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Evenly spacing in Detrended Fluctuation Analysis

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HIGHLIGHTS

- We analyze the effects of evenly spacing in Detrended Fluctuation Analysis (DFA).
- We compare evenly vs. logarithmic spacing with synthetic signals.
- Evenly spacing decreases by 36% the dispersion of estimates.
- Evenly spacing could allow the analysis of shorter time series.
- Evenly spacing should be systematically adopted in the application of DFA.

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ABSTRACT

Detrended Fluctuation Analysis is a widely used method, which aims at assessing the level of self-similarity in time series. This method analyzes the diffusion properties of the signal, by computing the linear regression slope in the diffusion plot, representing in log–log coordinates the relationship between the variability of the signal and the length of the intervals over which this variability is computed. We compare in this paper the results obtained with logarithmically spaced and evenly spaced diffusion plots. The study shows the substantial benefits of evenly spacing, especially in the reduction of the variability of estimation.

1. Introduction

The Detrended Fluctuation Analysis (DFA), initially introduced by Peng et al. [1], is a widely used analysis method which aims at determining the level of self-similarity in a time series. A better understanding of this method supposes a short introduction to the underlying model.

The DFA algorithm is based on the diffusion property of fractional Brownian motion (fBm), a family of stochastic processes introduced by Mandelbrot and Van Ness [2]. Here we focus on the discrete version of fBm, which corresponds to the nature of the series analyzed in experimental research. In such process variance is a power function of the length (n) of the interval over which it is computed. Consider a process x_i:

$$Var(x_i) \propto n^{2H}, \quad (1)$$

where H is the Hurst exponent, which can take any real value within the interval]0, 1[. For $H = 1/2$, x_i corresponds to ordinary Brownian motion, and variance is just proportional to the elapsed time (normal diffusion). For $H \neq 1/2$, x_i is characterized by anomalous diffusion: The process is said subdiffusive for $H < 1/2$, and superdiffusive for $H > 1/2$.

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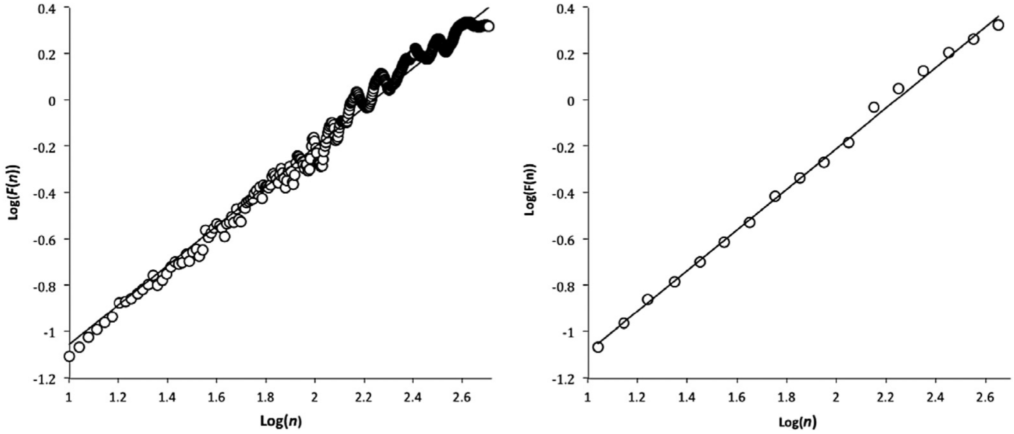

Fig. 1. Two example diffusion plots, obtained with the same series. The left panel represents the logarithmically spaced plot, and the right panel an evenly spaced plot. The slopes of the regression lines are 0.85 and 0.88, respectively.

A second family of stochastic processes, fractional Gaussian noise (fGn), is defined as the series of increments within a fBm. By definition, a fGn is the series of differences in a fBm, and conversely the summation of a fGn gives a fBm. Each fBm series is then related to a specific fGn, and both are characterized by the same H exponent. H determines the nature of correlations between successive values in the fGn: for $H < 0.5$, successive values are negatively correlated, and the series is said to be anti-persistent. Conversely for $H > 0.5$ successive values are positively correlated, and the series is persistent. For $H = 0.5$, successive values are uncorrelated, and the series corresponds to white noise. An important difference between these two classes of processes is that fBm are non-stationary processes, as suggested by Eq. (1), whereas fGn series present stationary mean and variance over time.

