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Negative dimensions: Theory, computation, and experiment

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Negative dimensions in probabilistic fractal measures are analyzed using the concept of level-independent multiplier distributions. By suitably manipulating these distributions we compute the positive and negative parts of the $f(\alpha)$ function. It is demonstrated that the multiplier method extracts the $f(\alpha)$ function with *exponentially less* work, and that it is more accurate than conventional box-counting methods. The utility of this method is demonstrated by applying it to a binary cascade with a triangular multiplier distribution and the dissipation field of fully developed turbulence.

In its present form, the multifractal formalism involves decomposing fractal measures into interwoven fractal sets each of which is characterized by its singularity strength. Examples of such measures are the invariant probability measure of a dynamical system, the harmonic measure of a diffusion-limited aggregation (DLA), or the spatial distribution of the dissipation field of fully developed turbulence. The simplest way of performing a multifractal analysis[1,2] is to partition the measure using boxes of fixed size ϵ. Then the measure in each box of size ϵ can be characterized by a singularity strength α by $P_i(\epsilon)\sim\epsilon^{\alpha_i}$, where the index $i=1,2,3,\ldots,1/\epsilon$ denotes the box number. The number of occurrences of a particular value of α defines $f(\alpha)$ (the fractal dimension of that iso-α set) by $N(\alpha)\sim\epsilon^{-f(\alpha)}$. The canonical way of computing $f(\alpha)$ directly (without Legendre transforming) is described in Refs. 3–5.

An alternative way of performing the analysis is to compute the sum (or partition function)

$$Z(q)=\sum_i P_i^q(\epsilon)=\epsilon^{\langle\tau(q)\rangle}, \tag{1}$$

and use the equations

$$\langle\alpha(q)\rangle=\frac{\partial\langle\tau(q)\rangle}{\partial q},\quad f(q)=q\langle\alpha(q)\rangle-\langle\tau(q)\rangle. \tag{2}$$

Typically one varies ϵ and checks for a unique $f(\alpha)$ function over some range of ϵ. The existence of such a unique function is believed to be a signature of statistical self-similarity.

However, when one performs a multifractal analysis on measures arising from experiments, in particular the dissipation field of turbulence, one notices[6,7] that the $f(\alpha)$ function fluctuates from sample to sample by an amount greater than the (least-squares) error bars on any one sample would indicate and that the dimension of the extremal iso-α sets are often negative.[8–11] In this paper we wish to understand the occurrence of the above two observations and provide an efficient method of computing both the positive and the negative parts of the $f(\alpha)$ function. The approach rests on the view that the scaling properties reflecting the self-similar structure of the measure can (for such probabilistic multifractals) be described in terms of a repeated composition of a level (scale) independent distribution of multipliers that define the rearrangement of the measure into smaller pieces. This issue has been discussed briefly in Refs. 10 and 12. We demonstrate that by suitably manipulating this multiplier distribution one can compute the entire $f(\alpha)$ function with exponentially less work (and correspondingly more accurately) than is possible by conventional box-counting methods, and apply the multiplier method to the dissipation field of fully developed turbulence.

The sample-to-sample fluctuation of the scaling properties of the measure implies that the partition function $Z(q)$ [defined by Eq. (1)] varies from sample to sample. To define thermodynamic quantities one must adopt an averaging procedure. One can average the logarithm of the partition function over different samples (quenched averaging) or average the partition function itself (annealed averaging) (in the context of multifractals see for example Refs. 9 and 13–17). In quenched averaging, one first computes $f(\alpha)$ for each sample. Since every *observed* α value will occur at least once, these curves will be strictly positive resulting in an averaged positive function. In annealed averaging, the resultant curve may not be positive everywhere because the dimension is now defined by $\langle N(\alpha)\rangle\sim\epsilon^{-f(\alpha)}$. Since $f(\alpha)$ is now the logarithm of an expectation value, a negative dimension will be associated with an iso-α set composed of α values that occur less

often than one per typical sample.

