CHAOS 19, 015108 (2009)

Hypothesis test for synchronization: Twin surrogates revisited

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(Received 15 December 2008; accepted 29 December 2008; published online 31 March 2009)

The method of twin surrogates has been introduced to test for phase synchronization of complex systems in the case of passive experiments. In this paper we derive new analytical expressions for the number of twins depending on the size of the neighborhood, as well as on the length of the trajectory. This allows us to determine the optimal parameters for the generation of twin surrogates. Furthermore, we determine the quality of the twin surrogates with respect to several linear and nonlinear statistics depending on the parameters of the method. In the second part of the paper we perform a hypothesis test for phase synchronization in the case of experimental data from fixational eye movements. These miniature eye movements have been shown to play a central role in neural information processing underlying the perception of static visual scenes. The high number of data sets (21 subjects and 30 trials per person) allows us to compare the generated twin surrogates with the "natural" surrogates that correspond to the different trials. We show that the generated twin surrogates reproduce very well all linear and nonlinear characteristics of the underlying experimental system. The synchronization analysis of fixational eye movements by means of twin surrogates reveals that the synchronization between the left and right eye is significant, indicating that either the centers in the brain stem generating fixational eye movements are closely linked, or, alternatively that there is only one center controlling both eyes. © *2009 American Institute of Physics*. [DOI: 10.1063/1.3072784]

In a typical laboratory experiment, in which phase synchronization of two systems is studied, the coupling strength between both systems is systematically increased, until both systems adapt their rhythms, and hence, become phase synchronized. In the case of passive experiments, it is not possible to systematically vary the coupling strength. This is the case in many natural systems, such as, the synchronization among the electrical activity of different brain areas. There, we have only access to one single value of the coupling strength. Computing the phase synchronization index in these cases is not enough to assess the statistical significance of the result. The method of twin surrogates has been proposed to overcome this problem, allowing the performance of a hypothesis test that assess the significance of the result. In this paper, we revisit the method of twin surrogates and derive new analytical expressions for the number of twins depending on the size of the recurrence neighborhood and the number of points of the trajectory. These results allow us to determine the optimal parameters for the generation of twin surrogates, which is a very relevant problem in the case of experimental data. Moreover, we validate the method of twin surrogates comparing the generated surrogates to "natural" surrogates in an experimental system consisting of fixational eye movements, and show that the phase synchronization of the left and right fixational eye movements is statistically significant.

I. INTRODUCTION

Synchronization of complex systems has been intensively studied in the last decade. This nonlinear phenomenon has been found in numerous technical and natural systems.[1] Recently, the conditions for synchronizability in complex networks has become a main focus of research.[1] In spite of the large number of papers about this topic, the problem of synchronization analysis of experimental data in passive experiments remains an open problem. Passive experiments are those in which it is practically impossible to systematically change the main parameters responsible for synchronization: the coupling strength or the frequencies of the two or more interacting systems. This is the case in many natural systems, such as, in geophysical and neurophysical ones. For example, synchronization is often analyzed between the electrical activity from different brain areas. In such cases, we obtain just one value for the synchronization index, and then, it is difficult to statistically judge whether the result is significant or not. In one of the standard textbooks for synchronization,[1] the authors state: "The general problem is, what kind of information can be obtained from a passive experiment. In particular, a natural question appears, whether one can detect synchronization by analyzing bivariate data.

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Generally, the answer to the formulated question is negative."

In Ref. 2 the authors encountered the same problem when analyzing phase synchronization (PS) between the heartbeats of pregnant women and their fetuses. To assess the significance of their results, they computed the synchronization index between a mother and the fetus of another pregnant surrogate woman. By means of this analysis, they obtained statistically significant results. However, the different women were shown to have rather different distributions of times between consecutive heartbeats, and therefore, it was not clear whether the synchronization results were significant just due to the physiological differences between the women.

In order to overcome this problem, we have recently proposed a mathematical algorithm to generate trajectories which correspond to the same underlying system but starting at different initial conditions.[3] This method, called twin surrogates (TS), generates an independent copy of the whole system. If we now compute the synchronization index between one subsystem from the original, and the other subsystem from the surrogate system (just as in the case of the pregnant women), we are able to assess the significance of the results. By means of this algorithm we avoid the difficulties with different statistical properties in different subjects or nonstationarities in the case of comparison between different realizations of the same subject. Therefore, the method of twin surrogates allows testing for synchronization of complex systems even in the case of passive experiments, which is a prevalent problem in synchronization research.

In this paper, we first review the method of twin surrogates (Sec. II) and then thoroughly analyze the influence of the parameters of the method on the quality of the generated surrogates. We derive analytical expressions for the average number of twins in the underlying trajectory depending on the parameters of the method and compare the theoretical expressions with numerical simulations (Sec. III). Moreover, we compute several linear and nonlinear statistics for the surrogates and compare them with the ones obtained from trajectories starting at different initial conditions generated from the equations of the underlying system (Sec. IV). Having done all these computations, allows us to choose optimal parameters of the method to generate twin surrogates in the case of experimental data. Hence, we exemplify in Sec. V how to apply the method of twin surrogates to a passive experiment: phase synchronization of fixational eye movements. This experiment is very appropriate to validate the twin surrogate technique in the case of experimental data, because measurements from 21 subjects with 30 trials per person are available. Then, we can compare the generated twin surrogates to the different trials performed by the same subject. But first of all, we review the twin surrogates algorithm in the next section.

II. ALGORITHM FOR THE GENERATION OF TWIN SURROGATES

The algorithm to generate twin surrogates is based on the recurrence matrix

$$R_{i,j} = \Theta(\delta - \|\vec{x}(i) - \vec{x}(j)\|), \quad i,j = 1, \ldots, N, \tag{1}$$

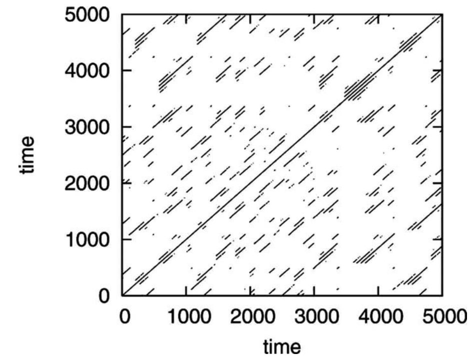

FIG. 1. Recurrence plot of a trajectory from the Lorenz system [Eq. (A2)].

where $\Theta(\cdot)$ denotes the Heaviside function, $\|\cdot\|$ a norm (e.g., Euclidean or maximum norm), and δ is a predefined threshold. $\vec{x}(i)$ denotes the vector of the trajectory of the system in phase space at time $t = i\Delta t$, with Δt being the sampling time of the trajectory and $i = 1, \ldots, N$. In the case that only a scalar time series has been observed, the trajectory of the system has to be reconstructed using some embedding technique, such as, the delay coordinates.[4,5] Coding the "1's" in the matrix as black dots and the "0's" as white ones, we obtain the recurrence plot (RP) of the trajectory. The method of RPs was introduced in Ref. 6 to visualize the trajectories of dynamical systems in phase space. This method and the related "Recurrence Quantification Analysis" have proven to be very useful for the analysis of data, as can be shown by the numerous publications in many different fields of research.[7] In Fig. 1 the RP of a trajectory of the Lorenz system in the chaotic regime [Eq. (A2)] is represented for illustration. Note that the RP consists mainly of diagonal lines of different lengths. A diagonal line indicates that the trajectory recurs to the neighborhood of a former visited point of phase space, and that the trajectory evolves similarly to the past during a certain time interval, which is given by the length of the diagonal line. Since the system is chaotic, after some time interval two segments of the trajectory starting at slightly different initial conditions diverge, and therefore, the diagonal lines in the RP are interrupted. There are different statistics based on the distribution of the diagonal lines in RPs, which are the basis for the RQA.

Furthermore, it has been shown that it is possible to estimate several invariants of the dynamics using the recurrence matrix,[8] and even the rank order of a univariate time series can be reconstructed from its recurrence matrix.[9,10] These facts suggest that the recurrence matrix contains the topological information about the underlying system.

Hence, a first idea for the generation of surrogates is to change the structures in a RP consistently with the ones produced by the underlying dynamical system and then reconstruct the trajectory from the modified RP. Furthermore, we use the fact that in a RP there are identical columns, i.e., $R_{k,i} = R_{k,j} \forall k$. This is because two different points of the trajectory can have exactly the same set of neighbors with respect to the threshold δ. Thus, there are points which are not only neighbors [i.e., $\|\vec{x}(i) - \vec{x}(j)\| < \delta$], but which also share the same neighborhood. These points are called *twins*. Twins are special points of the time series as they are dynamically indistinguishable considering their neighborhoods but in general different and hence, have different pasts and, more important, different futures. The key idea of how to introduce the randomness needed for the generation of surrogates of a deterministic system is that one can jump randomly to one of the possible futures of the twins. A surrogate trajectory $\vec{x}^s(i)$ of $\vec{x}(i)$ with $i=1,\ldots,N$ is then generated as follows:

1. Identify all pairs of twins, i.e., all pairs $\vec{x}(i)$ and $\vec{x}(j)$ such that $R_{i,k}=R_{j,k}$ for $k=1,\ldots,N$.
2. Choose an arbitrary starting point $\vec{x}(l)$ and set $\vec{x}^s(1)=\vec{x}(l)$.
3. Next, we generate the twin surrogate iteratively. The jth entry of the surrogate may be given by $\vec{x}^s(j)=\vec{x}(m)$. If $\vec{x}(m)$ has no twins, set $\vec{x}^s(j+1)=\vec{x}(m+1)$. If, on the other hand, $\vec{x}(n)$ is a twin of $\vec{x}(m)$, set $\vec{x}^s(j+1)=\vec{x}(m+1)$ or $\vec{x}^s(j+1)=\vec{x}(n+1)$ with equal probability.[28]

Step (3) is then iterated until the surrogate time series has the same length as the original one.

