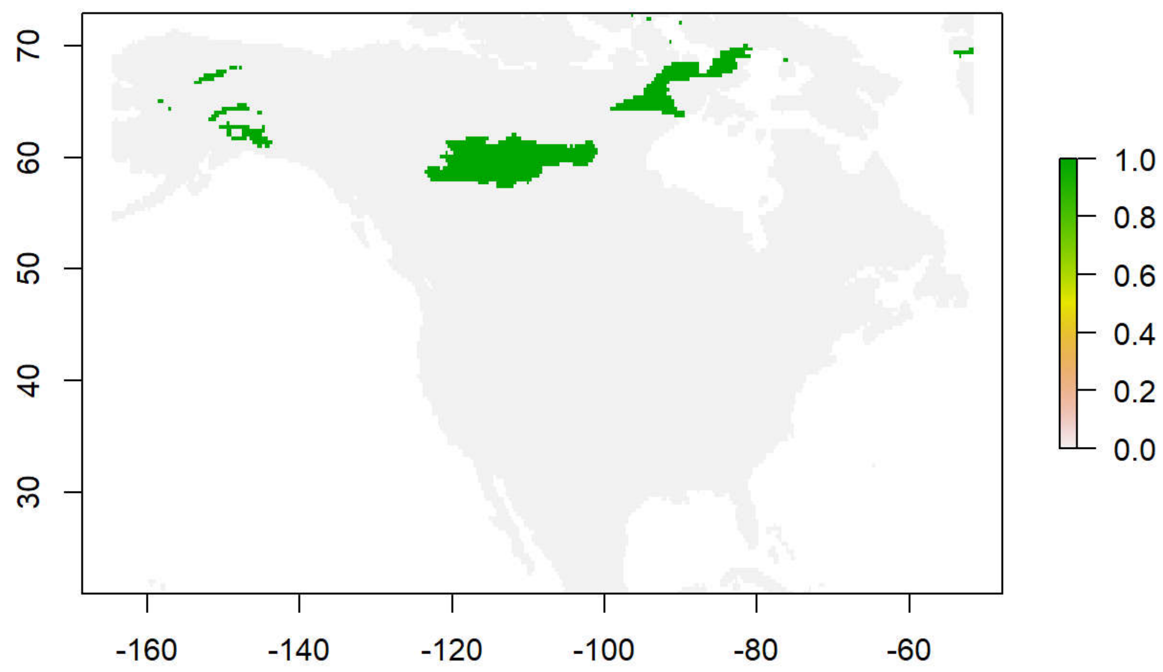
```
qtlRaster(asn, threshold = 0.1, thresholdType = 1)
```