There are at least two situations where negative dimensions are of interest. First, one may have a cascade process which is inherently probabilistic and the negative dimensions will describe the rarely occurring events. Second, the experimental procedure itself may force one to adopt a probabilistic view of a deterministic process. For example, one-dimensional hot wire measurements of the dissipation field of turbulence may be considered as randomly oriented one-dimensional cuts through a three-dimensional turbulent dissipation field, even if the latter arises from a strictly deterministic process. Events occurring with low probability in three-dimensional space would be missed by any single typical cut, but averaging (supersampling[9]) over many such cuts would enable one to gather information about such events.[18] Notice that a negative exponent in Eq. (1) means that as $\epsilon \rightarrow 0$ the number of occurrences of these α values actually *decreases*. Thus as one refines the measure, i.e., increases n, one needs an *exponentially increasing* number of samples to observe the same α value.[9] Correspondingly, for a fixed number of samples, increasing the level of refinement of each sample would show lesser negative parts of the $f(\alpha)$ curve.[9] This statement, although correct, is paradoxical: *a priori* it stands to reason that refining a measure should lead to better information about its scaling properties. And yet, following the supersampling procedure one does increasingly worse as the level of refinement increases. The attempt to resolve this apparent paradox is what has led us to explore the multiplier method.

Consider a simple binary process[19] in which at each level of refinement every piece divides into two equal ones but distributes its measure in the unequal ratio $\frac{7}{3}$. This is a special case of a probabilistic cascade, where the refinement process of each piece is (randomly) either [0.7,0.3] [i.e., the left piece (of the next generation) receives 70% of the measure and the right piece receives 30%] or vice versa, i.e., [0.3,0.7]. At the nth level, there are 2^n different combinations of multipliers that give rise to various α values. Since there are also exactly 2^n boxes at the nth level, all possible α values will be found in a single sample, leading to a well-defined and sample-independent $f(\alpha)$ curve. The extremal iso-α sets composed of boxes corresponding to the multipliers 0.7,0.7, $0.7,\ldots,n$ times [$\alpha=\log(0.7)/\log(0.5)=0.514\ldots$] and $0.3,0.3,0.3,\ldots,n$ times [$\alpha=\log(0.3)/\log(0.5)=1.71\ldots$] will occur exactly once at each level, and thus have zero dimension. All other combinations of the multipliers will occur more often and hence $f(\alpha)\geq 0$ everywhere. Consider a simple generalization,[20] where now the multipliers can be picked randomly from four rules: [0.7,0.3], [0.3,0.7], [0.8,0.2], and [0.2,0.8]. The extremal iso-α sets will be composed of boxes with multipliers 0.8,0.8, $0.8,\ldots,n$ times ($\alpha=0.138\ldots$) and $0.2,0.2,0.2,\ldots,n$ times ($\alpha=2.321\ldots$). However, these boxes will occur with probability $(\frac{1}{4})^n$. Since there are only 2^n boxes per sample, these extremal singularity strengths will be observed only once every $(2^n 4^{-n})^{-1}=2^n$ samples. Thus the $f(\alpha)$ curve will fluctuate from sample to sample and one will have to average over 2^n samples to observe the entire curve (this being the idea behind supersampling). The dimension of the singular set corresponding to $\alpha=2.321\ldots$ is $\log(2^{-n})/\log(2^n)=-1$, and the $f(\alpha)$ function, now quantifying the relative frequency of observing a singularity strength α in a given number of samples of finite size,[9] ranges from -1 to 1. This example suggests that all the scaling properties can be understood in terms of multipliers and the frequency with which various combinations occur. In particular the existence of a unique $f(\alpha)$ curve over different levels of resolution implies the existence of a scale-invariant multiplier distribution, whose repeated composition gives rise to the scaling properties. This means that, for each value of α, there exists a value of the multiplier M^* which, when composed n times, would produce the same α value, i.e., $M^*\sim 2^{-\langle\alpha(M^*)\rangle}$. The probability $P(M^*)$ of choosing the multiplier M^* is related to the dimension of the iso-α set by $P(M^*)=2^{+[f(M^*)-D_0]}$. It is important to note that $P(M^*)$ is a scale-invariant multiplier distribution derived from $P(M)$ but different from it.

