## Animal movement simulation

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1 Generating individual animal step lengths data (utilization distribution)

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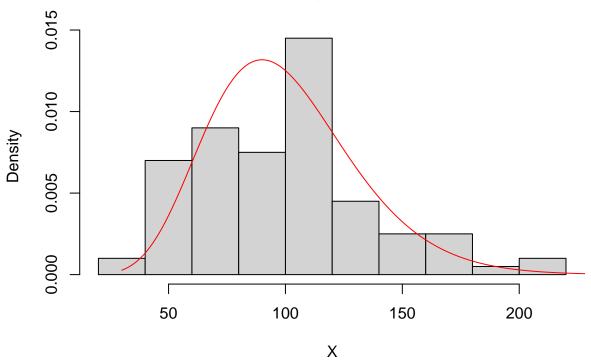
# 1 Generating individual animal step lengths data (utilization distribution)

Probability of obtaining a sample at some distance,  $l'_{t,i}$  from the previous observed point  $(l'_{t,i} = ||x'_{t,i} - x||)$  is given by the gammaPDF:

$$g(l'_{t,i}|b_1, b_2) = \frac{1}{\Gamma(b_1).b1^{b_2}} l'_{t,i}^{b_1-1}.e^{-\frac{l'_{t,i}}{b_2}}$$

```
b1 <- 10 ; b2 <- 10
n <- 100
X <- rgamma(n, scale = b1, shape = b2)
hist(X, freq=F)
x <- seq(30, 300, by = 0.1)
lines(x, dgamma(x, scale = b1, shape = b2), col = "red")</pre>
```

# Histogram of X

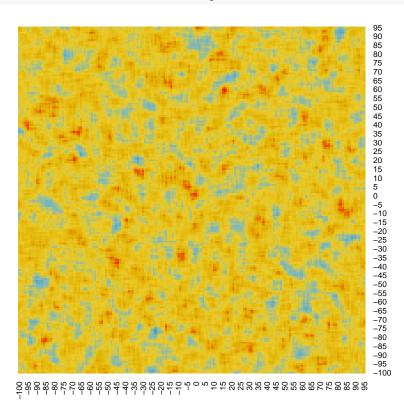


```
# Environment grid ver2
lat <- seq(-100,100, 1)
long <- seq(-100,100, 1)
n <- length(lat)
m <- length(long)
envi <- matrix(data = runif(n*m),nrow = n, ncol = m)
colnames(envi) <- lat
row.names(envi) <- long</pre>
```

```
#autocorection
p <- 5 #spatial unit

#sliding window
for (i in 1:(n-p)){
  for (j in 1:(m-p)){
    sub <- envi[i:(i+p),j:(j+p)]
    envi[i,j] = mean(sub)
}</pre>
```

```
pal <- wes_palette(40401,name = "Zissou1", type = "continuous")
heatmap(envi, Rowv = NA, Colv = NA, col = pal)</pre>
```



```
# habitat selection step
mu <- 1.7918
# chose moving length always ||x-x(t)|| = 1
omega <- 1
# #local habitat quality
envi_dt <- as.data.frame(envi)</pre>
 \hbox{\it\# apply truncated redistribution calculus kernel to the whole $\operatorname{grid-landscape}$ }
envi_exp <- exp(omega*envi-mu)</pre>
# adding two null columns at the "borders"
envi_exp <- cbind(rep(0, times = nrow(envi_exp)),</pre>
                   envi_exp,
                   rep(0, times = nrow(envi_exp)))
# adding two null rows at the "borders"
# adding two null columns at the "borders"
envi_exp <- rbind(rep(0, times = ncol(envi_exp)),</pre>
                   envi_exp,
                   rep(0, times = ncol(envi_exp)))
```