As presented in the first paragraphs of this article, fGn and fBm are defined as two distinct families, which can be considered superimposed, with their relationships of summation/differencing. A number of authors, however, have proposed to consider these two families as a continuum, surrounding the mythical border of "ideal" $1/f$ noise [3–6].

The *Detrended Fluctuation Analysis* (DFA), Ref. [1] can be applied to both fGn and fBm signals. The details of the DFA algorithm will be detailed later in this paper. Here we just present its general principles, in order to introduce the hypotheses underlying the present work. This method exploits a typical scaling law, which states that the standard deviation of the integrated series is a power function of the interval length over which it is computed, with an exponent α. Considering a time series x_i:

$$\begin{cases} X_i = \sum_{k=0}^{i} x_k \\ SD(X_i) \propto n^{\alpha}. \end{cases} \tag{2}$$

This scaling just derives from the original definition of fBm, expressed in Eq. (1). fGn series are characterized by α exponents ranging from 0 to 1, and fBm by exponents ranging from 1 to 2. $\alpha = 1$ corresponds to $1/f$ noise. If the series x_i is a fGn, X_i is the corresponding fBm and α is the Hurst exponent. If x_i is a fBm, X_i belongs to another family of over-diffusive processes, characterized by α exponents ranging from 1 to 2, and in that case $\alpha = H + 1$ [1].

The DFA algorithm works as follows: The series is first integrated, and then this integrated series is divided into non-overlapping intervals of length n. Within each interval the series is detrended, and the standard deviation of the residuals is computed. Then one calculates the average (detrended) standard deviation for the intervals of length n, noted $F(n)$. This computation is repeatedly performed over all n values. In practice, the shortest interval length is chosen for allowing a valid estimate of standard deviation (for example $n = 10$), and the lengthiest for allowing at least two distinct estimates (e.g., $n = N/2$). Then $F(n)$ is plotted against n in log–log coordinates, forming the so-called *diffusion plot*, and the exponent α is obtained as the slope of the linear regression (see Fig. 1, left panel).

An important consequence of this logarithmic transformation is that the density of points along the abscissa axis increases as interval length increases (see Fig. 1, left panel). And as regression analysis works on plane geometric principles, the weight of long intervals in the calculation of the slope becomes higher than that of short intervals. Moreover, the long-term region of the diffusion plot often presents irregularities around the linear trend, especially because the number of intervals involved in the computation of $F(n)$ is smaller for long time scales [7]. This results in a greater uncertainty in the determination of the slope in the long-term region of the diffusion plot, where most points are concentrated. A solution for overcoming this problem is to define the diffusion plot over a set of points evenly spaced in the logarithmic scale (Fig. 1, right panel).

Several methods have been proposed for obtaining a series of evenly spaced points in the log–log plot. Some authors have proposed to select a set of interval lengths, evenly spaced on the logarithmic scale. This idea was initially introduced by

Peng et al. [8]. For example Jordan, Challis, and Newell [9] used fifty interval lengths distributed between 4 and $N/4$ [10–16]. This method will be designed thereafter as *evenly spaced DFA*.

However, this arbitrary selection of isolated, evenly spaced points in the original diffusion plot could raise some problems, especially in the long-term region of the diffusion plot, where points often present strong deviations from the regression line. A solution for accounting with this potential problem is to divide the range of $\log(n)$ into a series of intervals of equal length, and then to average the points that fall within each interval [17–19]. This method allows to exploit the whole information contained in the original diffusion plot, while satisfying the evenly spacing principle. This method will be designed thereafter as *evenly spaced averaged DFA*.

While theoretically convincing, the advantages of evenly spacing have never been rigorously assessed, and a number of recent papers still work with logarithmically spaced points [20–31]. The aim of this paper is to assess the benefits of evenly spacing, in terms of accuracy and consistency of estimates. We hypothesize that evenly spacing should produce a lower variability in the estimation of exponents, and should allow working with shorter series. We also hypothesize that the evenly spaced averaged method should gave better results than simple evenly spacing.