In order to compute the scaling exponents from $P(M)$ one averages in the standard way the partition function over K samples (supersampling) of equal size so that

$$\langle\tau(q)\rangle=\frac{\log\langle Z(q)\rangle}{\log(\epsilon)}=\frac{\log\left[\left(\frac{1}{K}\right)\sum_{j=1}^{K}\sum_{i=1}^{a^n}P_{ij}^q(\epsilon)\right]}{\log(\epsilon)}, \tag{3}$$

where $\epsilon=a^{-n}$ (2^{-n} for binary cascades) and $P_{ij}(\epsilon)$ is the measure in the ith box of the jth realization of a cascade at level n. Since this relation should hold at any n due to the self-similarity of the measure, we set $n=1$. (Note that in doing so, we are assuming that no level-to-level correlations exist in the cascade. If they do then one should set n to a larger number so that the two boxes being compared are uncorrelated.[21] In the limit of infinite range correlations the multiplier method reduces to conventional box counting. However, systems with such long-range correlations are by definition not random multiplicative processes. It is therefore useful to run a conventional box-counting analysis on the data before using the multiplier method and establish self-similarity. Disagreement between the results of a multiplier analysis with conventional box counting then can be understood not as a breakdown of self-similarity but of the presence of strong level-to-level correlations in the cascade.) Having set $n=1$, we have a collection of K sets of boxes, where the measure in any one box is simply a multiplier picked randomly from $P(M)$ (subject to the constraint of conservation of the measure). Denoting the multiplier by M, and remembering that for $n=1$ the measure in the ith box is $P_{ij}=M_{ij}$, we can write[9]

$$\langle\tau(q)\rangle=-D_0-\frac{\log(\langle M^q\rangle)}{\log(a)}, \tag{4}$$

and correspondingly

$$\langle\alpha(q)\rangle=\left\langle\frac{\partial\tau(q)}{\partial q}\right\rangle=\frac{-\langle M^q\log(M)\rangle}{\langle M^q\rangle\log(a)}, \tag{5}$$

with $f(q)$ given by Eq. (2). Note that the averages are over the distribution of the multipliers $P(M)$. As q in Eq. (5) moves from $-\infty$ to ∞, different multipliers ranging from $M_{\min}$ to $M_{\max}$ get accentuated reproducing the en-

tire $f(\alpha)$ curve. The problem of computing the positive and negative parts of the $f(\alpha)$ function is thus reduced to the problem of computing $P(M)$. The simplest way of computing $P(M)$ is to cover a measure at the nth stage of refinement with boxes of size $2^{-(n-1)}$, and evaluate P_i $(i=1,2,3,\ldots,2^{(n-1)})$, then subdivide each of these boxes in two pieces and compute the ratios of the measures in the original box to any one of the two subdivided boxes. Each subdivided box will give a value for M, and using the entire measure one can compute $P(M)$ to a precision of 2^{-n}.[22]

Consider why the multiplier method is a substantial improvement over supersampling. From the definition of $P(M^*)$, α values corresponding to $P(M^*) < \frac{1}{2}$ will occur with probability less than $(\frac{1}{2})^{-n}$, and supersampling handles this by increasing the number of samples. If one supersamples over K different samples (of a binary cascade) then the minimum α value observed follows from the equation $(2^n K)[P(M^*)]^n = 1$. For $K = 2^n$, one can observe all α values corresponding to $P(M^*) \geq \frac{1}{4}$. Supersampling is thus a linear technique for increasing the probability of observing iso-α sets. Since the probability of encountering iso-α sets of negative dimension decreases exponentially with increasing level of resolution, one must increase the number of samples exponentially every time the measure is refined in order to keep the same resolution in $f(\alpha)$. On the other hand in the multiplier method, since one is measuring only the relative probability of occurrence of multipliers rather than the relative probability of occurrence of strings of n multipliers, one has much better precision. Further, as n increases, the multiplier method gets better as one can compute $P(M)$ to better precision, while the supersampling method gets exponentially worse. It is in this sense that the multiplier method requires exponentially less work besides being able to compute $f(\alpha)$ with better precision in comparison to supersampling.

