Microsaccade Toolbox 0.9

Authors: Ralf Engbert, Petra Sinn, Konstantin Mergenthaler, Hans Trukenbrod
Affiliation: Universität Potsdam, Germany
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Description

The Microsaccade Toolbox is a collection of functions to analyze fixational eye movements based on data recorded via high-resolution (>200 Hz) eye-tracking. The topics implemented in the current version 0.9 are detection of microsaccades, statistical analysis using surrogate data, and random-walk analysis of fixational eye movements. Microsaccade detection (Fig. 1) is based on an algorithm that implements a velocity threshold to identify (micro)saccades in eye-tracking traces [1–3]. Statistical tests of microsaccade detection can be performed against phase-randomized surrogate data [4] to evaluate the reliability of the detection threshold and data quality (Fig. 2). For more general statistical properties of fixational eye movements, random-walk [5, 6] and box-count [2] analyses are implemented to investigate the interaction between slow fixational eye movements (drift) with microsaccades (Fig. 3).

Usage

Input data must be provided containing horizontal and vertical components (vector-valued) of eye position `x`. The `demo` file contains an implementation of all functions of the toolbox for a small dataset.

Microsaccade detection

- `smoothdata(x)` – Preprocessing of raw data by applying a five-point running average.
- `vecvel(x, SAMPLING)` – Computation of two-dimensional (2D) velocity from eye-position data. The constant `SAMPLING` is the sampling rate (typically 250, 500, 1000 Hz).
- `microsacc(x, VFAC, MINDUR, SAMPLING)` – Estimation of monocular epochs containing candidate sequences for microsaccades using the basic algorithm. The velocity threshold is computed from `median(x)*VFAC`. The 2D velocity must pass a corresponding threshold for a minimum duration of `MINDUR` data samples.
- `binsac(microsacc_Right, microsacc_Left)` – Identification of binocular microsaccades from a temporal overlap criterion of the monocular candidate sequences in right and left eyes by function `microsacc()`.
- `sacpar(binsacs)` – Calculation of characteristic parameters for binocular microsaccades.

Default parameters for a 500 Hz eye-tracking device are `VFAC=5`, `MINDUR=3` (3 samples or 6 ms), and `SAMPLING = 500` (Hz).

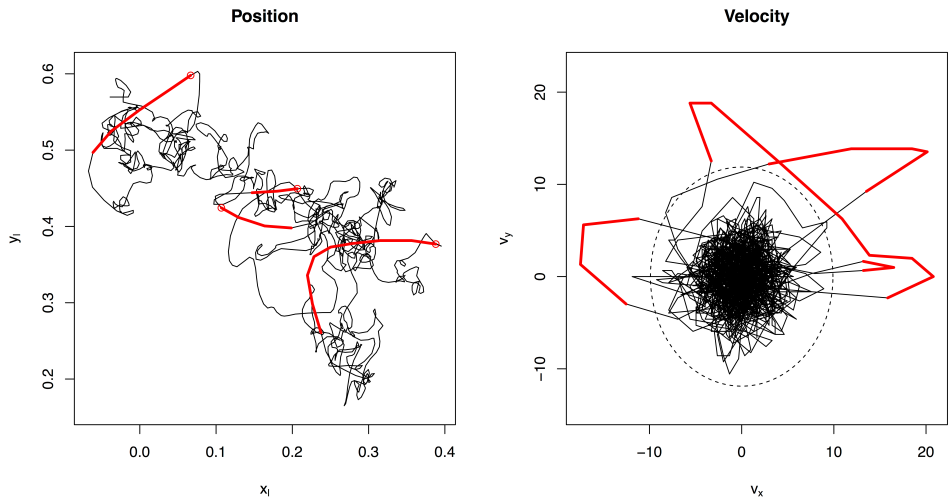

Figure 1. Trajectory and velocity of fixational eye movements. Microsaccades are marked by red color; the 2D threshold is indicated by the dotted ellipse.

Surrogate analysis for microsaccade detection

- `surrogate(x, SAMPLING)` – Main function for the generation of surrogate time series based on the following functions.
- `aaft(x)` – Amplitude-adjusted Fourier transformation (Algorithm II, Ref. [4], p. 183).
- `ftpr(x)` – Phase-randomization algorithm (Algorithm I, Ref. [4], p. 183) based on fast Fourier and inverse fast Fourier transforms.
- `fftsh(x)` – Discrete (fast) Fourier transform with zero frequency shifted to center (for R language)
- `ifftsh(x)` – Inverse discrete (fast) Fourier transform.

