

A Methodological Note on Nonlinear Time Series Analysis: Is the Open- and Closed-Loop Model of Collins and De Luca (1993) a Statistical Artifact?

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ABSTRACT. The authors reexamined, theoretically and empirically, the method proposed by J. J. Collins and C. D. De Luca (1993) for the analysis of center-of-pressure trajectories. The main argument in this article is that Collins and De Luca's approach is not adapted to the analysis of bounded time series and leads to statistical artifacts such as underestimation of the diffusion process for long-term intervals. The open- and closed-loop model developed by Collins and De Luca is a direct consequence of those statistical problems. Applying more classical methods, such as rescaled range analysis or detrended fluctuation analysis, the authors show that center-of-pressure trajectories can be modeled as continuous, antipersistent fractional Brownian motion. More specifically, those trajectories behave like $1/f$ noise, a ubiquitous feature in adaptive biological systems.

Key words: center-of-pressure profile, correlated noise, stochastic processes, time series analysis

In human movement studies, a number of variables measured in steady-state conditions have been classically conceived of as randomly varying around a stable mean value (e.g., heartbeats and stride duration). In other words, investigators have viewed measurement fluctuations as meaningless white noise and have generally eliminated them by averaging (Slifkin & Newell, 1998). In those traditional approaches, the dynamics of the measured variables was clearly ignored (e.g., the temporal ordering of the series, the magnitude and direction of displacements between successive points).

During the last decade, a number of attempts were made to analyze more specifically the dynamics of such biological time series (e.g., Collins & De Luca, 1993; Hausdorff,

Peng, Ladin, Wei, & Goldberger, 1995; Peng, Havlin, Stanley, & Goldberger, 1995). Those investigators used a set of analysis methods designed to reveal the hidden fractal properties of time series. For example, Hausdorff et al. (1995) showed that the apparently noisy fluctuations in stride duration during walking display complex fractal properties: When healthy participants walked at their preferred paces, stride variability was not attributable simply to uncorrelated random fluctuations but exhibited long-range power-law correlations and self-similarity, indicative of a fractal process.

Our aim in the present article was to discuss some potential methodological and statistical problems concerning the method proposed by Collins and De Luca (1993) for the analysis of center-of-pressure (COP) trajectories during quiet stance. Their method, as well as other mathematical techniques widely used in that domain, is fully explored in the following paragraphs and in the Appendix.

Fractional Brownian Motion

The point departure of those approaches was the seminal work of Einstein (1905), who studied Brownian motion (an integration of white noise) and showed that the variance of

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the displacement was in that case proportional to the expended time:

$$\text{Var}(\Delta x) = 2D\Delta t, \quad (1)$$

where the parameter D is the diffusion coefficient. D is an average measure of the stochastic activity of the white noise process that caused the displacement and is directly related to its frequency, amplitude, or both. The variance of displacement can be expressed as follows:

$$\begin{aligned} \text{Var}(\Delta x) &= E\{[\Delta x - E(\Delta x)]^2\} \\ &= E(\Delta x^2) - E(\Delta x)^2 \\ &= E(\Delta x^2), \end{aligned} \quad (2)$$

as, in the case of Brownian motion, $E(\Delta x) = 0$. One can estimate $E(\Delta x^2)$ by using the empirical mean squared displacement, computed over a given time interval, $\langle \Delta x^2 \rangle$.¹ The Einstein relation then takes the following form:

$$\langle \Delta x^2 \rangle = 2D\Delta t, \quad (3)$$

signifying that, on average, the displacement is proportional to the square root of the time.

The basic relation given by Equation 1 was generalized by Mandelbrot and van Ness (1968) to account for a family of stochastic processes that they termed *fractional Brownian motion* (fBm). They proposed the following scaling law:

$$\text{Var}(\Delta x) \propto \Delta t^{2H}, \quad (4)$$

where the scaling exponent H can be any real number in the range $0 < H < 1$. The fBm is the integral of a process called *fractional Gaussian noise* (fGn), which then represents the series of successive increments generating the fBm. Brownian motion represents a special case in the family of stochastic processes in which $H = .5$. In that case, the underlying fGn is a white noise process. The determination of the actual nature (fBm or fGn) of the time series obtained in a given experiment constitutes a crucial step in fractal analysis (Eke et al., 2000). Fundamentally, fGn is a stationary process with constant expected mean value and constant variance. Conversely, fBm is a nonstationary process with time-dependent variance.

An important feature of fBm is the presence of long-term correlations between past increments and future increments. Such motion exhibits long-memory processes, and each value is dependent upon the global history of the series. Long-term correlations (or dependence) do not necessarily imply that the current value influences subsequent values in a deterministic fashion (e.g., as in autoregressive moving average processes) but indicate that, on average, the fluctuations on one time scale are statistically similar to the fluctuations on other time scales.

When $H > .5$, the stochastic process is positively correlated: If at some time in the past, there was an increment on the variable average value, then an increasing trend will appear in the future. The series exhibits persistent behavior, and there is a long-term memory process. Conversely, when $H < .5$, the

series exhibits antipersistent behavior: If the system has a decreasing trend in the past, a probable increasing trend in the future is implied, and vice versa. $H = .5$ constitutes an exceptional case (pure Brownian motion) in which successive displacements are uncorrelated.²

Fractal Analysis Methods

Investigators have developed a number of methods for applying those principles to either simulated or empirical time series and for calculating the scaling exponent. Those methods differ in many points, but each is an attempt generally to assess, in multiple temporal intervals of various lengths, the dispersion or the displacement of the variable. The scaling exponent is then estimated as the slope of the double-logarithmic plot of fluctuation or the (squared) displacement as a function of the length of the corresponding time intervals.

The most classical method is the rescaled range analysis proposed by Hurst (1951, 1965; see Appendix for details). Hurst's approach is based on the assessment, for each interval, of the range of displacements of the locally integrated time series. One then rescales that range (R) by dividing it by the local standard deviation (S) of the original series. Finally, the rescaled range (R/S) is averaged over all intervals of equal length. The scaling exponent is then estimated as the slope of the double-logarithmic plot of R/S , as a function of interval length. R/S analysis is a very common method, widely used in econometry (Leland, Taqqu, Williger, & Wilson, 1994; Peters, 1994), geophysics (Marsan, Bean, Steacy, & McCloskey, 1999; Nickolaenko, Price, & Iudin, 2000), biology (Churilla et al., 1996; Hoop, Burton, Kazemi, & Liebovitch, 1995; Hoop, Kazemi, & Liebovitch, 1993), and motor control (Chen, Ding, & Kelso, 1997; Treffner & Kelso, 1999; Yamada, 1995).