This algorithm creates twin surrogates (TS) which are shadowed[11] by (typical) trajectories of the system in the limit of an infinitely long original trajectory. Note that the TS are multivariate surrogates, i.e., if the original trajectory is d-dimensional, the TS are also d-dimensional. In Ref. 3 it has been shown that already for a trajectory of finite length, the *errors* or *jumps* $\|\vec{x}(i)-\vec{x}(j)\|$ introduced by the TS generation are rather small (i and j denote the time indices of two twins) and that longer time series lead to even smaller jumps.

Note that other existing algorithms for the generation of surrogates are not so appropriate to test for PS. For example, the linear surrogates based on randomization of the Fourier phases (e.g., the iterative amplitude adjusted Fourier transform surrogates) or wavelet based surrogates,[12] mimic the probability distribution, the individual spectra of both components of the original bivariate series as well as their cross-spectrum, i.e., their linear properties, but not the higher order moments. In this case, the corresponding null-hypothesis is that the putative synchronization in the underlying system can be explained by a bivariate linear stochastic process observed through a nonlinear measurement function. The statistical specificity—considered as a count of false positives[13]—of such a test is not always satisfactory, because the concept of PS assumes the mutual adaption of self-sustained oscillators, i.e., nonlinear deterministic systems. On the other hand, the algorithm for the generation of the pseudoperiodic surrogates[14] might appear to be rather similar to the one for the twin surrogates. However, the pseudoperiodic surrogates have been proposed to test the null hypothesis that an observed time series is consistent with an (uncorrelated) noise-driven periodic orbit. The pseudoperiodic surrogates are closer to the surrogates needed to test for PS than the iterative amplitude adjusted Fourier transform surrogates, since they correspond to a trajectory of a deterministic system with noise. Nevertheless, they are still not appropriate to test for PS, because they are not capable of mimicking chaotic oscillators. Moreover, surrogates based on a time shifting algorithm have also been studied,[15] but the problem of truncating the time series or alternatively joining different blocks is still unsolved in that case. For an exhaustive comparison between twin surrogates and other types of surrogates mentioned above, please see Ref. 3.

In the next two sections we investigate the properties and quality of the TS depending on the parameters of the algorithm. We consider prototypical systems of different kinds of dynamics (chaotic maps, chaotic continuous systems, and discrete stochastic systems), since the algorithm to generate twin surrogates is, in principle, applicable to all kinds of dynamics. This study will allow us to decide objectively how to choose the parameters of the method before applying it to experimental data. Note that even though the method of the twin surrogates enables us to test for PS in passive experiments, we can generate twin surrogates of all kinds of systems, i.e., also systems which do not fulfill the assumptions necessary to have PS (e.g., chaotic one-dimensional maps or linear systems). Hence, the technique of twin surrogates can be also used to test for other kinds of synchronization, such as, generalized synchronization or even to test the direction of the coupling.[16] In the last section we exemplify the use of twin surrogates for testing phase synchronization in a passive experiment of fixational eye movements.

III. NUMBER OF TWINS

Regarding the algorithm for the generation of TS, the natural following question arises: How does the number of twins of the trajectory depend on the threshold δ and on the number of points N of the time series?

In order to address this basic question, we first consider a univariate time series $\{x_i\}_{i=1}^N$ consisting of random numbers uniformly distributed in the unit interval, for the sake of simplicity. This time series allows us to concentrate on the topology without having to take the dynamics into consideration. Note that two points are called twins if their neighbors are exactly the same. Assume that x_i and x_j are twins and that they are separated by the distance r, i.e., $|x_i-x_j|=r$. As the twins share their neighborhood, the nonoverlapping segments of their δ-intervals are empty (Fig. 2). Therefore, to compute the probability that two points of the time series are twins, we have to consider the probability that the nonoverlapping regions (NOR) are empty, or equivalently, the probability that the distance between two nearest neighbors is at least r (note that the length of the nonoverlapping segments is equal to r). As the considered time series is uniformly distributed, this probability is given by

$$P(\text{NOR of size } r \text{ empty}) = e^{-\lambda r}, \tag{2}$$

where λ is the density of points in the unit interval, and hence, proportional to the number of data points N of the time series.[17] Now, to compute the average number of twins of the time series, we have to integrate P (NOR of size r empty) considering the distribution of the distances $\rho(r)$ of the time series. For a uniformly distributed time series in the unit interval, it is easy to see that the distribution of the distances is given by $\rho(r)=2-2r$. Moreover, the average number of twins of the time series is proportional to the total number of points N. Hence, the average number of twins $\langle N_{\text{twins}}\rangle$ of the time series can be estimated as follows:

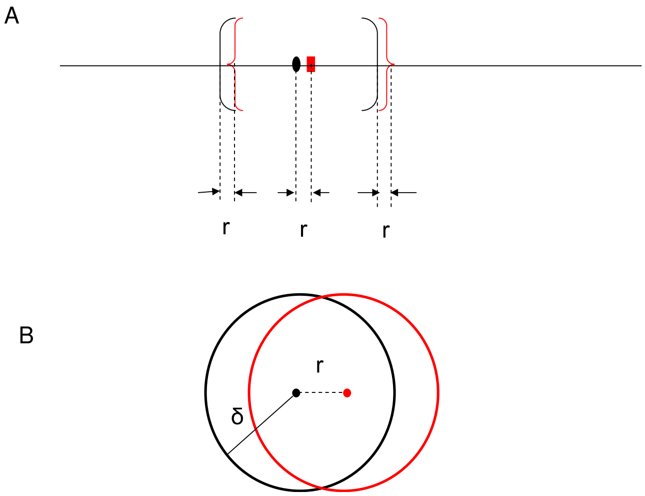

FIG. 2. (Color online) A: Two neighbors in the one-dimensional space with distance r. The nonoverlapping regions (NOR) have the length r. B: Two neighbors in the two-dimensional space with distance r. The nonoverlapping regions (NOR) depend on r and on the radius δ that defines the neighborhoods.

$$\langle N_{\text{twins}}\rangle \propto N\int_0^{\delta} e^{-\lambda r}(2-2r)dr$$

$$= \frac{2N}{\lambda^2}[e^{-\lambda\delta}(\lambda(\delta-1)+1)+\lambda-1]. \quad (3)$$

Note that we integrate between 0 and δ, because x_i and x_j must first be neighbors in order to be twins. Since λ is proportional to N,[17] we can plot our estimation of $\langle N_{\text{twins}}\rangle$ depending on δ and N [Figs. 3(a) and 3(b), respectively]. We see that the average number of twins depending on δ reaches very fast a maximum and then remains constant. On the other hand, the average number of twins depending on N is almost constant. These analytical findings reproduce the obtained numerical simulations for uniformly distributed random noise [Figs. 3(c) and 3(d)], but also for uniformly distributed one-dimensional chaotic maps, such as, the Bernoulli map [Figs. 3(e) and 3(f)] or the logistic map for $r=4$ (not shown here).

The two-dimensional case must be considered separately, since the above arguments do not hold exactly there. A heuristic derivation for the number of twins in this case is as follows: For the sake of simplicity, suppose again that we have a bivariate uniformly distributed time series $\{\vec{x}_i\}_{i=1}^N$ (note that it is not necessary to consider the dynamics, but just the distribution of the points of the time series). Two neighboring points $\vec{x}_i$ and $\vec{x}_j$ with distance r are twins if the nonoverlapping regions (NOR) are empty. Since we are now in the two-dimensional space, the area of NOR is not only dependent on r but also on the size δ of the neighborhood (see Fig. 2). If we use the Euclidean norm, the NOR in the two-dimensional case can be approximated by $\pi\delta r$. Note that in the two-dimensional case the probability that NOR is empty is not equivalent anymore to the probability that the distance between nearest neighbors is equal to r. Therefore, we can just estimate P (NOR empty) by assuming that it is inversely proportional to the area of NOR and to the density of points λ, and integrating over the distribution of distances $\rho(r)$. Furthermore, the average number of twins of the time series will be proportional to the probability that two points of the bi-