We demonstrate these arguments by two examples. In the first example the multipliers of a binary cascade process are chosen randomly from a triangular distribution, i.e., $P(M) = 4M$ for $0 < M < \frac{1}{2}$ and $P(M) = 4(1-M)$ for $\frac{1}{2} < M < 1$. We compare both box-counting and multiplier methods with the analytical result. Figure 1 shows this comparison for the cascade at $n = 15$. The difference between the $f(\alpha)$ computed using the multiplier method (circles) from a single sample and the analytical $f(\alpha)$ (solid line) is not discernable. Since box counting a single sample of the same length would not give us any negative dimensions, we arbitrarily averaged (supersampled) 15 different realizations (each at $n = 15$). Figure 1 shows that supersampling (diamonds) produces good results for most of the positive $f(\alpha)$ curve but there is some error near the tails. Some negative values can be seen, but the convergence is clearly very slow and the accuracy poor.

The second example is the application to the dissipation field of fully developed turbulence in the atmospheric surface layer. The scaling properties of this quantity are rather important in order to be able to make statements about universality. In addition, the examination of the multiplier distribution itself may be quite useful for understanding the underlying fractal structure of turbulence.[23–26] Figure 2 shows a comparison between box counting and the multiplier method for a record length of 720000 points of the atmospheric dissipation field obtained from hot wire measurements.[6] We see that the multiplier method yields negative dimensions which could not be obtained from supersampling: Simple estimates[10,17,27] show that to observe α values corresponding to dimension of say -2, the latter method would require over 10×10^6 samples (roughly 10^{11} data points) requiring several years of data acquisition.

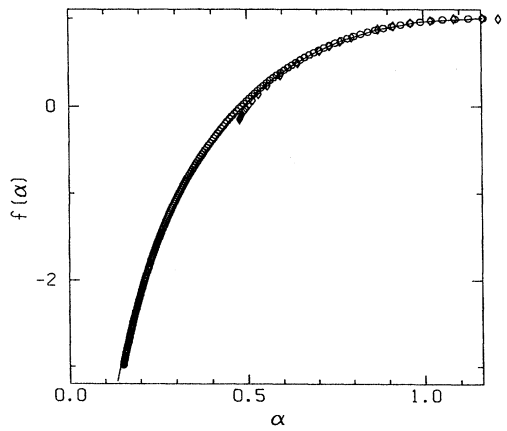

FIG. 1. Comparison between analytic results (solid line), multiplier method (circles), and supersampling (diamonds), for a binary cascade at $n = 15$ where the multipliers have been chosen randomly from a triangular distribution. The results of the multiplier method are for a single sample of 2^{15} points whereas, to improve statistics of the supersampling method, data for it were averaged over 15 different realizations. Results are shown only for $q > 0$. For $q < 0$, results from both methods can have large errors (Ref. 17).

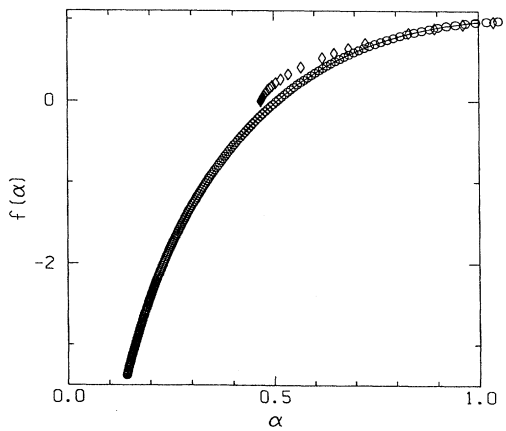

FIG. 2. Comparison between supersampling (diamonds) and the multiplier method (joined circles) for the dissipation field of fully developed turbulence in the atmospheric surface layer using 720000 data points. Shown is the portion of the $f(\alpha)$ curve which corresponds only to the singular region ($\alpha < 1$) of the dissipation field. Multipliers were obtained from box sizes ranging approximately from 100 to 2000 Kolmogorov scales assuming a binary cascade.

It appears that this reasoning holds true for most natural systems. In the study of fractals one is interested in looking either at the limit $\epsilon \rightarrow 0$, i.e., very fine resolution, or examining scaling behavior over a large range of resolution. However, for purposes of computing negative dimensions, the higher the level of refinement, the worse box counting gets while the multiplier method gets better. We therefore hope that the multiplier method will prove to be useful for the study of multifractal scaling behavior in a wide variety of systems. Indeed, we urge its usage whenever sample-to-sample fluctuations in the $f(\alpha)$ curve occur [as in the DLA (Ref. 28)] or where one expects the underlying mechanism to be probabilistic.

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