Top 10% by Cumulative Probability for a



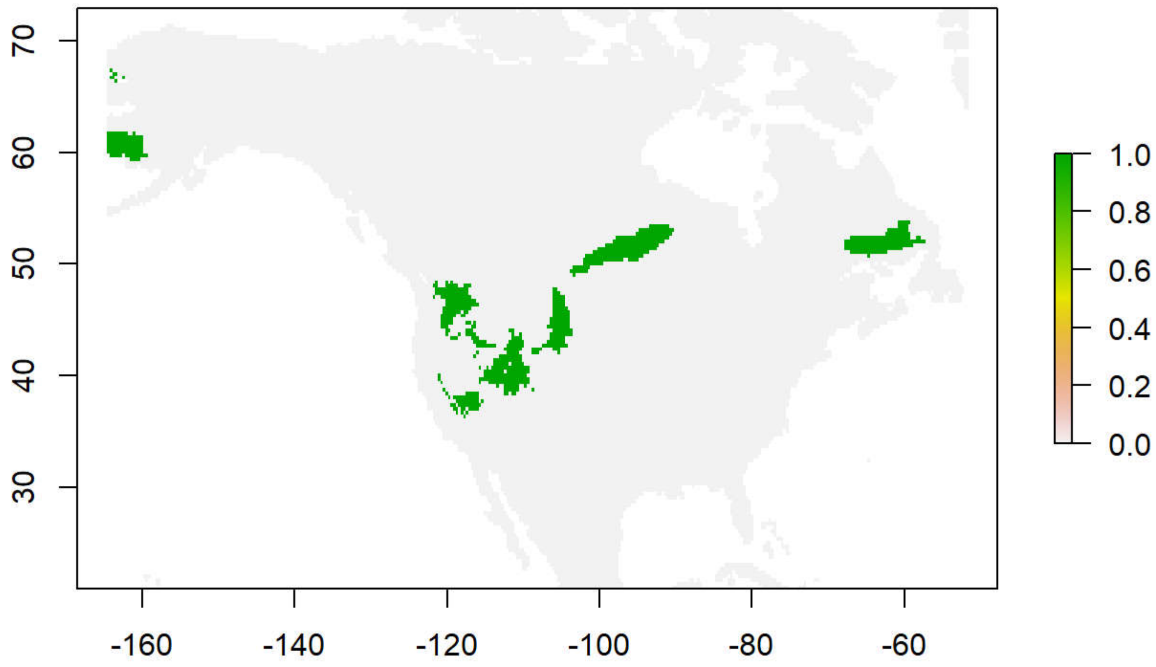
Top 10% by Cumulative Probability for b

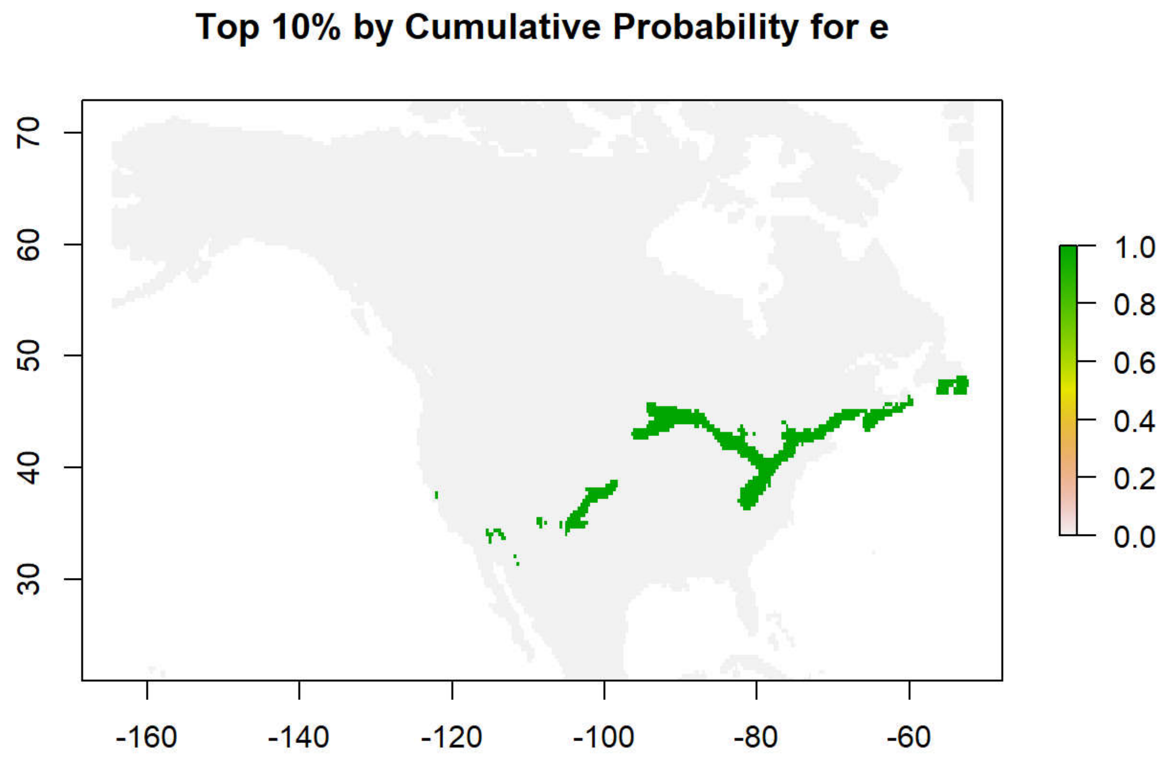


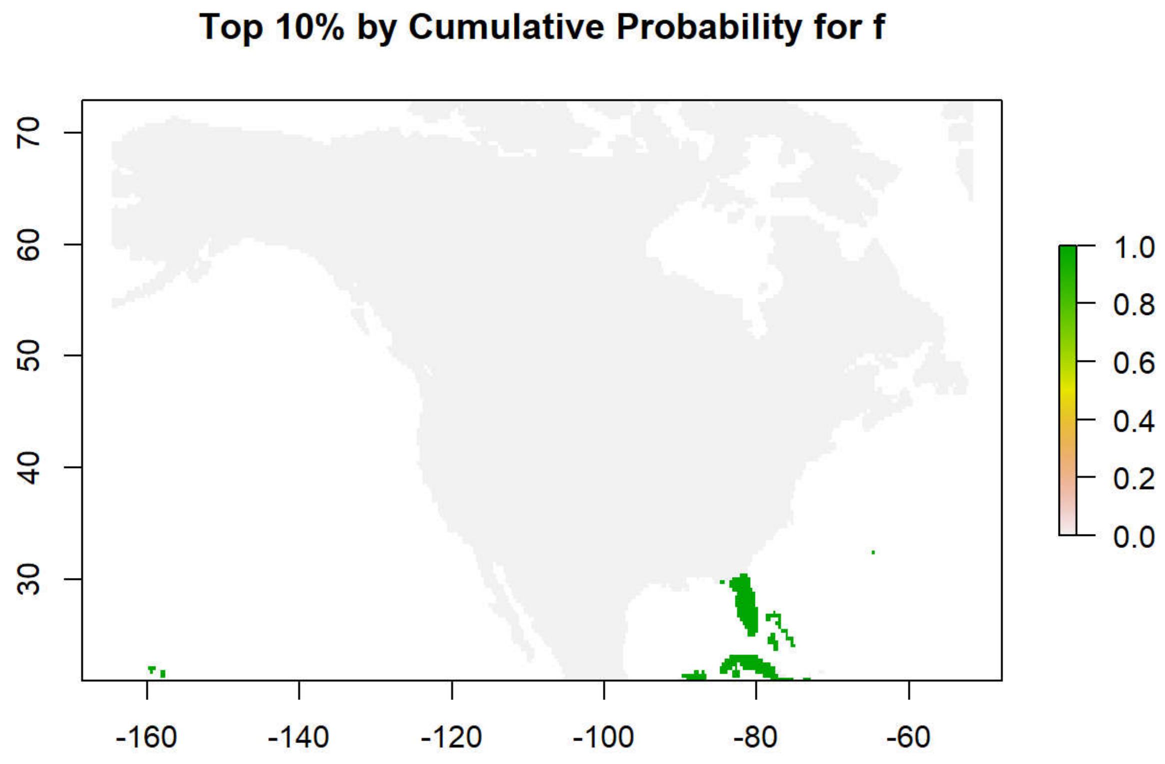


Top 10% by Cumulative Probability for c

Top 10% by Cumulative Probability for d



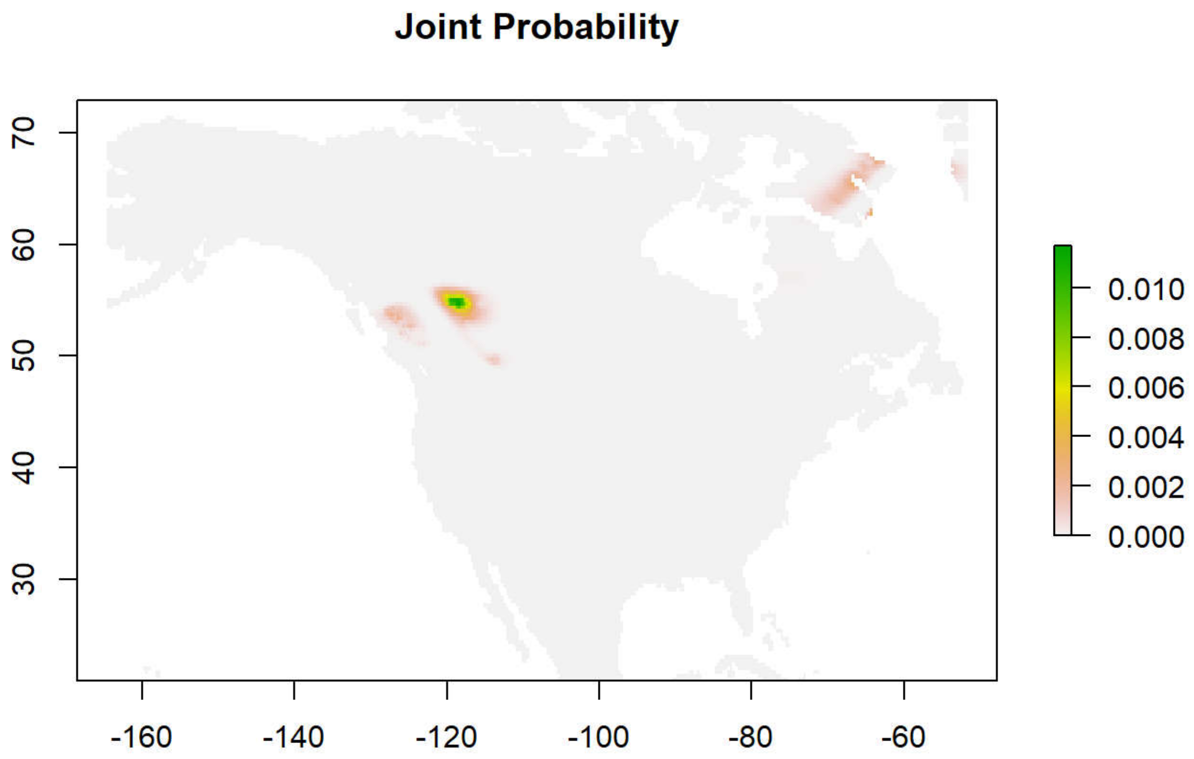

Top 10% by Cumulative Probability for e
70
60
50
40
30
-160
-140
-120
-100
-80
-60
1.0
0.8
0.6
0.4
0.2
0.0



```