2. Methods

2.1. Series simulation

In order to assess the performances of DFA over the whole fGn/Bm model, we simulated series with the algorithm proposed by Davies and Harte [32]. This method is known to generate fGn series that preserve the expected correlation structure for a given H value. This algorithm has been used in a number of previous studies aiming at analyzing exact fractal series [4,33–35]. We first generated fGn series for H values ranging from 0.1 to 0.9, by steps of 0.1. A second set of fGn series was generated, for H values ranging from 0.1 to 0.9, by steps of 0.1, and these series were summed for obtaining fBm series for each corresponding H values. In each case we generated 120 series of 1024 data points.

2.2. Detrended Fluctuation Analysis

Here we present in detail the original algorithm of DFA [1]. Consider a series x_i of length N. The series is first integrated, by computing for each i the accumulated departure from the mean of the whole series:

$$X_i = \sum_{j=1}^{i} \left(x_j - \bar{x}\right). \tag{3}$$

This integrated series is divided into k non-overlapping intervals of length n. The last $N - kn$ data points are excluded from analysis. Within each interval, a least squares line is fitted to the data (representing the trend in the interval). The series X_i is then locally detrended by subtracting the theoretical values X_i^{Th} given by the regression. For a given interval length n, the characteristic size of fluctuation for this integrated and detrended series is calculated by:

$$F(n) = \sqrt{\frac{1}{N - kn} \sum_{i=1}^{N-kn} \left(X_i - X_i^{Th}\right)^2}. \tag{4}$$

This computation is repeated over all possible interval lengths. In the present paper we considered interval lengths ranging from $n = 10$ to $n = N/2$. Typically, F increases with interval length n. A power law is expected, as

$$F(n) \propto n^{\alpha}. \tag{5}$$

α is expressed as the slope of the double logarithmic plot of $F(n)$ as a function of n (see Fig. 1, left panel).

2.3. Evenly spaced DFA

The papers using evenly spaced DFA remain often elusive about the selection of the points to introduce in the diffusion plot. Generally the shortest and lengthiest intervals are explicitly defined, and sometimes the number of points included in the diffusion plot. Quite often, however, this information is only accessible through the visual examination of the diffusion plots, when provided. The main idea is that the series of selected interval lengths should present a geometric progression:

$$n_i = a n_{i-1} \tag{6}$$

where a is a constant [8,10,15]. Here we propose a generic solution, considering the number of points to include in the diffusion plot (k), the minimum and maximum interval lengths ($n_{\min}$ and $n_{\max}$, respectively). The k interval lengths, noted n_i ($i = 1, 2, \ldots, k$), are defined as:

$$\begin{cases} n_1 = n_{\min} \\ n_i = \left[n_{i-1} 10^{\frac{\log_{10}(n_{\max}) - \log_{10}(n_{\min})}{k-1}} \right]. \end{cases} \tag{7}$$

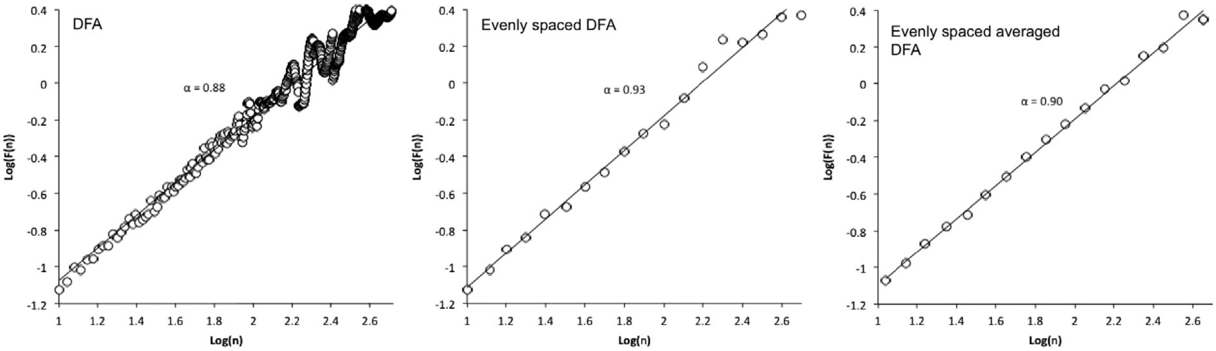

Fig. 2. Example diffusion plots, obtained with a series with true $\alpha = 0.9$. Left: DFA; middle: evenly spaced DFA; right: evenly spaced averaged DFA.

