Supplementary Information

Temporal fractals in seabird foraging behaviour: diving through the scales of time

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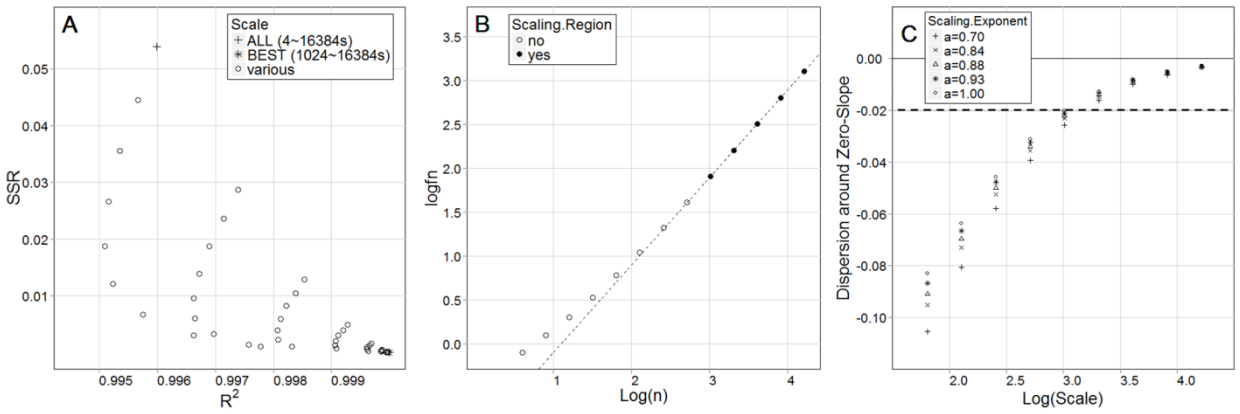
Supplementary Figure S1. Validation of scaling regions in pseudo-randomized surrogate sequences generated by the shuffling of observed sequences



Supplementary Figure S1. There is maximization in the coefficient of determination and minimization in the sum of squared residuals (*) in the shuffled data (A), suggestive of a best scaling region. However, this region includes only the minimum number of scales examined (filled circles shown in B) and it is clear that there is a progressive increase in the fit of the regression line with increasing scale (C), unlike the case for the observed sequences. The estimates of α_{DFA} for the best scaling region (0.993) is not comparable to that of the full range of scales (0.900), and indeed the estimates increased steadily with scale from a minimum of 0.727 to a maximum of 0.993 represented by the best scaling region. Therefore, these sequences clearly do not exhibit power-law behaviour, despite the appearance of linearity across certain sections of the log-log plot. See main text for a description of validation methods used.

Supplementary Table S1. DFA results of simulating effects of foraging trip length and diving probability distribution in binary sequences.

Sequence Length	Probability Distribution (diving frequency: time underwater)				
	0.25	0.33	0.50	0.66	0.75
2048	0.90±0.005	0.81±0.012	0.49±0.028	0.81±0.015	0.90±0.007
4096	0.91±0.005	0.83±0.010	0.50±0.036	0.83±0.009	0.91±0.006
8192	0.92±0.004	0.86±0.006	0.50±0.016	0.85±0.007	0.92±0.005
16384	0.92±0.003	0.87±0.004	0.50±0.019	0.86±0.004	0.92±0.002
32768	0.93±0.001	0.88±0.002	0.50±0.010	0.87±0.002	0.93±0.001
65536	0.94±0.001	0.89±0.002	0.50±0.008	0.88±0.002	0.94±0.001

Results are based on 100 simulations for each length/distribution combination

Fractal Analysis of Surrogate Sequences

The results of the surrogate sequences were somewhat surprising. For DFA_b and H_{AV}, the surrogate sequences behaved as predicted for sequences lacking serial correlation, producing mean±s.d. α_{DFAb} and H_{AV} values of 0.50±0.02 and 0.50±0.03, respectively. Similarly, box counts of surrogate sequences produced D_b=2 in all cases, which is also predicted for fractal dimension estimates of curves generated by Brownian (random) motion. However, applying the linear form of DFA to the surrogate sequences produced scaling exponents similar to those of the observed sequences at 0.84±0.11; far from the predicted values of 0.5. Upon further exploration we see that, indeed, these randomized sequences do appear to contain scaling regions, as points converge to maximize the coefficient of determination and minimize the sum of squared residuals in the R^2 – SSR procedure (Supplementary Fig. S1A). However, that is where the similarities between observed and surrogate sequences stop, because apparent scaling regions occur only at the largest scales and with the minimum number of scales (N=5) included in the regression (Supplementary Fig. S1B). This is also seen in the compensated slope procedure (Supplementary Fig. S1C); if the sequence were to persist across even larger time windows, the best scaling regions would presumably continue to move with increasing scale. Therefore, the scaling observed in these sequences does not reflect true scaling behaviour, but is instead an artefact of certain characteristics of the original observed sequences.

Fractal Analysis of Simulated Sequences

We determined which characteristics of observed sequences led to the appearance of scaling in the surrogate sequences in DFA by simulating random binary sequences. The results of these analyses are displayed in Supplementary Table S1, and it is clear that the probability

distribution exhibits marked effects on α_{DFA} values; predicted values of αDFA (0.5) are only obtained when the distributions of the behaviour and its lag are roughly equal, i.e. generated by a random process. Biases in α_{DFA} then increase as the probability distribution is skewed in either direction away from parity. Sequence length appears to have only an interactive impact on αDFA in the surrogate sequences; as length increases, the effects of the distribution on α_{DFA} are slightly exaggerated.

Given that all of the other fractal methods used in this study produced expected values for non-correlated sequences (i.e. 0.5 for Hurst estimators and 2 for the fractal dimension estimator), it seems strange that the linear form of DFA as implemented in the R package used ('fractal' [1]) should exhibit this bias. However, we must reiterate that scaling exponents estimated by each of our 4 methods used correlated strongly and fit very well the theoretical relationships expected of them. As a result, the bias shown by DFA here is unlikely to have influenced the results regarding our observed sequences in any way. These results clearly show that any related future studies should include multiple fractal analyses and multiple methods to validate observed scaling regions before concluding for the robustness of their results.

References

1 Constantine, W. & Percival, D. *fractal: fractal time series modeling and analysis. R package version 1.1-1*, <http://CRAN.R-project.org/package=fractal> (2011).