Fractal phenomena and fractal analysis in epidemiological studies

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Abstract

The paper discusses an approach to analysing time series in epidemiology using fractal analysis and discusses possible practical use of these theories in epidemiology.

Introduction

Standard methods of statistical epidemiology generally include some assumptions about the distributions of predictor variables or outcome variables. We typically assume that epidemiological studies contain hidden, random noise, which can be measured and corrected for in the statistical analysis.

However, standard analytical approaches assume that the noise can be described with a mean and a variance. If this is not the case, it may be necessary to use more non-traditional mathematical approaches linked to studies of non-linear systems. A basic introduction to the thinking behind this "non-linear" science may be found in Prigogine (1997). The starting point for Prigogine and others is that traditional mathematical theory is limited to the linear area. Life obviously does not appear to be linear, but exists in a next-to chaotic area, and only this area allows for the huge variability necessary for life and evolution to exist.

In epidemiology, infectious dynamics is a classic example of non-linear dynamics (Liebovitch, 1998). The main mathematical approach to studying these kind of systems has been to apply fractal theories (Liebovitch, 1998; Peitgen et al., 2004). Fractal theories have however remained considered as esoteric theories without much proven value for most biologists – including epidemiologists.

Inside chaos theory, one usually distinguishes between deterministic chaos and statistical chaos patterns. Deterministic chaos is famously described with the butterfly effect, but can also be visualised in epidemic outbreak patterns. The main aspect of deterministic chaos systems are their sensitivity to initial conditions (Liebovitch, 1998) – as often observed in infectious dynamics where small changes in conditions may cause a system breakdown and a major epidemic. Fractal patterns have been shown for measles epidemiology (Bolker and Grenfell, 1996) and rotavirus infections (Jose and Bishop, 2003).

Statistical chaos is seen in other time-series, where seemingly random fluctuations in trends may hide fractal patterns (Liebovitch, 1998). Epidemiological time-series with documented fractal

patterns include incidence rates for cancer (Nygaard and Glattre, 2003) and meta-analysis of breast-cancer studies (Glattre and Nygaard, 2004). In many epidemiological studies we study covariate variables over time, and the time series pattern may contain information hidden from standard analysis but of major importance if causal inference is to be drawn. Fractal patterns in cohort covariates may introduce severe bias of estimates.

Objective

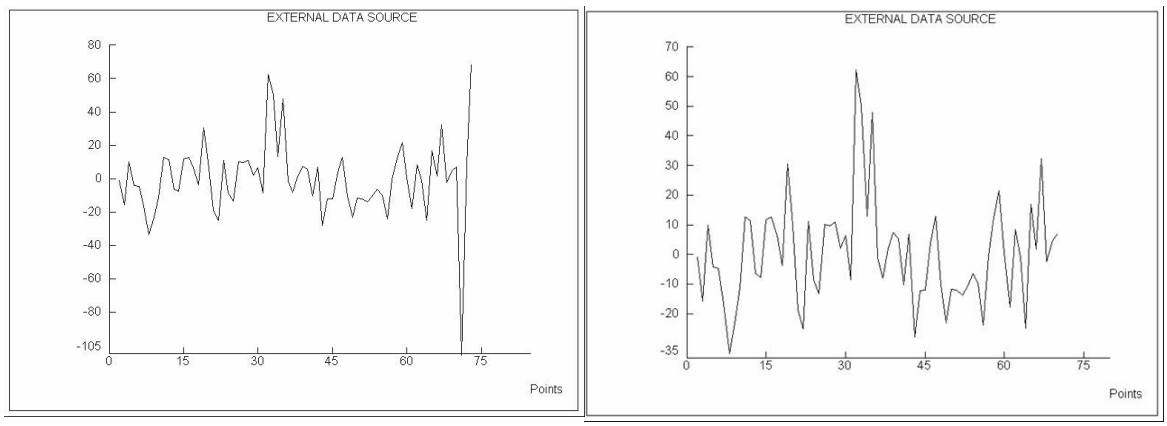
The objective of this study was to assess whether fractal theories may be used in certain areas of epidemiology and suggest practical analytical approaches for distinguishing between studies where a fractal approach may be used and more linear areas where traditional approaches will be valid.

Methods

Starting from a dataset on incidence rate in cancer (Nygaard and Glattre, 2003), we examine a dataset on *Campylobacter* incidence in humans in Norway for fractal patterns. After reducing trends in the data, we used the software Benoit version 1.31. (TruSoft Int'l Inc) to examine the data.

Results

Figure 1 (left) shows the time series of the residual of *Campylobacter* incidence after removing trends over year/month using a standard Poisson regression. Using the wavelet approach in Benoit, this series corresponds to a Hurst coefficient of 0.29 and a fractal dimension of 1.71. Removing the extremes in the time-series (right) increases the fractal dimension to 1.98 and a Hurst coefficient of 0.02. These values demonstrate a time series with fractal properties and rather strong negative autocorrelations.



Discussion

We can show a certain fractal pattern in the data analysed, with a strong negative autocorrelation. An interpretation of this may be a system with strong memory, but the biological mechanism behind may remain obscure. Most probably endemic infectious diseases belong to a class of biological systems represented by self-organising criticality (SOC). Previous papers have used a special method called de-trended fluctuating analysis (DFA) (Glattre and Nygaard, 2004) to analyse these kind of time series, and our presentation is a simplistic approach.

Disease mechanisms showing complex patterns represent a major challenge if the aim of a study is to establish a prediction. As previously shown (Glattre and Nygaard, 2004), the results of a meta-analysis may change considerably if fractal analysis is undertaken, and this and a working paper (Glattre et al., 2006) suggest a way to distinguish between time series with fractal properties and series where a traditional approach may be used. The main point here is that if a time series shows strong fractal patterns, we cannot expect to reproduce the results from a study, and continuing research in the area may be meaningless. Thus, controversial causal relations will still be controversial and contradictory even if more studies are added. A stopping rule in searching a possible prediction and causal relationship may be established using fractal analysis (Glattre et al., 2006).

While fractals and nonlinear system dynamics remain a controversial issue in biology, we argue that some pitfalls of statistical inference in epidemiological studies may be avoided if fractal analysis is used in certain types of studies. We would like to invite interested, perhaps more competent groups, to join us in this work.

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