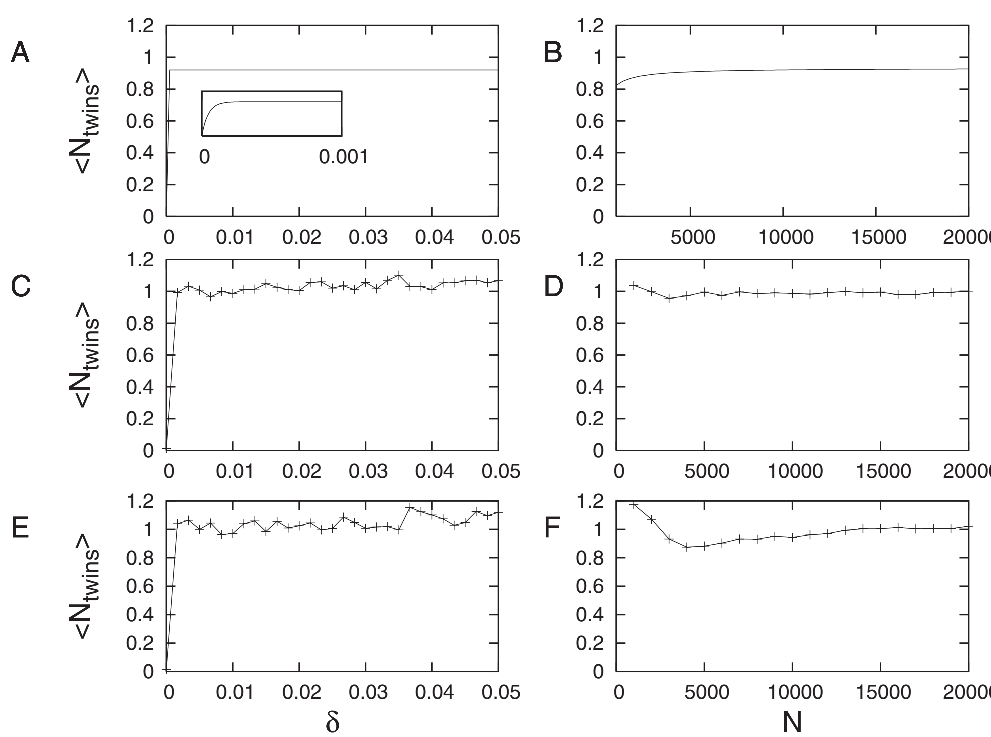

FIG. 3. Computation of the average number of twins depending on the threshold δ and the number of points N of the time series in the one-dimensional case: A, B [analytical, Eq. (3)], C, D (random uniformly distributed time series), and E, F (chaotic Bernoulli map). The inset in A presents a zoom to show that for $\delta=0$ the analytical expression for the average number of twins is equal to zero, in accordance with the numerical simulations.

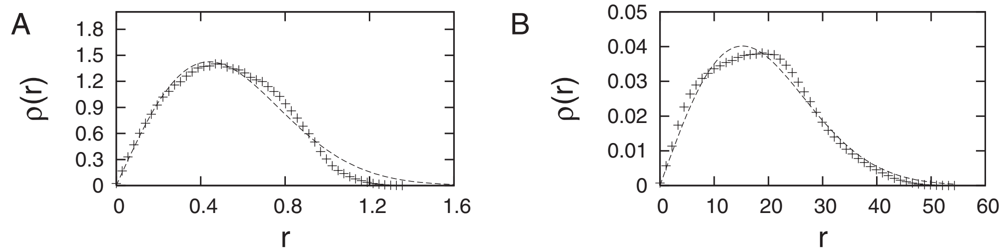

FIG. 4. A: Distribution of distances of the bivariate random uniformly distributed time series (points: numerical simulations; solid: curve fitted). B: Distribution of distances of the Lorenz system [Eq. (A2)] (points: numerical simulations; solid: curve fitted). The curve fitted in both cases has the form $\alpha x \exp(-\beta x^2)$.

variate time series are neighbors, and to the total number of points N of the time series

$$\langle N_{\text{twins}}\rangle \propto N \int_0^\delta \frac{1}{\lambda \pi \delta r}\rho(r)dr \int_0^\delta \rho(r)dr. \tag{4}$$

According to numerical simulations, the distribution of distances $\rho(r)$ seems to have the same form for many two and higher dimensional systems, such as, a bivariate random time series and the Lorenz system (Fig. 4). This form can be fitted by $\rho(r)=\alpha x \exp(-\beta x^2)$. Substituting this distribution in Eq. (4), we obtain

$$\langle N_{\text{twins}}\rangle \propto \frac{N}{\lambda}\frac{\alpha^2}{4\beta^{3/2}\pi^{1/2}}\frac{\text{erf}(\sqrt{\beta}\delta)(1-\exp(-\beta\delta^2))}{\delta}. \tag{5}$$

Next, we can represent the average number of twins $\langle N_{\text{twins}}\rangle$ depending on the threshold δ and the number of points N in the time series, considering that in the two-dimensional case, λ scales as N^2. The results from the analytical and numerical computations are shown in Fig. 5. Note that $\langle N_{\text{twins}}\rangle$ has a very well pronounced maximum for small values of δ. This behavior is rather different from the one-dimensional case. Furthermore, we see that the average number of twins decreases with the length of the time series. That means, that the longer the time series, the more improbable is that two points of the time series are twins. This is also very different from the one-dimensional, where the average number of twins does not depend on the number of points of the time series. However, note that for the two-dimensional case the average number of twins decreases fast for short lengths of the time series, but for longer time series, the average num-

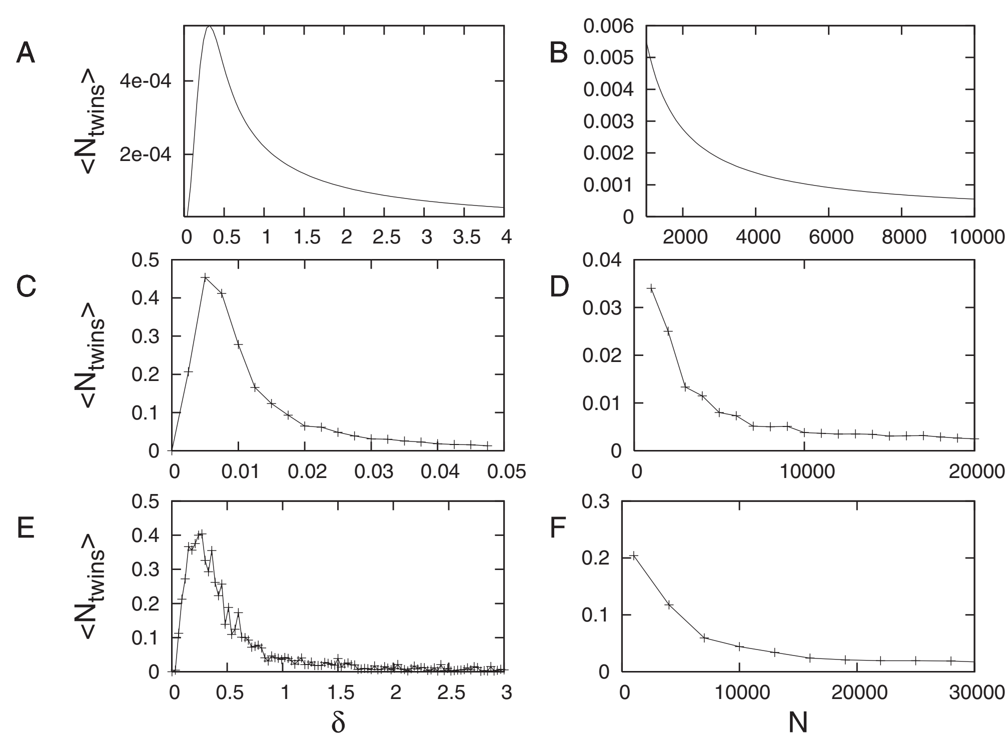

FIG. 5. Computation of the average number of twins depending on the threshold δ and the number of points N of the time series in the two-dimensional case: A, B [analytical estimation, Eq. (4)], C, D (bivariate random uniformly distributed time series), and E, F [chaotic Lorenz system, Eq. (A2)]. The length of the time series used for the left panels was N=10 000 (A, C, E) and the values for the thresholds were δ=0.3 (B), δ=0.1 (D) and δ=1.0 (F).

ber of twins decreases very slowly. Moreover, the analytical estimation reproduces rather well the numerical results for very different kinds of dynamics, such as, bivariate uniformly distributed noise [Figs. 5(c) and 5(d)] and the chaotic Lorenz system [Figs. 5(e) and 5(f)]. Numerical simulations show that for higher dimensional systems, the dependence of $\langle N_{\text{twins}} \rangle$ on δ and N is the qualitatively the same as for the two-dimensional case.

Next, we estimate the number of different twin surrogates that are possible to generate given a trajectory of length N and total number of twins N_{twins}. Suppose that the twins are distributed uniformly within the trajectory and that triplets do not occur (i.e., each point of the trajectory can have maximally one twin). Furthermore, we assume that we can jump also backwards and stop the algorithm when the length of the surrogate has reached N. Then, the number of possible twin surrogates scales as $2^{N_{\text{twins}}}$. Moreover, since it is possible to start the twin surrogate at each point of the original trajectory, the number of possible twin surrogates is also proportional to the length of the trajectory N. Hence, the total number of possible twin surrogates can be estimated as $N2^{N_{\text{twins}}}$. Therefore, even in the case that the total number of twins is rather low, the number of different twin surrogates that can be generated is extremely high. For example, in the Lorenz system with $\delta=3.0$ and $N=10\,000$ points, we have 14 twins [Fig. 5(e)], and therefore, we can generate 1.64×10^8 twin surrogates.

In the next section we compare in detail the twin surrogates to original trajectories of the underlying system with respect to different linear and nonlinear statistics and compute the errors made by the twin surrogates depending on the parameters of the method.

IV. COMPARISON OF TWIN SURROGATES WITH ORIGINAL TRAJECTORIES

As we have seen in Sec. II, the algorithm for the generation of twin surrogates depends mainly on the parameter δ, which defines the size of the neighborhood to which the trajectory recurs [Eq. (1)]. Therefore, it is crucial to know how the quality of the twin surrogates depends on this parameter. Furthermore, if only a scalar time series can be observed, the trajectory in phase space has to be reconstructed. Hence, an important question is also how the quality of the TS depends on the choice of the embedding parameters. Moreover, it is interesting to study the dependence on the used number of points of the trajectory.

