meters, divergences pose no problem of principle. Even theories with non-renormalizable divergences, suitably restricted, are perfectly sensible[3–5]. The demand that quantum field theories have no divergences is misguided and physically unnecessary.

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Uncorrelated DNA walks

SIR — Peng *et al.*[1] represent DNA sequences as random walks on which a pyrimidine represents a step up and a purine a step down. On the basis of their analysis of such walks they report "long-range correlations" in the nucleotide sequences of intron-containing genes and suggest that these reveal fractal properties of genome organization which may be connected with non-equilibrium dynamic processes. This could well be true. Here I put forward a different framework for thinking about their observations which readily suggests explanations in terms of molecular biology.

Consider a random walk which is uncorrelated, that is, the direction of each step, up or down, is independent of the direction of previous steps. The walk may or may not be biased. If the probability of stepping up is the same everywhere then the root mean square fluctuation function of the walk, $F(l)$, has a slope of 0.5 on a double-log plot (this slope is the fundamental statistic of the analysis). However, if the probability of stepping up differs in different regions then, simulation shows, the slope is greater than 0.5 and can, indeed, be much greater. So the observations of Peng *et al.* of slopes greater than 0.5 in their DNA walks do not necessarily imply long-range correlations in the sense of a lack of independence at long ranges. They may instead reveal that, for example, introns and exons are statistically different with a biased walk in the exons and an unbiased walk in the introns. That the walk is biased in the exons is strongly suggested by Peng *et al.*'s descriptions of the cDNA walks. Furthermore, if we calculate the probability of stepping up at the level of the codon, using the amino-acid frequency data in ref. 2 and the codon usage data in ref. 3, we find that the probability of a step up is 0.46 in GC-rich regions of the human genome and 0.48 in AT-rich regions.

What these latter data do not reveal is the origin of the bias reversals which seem present in Peng *et al.*'s cDNA. The global min–max partitioning procedure used by Peng *et al.* to analyse their walks will restore slopes of 0.5 as long as there are no more than three statistically distinct regions on the walk. That this procedure 'works' for the cDNA means that there are not many reversals of bias in the coding regions of genes. This suggests that the ultimate source of the bias reversals may be the mosaic structure of genomes with regard to GC content, which is more complex than a GC-rich/AT-rich dichotomy (ref. 4).

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Scientific Correspondence
Scientific Correspondence is intended to provide a forum in which readers may raise points of a scientific character. They need not arise out of anything published in *Nature*. In any case, priority will be given to letters of fewer than 500 words and five references.

Selfish genes in mosquitoes

SIR — Hurst and colleagues[1,2] state that "within any population of [the mosquito] *Culex pipiens* there are two sorts of individual, those that bear/harbour . . . *Wolbachia* [bacteria] and those that do not". But, according to Yen and Barr[3], all wild-type *C. pipiens* appropriately examined before 1973 were found to carry *Wolbachia*. It was only when Yen and Barr produced uninfected individuals artificially by tetracycline treatment that it was found that matings of uninfected females × infected males were sterile, whereas all matings by uninfected males were fertile.

Laven[4] test-crossed allopatric *C. pipiens* strains and found unidirectional or bidirectional incompatibility (sterility) in many cases. The crossing types are cytoplasmically inherited and the relationships between various strains are too complex to explain by a simple 'presence–absence' hypothesis. The same applies to variability in compatibility type found within wild populations[5,6]. It is presumed that different strains have genetically different *Wolbachia* whose interactions somehow cause the observed incompatibility[2,3]. The presumed differences in the *Wolbachia* between *C. pipiens* strains should be detectable by molecular techniques, for example as described in ref. 7.

It has long been realized that a mixed population of two unidirectionally cytoplasmically incompatible types would be expected to show selection for the type whose females are not sterilized in cross matings[2,4,8,9]. Strong selection for *Wolbachia*-infected *Drosophila* has been observed in Californian wild populations[10].

Cytoplasmic incompatibility has never been reported in *Anopheles* (malaria) mosquitoes and two *Anopheles* species examined by Yen (cited in ref. 11) did not carry *Wolbachia*. The *Wolbachia* associated with cytoplasmic incompatibility in diverse insects are very closely related[7].

It might be possible to introduce them into *Anopheles* mosquitoes by injection, or even by feeding. If the normal 'rules' about unidirectional incompatibility and maternal inheritance apply, it should be possible to initiate selective replacement of an uninfected wild-type *Anopheles* population by 'seeding' with a few of the artificially infected *Anopheles*. If a gene for inability to transmit malaria[12,13] could be inserted into the *Wolbachia* before introducing the bacteria into the vector population, the selective replacement process should render the population harmless to man without the need for mass release of the non-transmitting strain. This method may prove more feasible than the use of a transposable element such as a *P* factor[14].

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