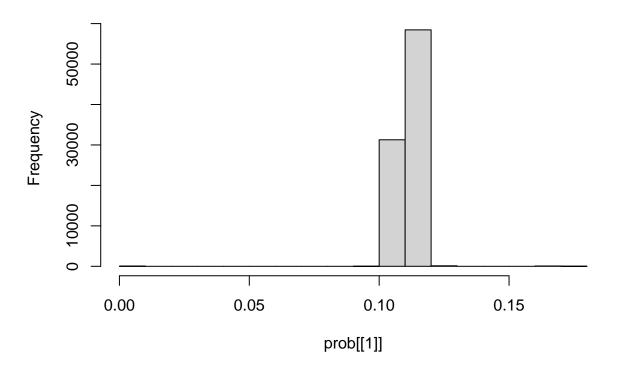
```
envi_exp <- as.data.frame(envi_exp)</pre>
# number of burn-in steps
step1 <- 2*length(envi)^2</pre>
# number of simulate steps
step2 <- 10<sup>5</sup>
# # starting point
# bird <- which(envi == max(envi), arr.ind = TRUE)</pre>
moves <- function(steps){</pre>
  # matrix of avaible movements
  code <- cbind(rep(c(1, 0, -1), 3), rep(c(-1, 0, 1), each = 3))
  # starting point (and
  coordinates <- which(envi_exp == max(envi_exp), arr.ind = TRUE)</pre>
  latitude <- coordinates[1,1]</pre>
  longitude <- coordinates[1,2]</pre>
  kernel <- envi_exp[(latitude-1):(latitude+1),</pre>
                       (longitude-1):(longitude+1)]
  # truncated redistribution kernel calculus
  prob_avail <- kernel/sum(kernel)</pre>
  prob_avail <- prob_avail %>% as_vector()
  names(prob_avail) <- 1:9</pre>
  num_cell <- which(rmultinom(1, 1, prob_avail)==1)</pre>
  move <- code[num cell,]
  coordinates <- rbind(coordinates,</pre>
                         c(latitude+move[1], longitude+move[2]))
  list_avail <- list(prob_avail, num_cell)</pre>
  for(i in 2:steps){
    latitude <- coordinates[i,1]</pre>
    longitude <- coordinates[i,2]</pre>
    # # dealing with "out of bounds" steps
    # if (latitude==nrow(envi_dt) | longitude==ncol(envi_dt) |
          latitude==1 | longitude==1){
    # warning(pasteO('stopping the algorithm at the ',i,'th step:
               animal reached the border of the "landscape"'))
    \# coord_dt <- as.data.frame(coordinates, row.names = FALSE)
    # return(list(coord_dt, list_avail))
    # }else{
    kernel <- envi_exp[(latitude-1):(latitude+1),</pre>
                      (longitude-1):(longitude+1)]
    # }
    # truncated redistribution kernel calculus
    # sub <- exp(omega*kernel-mu) # done earlier outside the function
    prob_avail <- kernel/sum(kernel)</pre>
    prob_avail <- prob_avail %>% as_vector()
    names(prob_avail) <- 1:9</pre>
    num_cell <- which(rmultinom(1, 1, prob_avail)==1)</pre>
    move <- code[num_cell,]</pre>
    coordinates <- rbind(coordinates,</pre>
```

```
c(latitude+move[1], longitude+move[2]))
list_avail[[1]] <- rbind(list_avail[[1]], prob_avail)
list_avail[[2]] <- rbind(list_avail[[2]], num_cell)
}
coord_dt <- as.data.frame(coordinates, row.names = FALSE)
return(list(coord_dt, list_avail))
}
res <- moves(10000)</pre>
```

```
res <- moves(10000)
coord <- res[[1]]
prob <- res[[2]]

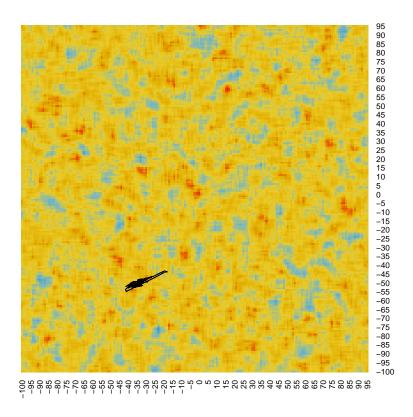
hist(prob[[1]])</pre>
```

### Histogram of prob[[1]]



```
# sub <- which(envi == max(envi), arr.ind = TRUE)
# sub <- exp(omega*sub-mu)
# prob <- sub/sum(sub)
# prob_vect <- envi[1:3, 1:3] %>% as.data.frame() %>% as_vector()
# names(prob_vect) <- 1:9
# num_cell <- which(rmultinom(1, 1, prob_vect)==1) ; num_cell</pre>
```

```
heatmap(envi, Rowv = NA, Colv = NA, col = pal)
lines(envi_exp[coord$row, coord$col], lwd = 0.2)
```



```
# points(envi_exp[coord$row, coord$col], lwd = 0.1, pch = 3, cex = 0.2)
```

 $\#\ seal\ <-\ read.csv("https://www.datarepository.movebank.org/bitstream/handle/10255/move.451/Grey\%20 seal) = -\ read.csv("https://www.datarepository.movebank.org/bitstream/handle/10255/move.451/Grey%20 seal) = -\ read.csv("https://www.datarepository.movebank.org/bitstream/handle/10255/movebank.org/bitstream/handle/10255/movebank.org/bitstream/handle/10255/movebank.org/bitstream/handle/10255/movebank.org/bitstream/handle/10$ 

```
# seal %>%
# mutate(timestamp = ymd_hms(timestamp)) %>%
# select(timestamp)

# seal %>%
# filter(tag.local.identifier == 106705) %>%
# ggplot() + aes(x = location.long, location.lat) +
# geom_point() +
# geom_line()
```