In order to study these dependencies, we will compute M twin surrogates for prototypical models of dynamical systems on the one hand {the logistic map [Eq. (A1)], the Lorenz system [Eq. (A2)], and an autoregressive (AR) model of first order [Eq. (A3)]}, and on the other hand we will generate M further trajectories of the same system starting at different initial conditions (random uniformly distributed) but using the equations of these models. Then, we can quantify how closely twin surrogates mimic basic dynamical properties of the underlying system by computing several linear and nonlinear statistics for both the twin surrogates and the further trajectories, namely, autocorrelation function (ACF), mutual information (MI), mean diagonal line (MDL), and mean vertical line (MVL) from the respective recurrence plots (see the Appendix). We compute each of the statistics for each of the twin surrogates, and determine the mean value and standard deviation. We do the same for the other ”real” trajectories and calculate the error (see the Appendix). In the next subsections we present the errors obtained for each of the former statistics depending on the parameters of the algorithm for generating twin surrogates for the three prototypical examples mentioned above.

A. Dependence on δ

In Fig. 6 we show the comparison between the twin surrogates and the “real” trajectories depending on the threshold δ for the logistic map [Eq. (A1)]. Note that the difference in all statistics computed is very small for a broad interval of values of the threshold δ. Only for values of $\delta > 0.5$, the errors in some statistics (MI and MDL) increase significantly. Taking into consideration that for $\delta \geqslant 0.5$ the whole unit interval is covered by the ball, and then such values for the choice of δ are not reasonable any more, this result indicates that the twin surrogates method does not sensitively depend on the choice of the threshold δ. In Figs. 7 and 8 we present the results depending on δ for the Lorenz system [Eq. (A2)] and the AR model [Eq. (A3)]. As in the case of the logistic map, we find a broad interval of values of δ where the errors in the considered statistics are very small.

B. Dependence on embedding parameters

Dealing with experimental time series, usually only one observable of the system is available, i.e., we have only a scalar time series. Since the twin surrogates are computed from the recurrence matrix of one trajectory in phase space, the trajectory has to be reconstructed first in order to apply the algorithm. This can be done by, e.g., delay embedding.[4] Therefore, it is important to investigate how robust is the twin surrogates algorithm with respect to the choice of the embedding parameters m (embedding dimension) and τ (embedding delay).

In order to study this dependence, we compute the errors in the statistics ACF, MI, MDL, and MVL for different values of the embedding dimension m and delay embedding τ. We exemplify the results in the case of the Lorenz system [Eq. (A2)], using the z-component as observable. Note that the results using the x- or y-components are qualitatively the same. The length of the time series used is 10 000 and the time step between two points is 0.03. We see that for the embedding dimension $m=3$, the delay τ must be chosen larger than 4. For other choices of m, the error does not depend strongly on the value of τ. For $m=5$ and $m=6$ a value of $\tau>7$ seems to be more appropriate (Fig. 9). In general, the error remains rather small for all values of the embedding parameters. This is the reason why the curves in Fig. 9 for different values of m are difficult to distinguish. Hence, we can conclude that the performance of the twin surrogates does not depend strongly on the choice of the embedding parameters.

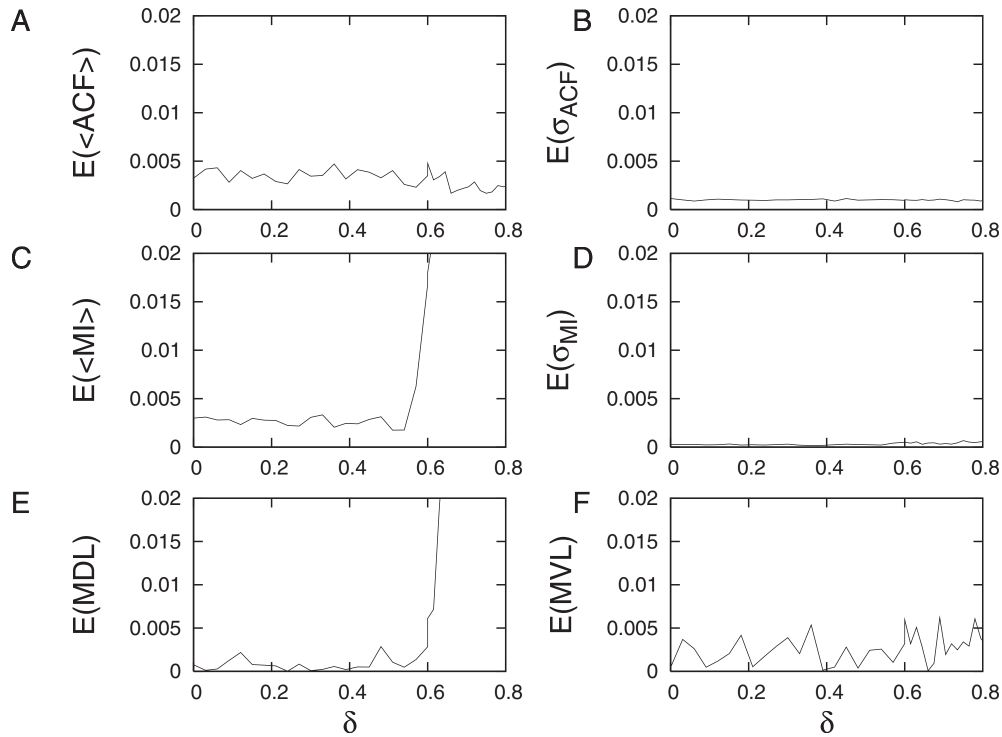

FIG. 6. Comparison between the twin surrogates and the "real" trajectories for several statistics for the logistic map [Eq. (A1)] depending on the threshold δ of the recurrence matrix. A: Mean value of the ACF. B: Standard deviation of the ACF. C: Mean value of the MI. D: Standard deviation of the MI. E: MDL, and F: MVL.

C. Dependence on the number of data points

Another important factor for the performance of the twin surrogates is the length N of the time series.

In order to investigate the effect of N on the quality of the twin surrogates, we again compute the errors in the statistics ACF, MI, MVL, and MDL depending on N. The results for the logistic map, the Lorenz system, and the AR model are represented in Figs. 10–12, respectively.

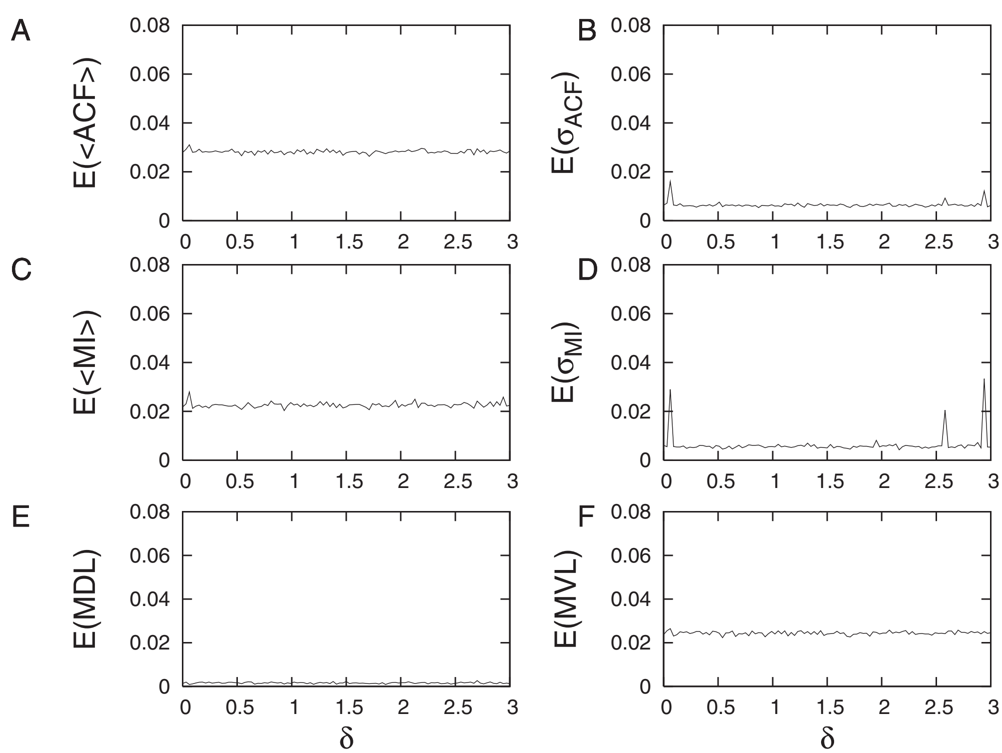

FIG. 7. Comparison between the twin surrogates and the "real" trajectories for several statistics for the Lorenz system [Eq. (A2)] depending on the threshold δ of the recurrence matrix. A: Mean value of the ACF. B: Standard deviation of the ACF. C: Mean value of the MI. D: Standard deviation of the MI. E: MDL, and F: MVL.