## class      : RasterStack
## dimensions : 156, 339, 52884, 6  (nrow, ncol, ncell, nlayers)
## resolution : 0.3333332, 0.3333332  (x, y)
## extent     : -164.6667, -51.66672, 20.91662, 72.9166  (xmin, xmax, ymin, ymax)
## crs        :  proj=longlat  datum= GS84  no_defs  ellps= GS84  towgs84=0,0,0
## names      : a, b, c, d, e, f
## min values : 0, 0, 0, 0, 0, 0
## max values : 1, 1, 1, 1, 1, 1
```

oint probability for individuals of common origin

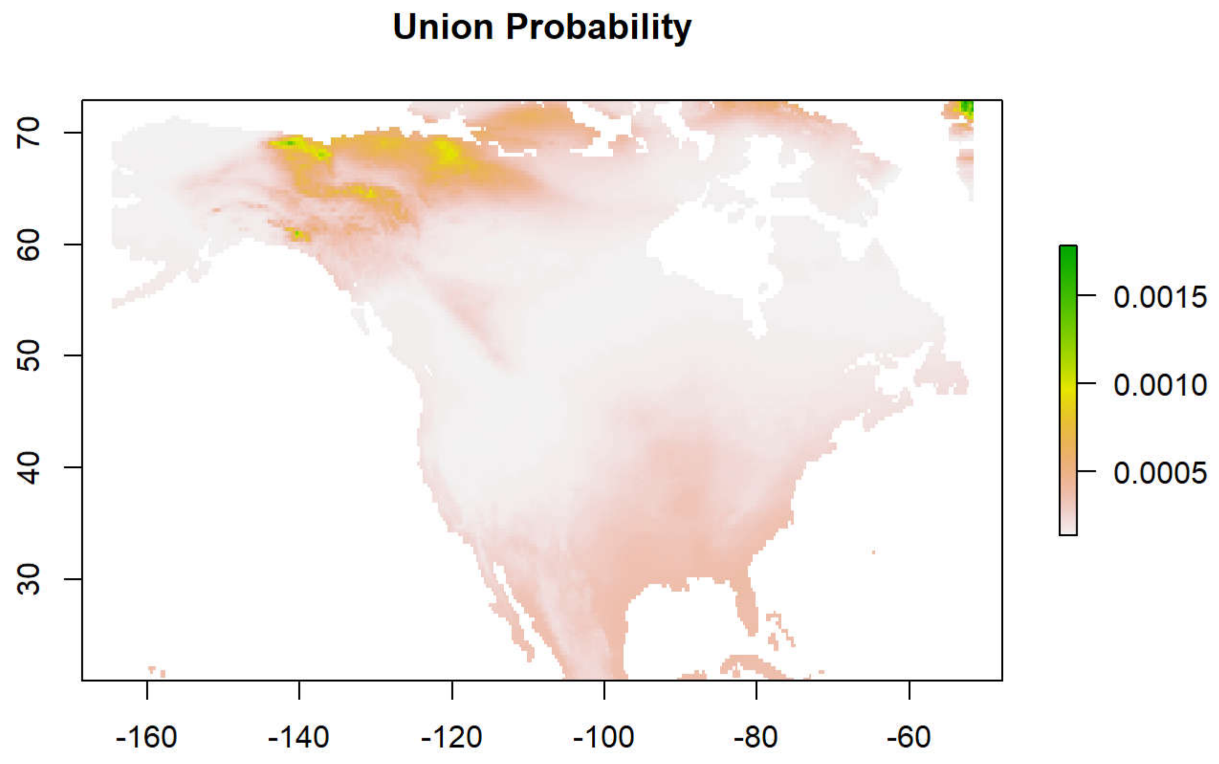
```
jointP(asn)
```



```
## class      : RasterLayer
## dimensions : 156, 339, 52884  (nrow, ncol, ncell)
## resolution : 0.3333332, 0.3333332  (x, y)
## extent     : -164.6667, -51.66672, 20.91662, 72.9166  (xmin, xmax, ymin, ymax)
## crs        :  proj=longlat  datum= GS84  no_defs  ellps= GS84  towgs84=0,0,0
## source     : memory
## names      : Joint_Probability
## values     : 1.031402e-44, 0.01170466  (min, max)
```

