Report for Short Term Scientific Mission (STSM):

A biologically-informed algorithmic framework for the analysis of animal movement

Guest:	**Host:**
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University of Zurich	Technical University of Eindhoven
Switzerland	the Netherlands

Aim of visit

The main purpose of this STSM was to further develop our algorithmic framework for the analysis of (simultaneous) animal movement data, and to coordinate the process of making it freely available to the end-user community as a "package" in the programming language R, later this year. In particular, we aimed to explore the possibility of explicitly incorporating temporal heterogeneity of movement into the pre-existing algorithm. Moreover, we set out to define the scope, content and time-line of two forthcoming publications, and wanted to identify suitable funding schemes to prolong our collaboration beyond the current COST action.

Summary of main results

Significant progress was made on three distinct fronts:
- Algorithm development, refinement and implementation
    - Design and implementation in R of a Brownian Bridge derived speed algorithm proved a challenge, but in the end succeeded.
    - Several fine-tuning tweaks in function calls to enhance end-user friendliness
    - A new MSc-project at the host institute was initiated on trajectory segmentation, a prerequisite for a "dynamic" Brownian Bridge movement model that allows for heterogeneity in movement within the course of a single trajectory (more truthfully reflecting animal movement)
- Publication plan
    - Meeting with a co-author on forthcoming paper (Dr Emiel van Loon) resulting in a subtle, yet important, reformulation of the main aim of the manuscript. Target is to submit the manuscript by the end of May.
    - Extensive discussion on the focus of a second paper in which the R-package will be presented to the movement ecology community: the aim will be a high impact ecological journal (e.g. Ecology) and writing commences once package with its current functionality is finalised (target: end of April/beginning of May)
- Future plans and funding
    - Continued collection of movement data on primates in South Africa by two MSc-students and 1 PhD-student at the institute of guest. Funding for data-collection has been secured for an additional 15 months.
    - Collaboration with Max Planck Institute in Radolfzell (MOVEBANK) was discussed and has already been consolidated by a working visit (21 – 22 March)
    - Suitable funding opportunities for guest and host to formalise their collaboration appear rare, but both remain enthusiastic and committed.

Brief elaboration on upcoming publication

In the first forthcoming paper (an invited contribution to the newly erected journal "Movement Ecology"), we demonstrate two related but crucially different ways in which our Brownian Bridge Movement Model (BBMM) can be fused with the movement ecology paradigm as proposed by Nathan et al. 2008.

We distinguish between an *a priori* approach (exemplified by a dataset on migrating European bee-eaters from one of our collaborators), in which environmental information is used to calculate a crucial parameter of the BBMM (the diffusion coefficient), and an *a posteriori* approach, in which the outcome of a "contextually naïve" BBMM is related to local environmental conditions (exemplified by a dataset on home range use by a group of vervet monkeys from the guest of this STSM). Moreover, for both approaches we illustrate the extended usefulness of our framework by not simply considering the respective utilisation distributions (*i.e.* the primary building block of any probabilistic movement model) but rather a derived movement parameter, speed. Below, I briefly expand on the second approach using data from free-ranging vervet monkeys.

In this example, data stem from a single group of wild monkeys, ranging freely in a South African wooded savannah landscape. As typical for wildlife biology, telemetric data were obtained from a GPS logger, deployed on 1 individual within the group (see Figure 1).
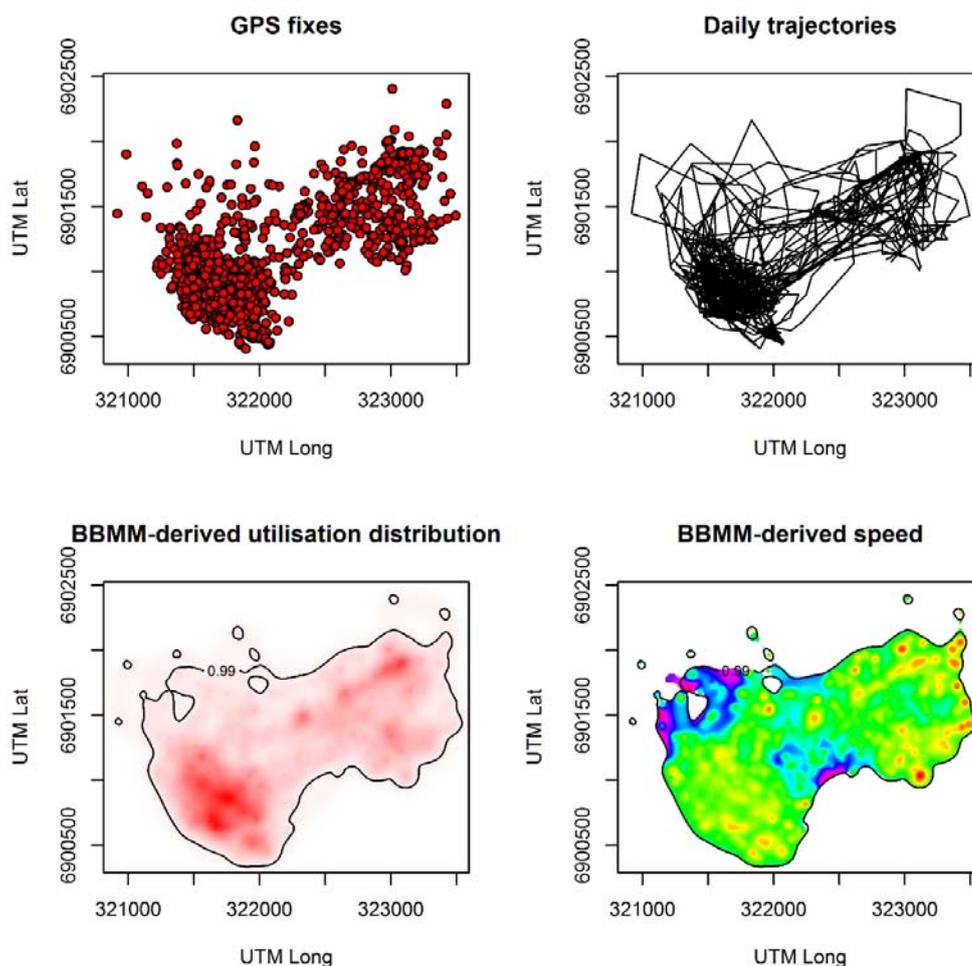