Peng et al. (1995) developed more recently a second method, detrended fluctuation analysis, DFA (see Appendix for details). They designed that method especially for the analysis of biological time series, which are often highly nonstationary. The series is first integrated and then detrended within each considered interval. Finally, the standard deviation of the integrated and detrended series is computed. The scaling exponent is then estimated as the slope of the double-logarithmic plot of standard deviation, as a function of interval length. DFA has been used in a number of experiments dealing with biological times series, in particular heartbeat time series (Absil, Sepulchre, Bilge, & Gérard, 1999; Matcharashvili & Janiashvili, 2001; Peng et al., 1995; Peng et al., 1993) and gait stride interval series (Hausdorff et al., 1997; Hausdorff et al., 1995; Hausdorff et al., 1996).

A third method, proposed by Collins and De Luca (1993), was mainly exploited in the analysis of COP trajectories during unperturbed stance (Collins & De Luca, 1993; Newell, Slobounov, Slobounova, & Molenaar, 1997; Riley, Mitra, Stoffregen, & Turvey, 1997; Riley, Wong, Mitra, & Turvey, 1997; Rougier, 1999; Rougier & Caron, 2000; Rougier &

Farenc, 2000). That method is extremely simple; one computes the square of the displacement, $(\Delta x)^2$, between all pairs of points separated by a specified time interval Δt . Those squared displacements are then averaged, and that process is repeated for increasing values of Δt . The H exponent is then determined as the slope of the double-logarithmic plot of $\langle \Delta x^2 \rangle$ as a function of Δt (stabilogram–diffusion plot). In the aforementioned experiments, the profile of the COP trajectory was found to reflect fBm that had two component processes, a short-term process (for $\Delta t < 1$ s), with H exponents revealing persistent behavior ($H > .5$), and a long-term process (for $\Delta t > 1$ s), with H exponents suggesting antipersistence ($0 < H < .5$). Those results were revealed by an inflexion of the double-logarithmic plot, which was modeled with two distinct straight lines intersecting approximately at $\Delta t = 1$ s. In an experiment in which participants attempted to actively balance an inverted pendulum (an aluminum rod), Treffner and Kelso (1995) obtained similar results with the same method.³

Collins and De Luca (1993) interpreted their results by postulating a two-component, open- and closed-loop control mechanism. Riley, Mitra, et al. (1997) suggested an alternative hypothesis—that the short-term region could refer to exploratory processes (considering persistence as information gathering) and the long-term region to performance processes (considering antipersistence as adjusting on the basis of obtained information). Subsequent experiments showed systematic evolutions of the parameters of the model (H exponents for short- and long-term processes, coordinates of the point of inflexion), under the manipulation of factors such as vision, leaning, or haptic touch (Riley, Mitra, et al., 1997; Riley, Wong, et al., 1997).

Fractal Processes and Biological Time Series

Nevertheless, the mapping of biological time series to formal stochastic processes raises a number of methodological problems. Of crucial importance is the fact that a pure fBm is typically unbounded: The fluctuations grow with the time interval length in a power-law way, and the expected displacement increases indefinitely with time. In other words, the diffusion with time of a pure fBm is unlimited. In contrast, biological time series are generally bounded within physiological limits. That is the case, for example, for the aforementioned heart rate and gait time series and for the trajectory of the COP, which is obviously bounded within the area of support of the participant's feet. As a consequence, the diffusion process remains limited, and the variance of such biological time series cannot exceed a ceiling value and, at least beyond a critical time interval (necessary to reach that ceiling value), should become more or less independent of time. That limitation should naturally yield to a crossover phenomenon in the relationship between variance (or displacement) and time interval, with persistence at short time intervals and antipersistence at long time intervals. In several experiments, evidence of such results was obtained in the fractal analysis of biological

time series (Churilla et al., 1996; Collins & De Luca, 1993; Treffner & Kelso, 1995, 1999), and one could hypothesize that the bounded character of the series under study could cause that typical feature. Liebovitch and Yang (1997), who considered that hypothesis, showed that a simulated bounded random walk yielded similar results, with comparable crossover phenomena.

At this point in the discussion, the fundamental argument is that the generalized relation of Mandelbrot and van Ness (1968) given by Equation 4 cannot directly hold for such bounded biological series. In a pure fBm, the diffusion process is directly related to the degree of persistence of the series of successive displacements. In the case of bounded series, the long-term diffusion is constrained within the range defined by the upper or lower boundaries. Whatever the actual degree of persistence of the series, the observed diffusion reflects only the narrowness of that range. Consequently, in an analysis based on diffusion, one could be unable to distinguish between a bounded fBm and an uncorrelated noise.

An elegant solution for that problem is to study the fractal properties of the integrated time series, rather than those of the original signals (Feder, 1988; Hurst, 1965; Peng et al., 1995). If the original signal is constrained within physiological boundaries, then the integrated series is not bounded and it exhibits fractal properties that can be quantified on the basis of Equation 4. Such a procedure allows one to distinguish between the uncorrelated noise, which gives a Brownian motion after integration, and a bounded fBm, which should exhibit after integration a higher diffusion than does Brownian motion. In other words, the solution is to infer the fractal properties of the original signal from the diffusion properties of its integrated series.

Then, mapping the original bounded time series to an integrated signal appears essential in biological time series analysis. Such a procedure constitutes the first step of the aforementioned DFA (see Appendix for details). That explains why a DFA's α scaling exponent equal to .5 characterizes a white noise process and not a Brownian motion, as in the relation of Mandelbrot and van Ness (1968). If the original signal is a purely random, uncorrelated process, then its integration leads to a random walk (Brownian motion), revealed by that typical exponent.

R/S analysis also includes as a first step the just-described kind of integration procedure (see Appendix for details). Nevertheless, the usefulness of that integration step for counteracting the bounding effect depends on the nature of the series used as input in the rescaled range method. A number of authors have suggested that the correct use of the method is to apply *R/S* analysis not on the original time series but on the series of increments between successively measured values (Bassingthwaighe, Liebovitch, & West, 1994; Caccia, Percival, Cannon, Raymond, & Bassingthwaighe, 1997; Liebovitch & Yang, 1997). In other words, the input series should be fGn rather than fBm. In that case, the integration procedure restores the original fBm, and the resulting expo-

ment corresponds to the H exponent of Equation 4. Nevertheless, if the original series is a bounded process, then the integration of the differenced series restores that characteristic, and the R/S analysis should logically evidence crossover phenomena. In some experiments in which R/S analysis has been used on biological data (Churilla et al., 1996; Treffner & Kelso, 1999) and on physical data (Berge, Rakotomalala, Feder, & Jossang, 1994), that kind of results has been obtained. In all of those experiments, R/S analysis was applied on fGn.