Probability that at least one individual came from the location (union of probabilities)

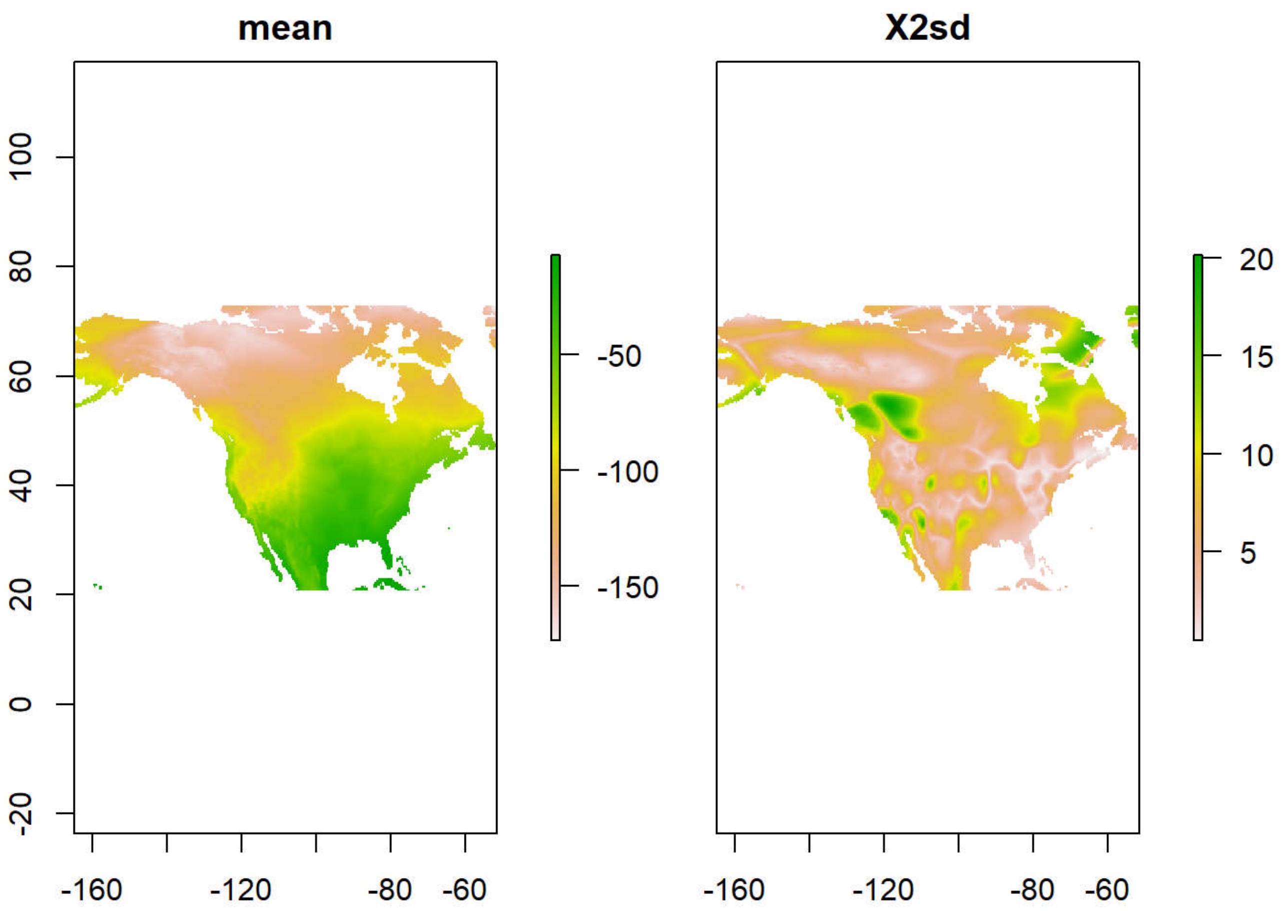
```
unionP(asn)
```



```
## class      : RasterLayer 
## dimensions : 156, 339, 52884  (nrow, ncol, ncell)
## resolution : 0.3333332, 0.3333332  (x, y)
## extent     : -164.6667, -51.66672, 20.91662, 72.9166  (xmin, xmax, ymin, ymax)
## crs        :  proj=longlat  datum= GS84  no_defs  ellps= GS84  towgs84=0,0,0 
## source     : memory
## names      : layer 
## values     : 0.0001361405, 0.001787688  (min, max)
```

