A General Hidden State Random Walk Model for Animal Movement - R functions

Aurelien Nicosia

A two state general random walk model for a caribou

First we have to load the source file of usefull fonctions and the data set.

Before applying the model, we can check for basic descriptive statistic on the direction and step length.

```
direction <- as.circular(jeu$y)
summary(direction)
```

```
##          n       Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## 617.00000  -0.33650   1.39300   2.77900   2.68200  -1.90500  -0.36770
##       Rho
##   0.03798
```

```
summary(jeu$d)
```

```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
##  0.001533  0.064210  0.125900  0.312000  0.249000 10.040000
```

We can fit an angular concensus regression model to inspect if the exploratory variables have an effect on the direction of the animal

```
n <- length(jeu$y)
yprec <- c(0, jeu$y[ - n])
mc <- consensus(formula = y ~ yprec + xcut + xcenter, data = jeu)
names(mc)
```

```
##  [1] "MaxLL"       "parameters"  "varcov1"      "varcov2"      "parambeta"
##  [6] "varcovbeta1" "varcovbeta2" "autocorr"     "matx"         "matz"
## [11] "y"           "long"         "mui"          "iter.detail" "call"
```

```
mc$parameters
```

```
##          estimate    stderr1    stderr2
## yprec   0.1058897 0.05752115 0.05750388
## xcut    0.1555772 0.06401522 0.06397484
## xcenter 0.2771297 0.06412821 0.06343050
```

Let's now present the two state general random walk model for this caribou

```
# preparation of the initials parameters
kappac <- cbind(mc$parameters[, 1], mc$parameters[, 3])
library(fitdistrplus)
```

```
## Loading required package: MASS
```

```
mel.d = mledist(jeu$d, distr = "gamma")
pi0 <- c(0.7, 0.3)
kappainit <- rbind(c(kappac[1, 1], kappac[2:3, 1]), c(kappac[1, 1], kappac[2:3, 1]))
thetalininit <- rbind(c(mel.d$estimate[1], 1/mel.d$estimate[2]),
                      c(mel.d$estimate[1], 1/mel.d$estimate[2]))
colnames(thetalininit) = c("shape", "scale")
paraminitiaux <- list(pi0 = pi0, kappainit = kappainit,
                      thetalininit = thetalininit, Pinit = NULL)
K = 2
```

```
# data set for the fit
target <- cbind(jeu$xcut, jeu$xcenter)
colnames(target) = c("xcut", "xcenter")
p <- length(target[1, ])
z = matrix(1, n, p)
jeu <- list(x = as.matrix(target), y = as.vector(jeu$y),
            z = z, d = as.vector(jeu$d))
```

```
# FIT
GM <- GHRandomWalk(jeu, K, paraminitiaux,
                   nb_init = 5, dist = "gamma", semi = TRUE)
```

```
## [1] "short-run EM algortim"
## [1] "20% of the short-run EM algorithm done"
## [1] "40% of the short-run EM algorithm done"
## [1] "60% of the short-run EM algorithm done"
## [1] "80% of the short-run EM algorithm done"
## [1] "long-run EM algorithm..."
```

Markov specification

There is the results for the Markov specification of the hidden process

```
names(GM$Markov)
```

```
## [1] "param"          "P.Markov"       "kappa.Markov"   "lambda.Markov"
## [5] "fit.Markov"
```

The transition matrix of the hidden Markov chain is :

```
GM$Markov$P.Markov
```

```
##     estimate (P1.) s.e. (P1.) estimate (P2.)   s.e. (P2.)
## P.1     0.7211776  0.0890572     0.02308734 0.009754052
```

That we can write

$$P = \begin{pmatrix} 0.721 & 0.279 \\ 0.023 & 0.977 \end{pmatrix}$$

which is well reprensented by

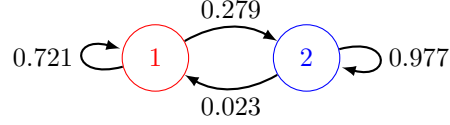The parameters of the observed direction are estimated as