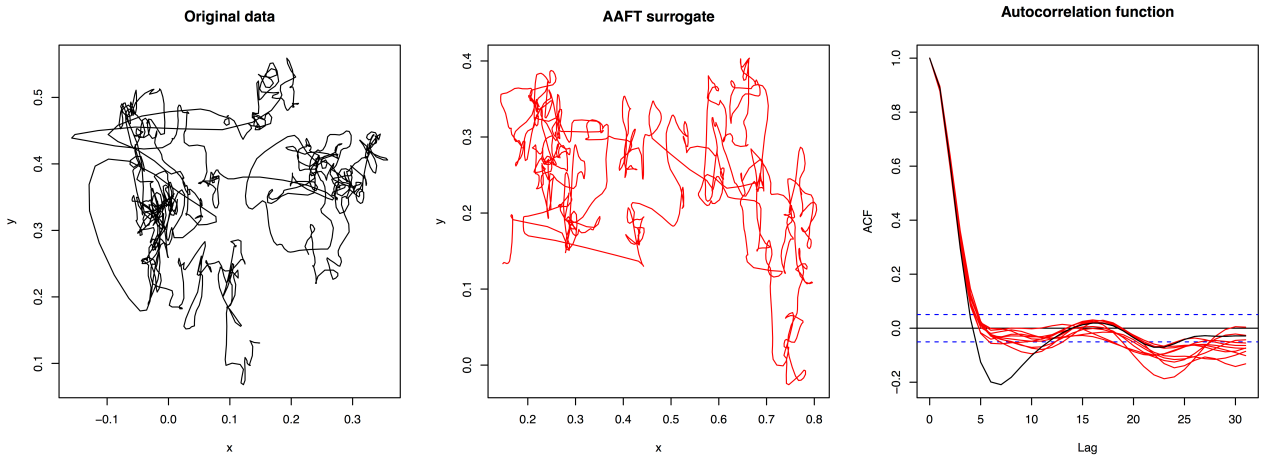

Figure 2. Trajectory of original data *(left)* and AAFT surrogate data *(center)*. The autocorrelation function *(right)* is plotted for original data (black) and ten realizations of surrogates (red).

Random-walk and box-count analyses

- `lagdist(x)` – Computation of lagged squared-distance estimator [5, 6].
- `acorr(x)` – Calculation of the autocorrelation function (for MATLAB).
- `boxcount(x, dx)` – Estimation of the number of boxes with linear dimesion `dx` that are needed to cover all samples of the trajectory `x`.

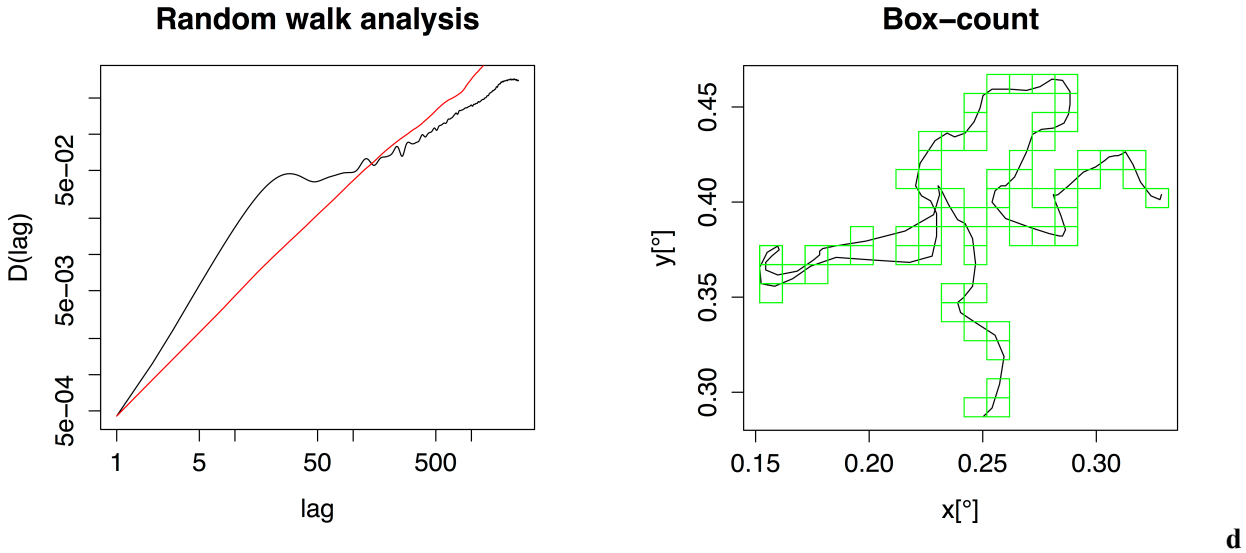

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Figure 3. Random-walk analysis *(left)* and estimation of box-count *(right)* for a sample trajectory.

Availability

The Microsaccade Toolbox is available for *The R Project for Statistical Computing* (www.r-project.org) and for MATLAB (www.mathworks.com) and can be downloaded from Potsdam Mind Research Repository (PMR^2; http://read.psych.uni-potsdam.de)

References

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