Quality analysis of geographic assignment

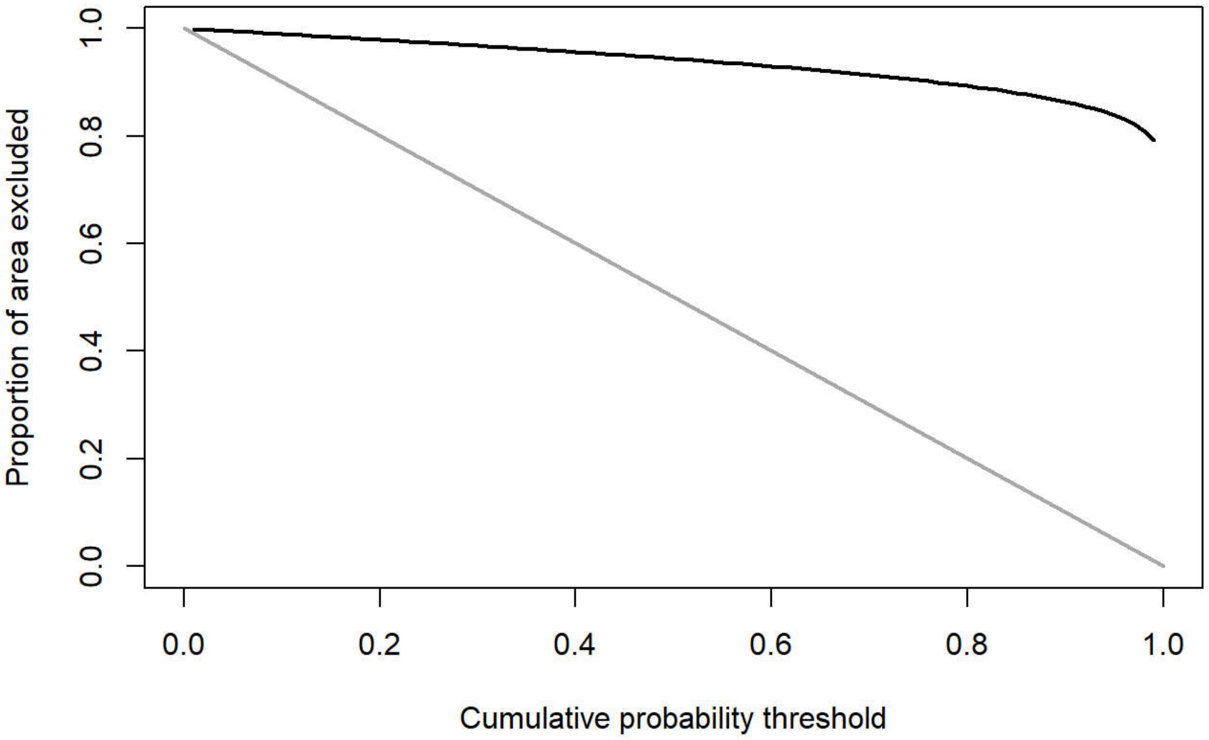
```
# oxygen and hydrogen isotopes of known-origin bird
data(bird_isotope)

# crop the world hydrogen data to North America
r <- crop(d2h_world, naMap)
plot(r)
```