Figure 1: Hidden Markov process

```
GM$Markov$kappa.Markov
```

```
##         estimate (k=1) s.e. (k=1) p.value (k=1) estimate (k=2) s.e. (k=2)
## yprec       1.2666354  0.3327569        0.0001     0.02740224 0.06181979
## xcut        0.1601465  0.3013192        0.2975     0.14543757 0.06979821
## xcenter     0.3732653  0.2994235        0.1063     0.25900191 0.06944963
##         p.value (k=2)
## yprec          0.3288
## xcut           0.0186
## xcenter        0.0001
```

The observed direction y_i is model as a von Mises distribution with mean direction $\mu_i^{(k)}$ and concentration parameter $\ell_i^{(k)}$. Moreover, since we use the consensus version for the concentration, $\mu_i^{(k)}$ and $\ell_i^{(k)}$ are the direction and length of the vectors $V_t^{(k)}$, $k = 1, 2$:

$$V_t^{(1)} = \mathbf{1.27} \begin{pmatrix} \cos(y_{t-1}) \\ \sin(y_{t-1}) \end{pmatrix} + 0.16 \begin{pmatrix} \cos(x_\text{xcut}) \\ \sin(x_\text{xcut}) \end{pmatrix} + 0.37 \begin{pmatrix} \cos(x_\text{xcenter}) \\ \sin(x_\text{xcenter}) \end{pmatrix}$$

and

$$V_t^{(2)} = 0 \begin{pmatrix} \cos(y_{t-1}) \\ \sin(y_{t-1}) \end{pmatrix} + \mathbf{0.3} \begin{pmatrix} \cos(x_\text{xcut}) \\ \sin(x_\text{xcut}) \end{pmatrix} + \mathbf{0.11} \begin{pmatrix} \cos(x_\text{xcenter}) \\ \sin(x_\text{xcenter}) \end{pmatrix}$$

The observed distance are model as gamma distribution with parameters:

```
GM$Markov$lambda.Markov
```

```
##       estimate (k=1) s.e. (k=1) estimate (k=2) s.e. (k=2)
## shape      0.6477965  0.1372759      1.2626090 0.07735345
## scale      3.0444805  0.8450568      0.1351119 0.01199943
```

Finally, the fit under the Markov assumption can be obtained by

```
GM$Markov$fit.Markov
```

```
## $likelihood.Markov
##          [,1]
## [1,] -794.91
##
## $AIC.Markov
##          [,1]
## [1,] 1613.82
##
## $BIC.Markov
##          [,1]
## [1,] 1666.918
```

Semi-Markov specification

```
GM$SemiMarkov
```

```
## $Dwell.SemiMarkov
##         size       s.e        prob         s.e
## p1 0.3175366 0.2666360 0.13718828 0.11365594
## p2 0.5992177 0.3811016 0.01581297 0.01242247
##
## $kappa.SemiMarkov
##         estimate (k=1)      s.e. estimate (k=2)        s.e.
## yprec        1.2588961 0.3366317     0.02574442 0.06203552
## xcut         0.1269109 0.3039780     0.14648343 0.06990856
## xcenter      0.4241228 0.2992742     0.25654797 0.06960431
##
## $lambda.SemiMarkov
##       lambda (k=1)        s.e lambda (k=2)        s.e
## shape    0.6653796 0.1360421    1.2712366 0.07831696
## scale    2.9259282 0.8107420    0.1330343 0.01205461
##
## $fit.SemiMarkov
## $fit.SemiMarkov$likelihood.SemiMarkov
##           [,1]
## [1,] -793.265
##
## $fit.SemiMarkov$AIC.SemiMarkov
##          [,1]
## [1,] 1614.53
##
## $fit.SemiMarkov$BIC.SemiMarkov
##          [,1]
## [1,] 1676.478
```

The results of both specification of the hidden process are summarized in Table~1.