A solution for avoiding that problem with such bounded series could be to apply R/S analysis directly on raw data, as proposed in the DFA method (Peng et al., 1995). It is important to note that in that case, the range R is calculated on the cumulative sum of the original series. As a result, a shift appears in the obtained exponents. $H_{R/S}$ is .5 if the original series is an uncorrelated white noise and is 1.0 for a Brownian motion. More generally, the H exponent of Equation 4 is $H_{R/S}$ less .05 (De la Fuente, Martinez, Aguirregabiria, & Vaguillas, 1998; Yamada, 1995).

A quite interesting result in that regard was reported by Chen, Ding, and Kelso (1997). In their experiment, participants had to perform continuous tapping in synchrony with an auditory metronome. R/S analysis was first applied to the synchronization error series, and the diffusion plot displayed a single straight line, revealing long-range correlation, with an $H_{R/S}$ of about .8. R/S analysis was also applied to the series of intertap intervals, and in that case it evidenced a crossover from persistence to antipersistence similar to those observed in the aforementioned experiments. According to the authors, such results were not informative in terms of revealing the underlying long memory and "should not be construed as giving multiple values of H " (Chen et al., 1997, p. 4503). They proposed the concept of fundamental time series to designate series able to reveal, when used as input in fractal analysis, the long-range correlation properties of the system. Most interesting, they noted that the two series were not independent, because the error series appeared as the cumulative sum of the intertap interval series. In other words, they suggested that under such circumstances, R/S analysis should be applied on fBm rather than on fGn. Note that in that particular case, the intertap intervals series was not, as in previous experiments, bounded within biological limits. But one could consider that the auditory beeps of the metronome gave a periodic feedback to the participants, generating a kind of recovering force. Liebovitch and Yang (1997) showed that such underlying dynamics also led to a crossover from persistence to antipersistence.

Collins and De Luca (1993), who applied their method directly on the raw trajectory of the COP, did not consider those methodological problems. Recall that their method did not include any integration step. One can hypothesize that, in that respect, the flattening of the slope of the double-logarithmic plot beyond a critical point, described by Collins and De Luca, was simply the consequence of the bounded character of their original series. Furthermore, the length of the

short-term region represented the average time the variable needs, from a given point of the allowed space, to reach one of the physiological boundaries. In other words, the two-processes model they proposed to account for their COP trajectories could simply have been a statistical artifact.

Oscillatory Behavior and Fractal Analysis

Another problem with the method of Collins and De Luca (1993) is related to the oscillatory character of many biological time series, especially in the case of displacement data. The displacement of the COP, or the displacement of the bottom of the rod in the experiment of Treffner and Kelso (1995), resulted from the behavior of a complex system, composed of many interacting oscillatory components. Fourier analysis generally reveals a rich spectrum of periodicities, and, in the case of COP displacement, Powell and Dzendolet (1984) showed that the most power was concentrated in the region of about 0.3–0.4 Hz, revealing the presence of low-frequency oscillatory components.

Working on the basis of the squared differences between points separated by given time lags, the method of Collins and De Luca (1993) should be sensitive to those periodicities. With an original signal containing a main underlying component of frequency f , the stabilogram–diffusion plot should exhibit wave behavior, with minima corresponding to $\Delta t = k(1/f)$, ($k \in \{1, 2, 3, \dots\}$) and maxima corresponding to $(k/2)(1/f)$, ($k \in \{1, 2, 3, \dots\}$). Such behavior was not evident in the stabilogram–diffusion plots presented by Collins and De Luca (1993), but one could think that the trial averaging realized by those authors hid those periodicities. In contrast, the single-trial stabilogram–diffusion plot reported in Treffner and Kelso (1995, see p. 85) clearly exhibited wave behavior, related, according to the authors, to the eigenfrequency of the rod used in the trial.

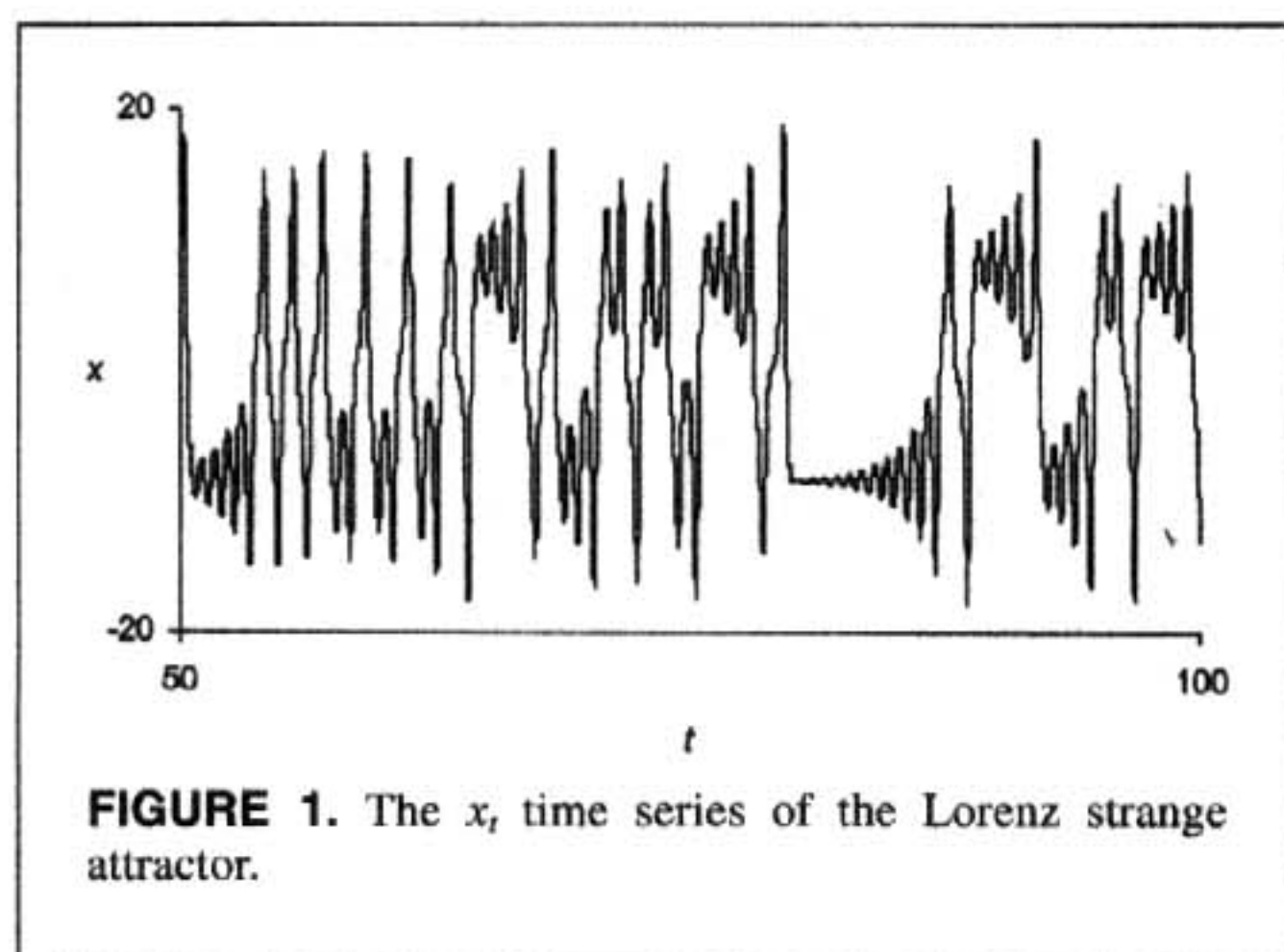
Treffner and Kelso (1999) recognized that there are problems with estimating H by using Collins and De Luca's method because periodicities in the underlying process might emerge as prominent low-frequency oscillations in the diffusion plot, thus eliminating the possibility of a valid linear fit. With R/S analysis and DFA, that problem can be avoided, because those methods work on the basis of the global behavior of the variable of interest within each interval (the maximal range for the first method, the detrended standard deviation for the second) and not only on the relative distance between the points corresponding to the temporal boundaries of each interval.