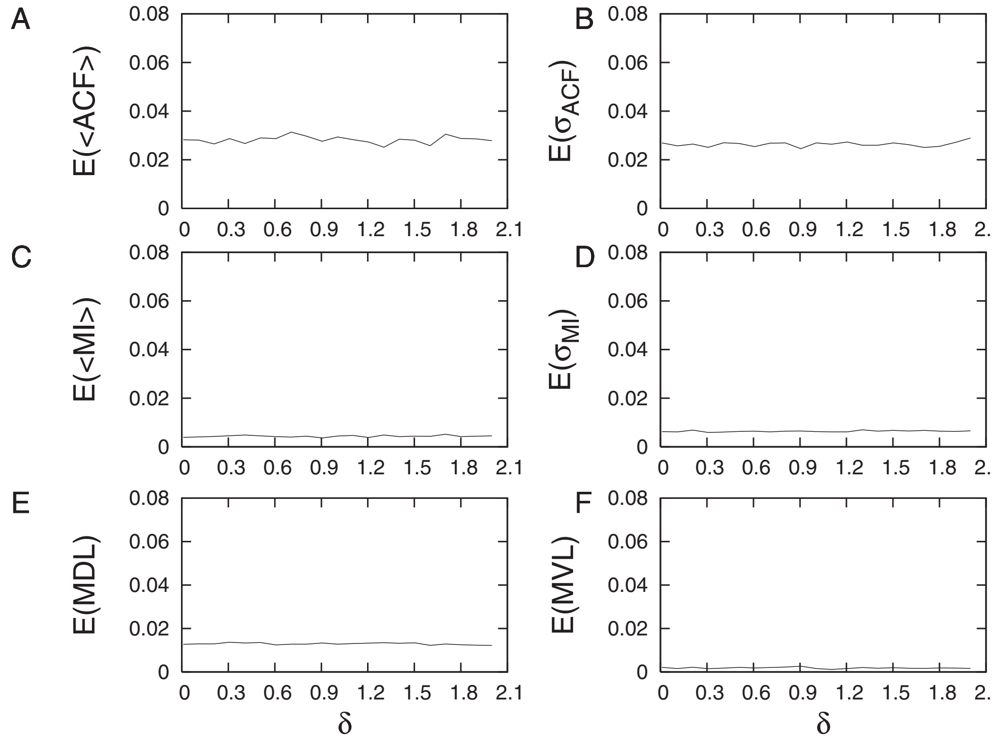

FIG. 8. Comparison between the twin surrogates and the "real" trajectories for several statistics for the AR-model [Eq. (A3)] depending on the threshold δ of the recurrence matrix. A: Mean value of the ACF. B: Standard deviation of the ACF. C: Mean value of the MI. D: Standard deviation of the MI. E: MDL, and F: MVL.

In all three cases, especially in the logistic map and in the AR model, the general trend is that the errors in the statistics decrease with the length of the time series, as expected. Nevertheless, note that even for rather short data sets, the errors are acceptable. For example, in the case of the ACF the errors for time series of only 1000 data points are of the order of magnitude of 1%.

V. APPLICATION TO EXPERIMENTAL DATA FROM A PASSIVE EXPERIMENT: SYNCHRONIZATION OF FIXATIONAL EYE MOVEMENTS

In the last decade it has been shown that fixational eye movements are very relevant in information processing and visual perception of the world around us. In this section we apply the method of twin surrogates to data from eye-movement experiments. The aim is to investigate the relationship between miniature (or fixational) movements from the left and right eyes. During fixation of a stationary target our eyes perform small involuntary and allegedly erratic movements to counteract retinal adaptation. There are three categories of fixational eye movements: microsaccades, ocular drifts, and ocular microtremor.[18] If these eye movements are experimentally suppressed, retinal adaptation to the constant input induces very rapid perceptual fading.[19] Fixational eye movements can be described by random walks, with statistical correlations showing a time scale separation from persistence to antipersistence.[20] Persistence on the short time scale counteracts retinal fading, whereas antipersistence on the long time scale contributes to stability of ocular disparity. According to current textbook knowledge, the fixational movements of the left and right eye are correlated very poorly at best.[21] Therefore, it is highly desirable to examine these processes from a perspective of phase synchronization.[22] In Ref. 23 it has been shown for the data of only two different subjects, that phase synchronization between the fixational eye movements from the left and right eye is significant.

Here we analyze a larger data set, which consists of eye movements obtained from 21 subjects. Each performed 30 trials, in which they fixated a small stimulus (black square on a white background, 3×3 pixels on a computer display) with a spatial extent of 0.12°, or 7.2 arc min during approximately 20 s. Eye movements were recorded using an Eyelink-II (SR Research, Toronto, Canada) with a sampling rate of 500 Hz and an instrument spatial resolution $<0.01°$ visual angle. Trials in which the subjects closed their eyes (blinked) were discarded and repeated. The availability of data from so many trials and subjects in this experiment allows us to investigate two different aspects: (i) the performance of the twin surrogates applied to experimental data, i.e., how close are the twin surrogates to further real realizations from the same subject, and (ii) the systematic test of phase synchronization in fixational eye movements.

Figure 13(a) shows a typical segment of the horizontal component of the eye movements of the left (red) and right (blue) eye for one person. The data were first high-pass filtered applying a difference filter $\tilde{x}(t)=x(t)-x(t-\tau)$ with $\tau=40$ ms in order to eliminate the slow drift of the data. After this filtering, we find an oscillatory trajectory [Fig. 13(b)], which has maximum spectral power in the frequency range between 6 and 8 Hz.[23]

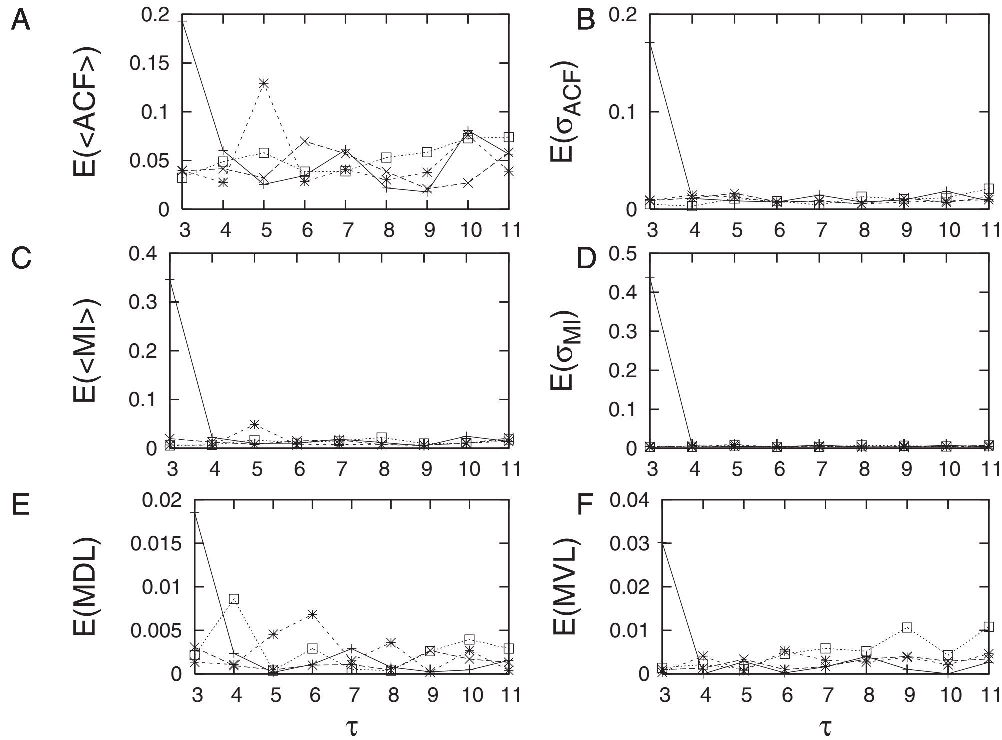

FIG. 9. Errors of the twin surrogates depending on the embedding delay τ for the Lorenz system. A: Mean value of the ACF. B: Standard deviation of the ACF. C: Mean value of the MI. D: Standard deviation of the MI. E: MDL, and F: MVL. The curves have been computed for the following values of the embedding dimension: $m=3$ (+ solid), $m=4$ (× long-dashed), $m=5$ (* short-dashed), and $m=6$ (□ dotted).

(i) To study the quality of the twin surrogates method applied to experimental data, we generate 30 twin surrogates from one trial from one fixed subject. Then, we compare the generated twin surrogates with the 30 measured trials from the same subject. The comparison is made with respect to the statistics ACF, MI, MVL, and MDL, analogously to Sec. IV. Since both horizontal and vertical components of the trajectories of the eye movements are available, no delay embedding has been applied. The results for one trial of one fixed subject are shown in Fig. 14. There, we have computed the

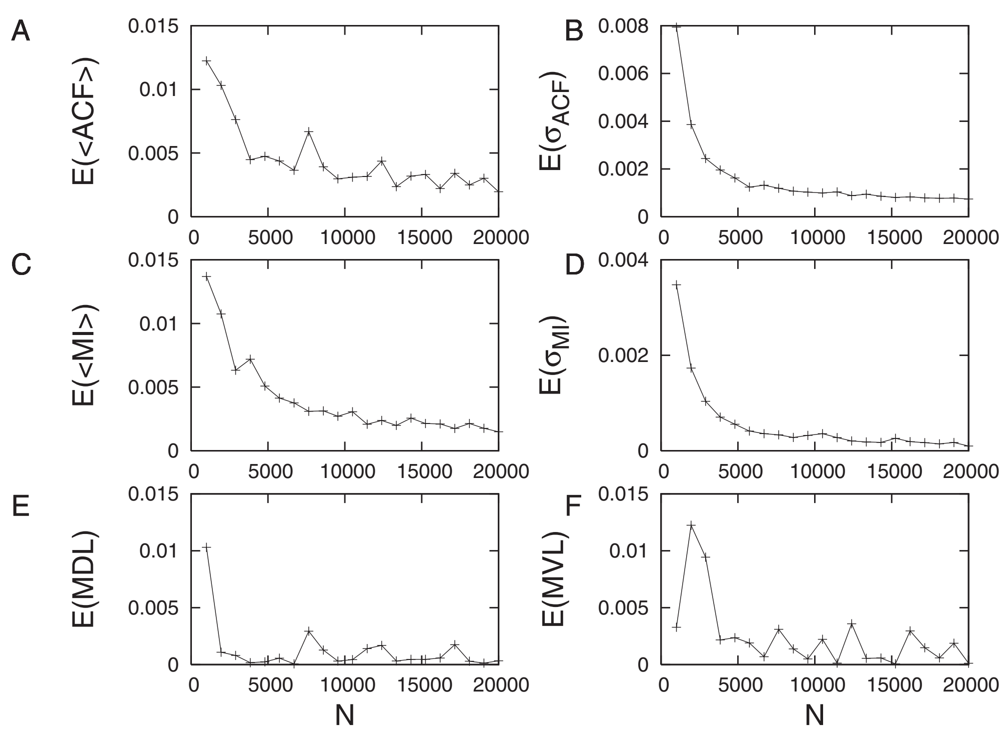

FIG. 10. Errors of the twin surrogates depending on the length N of the time series for the logistic map. A: Mean value of the ACF. B: Standard deviation of the ACF. C: Mean value of the MI. D: Standard deviation of the MI. E: MDL, and F: MVL.

