HMM Workshop

Rocío Joo
Structure of the workshop

- Introduction to HMMs
- Data for application
- 3 HMM applications
  - Simple HMM with 3 states
  - HMM with 4 states with constraints in transitions
  - HMM with covariates conditioning transitions and observed variables
- Other stuff you can and can’t do with momentuHMM
- References
Hidden Markov Models:

- What are they?
- What assumptions?
Hidden Markov Models:

States: \[ A A A B B C C C A A A A \]

Observed variables: \[ X_0 \ X_1 \ X_2 \ X_3 \ \ldots \ldots \ X_{11} \]
Hidden Markov Models:

State: $S_{t-1} \rightarrow S_t \rightarrow S_{t+1}$

Obs: $Z_{t-1} \quad Z_t \quad Z_{t+1}$
Hidden Markov Models:

State: \( S_{t-1} \rightarrow S_t \rightarrow S_{t+1} \)

Obs: \( Z_{t-1} \rightarrow Z_t \rightarrow Z_{t+1} \)

- Underlying unobserved Markov process \( \{S_t\} \):
  \[
P(S_t = s_t \mid S_{t-1} = s_{t-1}) = P(S_t = j \mid S_{t-1} = i) = \gamma_{ij}
  \]
Hidden Markov Models:

State: \( S_{t-1} \rightarrow S_t \rightarrow S_{t+1} \)

Obs: \( Z_{t-1} \rightarrow Z_t \rightarrow Z_{t+1} \)

- Underlying unobserved Markov process \( \{S_t\} \):
  \[
P(S_t = s_t \mid S_{t-1} = s_{t-1}) = P(S_t = j \mid S_{t-1} = i) = \gamma_{ij}
  \]

- State-dependent observation process \( \{Z_t\} \):
  \[
P(Z_t = z_t \mid S_t = s_t)
  \]
Data for application: seals

- Southern elephant seal (*Mirounga leonina*)
- Trips from 15 animals (eight adult females and seven subadult males) tagged with Argos at Kerguelen Island.
- Previous filtering with SSMs was performed.

Let’s start preparing the data for modelling first. We need observed variables.

```r
path_data <- "./Data/"
trackData <- read.csv(paste0(path_data,"seal_tracks.csv"))
```
head(trackData)

## ID  lon  lat  date
## 1   1  70.60946 -49.60737 2014-02-11 10:34:58
## 2   1  70.82908 -50.08287 2014-02-11 20:10:58
## 3   1  70.90029 -50.32835 2014-02-12 05:46:58
## 4   1  70.85766 -50.54746 2014-02-12 15:22:58
## 5   1  70.63792 -50.90529 2014-02-13 00:58:58
## 6   1  70.48480 -50.99666 2014-02-13 10:34:58

str(trackData)

## 'data.frame': 7353 obs. of 4 variables:
## $ ID : int 1 1 1 1 1 1 1 1 1 1 ...
## $ lon : num 70.6 70.8 70.9 70.9 70.6 ... 
## $ lat : num -49.6 -50.1 -50.3 -50.5 -50.9 ... 
## $ date: Factor w/ 7353 levels "2013-02-13 22:27:43",..: 44
Just checking if the time steps are regular

```r
dates <- as.character(trackData[,4])
time_dif <- diff.Date(as.POSIXct(dates, tz = "GMT"))
head(time_dif)
```

```r
## Time differences in hours
## [1]  9.6  9.6  9.6  9.6  9.6  9.6  9.6
```

Calling the package

```r
library(momentuHMM)
```

Now, use the prepData for two reasons:

1. derive the observed variables through that function
2. transform the dataframe into a momentuHMMData object
data <- prepData(trackData, type = "LL",
    coordNames = c("lon", "lat"))

head(data)

## ID step  angle  date        x
## 1 1  55.19656  NA 2014-02-11 70.60946 -49.60737
## 2 1  27.77600 -0.1051839 2014-02-11 70.82908 -50.08287
## 3 1  24.56027 -0.3069499 2014-02-12 70.90029 -50.32835
## 4 1  42.72315 -0.2468352 2014-02-12 70.85766 -50.54746
## 5 1  14.80219 -0.4426067 2014-02-13 70.63792 -50.90529
## 6 1  27.87312  0.9141237 2014-02-13 70.48480 -50.99666
You can also plot the tracks and the series of steps and angles with

\[
\text{plot(}x=\text{data, compact=TRUE, ask=FALSE)}
\]
Modeling movement with a 3-state HMM

- 3 movement modes are expected: travelling (T), searching (S) and foraging (F)
- Observation variables: step length and turning angles
- No covariates