Trajectory with smooth probabilities

We can use the smooth probability $\mathbb{P}(S_t = k|\mathcal{F}_T)$ in the E step of the EM algorithm to caracterize the behavior (state 1 or 2) of the animal across the time

Table 1: Estimation of the parameters of multistate models, with gamma distributed distances; $\lambda_1^{(k)}$ and $\lambda_2^{(k)}$ denote the shape and scale parameters of the gamma distribution in the state k; n_k and q_k are the size and probability of the negative binomial distribution of the state k's dwell time.

|	Markov		Semi-Markov	
	Estimate	S.e.	Estimate	S.e.
q_1	0.2799	0.0891	0.1290	0.1087
n_1	1	.	0.3046	0.2529
q_2	0.0231	0.0097	0.0157	0.0124
n_2	1	.	0.6034	0.3828
$\kappa_{persist.}^{(1)}$	1.2666	0.3327	1.2617	0.3368
$\kappa_{center}^{(1)}$	0.3732	0.2994	0.4251	0.2995
$\kappa_{cut}^{(1)}$	0.1601	0.3013	0.1274	0.3043
$\lambda_1^{(1)}$	0.6477	0.1372	0.6670	0.1366
$\lambda_2^{(1)}$	3.0444	0.8450	2.9361	0.8122
$\kappa_{persist.}^{(2)}$	0.0274	0.0618	0.0263	0.0619
$\kappa_{center}^{(2)}$	0.2590	0.0694	0.2563	0.0695
$\kappa_{cut}^{(2)}$	0.1454	0.0679	0.1462	0.0698
$\lambda_1^{(2)}$	1.2626	0.0774	1.2704	0.0779
$\lambda_2^{(2)}$	0.1351	0.0119	0.1332	0.0119
(l,AIC,BIC)	(-794.91,1613.82,**1666.91**)		(-793.11,1614.22,1676.17)	
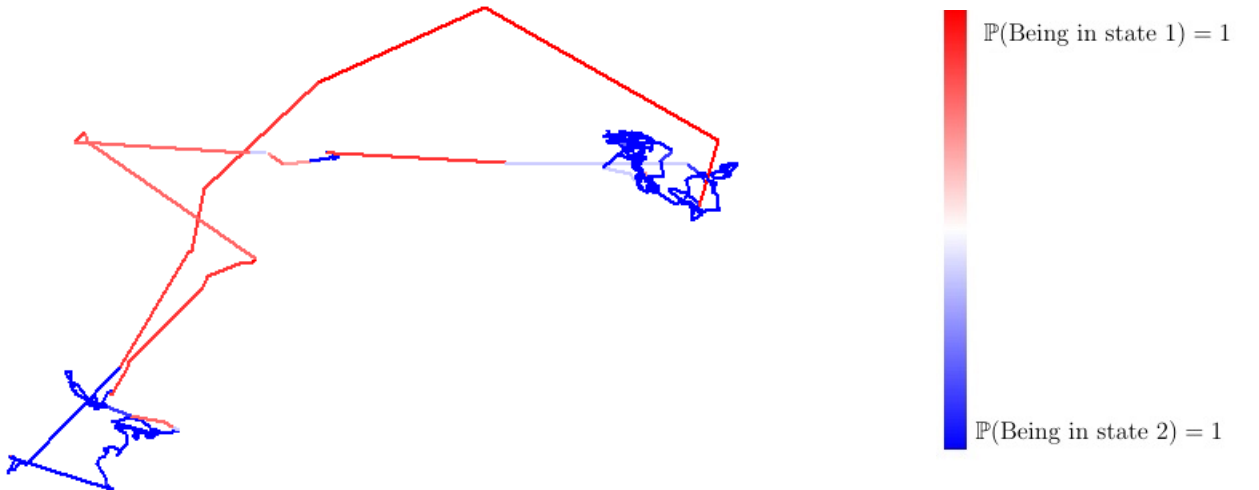
Figure 2: Hidden state probabilities at each time step of the trajectory of the caribou.

$\mathbb{P}(\text{Being in state } 1) = 1$

$\mathbb{P}(\text{Being in state } 2) = 1$