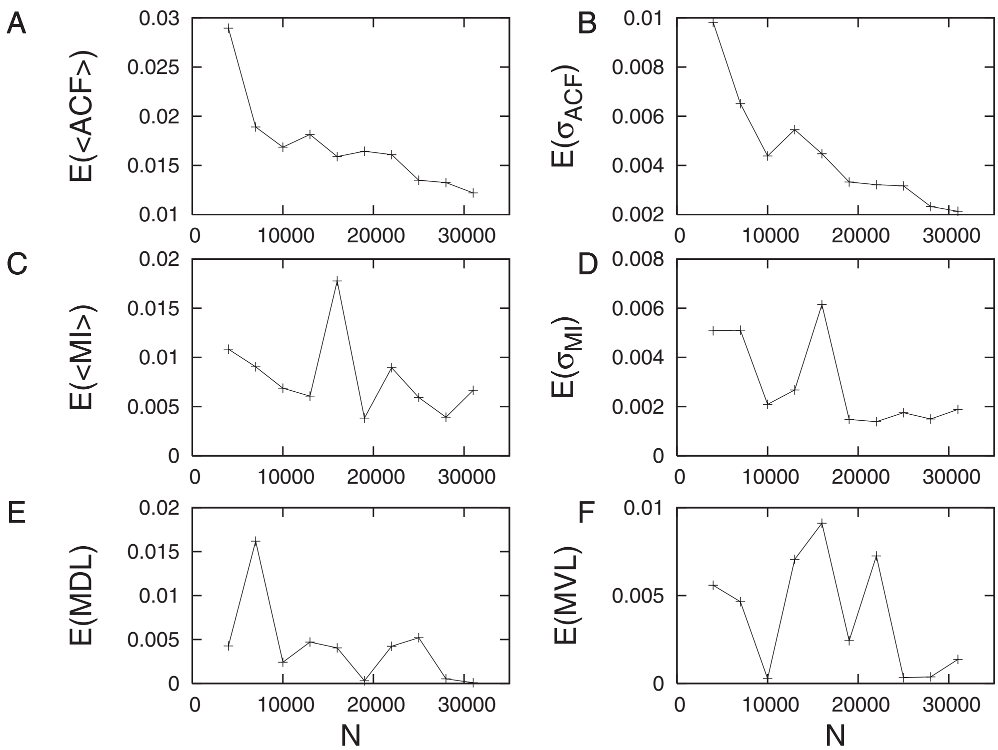

FIG. 11. Errors of the twin surrogates depending on the length N of the time series for the Lorenz system. A: Mean value of the ACF. B: Standard deviation of the ACF. C: Mean value of the MI. D: Standard deviation of the MI. E: MDL, and F: MVL.

errors in the statistics ACF, MI, MVL, and MDL depending on the threshold δ. For a rather broad range of values of δ covering up to 20% of the phase space, the errors in the statistics remain rather small. This indicates, that the twin surrogates perform very well also in the case of experimental data, and furthermore, that the performance of the twin surrogates is not sensitive to the choice of the threshold δ.

In Fig. 15, we show one twin surrogate generated from one trial of one subject with $\delta=0.02$ (A) in comparison with other measured trial from the same subject. The twin surrogate reproduces the structure of the real time series very well.

(ii) Knowing from the former study that the twin surrogates for the fixational eye movements perform well,[10] we test for phase synchronization between right and left fixational eye movements systematically generating 100 twin

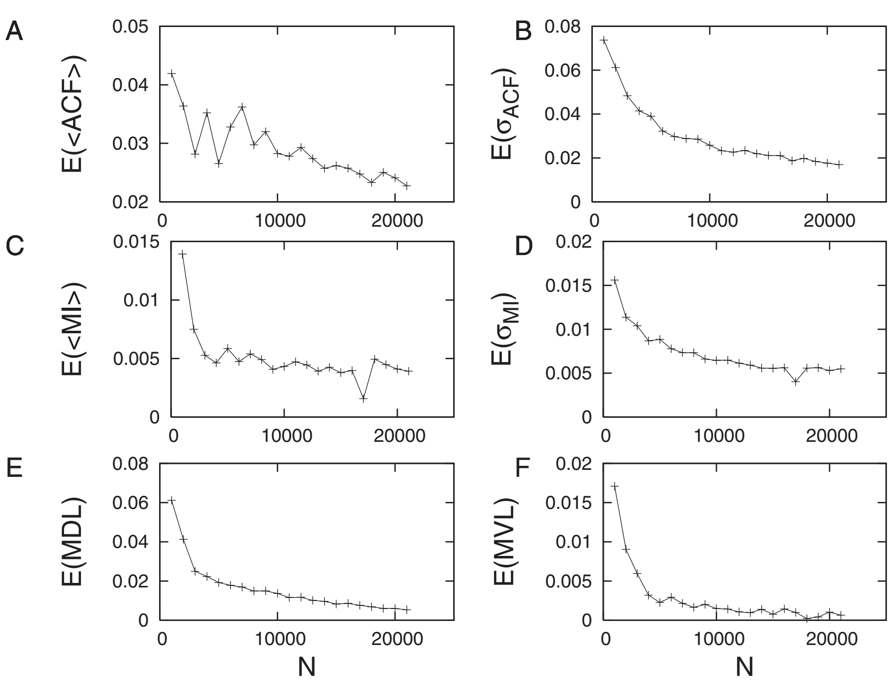

FIG. 12. Errors of the twin surrogates depending on the length N of the time series for the AR-model. A: Mean value of the ACF. B: Standard deviation of the ACF. C: Mean value of the MI. D: Standard deviation of the MI. E: MDL, and F: MVL.

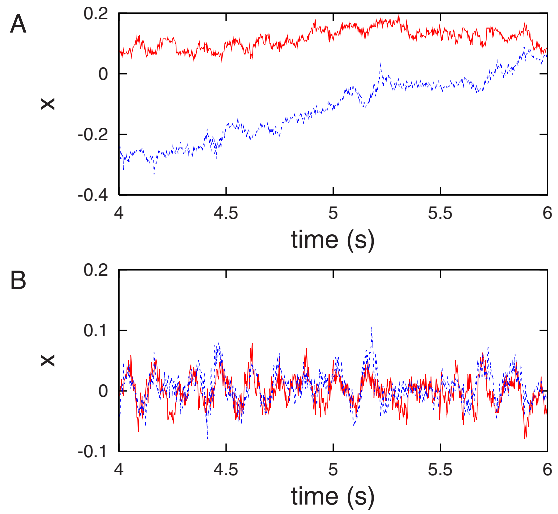

FIG. 13. (Color online) Simultaneous recording of left and right fixational eye movements. A) Horizontal component of the left (red, solid line) and right (blue, dashed line) eye. B) Detrended data.

surrogates for every trial of every subject with $\delta=0.02$.

Even though the filtered eye movements trajectories present an oscillatory behavior, the trajectories are rather noisy and nonphase coherent. Therefore, it is cumbersome to estimate the phase of these data. Hence we apply a measure of phase synchronization which is based on the probability of recurrence of a trajectory in phase space

$$P(\tau) = 1/N\sum_{i=1}^{N} R_{i,i+\tau}, \tag{6}$$

where $R_{i,i+\tau}$ is the recurrence matrix [Eq. (1)]. The correlation between the probabilities of recurrence of two interacting oscillators

$$\mathrm{CPR} = \langle \bar{P}_1(\tau)\bar{P}_2(\tau)\rangle/(\sigma_1\sigma_2) \tag{7}$$

[where $\bar{P}_{1,2}$ means that the mean value has been subtracted and σ_1 and σ_2 are the standard deviations of $P_1(\tau)$, respectively $P_2(\tau)$] has been proposed to detect PS in nonphase coherent and noisy oscillators, where the phase cannot be estimated directly.[24] Next, we compute 100 twin surrogates of the left and right eye's trajectory and compute the recurrence based synchronization index CPR^{s_i} between the left eye surrogates and the measured right eye's trajectory. In Fig. 16 the results of the test of one trial are visualized. The value obtained for CPR for the original data is well outside the distribution of values of CPR^{s_i} obtained for the twin surrogates, which indicates that the fixational right and left eye movements for these data are in PS.