**Parametrisation of the model:**

Transition probability matrix:

\[
\Gamma = \begin{bmatrix}
\gamma_{TT} & \gamma_{TS} & \gamma_{TF} \\
\gamma_{ST} & \gamma_{SS} & \gamma_{SF} \\
\gamma_{FT} & \gamma_{FS} & \gamma_{FF}
\end{bmatrix}
\]

6 parameters to estimate
Modeling movement with a 3-state HMM

Parametrisation of the model:

L: step length

\[ L_t | S_t = s_t \sim Gamma(\text{shape}, \text{scale}) \]

initial values:

\[ L_t | S_t = T \sim Gamma(40, 10) \]
\[ L_t | S_t = S \sim Gamma(20, 8) \]
\[ L_t | S_t = F \sim Gamma(8, 5) \]
Modeling movement with a 3-state HMM

Parametrisation of the model:

$\Theta$: turning angle

$\Theta_t | S_t = s_t \sim VM$ (location, concentration)

initial values:

$\Theta_t | S_t = T \sim VM(-0.001, 7)$

$\Theta_t | S_t = S \sim VM(0, 4)$

$\Theta_t | S_t = F \sim VM(\pi, 0.1)$

So 12 parameters to estimate for the observation model. 18 in total.
Now in R!

Initial values for parameters in the model

```r
stateNames <- c("travel","search","forage")
shape_0 <- c(40,20,8)
scale_0 <- c(10,8,5)
stepPar0 <- c(shape_0,scale_0)
location_0 <- c(-0.001,0,3.14)
concentration_0 <- c(7,4,0.1)
anglePar0 <- c(location_0,concentration_0)
```
And fitting the model

```r
m1 <- fitHMM(data=data, nbStates=3,
              dist=list(step="gamma", angle="vm"),
              Par0=list(step=stepPar0, angle=anglePar0),
              estAngleMean = list(angle=TRUE),
              stateNames = stateNames)
print(m1) #estimations
```
Reconstructing state sequences:

The Viterbi algorithm:

$$\arg \max_{S_0 = s_0, \ldots, S_t = s_t} P(S_0 = s_0, \ldots, S_t = s_t \mid Z_0 = z_0, \ldots, Z_t = z_t)$$

In R:

```r
states.1 <- as.factor(viterbi(m1))
prop.table(table(states.1))
```

```r
## states.1
## 1 2 3
## 0.2623419 0.2560860 0.4815721
```
You might want to compute the probability of the process being in a different state at each time point...

\[ \text{stateProbs}(m1) \]

It is computing \( P(S_t = s_t \mid Z_0 = z_0, ..., Z_t = z_t, ..., Z_{T-1} = z_{T-1}) \)

which is different than what viterbi does.
Modeling movement with a 3-state HMM

Plotting outputs

```r
plot(m1, plotCI = TRUE, plotTracks=FALSE)
```

## Decoding state sequence... DONE

---

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HMM Workshop
Modeling movement with a 3-state HMM

Checking residuals

plotPR(m1)

## Computing pseudo-residuals... DONE
Modeling movement with a 4-state HMM

- 4 movement modes are expected: outbound (O), searching (S), foraging (F) and inbound (I)
- Not all transitions are possible
- Observation variables: step length and turning angles
- No covariates

The observation model is almost the same, we add one state
Parametrisation of the model:

L: step length

\[ L_t | S_t = s_t \sim Gamma(\text{shape, scale}) \]

initial values:

\[ L_t | S_t = O \sim Gamma(40, 10) \]
\[ L_t | S_t = S \sim Gamma(20, 8) \]
\[ L_t | S_t = F \sim Gamma(8, 5) \]
\[ L_t | S_t = I \sim Gamma(40, 10) \]
Modeling movement with a 4-state HMM

Parametrisation of the model:

\( \Theta \): turning angle

\( \Theta_t | S_t = s_t \sim VM(\text{location, concentration}) \)

initial values:

\( \Theta_t | S_t = O \sim VM(-0.001, 7) \)
\( \Theta_t | S_t = S \sim VM(0, 4) \)
\( \Theta_t | S_t = F \sim VM(\pi, 0.1) \)
\( \Theta_t | S_t = I \sim VM(-0.001, 7) \)

So 16 parameters to estimate for the observation model.
In R:

```r
stateNames <- c("outbound","search","forage","inbound")
shape_0 <- c(40,20,8,40)
scale_0 <- c(10,8,5,10)
stepPar0 <- c(shape_0,scale_0)
location_0 <- c(-0.001,0,3.14,-0.001)
concentration_0 <- c(7,4,0.1,7)
anglePar0 <- c(location_0,concentration_0)
```
**Modeling movement with a 4-state HMM**

**Parametrisation of the model:**

Not all transitions are possible:

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**Modeling movement with a 4-state HMM**

**Parametrisation of the model:**

Not all transitions are possible:

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4 parameters to estimate. 20 in total.
Modeling movement with a 4-state HMM

Parametrisation of the model:

Not all transitions are possible:

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4 parameters to estimate. 20 in total.

