

# Analysis of Sampling Rate (TR) Dependence of Hurst Exponent of fMRI BOLD Time Series

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## Target Audience

fMRI researchers in the field of resting-state fMRI; researchers studying the long-range dependence and self-similarity properties of fMRI BOLD time-series.

**Purpose:** The purpose of this study is to accurately estimate the Hurst exponent (H-value) of fMRI BOLD time series obtained at different sampling rates (TR), as a means of demonstrating the change in H-value resulting from frequency aliasing due to a change in TR. Hurst values have been used in previous fMRI studies, e.g. to distinguish between healthy controls and patients with Alzheimer's Disease<sup>1</sup>. We seek to answer the following questions in this study: How does the H-value change with respect to the TR at which the data has been acquired, and if the change is subject-specific, and; Whether the change in H-value is limited to voxels in specific parts of the brain, or whether all regions can be randomly affected. Although dependence of H-value on TR has been speculated before, no concrete study using multi-subject, multi-TR data is available, and this study seeks to fill this gap.

## Methods

**Imaging:** fMRI was performed on 6 healthy subjects (mean age 23 years) in a 3.0 T Trio Tim Siemens MRI scanner equipped with a 12-ch head coil and parallel imaging acquisition using EPI with imaging parameters: GRAPPA = 2, 32 reference lines, TE = 25 ms, FOV = 22 x 22 cm, 14 slices in oblique axial direction covering the prefrontal cortex, brainstem and cerebellum, thickness/gap = 3.0 mm/1.0 mm, resolution 64 x 64, BW = 2170 Hz/pixel (echo spacing = 0.55 ms) and 200 time frames. For each subject, 20 different data sets corresponding to 20 different sampling rates (TR: {700, 800, 900, ..., 2600} ms) were used.

**Analysis:** The first method for H-value estimation of all voxel time series for each subject uses the wavelet-based estimator<sup>2</sup>. The wavelet-based estimator is sensitive to input signal length, and correct estimation of the H-value also depends on the mother wavelet used. To account for this, 5000 fractional Gaussian noise (fGn) sequences with H-values ranging from 0.1 to 0.9 with 0.1 increments were generated, and the H-value estimated using db2, db3, db4 and db5 wavelets. The best estimation was achieved using db3 wavelet, which was henceforth used for voxel time series. The second method for H-value estimation is based on Empirical Mode Decomposition (EMD)<sup>3</sup>, which is a data adaptive signal decomposition technique. Unlike wavelets, EMD does not assume a pre-defined basis, rather the decomposition is data-adaptive in nature. EMD iteratively decomposes a signal into a finite number of intrinsic mode functions (IMFs). EMD based H-value estimator<sup>3</sup> is similar to the wavelet-based estimator, and allows estimation of the H-value through variance progression of IMFs, by estimating the slope  $\theta$  of the graph of IMF variance  $\log_2(V[k])$  plotted against the IMF index  $k$ , using the relation  $H = 1 + \theta/2$ , given the relation  $V[k] = C \cdot 2^{2(H-1)k}$ . Decomposition using EMD is not affected by the signal length, hence EMD is a good choice for H-value estimation of short length time series. The H-values of all the voxel time series estimated using the wavelet-based estimator were found to adequately match the H-values estimated using EMD-based estimator, hence providing confidence in the estimated H-values for all voxel time series at all TRs.

**Results:** At each TR, the H-values for all voxel time series were averaged to find a mean H-value for each of the six subjects. The mean H-values per subject are plotted against the TR values in Fig. 1, demonstrating changes in mean H-values with a change in TR. Furthermore, this change in the mean H-value is subject-specific, with considerable difference in mean H-value of each subject at most TRs. For all subjects, an overall decreasing trend in mean H-values with an increase in TR is visible, e.g. it is more pronounced for subject #6, but much less for subject #4. Interestingly, the lowest mean H-values for all subjects occur at the typically used TR values, i.e. between 2 s and 2.6 s. The distribution of H-values for subject #6 is shown for two TRs (1.1 s and 2.4 s) in Fig. 2, where the highest (0.66) and lowest (0.49) mean H-values occur, respectively. As seen from Fig. 2, the decrease in mean H-value at TR = 2.4 s is caused by a decrease in the number of voxels having high H-values at this TR, thereby suggesting a change in the frequency spectrum of individual voxel time-series from low-frequency (higher H-value) to a (relatively) higher frequency (lower H-value) behavior (it should be remembered that the maximum frequencies in a time-series are limited by the sampling frequency represented by the TR).

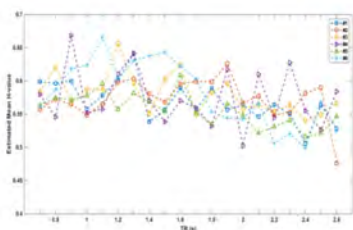


Fig. 1: mean H-values plotted against TR

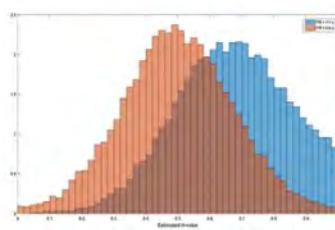


Fig. 2: Distribution of H-values at 2 TRs: Sub#6

$H \geq 0.8$  to  $H \leq 0.4$ , going from TR 1.1 s (with highest mean H-value of 0.66) to 2.4 s (with lowest mean H-value of 0.50). As reported in previous studies, the lower H-values are concentrated around the ventricles, however at a lower TR all these voxels had high H-values. Finally, Fig. 3(d) shows, for subject #4, the voxels having H-value  $H \geq 0.8$  at TR = 0.9 s (highest mean H-value of 0.67). Importantly, though, these voxels have a H-value of  $H \leq 0.4$  at TR 2.0 (mean H-value 0.49, the lowest for this subject), thereby demonstrating that voxels in regions of brain considered to be associated with certain H-values (high or low) can have different H-values depending on the TR and the subject.

**Discussion:** The results presented here demonstrate dependence of the H-value on the sampling rate at which the fMRI data has been obtained. It should be mentioned

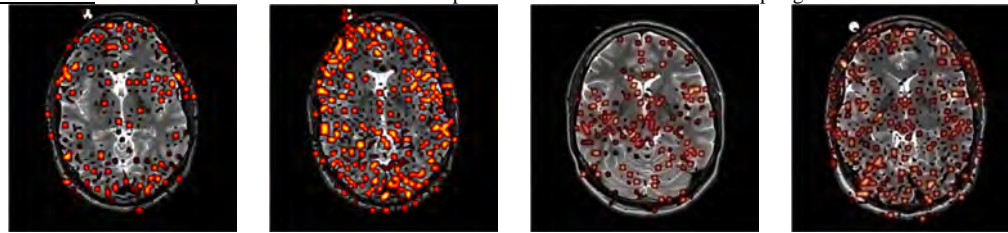


Fig 3: (a)

(b)

(c)

(d)

aliasing affects voxel time-series over a broad frequency spectrum. Our study also corroborates and quantifies previous findings relating the effect of aliasing by TR<sup>4</sup>.

**Conclusions:** We studied the Hurst exponent (H-value) of fMRI BOLD time series obtained at different TRs. The H-values were estimated using two different methods. The dependence of the H-value on the TR was illustrated, and its effect over all regions of the brain was demonstrated. This has important implications for works using the Hurst value for investigation of fMRI characteristics.

## References:

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