The brackets signify that n_i is rounded to the closest integer value. In the present analysis, for series of 1024 points, we set $k = 18$, $n_{\min} = 10$, and $n_{\max} = 512$ ($N/2$). We obtained the following n_i values: 10, 13, 16, 20, 25, 32, 40, 51, 64, 80, 101, 128, 161, 203, 322, 256, 406, 512. The regression slope was computed over the corresponding points.

2.4. Evenly spaced averaged DFA

For obtaining the evenly spaced averaged diffusion plots, we divided the (log) abscissa into k bins of length $(\log_{10}(n_{\max}/n_{\min}))/k$, starting from $\log_{10}(n_{\min})$. The k bins are then defined by:

$$bin_i = \left[\log_{10}(n_{\min}) + \left(\frac{i-1}{k}\right)\left(\log_{10}\left(\frac{n_{\max}}{n_{\min}}\right)\right); \log_{10}(n_{\min}) + \frac{i}{k}\left(\log_{10}\left(\frac{n_{\max}}{n_{\min}}\right)\right)\right[\tag{8}$$

with $i = 1, 2, \ldots, k$. The corresponding bins in the natural scale are defined as:

$$bin_i = \left[n_{\min} + (i-1)10^{\frac{1}{k}\log_{10}\left(\frac{n_{\max}}{n_{\min}}\right)}; n_{\min} + i10^{\frac{1}{k}\log_{10}\left(\frac{n_{\max}}{n_{\min}}\right)}\right[, \tag{9}$$

with $i = 1, 2, \ldots, k$. In this natural scale, the length of the successive bins (and hence the number of points that fall into each successive bin) presents a geometric progression:

$$length_{i+1} \simeq \left(10^{\frac{1}{k}\log_{10}\left(\frac{n_{\max}}{n_{\min}}\right)}\right) length_i. \tag{10}$$

Within each bin i, we computed the average interval length $\bar{n}_i$ and the average fluctuation size $\bar{F}(n)_i$, and determined the diffusion plot with these k average points. In the present analyses, we set $n_{\min} = 10$, $n_{\max} = 512$, and $k = 18$.

2.5. Statistical analyses

The results of these analyses were examined in terms of accuracy and consistency. Accuracy refers to the difference between the mean estimate for a set of series and the true exponent that was used for its simulation. This aims at determining systematic biases that could occur in some parts of the fGn/fBm model [33]. Consistency refers to the standard deviation of exponent estimates in a set of series simulated with the same true exponent. In order to assess the effect of series length, we performed additional analyses with shorter series of 512 and 256 data points. In both cases we considered the first segments of our simulated series.

3. Results

We present in Fig. 2 example diffusion plots obtained with the three methods on the same series. As expected, DFA produced a diffusion plot exhibiting large fluctuations around the linear trend in the long-term region. In contrast, the two other methods seem able to allow a more effective determination of the linear trend. Note that in this particular example, evenly spaced averaged DFA seems to present less deviations from the linear slope in the long-term region.

We present in Fig. 3 the results of the three methods, in terms of accuracy of the mean estimates. All methods gave similar results for fGn series, and mean α estimates appear very close to the corresponding true α. In contrast, DFA tends to underestimate α for fBm series. This bias is also present in the two evenly spaced methods, which both present similar results.

The length of series had no noticeable effect of the accuracy of methods for fGn series. Reducing length tended to increase the underestimation bias for fBm close to $1/f$.