In momentuHMM, $\gamma_{ij} = \text{logit}^{-1}(\beta X)$; $X$: covariates

If there are no covariates, then $\gamma_{ij} = \text{logit}^{-1}(\beta_0) = \frac{1}{1 + \exp -\beta_0}$

Then, for $\gamma_{ij} \approx 0$, $\beta_0$: large negative number; e.g. $-100$

Thus, for our case:

beta_M2=c(NA,-100,-100, -100, NA, NA, -100, NA, -100, -100, -100, -100)
And fitting the model

```r
m2 <- fitHMM(data=data, nbStates=4,
              dist=list(step="gamma", angle="vm"),
              Par0=list(step=stepPar0, angle=anglePar0),
              estAngleMean = list(angle=TRUE),
              fixPar=list(beta=beta_M2),
              stateNames = stateNames)
print(m2) #estimations
```
Reconstructing state sequences:

The Viterbi algorithm:

```r
states.2 <- as.factor(viterbi(m2))
prop.table(table(states.2))
```

```
## states.2
##       1       2       3       4
## 0.1365429 0.2461580 0.4920441 0.1252550
```
Modeling movement with a 4-state HMM

Plotting outputs

```r
plot(m2, plotCI = TRUE, plotTracks=FALSE)
```

## Decoding state sequence... DONE

---

### All animals

- **Outbound**
- **Search**
- **Forage**
- **Inbound**
- **Total**

---

**Plot for step density:**

- **X-axis:** Step
- **Y-axis:** Density

**Plot for angle (radians):**

- **X-axis:** Angle (radians)
- **Y-axis:** Density
Modeling movement with a 4-state HMM

Checking residuals

```r
plotPR(m2)
```

## Computing pseudo-residuals... DONE
4-state HMM with covariates

- 4 movement modes are expected: outbound (O), searching (S), foraging (F) and inbound (I)
- Not all transitions are possible
- Observation variables: step length and turning angles
- What if transitioning from outbound or into inbound depended on covariates?
- What if the observed model depended on covariates as well?
- Covariates: distance to the colony, time since departure from the colony

Let’s start by deriving the covariates in R:
We first to compute distances to the colony:

center <- matrix(c(70, -49), nrow=1, dimnames=list("colony"))
data <- prepData(data=trackData, type="LL", centers=center,
            coordNames = c("lon", "lat"))
head(data[,c(1:3,7,8)])

## ID  step       angle colony.dist colony.angle
## 1  1    55.1966   NA         80.79235    0.5847407
## 2  1   27.7760  -0.1052     134.55555   -2.9626223
## 3  1   24.5603  -0.307    161.40565   -2.9047384
## 4  1   42.7232  -0.2468    182.86506   -2.6678926
## 5  1  14.80219  -0.4426    216.80945   -2.5543702
## 6  1   27.8731  0.91412    224.79045   -2.1702936
Deriving time spent since it left the colony:

```r
time <- NULL
for(id in unique(data$ID)) {
  nbSub0bs <- sum(data$ID==id)
  # approximately in months for interval = 9.6h
  time <- c(time, (1:nbSub0bs)*9.6/(24*30))
}
data$time <- time
```

Now, back to the parameters of the model.
**4-state HMM with covariates**

**Parametrisation of the model:**

Not all transitions are possible:

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<tr>
<th></th>
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<tbody>
<tr>
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<td>$\gamma_{OO}$</td>
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</tr>
<tr>
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Parametrisation of the model:

Not all transitions are possible:

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Michelot et al (2017): ‘(...) Animals often make fast trips away from the colony and tend to switch into other movement modes once they have reached foraging grounds’
### 4-state HMM with covariates

#### Parametrisation of the model:

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Michelot et al (2017): ’(...) Animals often make fast trips away from the colony and tend to switch into other movement modes once they have reached foraging grounds’

\[
\gamma^{(t)}_{OS} = \text{logit}^{-1} (\beta^{(OS)}_0 + \beta^{(OS)}_1 d_t)
\]

\(d_t\): distance of the animal to the colony at time \(t\)
4-state HMM with covariates

**Parametrisation of the model:**

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Michelot et al (2017): '(...)