The results for all trials and all subjects are summarized in Table I. In almost all cases (95%), the PS index of the original data is significantly different from the ones of the surrogates, which strongly indicates that the concept of PS can be successfully applied to study the interaction between the trajectories of the left and right eye during fixation. This result also suggests that the physiological mechanism in the brain stem that produces the fixational eye movements con-

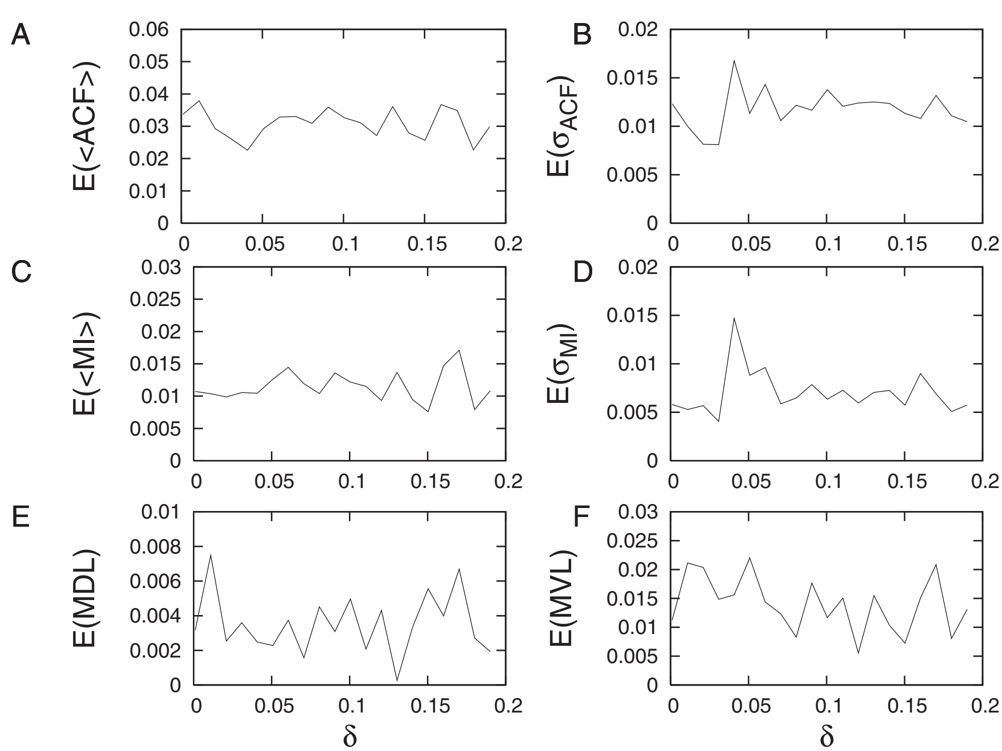

FIG. 14. Comparison between the twin surrogates and the "real" trajectories for several statistics for the fixational eye movements from one subject depending on the threshold δ of the recurrence matrix. A: Mean value of the ACF. B: Standard deviation of the ACF. C: Mean value of the MI. D: Standard deviation of the MI. E: MDL, and F: MVL.

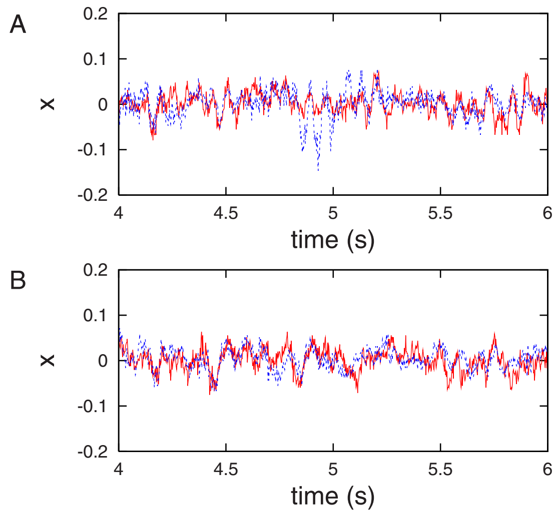

FIG. 15. (Color online) A) Twin surrogate of the left (red, solid line) and right (blue, dashed line) filtered fixational eye movements, horizontal component. B) Segment of another filtered trial of the same subject. The twin surrogates reproduce the structure of the measured time series very well.

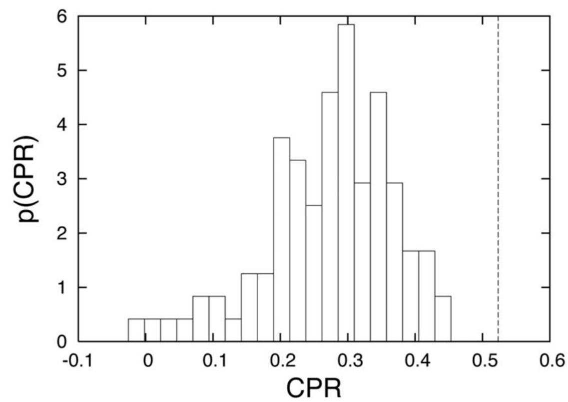

FIG. 16. Histogram of the values obtained for CPR^{s_i} with $i=1,\ldots,100$ (bars). The dashed vertical line indicates the value obtained for CPR for the original data. Hence, in this case the null hypothesis is rejected, which indicates that there is PS between the left and right fixational eye movements. This test was performed with the data from subject 2, trial 10.

trols both eyes simultaneously, i.e., there might be only one center in the brain that produces the fixational movements in both eyes or a close link between two centers. Our finding of PS between left and right eyes is in good agreement with current knowledge of the physiology of the oculomotor circuitry. In a single-cell study, 66% of abducens motor neurons fired in relation to the movements of either eye, while premotor neurons in the brain stem encode monocular movements.[25] Thus, motor neurons—as the final common pathway of neural control of eye movements—are candidates for the synchronization of left and right fixational movements.

VI. CONCLUSIONS

In this paper we have revisited the recurrence based method of twin surrogates, assessing the quality of the generated surrogates depending on the parameters of the method for different cases of prototypical dynamics. A twin surrogate corresponds to a trajectory of the underlying dynamical system starting at different initial conditions. Therefore, in order to quantify the quality of the generated twin surrogates, we have compared them with "real" trajectories of the underlying system starting at different initial conditions. The comparison between the surrogates and the real trajectories is performed in terms of linear and nonlinear statistics. We have shown that the precise choice of the threshold δ, the most important parameter of the method, does not influence the result. We have assumed that we have only scalar time series, since this is the case in most of the experimental situations, and therefore, reconstructed the phase space by delay embedding. We have shown that the quality of the surrogates is not strongly influenced by different choices of the embedding parameters. Moreover, the dependence of the quality of the surrogates on the length of the time series is as expected, i.e., the longer the original time series, the better the quality of the surrogates, even though our results show that already for rather short time series (1000 data points), the errors found are very small. The average number of twins of the underlying trajectory depending on the threshold δ and the number of points has also been studied. We have derived analytical expressions which are in accordance with numerical simulations for different kinds of dynamics. Moreover, we have estimated the total number of different twin surrogates that can be obtained from a time series of length N and average number of twins $\langle N_{\mathrm{twins}} \rangle$. We have seen that the total number of different twin surrogates that can be generated is very large, even in the case that the number of twins of the

TABLE I. Results for the test for PS between the trajectories of the left and right fixational eye movements performed for 30 trials for 21 subjects. Trials in which the participants blinked, were discarded. 100 twin surrogates were used for the test.

Participant	Total number of trials	No. of trials where the 0-hypothesis was rejected
1	30	23
2	29	26
3	30	30
4	30	30
5	30	30
6	30	30
7	30	30
8	30	30
9	30	25
10	30	30
11	28	24
12	30	30
13	30	30
14	30	21
15	30	30
16	30	30
17	29	29
18	27	27
19	29	29
20	30	29
21	30	29
total number of trials=622, rejections=592		

trajectory is rather low. The results of this thoroughly analysis have been confirmed in the case of experimental data from fixational eye movements. In this case, we have compared the generated twin surrogates with "real" further measured time series, and we have seen, that also in this case, the precise choice of the threshold δ does not influence the performance of the twin surrogates. Finally, we have performed systematically an hypothesis test using twin surrogates to infer the statistical significance of phase synchronization between fixational eye movements of left and right eyes. We have analyzed the data from approximately 30 trials from 21 subjects. In 95% of the cases, we have found that phase synchronization is significant. This finding is in agreement with physiological results about the functional role of oculomotor neurons. Contrary to popular belief, fixational eyes movements are a necessary condition for vision. Thus, an understanding of their dynamics is fundamental for perception and the associated control of spatial attention.[26]

ACKNOWLEDGMENTS

We thank Norbert Marwan for fruitful discussions. M. C. R. would like to acknowledge the Scottish Universities Life Science Alliance (SULSA) for the financial support. M. T. would like to acknowledge the RCUK academic fellowship from EPSRC. J. K. and R. E. acknowledge the Research Group of Computational Modeling of Behavioral and Cognitive Dynamics, funded by DFG.

APPENDIX: PROTOTYPICAL SYSTEMS AND STATISTICS USED FOR THE COMPARISON

We introduce the equations of the dynamical systems used for illustration and the definitions of the statistics used for the quantification of the quality of the twin surrogates compared to original trajectories of the underlying system.