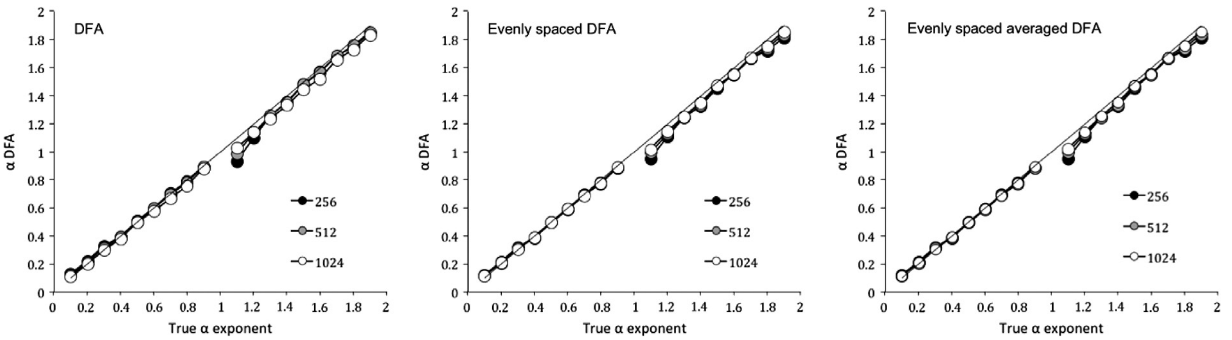

Fig. 3. Mean α estimates, as a function of true α exponents, for DFA (left), evenly spaced DFA (middle), and evenly spaced averaged DFA (right). The solid line represents the theoretical equality between estimated and true exponents.

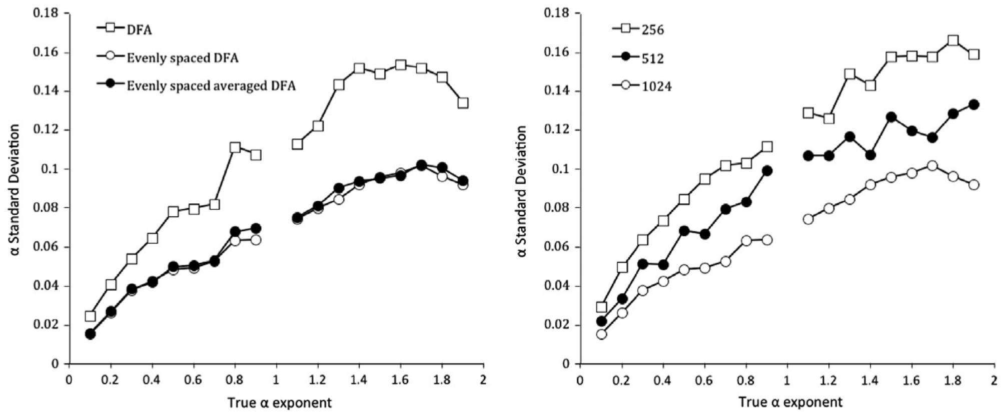

Fig. 4. Left: Standard deviation of the samples of estimated exponents, as a function of the true exponent, for the three tested methods. Right: Standard deviation of the samples of estimated exponents, as a function of the true exponent and according to series length (results obtained with evenly spaced DFA, evenly spaced averaged DFA gave similar results).

We present in Fig. 4 (left panel), for the three methods, the standard deviation of the samples of estimates, as a function of true α. In all cases variability increases as true α increases, with a kind of ceiling effect for $\alpha > 1.5$.

The most interesting result is the clear decrease of variability with the two evenly spaced methods, as compared with DFA. Note that the two evenly spaced methods gave similar results. The average decrease in variability is of about 36% for evenly spaced DFA, and 35% for evenly spaced averaged DFA, as compared with DFA.

We present in Fig. 4 (right panel) the standard deviation of α estimates as a function of series length, using evenly spaced DFA. As expected, variability increased as series length decreased. However, the examination of the two graphs shows that evenly spaced DFA presents a variability with series of 256 points which is roughly similar to that obtained with DFA, with series of 1024 points. Evenly spaced averaged DFA gave similar results.