Animals often make fast trips away from the colony and tend to switch into other movement modes once they have reached foraging grounds'

\[
\gamma^{(t)}_{OS} = \logit^{-1}(\beta_0^{(OS)} + \beta_1^{(OS)} d_t)
\]

$d_t$: distance of the animal to the colony at time $t$

\[
\gamma^{(t)}_{OS} = \frac{\exp(\beta_0^{(OS)} + \beta_1^{(OS)} d_t)}{1 + \exp(\beta_0^{(OS)} + \beta_1^{(OS)} d_t)}
\]
# 4-state HMM with covariates

## Parametrisation of the model:

Not all transitions are possible:

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Michelot et al (2017): ‘... time constraints to go back to the colony ...’
4-state HMM with covariates

Parametrisation of the model:

Not all transitions are possible:

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Michelot et al (2017): ‘... time constraints to go back to the colony ...’

\[
\gamma_{SI}^{(t)} = \frac{\exp(\beta_0^{(SI)} + \beta_1^{(SI)}(t - t_0))}{1 + \exp(\beta_0^{(SI)} + \beta_1^{(SI)}(t - t_0)) + \exp(\beta_0^{SF})}
\]

\[
\gamma_{SF}^{(t)} = \frac{\exp(\beta_0^{(SF)})}{1 + \exp(\beta_0^{(SI)} + \beta_1^{(SI)}(t - t_0)) + \exp(\beta_0^{SF})}
\]
### Parametrisation of the model:

What $\beta$ parameters to estimate? NA to those we need, 0 to those we don’t, and -100 when transitions are not likely to occur.

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</tr>
</tbody>
</table>


Parametrisation of the model:

What $\beta$ parameters to estimate? NA to those we need, 0 to those we don’t, and -100 when transitions are not likely to occur

In R:

```r
beta <- matrix(c(NA,-100,-100,-100,NA,NA,-100,NA,-100,
                 -100,-100,-100,
                 NA,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
                 nrow=3,byrow=TRUE)
formula <- ~ colony.dist + time
```
Parametrisation of the model:

What about the observed variables?

Idea: model outbound and inbound as BRWs, with repulsion from the colony for outbound and attraction towards the colony during inbound.

In momentuHMM, you can express it by:

```r
angleFormula <- ~ state1(colony.angle) + state4(colony.angle)
fixPar <- list(angle=c(-100,100,NA,NA,NA,NA),beta=beta)
```

-100: mean direction away from the colony

100: mean direction towards the colony

4 concentration parameters to estimate
4-state HMM with covariates

Parametrisation of the model:

Gamma distributions will be used for step length.

Instead of starting all over, we use the estimated values by the previous model as initial values to fit this model

```r
m2 <- fitHMM(data=data, nbStates=4,
              dist=list(step="gamma",angle="vm"),
              Par0=list(step=stepPar0, angle=anglePar0),
              estAngleMean = list(angle=TRUE),
              fixPar=list(beta=beta_M2),
              stateNames = stateNames)
```

```r
Par0 <- getPar0(model=m2, nbStates=4,
                 DM=list(angle=list(mean=angleFormula,
                                    concentration=~1)),
                 estAngleMean=list(angle=TRUE),
                 circularAngleMean=list(angle=TRUE),
                 formula=formula)
```
Now, fitting the model:

```r
m3 <- fitHMM(data=data, nbStates=4, 
    dist=list(step="gamma",angle="vm"), 
    Par0=list(step=Par0$Par$step, 
               angle=Par0$Par$angle), 
    beta0=Par0$beta, fixPar=fixPar, formula=formula, 
    DM=list(angle=list(mean=angleFormula, 
                     concentration=~1)), 
    estAngleMean=list(angle=TRUE), 
    circularAngleMean=list(angle=TRUE), 
    stateNames = stateNames)
```
4-state HMM with covariates

Reconstructing state sequences:

The Viterbi algorithm:

```r
states.3 <- as.factor(viterbi(m3))
prop.table(table(states.3))
```

```r
## states.3
## 1 2 3 4
## 0.1262070 0.2437101 0.5154359 0.1146471
```
4-state HMM with covariates

Checking residuals

\texttt{plotPR(m3)}

### Computing pseudo-residuals... DONE
Other stuff that you can do

- Introduce a dynamic activity center
- More complicated models (e.g. parameter bounds)
- Data imputation methods (e.g. using crawl)
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- Introduce a dynamic activity center
- More complicated models (e.g. parameter bounds)
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Stuff that cannot be done in momentuHMM

- Hidden semi-Markov models
- Random effects
Acknowledgments:

Théo Michelot

Thanks!