We consider three prototypical examples:

- the logistic map,

$$x_{n+1} = 4x_n(x_n - 1); \tag{A1}$$

- the Lorenz system,

$$\begin{aligned} \dot{x} &= 10(y - x), \\ \dot{y} &= 28x - y - xz, \\ \dot{z} &= xy - 8/3z; \end{aligned} \tag{A2}$$

- and one autoregressive (AR) model of first order,

$$x_{n+1} = 0.87x_n + \xi_n. \tag{A3}$$

The statistics that we use for the comparison of the twin surrogates with the original trajectories are the following:

- the autocorrelation function of a scalar time series $\{x(t)\}_{t=1}^{N}$,

$$\mathrm{ACF}(\tau) = \frac{1}{N-\tau}\sum_{t=1}^{N-\tau}\frac{(x(t)-\bar{x})(x(t+\tau)-\bar{x})}{\sigma_x^2}, \tag{A4}$$

  where $\bar{x}$ denotes the mean value and σ_x the standard deviation of the time series;

- the mutual information of a scalar time series $\{x(t)\}_{t=1}^{N}$,

$$\mathrm{MI}(\tau) = -\sum_{i,j} p_{i,j}(\tau)\ln\frac{p_{i,j}(\tau)}{p_i p_j}, \tag{A5}$$

  where p_i denotes the probability to find a time series value in the ith interval of the partition, and $p_{i,j}(\tau)$ the joint probability that an observation falls in the ith interval, and at time τ later, in the jth interval;

- the mean length of black diagonal lines, i.e., the average value of the black diagonal lines of the RP of a trajectory $\{\vec{x}(t)\}_{t=1}^{N}$, which is an estimate of the mean prediction time of the system[7]

$$\mathrm{MDL} = \sum_l l P_d(l), \tag{A6}$$

  where $P_d(l)$ denotes the probability to find a black diagonal line of length l in the RP of the trajectory. A black diagonal line of length l in the RP means that the trajectory runs close to another segment of the trajectory during l time steps. Note that we discard the main diagonal line of the RP, which has length N;

- the mean white vertical line, i.e., the average value of the white vertical lines of the RP of a trajectory $\{\vec{x}(t)\}_{t=1}^{N}$, which is an estimate of the information dimension of the system[27]

$$\mathrm{MVL} = \sum_l l P_v(l), \tag{A7}$$

  where $P_v(l)$ denotes the probability to find a white vertical line of length l in the RP of the trajectory. Note that a white vertical line of length l in the RP means that the trajectory needs l time steps to recur to the neighborhood of a fixed point of the trajectory.

We compute each statistic for each of the twin surrogates, and determine the mean value and standard deviation. We do the same for the other "real" trajectories and calculate the error.

The error in the mean of the autocorrelation function is computed as

$$E_{\langle \mathrm{ACF}\rangle} = \sqrt{\frac{\sum_{\tau=1}^{\tau_{\max}}(\langle \mathrm{ACF}(\tau)\rangle_{\mathrm{surr}} - \langle \mathrm{ACF}(\tau)\rangle_{\mathrm{real}})^2}{\tau_{\max}}}, \tag{A8}$$

where $\tau_{\max}$ is the maximal time lag considered and $\langle\cdot\rangle$ denotes the average. The error in the standard deviation of the autocorrelation function is

$$E_{\sigma(\mathrm{ACF})} = \sqrt{\frac{\sum_{\tau=1}^{\tau_{\max}}(\sigma(\mathrm{ACF}(\tau))_{\mathrm{surr}} - \sigma(\mathrm{ACF}(\tau))_{\mathrm{real}})^2}{\tau_{\max}}}, \tag{A9}$$

where $\sigma(\cdot)$ denotes the standard deviation. The error in the mutual information is computed analogously. In the case of the mean diagonal line MDL, the error is computed as follows:

$$E_{\mathrm{MDL}} = \frac{\sqrt{(\langle \mathrm{MDL}\rangle_{\mathrm{surr}} - \langle \mathrm{MDL}\rangle_{\mathrm{orig}})^2}}{2.96(\sigma(\mathrm{MDL})_{\mathrm{surr}} + \sigma(\mathrm{MDL})_{\mathrm{orig}})/2}, \quad \text{(A10)}$$

and the error in the mean white vertical line MVL is calculated analogously.

[1] A. S. Pikovsky, M. G. Rosenblum, and J. Kurths, Cambridge Nonlinear Science Series (2001), p. 12; S. Boccaletti, J. Kurths, G. Osipov, D. L. Valladares, and C. S. Zhou, Phys. Rep. **366**, 1 (2002); C. Zhou, A. E. Motter, and J. Kurths, Phys. Rev. Lett. **96**, 034101 (2006); A. Arenas, A. Diaz-Guilera, J. Kurths, Y. Moreno, and C. Zhou, Phys. Rep. **469**, 93 (2008).
[2] P. van Leeuwen, D. Geue, S. Lange, D. Cysarz, H. Bettermann, and D. H. W. Grönemeyer, BMC Physiology **3**, 2 (2003).
[3] M. Thiel, M. C. Romano, J. Kurths, M. Rolfs, and R. Kliegl, Europhys. Lett. **75**, 535 (2006).
[4] H. Kantz and T. Schreiber, *Nonlinear Time Series Analysis* (Cambridge University Press, 1997).
[5] L. M. Pecora, L. Moniz, J. Nichols, and T. L. Carroll, Chaos **17**, 013110 (2007).
[6] J.-P. Eckmann, S. O. Kamphorst, and D. Ruelle, Europhys. Lett. **5**, 973 (1987).
[7] N. Marwan, M. C. Romano, M. Thiel, and J. Kurths, Phys. Rep. **438**, 237 (2007).
[8] M. Thiel, M. C. Romano, P. L. Read, and J. Kurths, Chaos **14**, 234 (2004).
[9] M. Thiel, M. C. Romano, and J. Kurths, Phys. Lett. A **330**, 343 (2004).
[10] M. Thiel, M. C. Romano, and J. Kurths, Philos. Trans. R. Soc. London, Ser. A **366**, 545 (2007).
[11] E. Ott, *Chaos in Dynamical Systems* (Cambridge University Press, Cambridge, 1993).
[12] J. Theiler, S. Eubank, A. Longtin, B. Galdrikian, and J. Farmer, Physica D **58**, 77 (1992); D. Prichard and J. Theiler, Phys. Rev. Lett. **73**, 951 (1994); T. Schreiber and A. Schmitz, *ibid.* **77**, 635 (1996); Physica D **142**, 346 (2000); M. Palus, Phys. Lett. A **235**, 341 (1997); M. Palus and A. Stefanovska, Phys. Rev. E **67**, 055201(R) (2003); K. T. Dolan and A. Neiman, *ibid.* **65**, 026108 (2002); M. Breakspear, M. J. Brammer, E. T. Bullmore, P. Das, and L. M. Willians, Hum. Brain Mapp **23**, 1 (2004).
[13] B. Schelter, M. Winterhalder, R. Dahlhaus, J. Kurths, and J. Timmer, Phys. Rev. Lett. **96**, 208103 (2006).
[14] M. Small, D. Yu, and R. G. Harrison, Phys. Rev. Lett. **87**, 188101 (2001).
[15] R. G. Andrzejak, A. Kraskov, H. Stögbauer, F. Mormann, and T. Kreuz, Phys. Rev. E **68**, 066202 (2003).
[16] M. C. Romano, M. Thiel, J. Kurths, and C. Grebogi, Phys. Rev. E **76**, 036211 (2007).
[17] M. G. Reed and C. V. Howard, J. Microsc. **186**, 177 (1997).
[18] S. Martinez-Conde, S. L. Macknik, and D. H. Hubel, Nat. Rev. Neurosci. **5**, 229 (2004); R. Engbert and K. Mergenthaler, Proc. Natl. Acad. Sci. U.S.A. **103**, 7192 (2006); J.-R. Liang, S. Moshel, A. C. Zivotofsky, R. Engbert, R. Kliegl, and S. Havlin, Phys. Rev. E **71**, 031909 (2005); for an overview see, R. Engbert, Prog. Brain Res. **154**, 177 (2006).
[19] L. A. Riggs, F. Ratliff, J. C. Cornsweet, and T. N. Cornsweet, J. Opt. Soc. Am. **43**, 495 (1953); D. Coppola and D. Purves, Proc. Natl. Acad. Sci. U.S.A. **93**, 8001 (1996).
[20] R. Engbert and R. Kliegl, Psychol. Sci. **15**, 431 (2004); K. Mergenthaler and R. Engbert, Phys. Rev. Lett. **98**, 138104 (2007).
[21] K. J. Ciuffreda and B. Tannen, St. Louis, Mosby (1995).
[22] S. Moshel, J. Liang, A. Caspi, R. Engbert, R. Kliegl, S. Havlin, and A. Z. Zivotofsky, Ann. N.Y. Acad. Sci. **1039**, 484 (2005).
[23] M. C. Romano, M. Thiel, J. Kurths, M. Rolfs, R. Engbert, and R. Kliegl, *Handbook of Time Series Analysis* (Wiley-VCH, Berlin, 2006).
[24] M. C. Romano, M. Thiel, J. Kurths, I. Z. Kiss, and J. L. Hudson, Europhys. Lett. **71**, 466 (2005).
[25] W. Zhou and W. M. King, Nature (London) **393**, 692 (1998).
[26] R. Engbert and R. Kliegl, Vision Res. **43**, 1035 (2003); J. Laubrock, R. Engbert, and R. Kliegl, *ibid.* **45**, 721 (2005); M. Rolfs, R. Engbert, and R. Kliegl, Exp. Brain Res. **166**, 427 (2005).
[27] J. B. Gao, Phys. Rev. Lett. **83**, 3178 (1999).
[28] If triplets or multiplets occur, one proceeds analogously.