4. Discussion

The use of evenly spaced diffusion plots has been recommended for a long time in the literature, but its benefits have never been systematically assessed, and a number of recent papers still exploit logarithmically spaced diffusion plots. We show in this paper that evenly spacing provides substantial benefits, and especially increases the consistency of estimates. Evenly spacing provides reliable results with relatively short series, an important goal in psychological and behavioral sciences in the design of analysis methods [33].

We tested two distinct procedures, evenly spaced DFA and evenly spaced averaged DFA, hypothesizing that the second one should give better results. Our analyses did not comfort this hypothesis, and both methods gave similar results. One should keep in mind, however, that the present study was performed with synthetic signals. One could suppose that such signals present a more homogeneous correlation behavior over time, and fewer deviations around the regression line in the diffusion plot, as compared with empirical series. Despite the absence of statistically significant results in the present work, the evenly spaced averaged method could in our mind be favored.

Our results confirm the slight underestimation bias of DFA for fBm series, which has been already noticed in several studies [4,33]. It is important to keep in mind that DFA first integrates the series and then analyzes the diffusion properties of the resultant series. In other words the initial series is considered as increments, and DFA works on the diffusion properties of its cumulative sum. However, DFA is mainly sensitive to the correlation structure of the series of increments, and Delignières [36] showed that fGn and fBm presented completely different correlation structures. By definition, the cumulative sum of a fGn is a fBm, which possesses the diffusion property expressed in Eq. (1). In contrast, there is no guaranty that the correlation structure of fBm provides its cumulative sums with such a property. The global under-estimation bias with fBm series could be related to this problem. It seems important to notice that when the analyzed series is unambiguously characterized as fBm (e.g., with an α estimate higher than 1.2, see Ref. [33]), it could be considered to re-apply DFA, omitting the summation step. This procedure directly assesses the diffusion properties of the original signal (supposed to be a fBm), and gives an unbiased estimate of the Hurst exponent, which can be converted if necessary in α metrics ($\alpha = H + 1$).

Evenly spacing could also be of interest in the approach of crossovers, a rather common phenomenon in fractal analysis [37–39]. Scale invariance is theoretically revealed by the presence of a linear trend in the bi-logarithmic diffusion plot, over the whole range of time scales. Sometimes, however, correlations do not follow the same scaling law for all time scales, and a crossover can be observed between different scaling regions [37,40]. Such crossover could be related to the presence of a sinusoidal trend in the series, and in that case the timescale where this crossover occurs is inversely related to the oscillatory frequency that dominates the time series [38]. More generally, a crossover appears when series are bounded within upper and lower limits [41].

Because crossovers often appear in the long-term region of the diffusion plots, one could suppose that evenly spacing could allow a more accurate determination of the nature of the crossover [38], and in the case of genuine crossovers separating the diffusion plots in two clearly distinguishable scaling regimes, a better estimate of the crossover point, in order for example to filter out the troublemaking frequency [42].

The present paper focused more on evenly spacing than on DFA itself. However, some concluding remarks about this widely used method could represent an interesting complement. The DFA algorithm is based on the fGn/fBm model, and a number of experiments have proven the suitability of this model for accounting for the long-range correlation properties of a wide diversity of physiological signals. However, a blind application of DFA could yield irrelevant results, and one could wonder whether the fGn/fBm model can be used for any forms of physiological fluctuations [3,43]. Some recent experiments considered signals that clearly fell out of the scope of the fGn/fBm fluctuations [41,44]. Moreover, the fGn/fBm model presents an abrupt breakdown of correlation properties around the $1/f$ boundary, casting some doubts about its relevancy for accounting for $1/f$ behavior [36]. Some alternative models have been proposed for accounting for long-range correlation properties [45,46], which could be considered in order to design more suitable analysis methods.

Despite these reserves, evenly spacing yields substantial benefits, and it seems reasonable to promote the systematic use of this procedure, in order to improve the performances of DFA. Note that this recommendation could be extended to all methods exploiting power laws, including Power Spectral Density [4], Scaled Windowed Variance Analysis [47], Rescaled Range Analysis [48], or Dispersional Analysis [49,50].

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