In summary, we think that the application of the method proposed by Collins and De Luca (1993) to a bounded series leads automatically to a nonlinear log–log plot. For the smallest time lags considered, the plot should produce a straight line, revealing short-term dependency in position and direction. Beyond a given time lag, a flattening of the slope of the log–log plot should be observed, because $\langle \Delta x^2 \rangle$ bounded within physiological limits cannot increase indefinitely. Finally, when the original time series presents an oscillatory behavior, the plot should exhibit a typical wave-

form whose periodicities should be related to the eigenfrequencies of the system under study. Those expected alterations of the log-log plot are problematic because obtaining a straight line is generally considered to be an important test of the fractality of the data (Hurst, 1965; Peng et al., 1995).

A Formal Example: The Lorenz Strange Attractor

As a first example, we applied the Collins and De Luca (1993) method to the analysis of the time series of the $x(t)$ coordinate of the Lorenz strange attractor.⁵ That well-known, chaotic and bounded series was recently studied by De la Fuente et al. (1998), who found, by using R/S analysis, an exponent of value $H_{R/S} = .82$. Because they carried out that analysis by using raw data as input, the corresponding H exponent was about .32, revealing a long-range antipersistent correlation structure. The following analyses were carried out on a similar series (5,000 data points, starting at $t = 50$ and finishing at $t = 100$, by steps of 0.01, in arbitrary units, initial values at $t = 0$: $x = y = z = 1$; see Figure 1). Because De la Fuente et al. (1998) did not use the same initial values, the two series are not identical. That should not have a significant influence on the estimation of the scaling exponent.

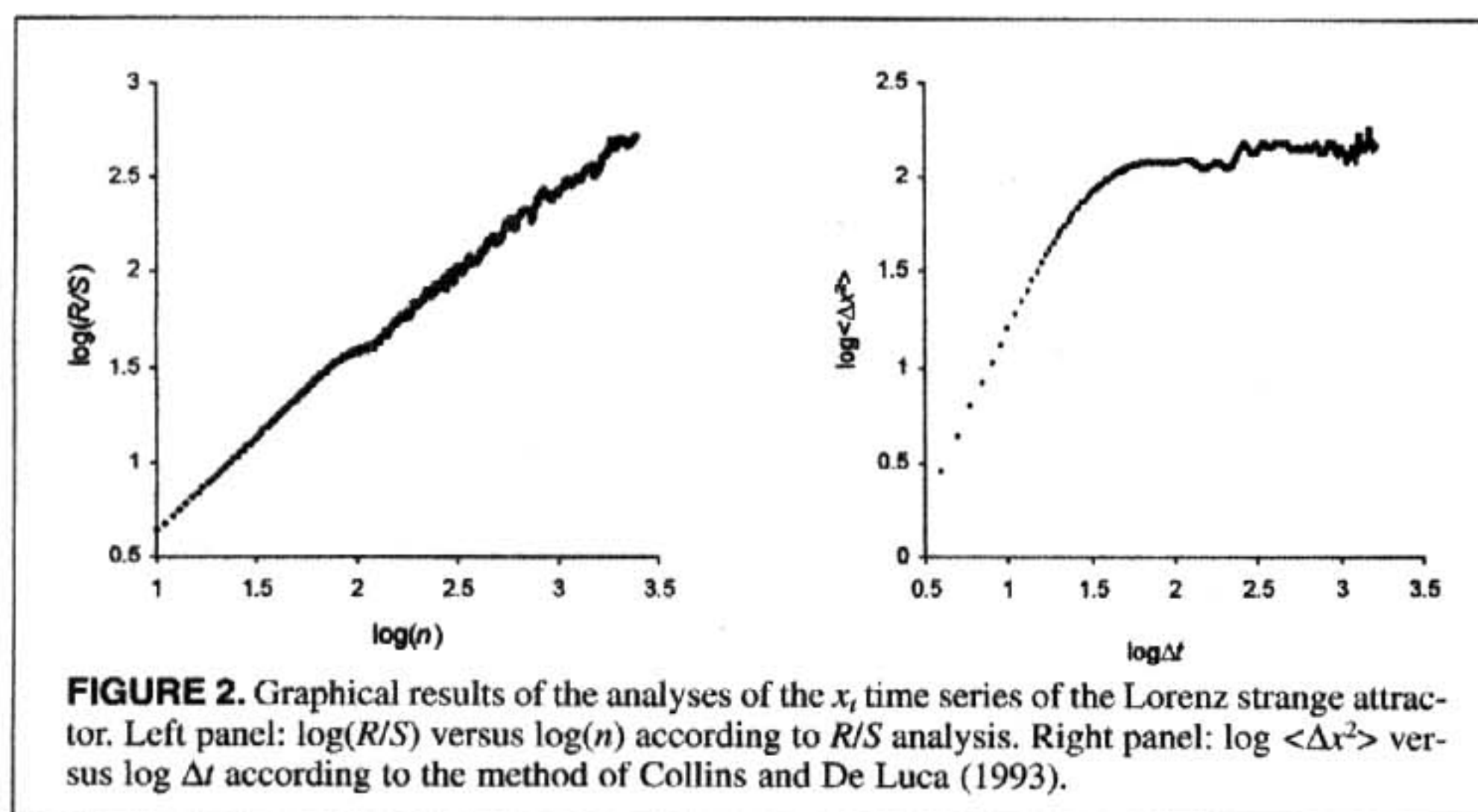


We first applied on that series the R/S analysis, which gave a scaling exponent of value $H_{R/S} = .83$, corresponding to an H exponent of about .33 (see Figure 2, left panel), confirming the result of De la Fuente et al. (1998). Then we applied the previously described Collins and De Luca (1993) method, which gave, as hypothesized, a nonlinear double-logarithmic plot (Figure 2, right panel), with two distinct regions, characterized by scaling exponents $H_s = .87$ and $H_l = .04$, respectively.⁶ The critical point appeared approximately at $\log_{10} n = 1.6$, revealing a short-term region of about .4, in arbitrary units. That first example showed that the typical results of Collins and De Luca could be obtained with formal series, when bounded within given limits. In other words, hypothetical biological processes underlying the time series do not necessarily cause a nonlinear plot.

