# A tutorial for Step Selection Function

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## Contents

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# 1 Introduction

In addition to Resources Selection Functions (RSF) another powerful tool for evaluating data on animal movements and habitat selection are Step Selection Functions (SSF). The latter are used to estimate resource selection by comparing observed habitat use with available structures. Given GPS locations of a collared individual each observation is connected by a linear segment. These segments are considered as steps. The time intervals influencing the step length should be choosen carefully (i.e. by conducting a pilot study) to meet the requirements of the study questions and the target species. The SSF than calculates random steps by taking measured angle and distance along steps and using the observed positions as starting points. These alternative steps represent the available habitat within a realistic step length of the observed positions. Finally, we can compare spatial attributes on both and test for effects that explain habitat selection by animals [1].

So far, SSF models were mainly done using Geospatial Modelling Environment (GME) that works with a GIS[1]. However, more and more packages for analyzing animal movements are provided in R. Non of these packages is designed for doing a SSF only but quite a number provide already helpful functions to perform single steps of the Selection Function. Therefore, the aim of this tutorial is to collect all functions necessary to conduct a SSF and order them in a way that intuitively makes you understand how to run a SSF with your own data. Each step will be explained using an exemplary dataset of GPS locations collected from seven Cougars (*Puma concolor*) in the year 2010 (in the following adressed as `xmpl`).

Figure 1 provides an overview of all necessary steps and potential options to conduct a SSF. This tutorial will guide you through each step and gives brief instructions on how to implement the functions and what to consider beforehand. To conduct a SSF using this tutorial we need you to store your initial data in two independant datasets:

1. A raster file of your spatial attributes (*Raster data*) and

2. GPS locations of your individuals assigned with a time stamp (*Waypoint data*).

We will start with the *Waypoint data* because these need to transformed a couple of times to be able to work with them. You can find the single steps on the right site of Figure 1. After loading the table into R you need to create an so-called `ltraj` object. This data class can now be further transformed by ... Random steps should only be calculated for equal time intervals. These can be defined by creating bursts. Each burst has an unique ID (often including an ID for the individual and the time stamp). While there are many options to adjust your *Waypoint data* the *Raster data* describing your spatial attributes needs not much of change. Once you created random steps for your observed positions you can extract the spatial attributes for each of those positions by using the function `extract`. At this point *Waypoint* and *Raster data* will be combined and your final model can be written.

DO WE NEED A EQUATION??

$$w(x) = exp(\beta 1x1 + \beta 2x2 + ... + \beta pxp)$$

Why did we not use the data (Wildboar) prepared for the adehabitatLT package? - No information on details, metadata provided, it is hard to understand when to use which dataset and why.

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[1]www.spatialecology.com/gme/

## 1.1 Preparations

Before you can actually start using the tutorial for conducting SSF you need to load a bunch of packages in R. Some of them require others so that you have to add all these to your library:

## 1.2 Packages - what we need

```
> # installing packages -----------------------------------------------------
> ## for implementing SSF
> # install.packages("adehabitat") # outdated version, not needed for this tutorial
> install.packages("adehabitatHR")
> install.packages("adehabitatHS")
> install.packages("adehabitatLT")
> install.packages("adehabitatMA")
> install.packages("tkrplot")
> install.packages("hab", repos = "http://ase-research.org/R/") # regular
> install.packages("hab", repos = "http://ase-research.org/R/", type = "source") # for
> # for handling ratser data
> install.packages("move")
> install.packages("raster")
> install.packages("rgdal")
> #install.packages("")
>
> # loading the packages
> # require(adehabitat) # keep fingers off this package. It is outdated.
> require(hab)
> require(adehabitatMA)
> require(adehabitatHR)
> require(adehabitatHS)
> require(adehabitatLT)
>
>
> ## for i dont know
>
> #require(move)
> #require(raster)
> #require(rgdal)
> #require(tkrplot)
> #require(raster)
> #require(sp)
>
```

# 2 All right site steps

## 2.1 Load telemetry data (*.csv, ESRI)

The data for the analysis should be safed in a simple *.csv format. Depending on your analysis you have to include