Figure 1 Schematic representation of how our movement model, which takes GPS fixes as its primary input, first reconstructs daily trajectories, subsequently calculates a probability density distribution function of location (*i.e.* the utilisation distribution), which in turn (and uniquely to our movement model) can be used to obtain a probabilistic estimate of movement speed (purple equals high, red low speed). The black outline in the bottom two figures demarcates the 99% volume isopleth, which in biology is more commonly referred to as the home range area.

In a previous paper (Buchin et al. 2012), we already mentioned the theoretical possibility inherent to our algorithmic framework to calculate derived movement parameters from these GPs coordinates, and in this paper we give a first implementation of this. To investigate how our speed estimates relate to the natural environment in which the animals are moving, we hypothesised that the monkeys travelled faster in the more open, less densely vegetated areas of their home range (due to greater exposure to predators and lower food availability), and slower in those areas of their home range in which the vegetation is more lush (more safety and food). We set out to investigate this hypothesis by relating our speed estimate to local vegetation density, which was proxied by a high resolution multi-spectral satellite image, from which the Normalised Difference Vegetation Index (NDVI) was calculated (Figure 2). High NDVI values correspond to high vegetation density, whereas low areas reflect sparse vegetation.
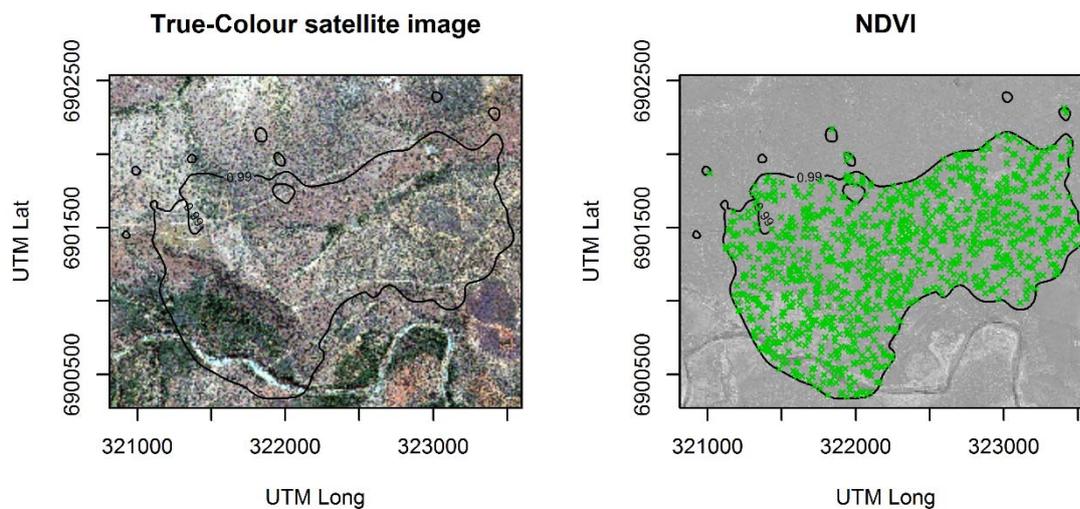

Figure 2 *High resolution (50 x 50 cm) multispectral satellite image of study area and the derived NDVI values (light shades correspond to high, dark shades to low vegetation density). Green crosses in right-hand figure indicate the locations of 1000 random sample locations.*

We firstly generated 1000 random sample locations throughout the home range of the animals and extracted both local NDVI and speed estimate values. Since data exhibited significant levels of spatial autocorrelation, statistical significance of a potential association between local vegetation density and speed of movement was assessed using geographically effective degrees of freedom (Dutilleul 1993). We found a significant negative correlation between NDVI and BBMM speed ($r_{Pearson}$= -0.155, $F_{(1, 228.81)}$, p< 0.05), in line with expectations and highly suggestive of the biological validity of our algorithmic framework.

Together with findings on the migrating bee-eaters, we feel that this paper provides a very convincing case for our BBMM algorithm, and as such that it will provide an ideal jumping board to our second intended paper, in which the release of our software package will be announced to the broader ecological community.