COP Series: The Collins and De Luca (1993) Approach

A second important test for our hypotheses was the application of the previously described methods to COP trajectories similar to those studied by Collins and De Luca (1993). To that end, we used 30-s data samples obtained during clinical testing with 5 healthy adult participants. The participants were instructed to maintain the normal Romberg position, with the minimum of movements. A high-resolution force platform with four piezoelectric capacitors (Kistler system) was used, with an acquisition frequency of 100 Hz.

The analyses for the present article were conducted separately on the x - and y -coordinate samples. We first applied the method proposed by Collins and De Luca (1993). As previously described, squared displacements between all data pairs separated by a given time interval Δt were computed for several values of Δt . We then plotted $\langle \Delta x^2 \rangle$ (and $\langle \Delta y^2 \rangle$) as a function of Δt , with the aim of determining the diffusion coefficients D (see Equation 3).⁷ Those plots confirmed the results of Collins and De Luca (1993) and revealed the presence of two scaling regions characterized



by different slopes. The slopes were calculated separately for the two regions and denoted D_{xs} and D_{ys} for the short-term region, and D_{xl} and D_{yl} for the long-term region. The time interval corresponding to the critical point (Δt_{xc} or Δt_{yc}) was determined as the abscissa of the intersecting point of the regression lines of the short- and the long-term regions.

Then, we plotted $\langle \Delta x^2 \rangle$ (and $\langle \Delta y^2 \rangle$) as a function of Δt in a double-logarithmic plot, with the aim of determining the H exponents. Those exponents were computed separately for each region and were denoted, respectively, H_{xs} and H_{ys} for the short-term region and H_{xl} and H_{yl} for the long-term region. Finally, we applied R/S analysis and DFA (see Appendix) to determine, respectively, the $H_{R/S}$ exponents (denoted $H_{R/Sx}$ and $H_{R/Sy}$) and the α exponents (denoted α_x and α_y).

The results of those analyses are reported in Table 1. As expected, the analyses performed according to the method of Collins and De Luca (1993) led, as in most previous studies, to the identification of two distinct regions in the plots (see Figure 3, panels *a* and *b*). The short-term region was characterized by high diffusion coefficients (mean values $D_{xs} = 18.151 \pm 16.96$ and $D_{ys} = 16.322 \pm 6.23$) and high H exponents (mean values $H_{xs} = .831 \pm .06$ and $H_{ys} = .766 \pm .08$). In contrast, the long-term region exhibited lower values ($D_{xl} = 0.437 \pm 0.71$, $D_{yl} = 0.716 \pm 0.77$, $H_{xl} = .056 \pm .05$, and $H_{yl} = 0.113 \pm 0.07$). The time coordinates of the critical point were respectively $\Delta t_{xc} = 0.828 \text{ s} \pm 0.23$ and $\Delta t_{yc} = 0.791 \text{ s} \pm 0.45$. Those results were generally consistent with those obtained in previous studies. One should note that the values for the D coefficients for the short-term region were higher than those reported by Collins and De Luca (1993)

but similar to those obtained in subsequent works (e.g., see Riley, Mitra, et al., 1997; Riley, Wong, et al., 1997).

Finally, if a straight line generally characterized the short-term region, allowing an accurate assessment of the slope, then the long-term region exhibited, as hypothesized, an oscillatory and periodic behavior. The dependence of the periodic behavior on the frequency composition of the original series is easy to verify. As an example, the spectral analysis of the x series of Participant 1 (which corresponds to the example plots in Figure 3) revealed two power peaks, at 0.15 Hz and 0.34 Hz, corresponding, respectively, to periods of 6.82 s and 2.97 s. One can check the presence in panel *a* of a minimum for $\Delta t = 6.74$ s, corresponding to the first period, and of minima for $\Delta t = 2.86$, 5.95, and 8.98 s, corresponding to multiples of the second period. That periodic behavior was present in all analyses, leading to a poor definition of the slopes for the long-term region.

COP Series: R/S analysis and DFA

The most important result for our present purpose was the obvious nonlinearity of the double-logarithmic plot, suggesting the presence of two successive scaling regimes in the trajectory of the COP. In contrast, R/S analysis and DFA provided in all cases a straight-line fit in the log-log plot. The mean values given by R/S analysis were $H_{R/Sx} = .848 \pm .06$ for x -coordinate samples (corresponding to $H = .348$) and $H_{R/Sy} = .865 \pm .03$ for y -coordinate samples ($H = .365$). The corresponding mean α values were $\alpha_x = 1.054 \pm 0.11$ and $\alpha_y = 1.103 \pm 0.04$. One should note that according to the theoretical relationship between H and α (see, in Appendix, Equation A8), R/S analysis seemed to provide

TABLE 1
Diffusion Coefficients (D_{xs} , D_{xl}), Critical Point Time Coordinate (Δt_{xc}), Scaling Exponents (H_{xs} , H_{xl}), and α_x Obtained for 5 Adult Participants

Participant	D_{xs}	D_{xl}	Δt_{xc}	H_{xs}	H_{xl}	$H_{R/Sx}$	α_x
<i>x coordinate</i>							
1	4.526	0.116	0.852	0.744	0.052	0.876	1.071
2	46.604	1.676	0.522	0.900	0.121	0.889	1.121
3	16.124	0.289	0.941	0.857	0.035	0.836	1.051
4	5.842	0.188	1.120	0.800	0.091	0.884	1.152
5	17.657	-0.085	0.704	0.853	-0.018	0.756	0.873
<i>M</i>	18.151	0.437	0.828	0.831	0.056	0.848	1.054
	D_{ys}	D_{yl}	Δt_{yc}	H_{ys}	H_{yl}	$H_{R/Sy}$	α_y
<i>y coordinate</i>							
1	7.259	-0.268	1.530	0.648	0.038	0.845	1.076
2	16.173	1.897	0.816	0.784	0.216	0.868	1.092
3	13.920	0.685	0.718	0.744	0.082	0.850	1.085
4	22.264	0.684	0.367	0.880	0.148	0.922	1.171
5	21.995	0.579	0.521	0.776	0.082	0.841	1.089
<i>M</i>	16.322	0.716	0.791	0.766	0.113	0.865	1.103