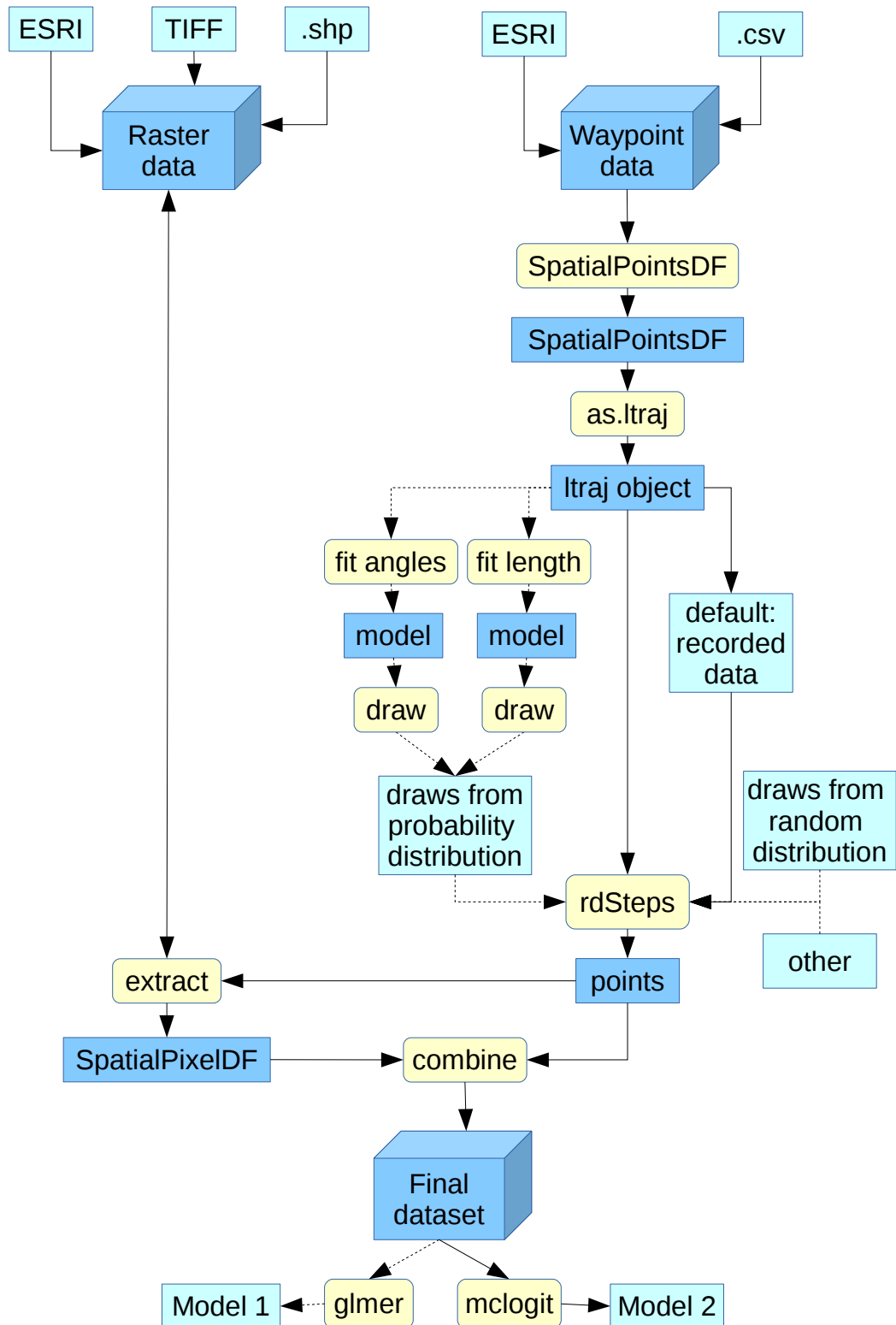1. coordinates

2. ID

3. date and/or time

Figure 1: Conducting a Step Selection Function using existing R-packages. The yellow boxes show the name of the fucntion applied while the blue boxes provide the type of object or data. Following the arrows a step by step instruction is provided ...

4. ...

## 2.2　Create a Spatial Points Data Frame

## 2.3　Create a ltraj object

## 2.4　Compute random steps

The function **rdSteps** removes the first and the last data point. That's what you want.

# 3　Spatial covariates

This section explains the use of spatial parameters that will be tested for selection by the target species. You should store these data in raster files (probably ESRI (*.adf) or *.tif) and for time reasons already clipped to your area. How you can do this in R please read the GIS instructions from the other group ;)

## 3.1　Load raster data (ESRI, *.tif, (*.shp))

With a simple function stored in the package **raster** you are able to upload any ratser file into R. Examplarily we are using the ratser data for ruggedness and canopy cover for the study area.

```
> #install.packages("RArcInfo")
> #require(RArcInfo)
> require(raster)
> require(rgdal)
> require(sp)
> #?raster
> #getwd()
> #setwd("/home/Peter/")
>
> ruggedness <- raster("/home/Peter/Dokumente/uni/WS_14_15/Best Practice R/Dataset/NEW
> # plot(ruggedness) # outcomment this if you just quickly want to run the script. Take
>
> landcover <- raster("/home/Peter/Dokumente/uni/WS_14_15/Best Practice R/Dataset/NEW (
> # plot(landcover) # outcomment this if you just quickly want to run the script. Takes
>
> canopycover <- raster("/home/Peter/Dokumente/uni/WS_14_15/Best Practice R/Dataset/NEW
> # plot(canopycover) # outcomment this if you just quickly want to run the script. Tak
>
> disthighway <- raster("/home/Peter/Dokumente/uni/WS_14_15/Best Practice R/Dataset/NEW
> # plot(disthighway) # outcomment this if you just quickly want to run the script. Tak
>
> distroad <- raster("/home/Peter/Dokumente/uni/WS_14_15/Best Practice R/Dataset/NEW GI
> plot(distroad) # outcomment this if you just quickly want to run the script. Takes a
>
```

## 3.2　Extract coordinates for comparison of used and random points

Peter is successfully doing this step!!

# 4 Final SSF model

Using the function `cs.` we get comparable values for each predictor. The according equation is:

$$f(x) = (x - \mathtt{mean})/\mathtt{sd}(x)$$

# 5 Acknowledgements

Don't forget to thank TeX and R and other opensource communities if you use their products! The correct way to cite R is shown when typing "`citation()`", and "`citation("mgcv")`" for packages.

# References

[1] Henrik Thurfjell, Simone Ciuti, and Mark S Boyce. Applications of step-selection functions in ecology and conservation. *Movement Ecology*, 2(1):4, 2014.