

Appendix 1: R code for the ecological illustration

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Data are contained in the object `trajbear.rda`. This is an object of the class `ltraj`.

```
library(adehabitat)
```

This package requires `ade4` to be installed

Type:

```
demo(rastermaps) for demonstration of raster map analysis
demo(homerange) for demonstration of home-range estimation
demo(managltraj) for demonstration of animals trajectory management
demo(analysisltraj) for demonstration of animals trajectory analysis
demo(nichehs) for demonstration of niche/habitat selection analysis
```

```
load("trajbear.rda")
trajbear
```

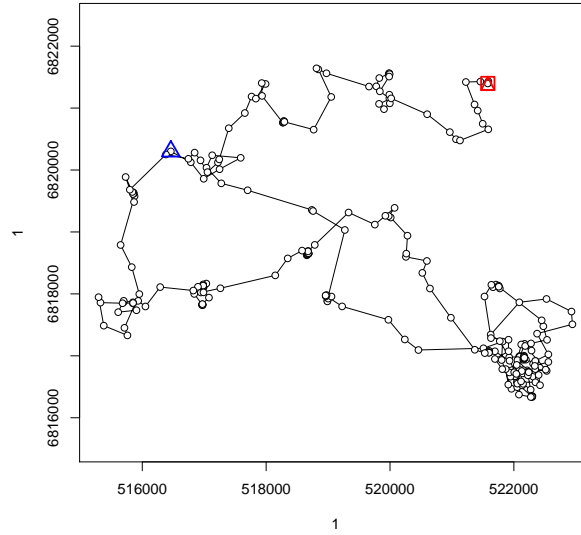
```
***** List of class ltraj *****
```

```
Type of the traject: Type II (time recorded)
Regular traject. Time lag between two locs: 1800 seconds
```

```
Characteristics of the bursts:
```

	id	burst	nb.reloc	NAs	date.begin	date.end
1	1	1	336	70	2004-07-01	2004-07-07 23:30:00

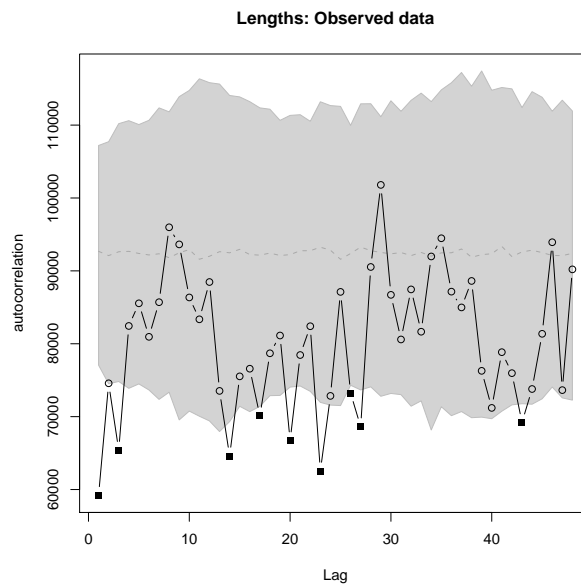
```
plot(trajbear)
```



It contains 336 relocations.

Correlogram for the length steps can be computed using the function `acfdist.ltraj`. Here, it is tested using 999 permutations.

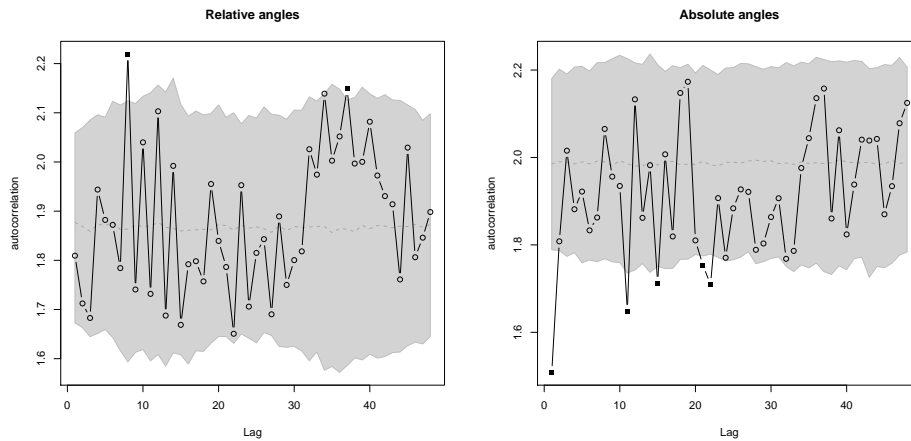
```
acfdist.ltraj(trajbear, lag = 48)
title(main = "Lengths: Observed data")
```



No structure is identified for the correlograms of absolute and relative angles:

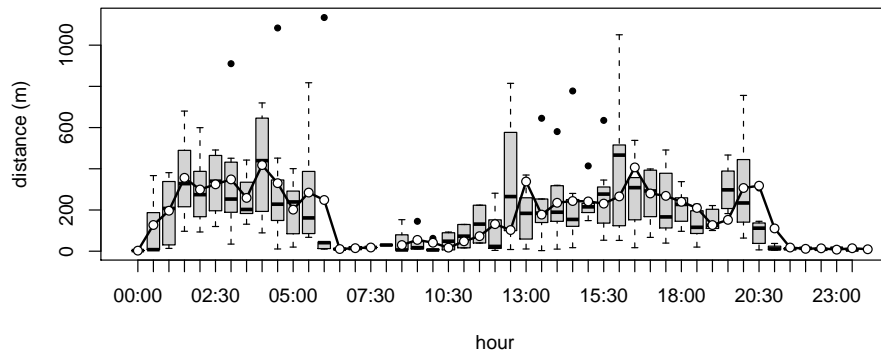
```
acfang.ltraj(trajbear, lag = 48, xlab = "Lag", which = "relative")
title(main = "Relative angles")
```

```
acfang.ltraj(trajbear, lag = 48, xlab = "Lag", which = "absolute")
title(main = "Absolute angles")
```



The average daily pattern of step lengths could then be represented:

```
boxplot(trajbear[[1]]$dist ~ substr(trajbear[[1]]$date,
  12, 16), col = "lightgrey", ylab = "distance (m)",
  xlab = "hour", pch = 20)
lines(1:48, tapply(trajbear[[1]]$dist, substr(trajbear[[1]]$date,
  12, 16), mean, na.rm = T), lwd = 2, ty = "l")
points(1:48, tapply(trajbear[[1]]$dist, substr(trajbear[[1]]$date,
  12, 16), mean, na.rm = T), pch = 21, bg = "white")
```



This structure corresponds to a circadian activity with two peaks. Detrending would then be performed on this data. A spatial weighting object is created to represent the temporal structure of the data:

```
library(spdep)
```

```
deldir 0.0-10
```

Please note: The process for determining duplicated points has changed from that used in version 0.0-9.

```
lw1 <- nb2listw(cell2nb(48 * 7, 1))
```

Then, a detrending is performed on the data. Residuals (i.e. detrended data) are stored in `trajresid` and predictions (i.e. structure corresponding to the circadian activity) are stored in `trajpred`:

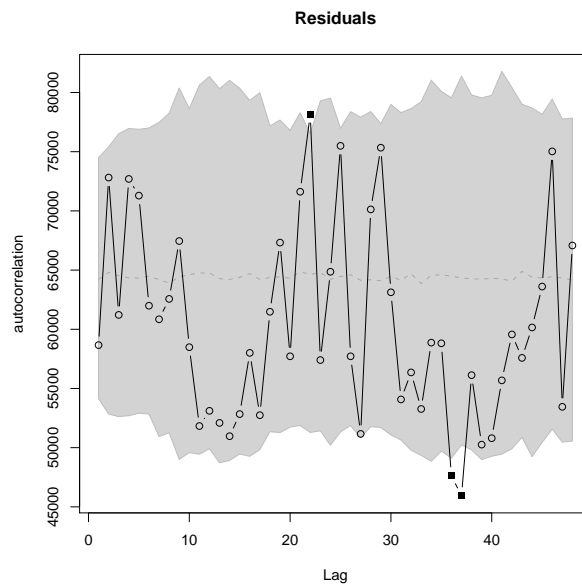
```
trajresid <- trajpred <- trajbear
y <- trajbear[[1]]$dist
y[is.na(y)] = mean(na.omit(y))
MEtest <- ME(y ~ 1, listw = lw1, nsim = 999, alpha = 0.05)
```

```
eV[,29], I: 0.2737 ZI: NA, pr(ZI): 0.001
eV[,6], I: 0.2481 ZI: NA, pr(ZI): 0.001
eV[,28], I: 0.2270 ZI: NA, pr(ZI): 0.001
eV[,31], I: 0.2063 ZI: NA, pr(ZI): 0.001
eV[,1], I: 0.1862 ZI: NA, pr(ZI): 0.002
eV[,62], I: 0.1653 ZI: NA, pr(ZI): 0.002
eV[,34], I: 0.1432 ZI: NA, pr(ZI): 0.003
eV[,7], I: 0.1224 ZI: NA, pr(ZI): 0.02
eV[,2], I: 0.1017 ZI: NA, pr(ZI): 0.034
eV[,48], I: 0.089 ZI: NA, pr(ZI): 0.046
eV[,27], I: 0.07595 ZI: NA, pr(ZI): 0.068
```

```
p <- ncol(MEtest$vector)
lm1 <- lm(trajbear[[1]]$dist ~ MEtest$vector[, 1:(p -
1)])
trajresid[[1]]$dist[!is.na(trajresid[[1]]$dist)] <- residuals(lm1)
trajpred[[1]]$dist[!is.na(trajpred[[1]]$dist)] <- predict(lm1)
```

Autocorrelation has been removed from the data. Residuals are then independent and can be used as response variable in subsequent analysis:

```
acfdist.ltraj(trajresid, lag = 48)
title(main = "Residuals")
```



The structure corresponding to the circadian activity has been completely identified by the detrending approach:

```
acfdist.ltraj(trajpred, lag = 48)
title(main = "Predictions")
```