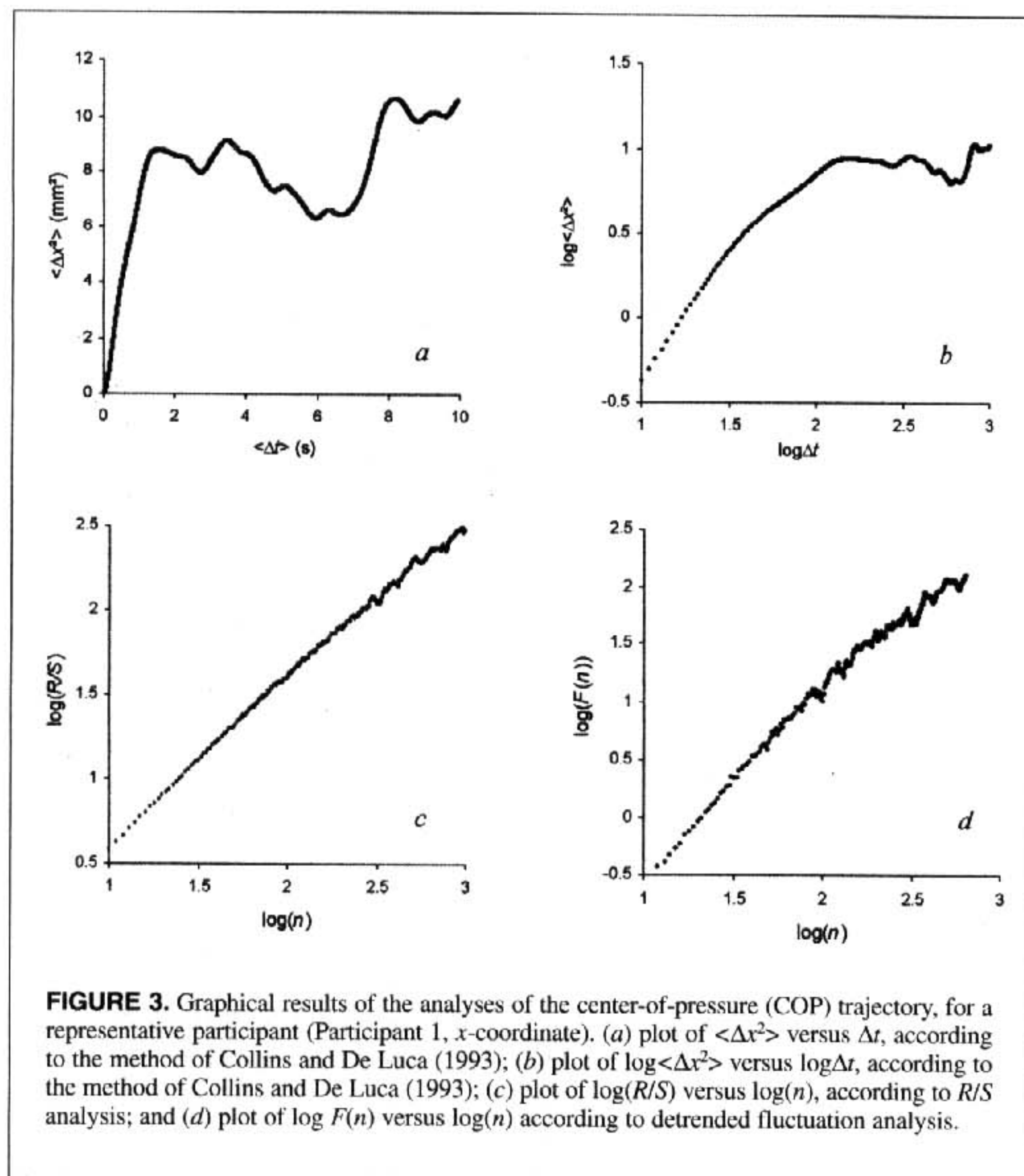


FIGURE 3. Graphical results of the analyses of the center-of-pressure (COP) trajectory, for a representative participant (Participant 1, x -coordinate). (a) plot of $\langle \Delta x^2 \rangle$ versus Δt , according to the method of Collins and De Luca (1993); (b) plot of $\log \langle \Delta x^2 \rangle$ versus $\log \Delta t$, according to the method of Collins and De Luca (1993); (c) plot of $\log(R/S)$ versus $\log(n)$, according to R/S analysis; and (d) plot of $\log F(n)$ versus $\log(n)$ according to detrended fluctuation analysis.

slightly higher estimates of the diffusion process than DFA did. Such slight discrepancies between different fractal analysis methods have been frequently reported (Caccia et al., 1997; Rangarajan & Ding, 2000; Schepers, van Beek, & Basingthwaite, 1992) and remain conceivable because those methods operate on the basis of different statistics and because of the relatively small number of data involved in the calculation (note that for that kind of analysis, the accuracy of parameters assessment is dependent on the length of the time series). Rangarajan and Ding (2000) advocated an integrated approach, that is, using simultaneously different methods to avoid false conclusions.⁸

The present results obtained with R/S analysis and DFA can be considered consistent, and they suggest that those times series are located, in the continuum defined by Mandelbrot and Van Ness (1968), between white noise and Brownian motion, just above the so-called pink noise, which is characterized by an H exponent of .25 and an α of 1.0. The two methods led to similar conclusions: The fluctuations of the COP are structured rather than random, and the trajectories exhibit antipersistent behavior. Clearly, the

results of those two classical time series analysis methods suggest that diffusion in COP trajectories is a single continuous process; in other words, the value of the scaling exponent is time independent.

To examine the empirical relationships between those diverse parameters, we applied those methods to a larger number of data samples ($N = 40$) that were obtained in similar conditions. Correlation analyses showed a good agreement between R/S analysis and DFA ($r = .952$). Lower, but significant correlations were evidenced between H_1 and $H_{R/S}$ ($r = .796$) and between H_1 and α ($r = .843$). That finding indicates that despite an evident ill definition of the slope of the log-log plot, H_1 contained significant residual information about the scaling behavior of the times series. One could note, nevertheless, that the theoretical relationship $H_{R/S} = H_1 + .5$ was not observed in our results (e.g., see Table 1), suggesting a global underestimation of H_1 . Finally, the correlations between H_s and $H_{R/S}$ and between H_s and α were not significant ($r_s = -.196$ and $-.299$, respectively). That finding suggests that H_s is not related to the phenomenon of long-term correlation that has been

classically determined with stochastic processes analyses. The obtained values ($H \cong .8$, see Table 1) revealed, in the short term, high persistence in successive displacements. As proposed by Liebovitch and Yang (1997), such persistent behavior for brief time intervals could be caused by inertia, a property that obviously cannot be ignored in postural sway. Inertia tends to keep the COP moving in the same direction and thus to produce persistent correlation, at least when the considered time interval is smaller than the relaxation time of the inertial movement.