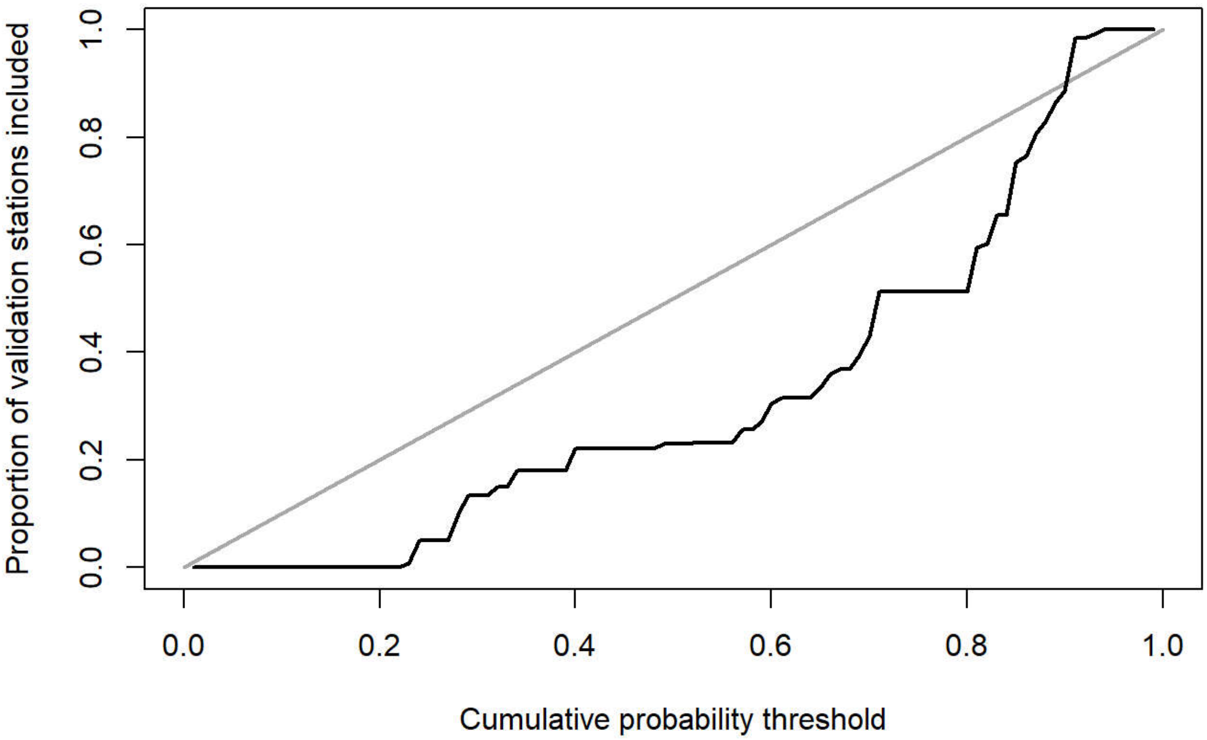


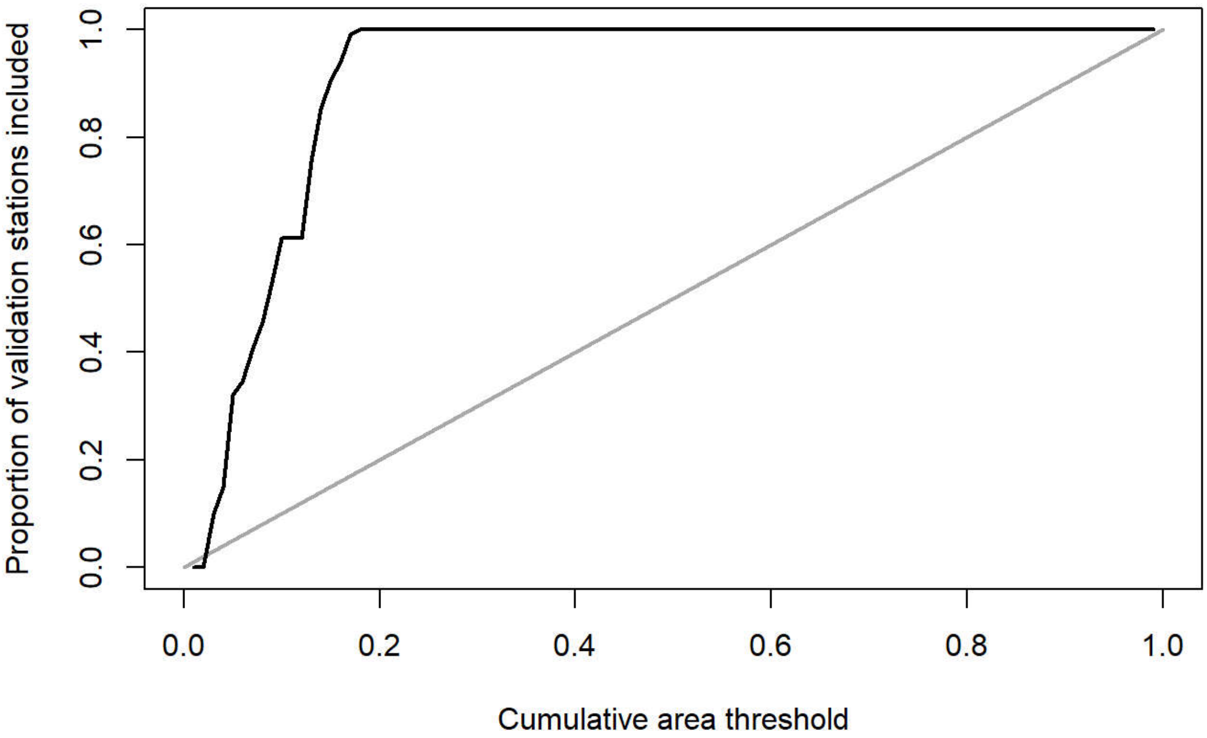
```
# convert 2 standard deviation from d2h_world to 1 standard deviation
r[[2]] <- r[[2]]/2

# seperate the hydrogen isotope for the known-origin bird
bird_d2h <- bird_isotope[1:20,c("Longitude", "Latitude", "d2H")]
coordinates(bird_d2h) <- c(1,2)
proj4string(bird_d2h) <- proj4string(d2h_world)

# run quality assessment based hydrogen isotope from precipitation and known-origin bi
rd
d2h_ A <-  A(isoscape = r, known = bird_d2h, valiStation = 2,
             valiTime = 5, setSeed = T)
```