The results of our approach clearly suggested that a continuous fractal process, characterized by antipersistent long-term correlations, underlies COP trajectories. That assumption clearly contradicts the two-stage model proposed by Collins and De Luca (1993), but one should note that that model was previously criticized by Newell et al. (1997), who showed that a linear stochastic process model, the Ornstein–Uhlenbeck equation, gave a satisfying account of COP trajectories. In that model, diffusion is also a continuous process rather than a two-step operation. According to those authors, the claim of dual open- and closed-loop diffusion processes needs to be examined carefully.

One could wonder, nevertheless, whether in our approach some essential features of COP trajectories could be hidden. We do not definitely deny any interest in the approach initiated by Collins and De Luca (1993). The time coordinate of the inflexion point proved to be an interesting variable, revealing the effect of various experimental conditions and pathological syndromes (Newell et al., 1996; Riley, Mitra, et al., 1997; Riley, Wong, et al., 1997; Rougier, 1999; Rougier & Caron, 2000; Rougier & Farenc, 2000). Nevertheless, if the inflexion of the stabilogram–diffusion plot reflects only some physical or physiological boundaries in the time series (Liebovitch & Yang, 1997), then we are not sure that fractal analysis methods constitute the most relevant approach. Liebovitch and Yang noted that the exact determination of the time coordinate of the inflexion point remains difficult because the values obtained with one method could be 10 times larger than those obtained with another method. Others approaches, based on the analysis of the range of the original series, could be more relevant in that respect.

We do not argue, on the other hand, that a unique H exponent for a given series constitutes the only acceptable result in fractal analysis. Peng et al. (1995) reported crossover phenomena in heartbeat time series, which were clearly not related, as in the previously discussed studies, to the boundedness of the series within physiological limits.

One could also note that in R/S analysis and DFA, the shortest time intervals are traditionally omitted in the estimation of the scaling exponent (see Appendix). The purpose for omitting those intervals is to avoid the calculation of range or standard deviation on small data samples, which could eventually hide specific features in the short-term region. That remark cannot be considered for the present analyses, because the threshold we used (10 data points)

was clearly below the transition point identified with the method of Collins and De Luca (1993).

Concluding Remarks

From our point of view, the main purpose for fractal analysis, in the biological domain, remains the precise assessment of long-term correlations and their possible alteration under experimentally controlled conditions. Our present analyses suggest that the approach of Collins and De Luca (1993) failed to satisfy that goal: Long-term correlations appeared to be clearly underestimated, and their assessment, at the individual level, seemed to be based on quite poorly defined diffusion plots because of an evident contamination by low-frequency oscillatory components.

We propose alternative methods, especially designed for the analysis of such bounded series and able to provide precise estimations of H exponents. In that respect, our results suggest that the COP trajectory can be considered as an fBm, close to the so-called $1/f$ noise (easily identifiable by the obtaining of α exponents close to 1.0 in DFA; see Appendix). $1/f$ noise constitutes a very special case of fBm and was discovered in a number of biological time series, such as heartbeat and stride interval (Hausdorff et al., 1997; Peng et al., 1995; see also Gilden, Thornton, & Mallon, 1995; Yamada, 1995). Most interesting, pink noise was often evidenced in the behavior of healthy and adaptive systems, whereas disabilities generally led to an alteration of the fractality of the time series. For example, Hausdorff et al. (1997) showed that the time series of successive stride intervals in healthy young adults presented a fractal structure, characterized by an α exponent close to 1.0. The exponent was lower in elderly participants and in participants with Huntington's disease, revealing that in those cases the stride-interval fluctuations were more random (i.e., less correlated).

When considering the power spectrum of the time series (see, in Appendix, Spectral Analysis), $1/f$ noise signifies that each frequency has power proportional to its period of oscillation (equivalently, power is proportional to $1/f$). As such, power is distributed across the entire spectrum and not concentrated at a certain portion. Consequently, fluctuations at some time scale are only loosely correlated with those at another time scale. That relative independence of the underlying processes acting at different time scales suggests that a localized perturbation at one time scale will not necessarily alter the stability of the global system. In other words, $1/f$ noise renders the system more adaptive to internal and external perturbations (West & Shlesinger, 1990).

A precise quantification of scaling exponents is essential in experimental research as well as in clinical applications (Peng et al., 1995). Several methods for characterizing fractal time series have been proposed during the last decade. Those methods were recently discussed and evaluated with regard to their ability to provide reliable estimates of the Hurst exponent of exact fractal time series (Caccia et al., 1997; Cannon, Percival, Caccia, Raymond, & Bassingthwaite, 1997; Rangarajan & Ding, 2000;

Shepers, van Beek, & Bassingthwaighe, 1992). A good methodological synthesis was proposed by Eke et al. (2000), who pointed out the necessity for using methods adapted to the very nature of the original series (i.e., fBm or fGn). Nevertheless, they did not address the specific problems raised by physiological data, which frequently lie at the boundary between fBm and fGn (West & Shlesinger, 1989) and appear generally bounded within biological limits. Our analyses showed that the use of unadapted methods with such series could produce misleading results and support erroneous interpretations.

We examined in this article two methods specially designed so that the specific features of such series can be taken into account. Working on the basis of the cumulative sums of the original series, those methods allow both the mapping of biological data onto pure (diffusion-free) fractal models and an accurate characterization of long-term correlation. The present methodological debate remains open, considering the current lack of consensus among scientists concerning the basic concepts of fractal theory (scaling exponent, persistence, and antipersistence, among others) and their application on experimental series (Cannon et al., 1997; Eke et al., 2000).