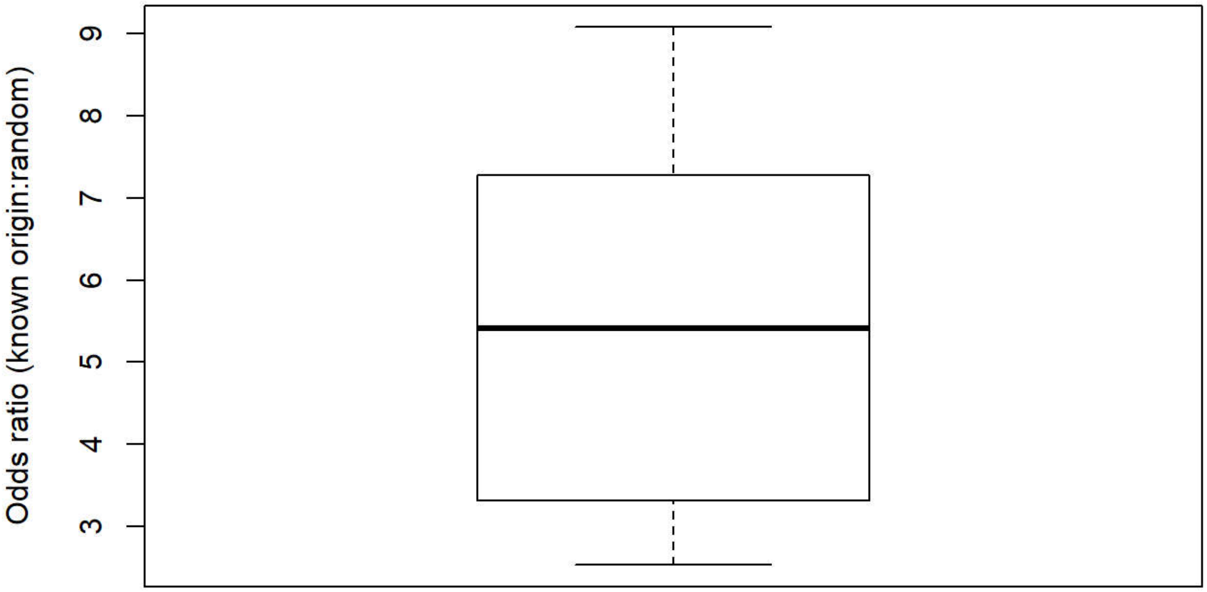
```
##

                                                                         0

   =============                                                        20

   ==========================                                           40

   =======================================                              60

   ====================================================                 80

   =================================================================   100
```

```
# plot the QA result
plot(d2h_ A)
```




Proportion of validation stations included
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0
Cumulative probability threshold


Proportion of validation stations included
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0
Cumulative area threshold


Odds ratio (known origin:random)
3
4
5
6
7
8
9