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NOTES

1. The brackets denote an average over time.
2. According to that definition, persistence and antipersistence are defined in terms of successive increments. As such, the boundary between persistence and antipersistence, in terms of fBm, is Brownian motion. Persistence is characterized by a higher diffusion than Brownian motion is; and conversely, antipersistence is characterized by a lower diffusion than is Brownian motion. That definition was recently adopted, for example, by Caccia et al. (1997) and by Eke et al. (2000). Some authors, nevertheless, have defined persistence in terms of successive positions (e.g., Peng et al., 1995; Yamada, 1995). According to that definition, the boundary between persistence and antipersistence is white noise. As a consequence, pink noise, or $1/f$ noise, which constitutes a compromise between white noise and Brownian motion, has sometimes been qualified as antipersistent (according to the first definition) and other times as persistent (according to the second definition).
3. Collins and De Luca (1993) also proposed an estimation of the diffusion coefficient D (see Equation 3) on the basis of an assessment on the slope of the natural plot of $\langle \Delta x^2 \rangle$ as a function of Δt . Such an estimation appears awkward, because the original relation of Einstein (1905) holds only for Brownian motion.
4. To avoid any confusion, we have termed the exponent obtained with R/S analysis $H_{R/S}$.
5. The Lorenz attractor is generated by the following set of differential equations:

$$\begin{aligned}\dot{x} &= \sigma(y - x), \\ \dot{y} &= \rho x - y - xz, \\ \dot{z} &= xy - \beta z,\end{aligned}$$
 with $\alpha = 10$, $\rho = 28$, $\beta = 8/3$.
6. Most interesting, the method of Collins and De Luca (1993)

appeared unable, beyond the transition point, to distinguish the Lorenz series from white noise ($H = 0$). That result illustrates the fact that for a strictly bounded series, the mean squared displacement becomes independent of interval length for long intervals.

7. We determined the diffusion coefficient D in order to replicate the analyses of Collins and De Luca (1993). Theoretically, D is an accurate index of stochastic activity only when $H = .5$ (see Note 3).

8. We consider R/S analysis and DFA to be complementary. Note, nevertheless, that we expected R/S analysis to overestimate H for time series with $H < .7$, and to underestimate H for $H > .7$ (Caccia et al., 1997; Liebovitch & Yang, 1997; Shepers et al., 1992). On the other hand, DFA is related to scaled windowed variance methods, which seem to provide satisfying results for the analysis of fBm (Cannon et al., 1997).

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APPENDIX

Rescaled Range Analysis

Consider the time series of N numbers as $x(t)$. The series is divided into nonoverlapping intervals of length n . Within each interval, an integrated series $X(t, n)$ is computed as follows:

$$X(t, n) = \sum_{k=1}^t \{x(k) - \langle x \rangle_n\}, \quad (\text{A1})$$

where $\langle x \rangle_n$ is the local average of the n data:

$$\langle x \rangle_n = \frac{1}{n} \sum_{t=1}^n x(t). \quad (\text{A2})$$

For each interval, the difference between the maximum and the minimum integrated data $X(t, n)$ is the range R .

$$R = \max X(t, n) - \min X(t, n), \quad (\text{A3})$$

where $1 \leq t \leq n$.

That range is then divided for normalization by the local standard deviation (S) of the original series $x(t)$. That computation is repeated over all possible interval lengths (in practice, the shortest length is around 10, and the largest is $N/2$, giving two adjacent intervals). Finally, the rescaled ranges R/S are averaged for each interval length n . R/S is related to n by a power law:

$$R/S = (an)^{H_{R/S}}, \quad (\text{A4})$$

where a is a constant. $H_{R/S}$ is expressed as the slope of the double-logarithmic plot of R/S as a function of n (see Figures 2 and 3), and can vary between 0 and 1.

For obtaining an $H_{R/S}$ corresponding to the H exponent of Equation 4 ($H = .5$ for a pure Brownian motion), R/S analysis should be applied on fGn, that is, the series of increments in fBm. As such, the series exhibits persistent behavior when $H_{R/S}$ is higher than .5, and antipersistent behavior when $H_{R/S}$ is lower than .5.

We proposed, in this article, to apply R/S analysis directly on fBm in the special case of biological bounded series. That method induces a shift in the obtained values, with $H_{R/S} = 1$ for Brownian motion and .5 for white noise. As a consequence, $H = H_{R/S} - .5$. Because $H_{R/S}$ cannot exceed 1.0, that particular application of the method is not possible if $H > .5$ (persistent series).

Detrended Fluctuation Analysis

Consider the time series of N numbers as $x(t)$. In a first step, one integrates the original series by computing for each t the accumulated departure from the mean of the whole series:

$$X(k) = \sum_{i=1}^k [x(i) - \bar{x}] \quad (\text{A5})$$

The integrated series is divided into nonoverlapping intervals of length n . In each interval, a least squares line is fit to the data (representing the trend in the interval). One then detrends the series $X(t)$ locally by subtracting the theoretical values $X_n(t)$ given by the regression. For a given interval length n , the characteristic size of fluctuation for the integrated and detrended series is calculated by

$$F(n) = \sqrt{\frac{1}{n} \sum_{k=1}^N [X(k) - X_n(k)]^2} \quad (\text{A6})$$

That computation is repeated over all possible interval lengths (in practice, the shortest length is around 10, and the largest is $N/2$, giving two adjacent intervals). Typically, $F(n)$ increases with interval length n . A power law is expected, as

$$F(n) = an^\alpha, \quad (\text{A7})$$

where a is a constant and α is the scaling exponent. Scaling exponent α is expressed as the slope of a double-logarithmic plot of $F(n)$ as a function of n and can vary between 0 and 1.5. In its original formulation, the DFA was conceived to be applied directly on raw data. When α is 0.5, the original series is an uncorrelated random process (white noise). A scaling exponent $\alpha = 1.0$ corresponds to a special case, pink or $1/f$ noise, which lies at the boundaries between

stationarity ($\alpha < 1.0$) and nonstationarity ($\alpha > 1.0$). When $\alpha = 1.5$, the original series is a Brownian motion. Higher values are mathematically obtainable (up to 2.0), for persistent series. Nevertheless, the reliability of such high exponents is still unknown.

α and H are linked according to the following equations:

$$\alpha = (4H + 1)/2 \text{ or } H = (2\alpha - 1)/4. \quad (\text{A8})$$

Spectral Analysis

A third classical method for assessing stochastic processes operates on the basis of the periodogram obtained by Fourier analysis. The relation of Mandelbrot and van Ness (1968) can be expressed as follows:

$$S(f) \propto 1/f^\beta, \quad (\text{A9})$$

where f is the frequency and $S(f)$ the corresponding squared amplitude. One estimates β by calculating the negative slope of the line relating $\log S(f)$ to $\log f$, as

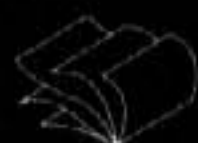
$$\log S(f) \propto (\log f)^{-\beta}. \quad (\text{A10})$$

For a white noise process, $\beta = 0$ (signifying that all squared amplitudes are equivalent, whatever the frequency). $\beta = 2$ for Brownian motion. In the special case of pink noise, $\beta = 1.0$: In other words, $S(f)$ is proportional to $1/f$.

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