Title

Axial variation of deoxyhemoglobin density as a source of the low-frequency time lag structure in
blood oxygenation level-dependent signals.

Authors

Toshihiko Aso[1,2*], Shinnichi Urayama[2,3], Fukuyama Hidenao[2,3], Toshiya Murai[1]

Affiliations

[1]Department of Psychiatry, Kyoto University Graduate School of Medicine, Kyoto, Japan

[2]Human Brain Research Center, Kyoto University Graduate School of Medicine, Kyoto, Japan

[3]Research and Educational Unit of Leaders for Integrated Medical System, Center for the Promotion
of Interdisciplinary Education and Research, Kyoto University, Kyoto, Japan

* Correspondence:

Toshihiko Aso
aso.toshihiko@gmail.com

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Abstract

Perfusion-related information is reportedly embedded in the low-frequency component of blood
oxygen level-dependent (BOLD) fMRI signal. The blood-propagation pattern through the cerebral
vascular tree is detected as an interregional lag variation of spontaneous low-frequency oscillations
(sLFOs). Mapping of this lag, or phase, has been implicitly treated as a projection of the vascular
tree structure onto real space. While accumulating evidence supports the biological significance of
this signal component, the physiological basis of the "perfusion lag structure," a requirement for an
integrative fMRI-signal model, is lacking. In this study, we conducted analyses furthering the
hypothesis that the sLFO is not only largely of systemic origin, but also essentially intrinsic to blood
and hence, behaves as a virtual tracer. By summing the small fluctuations of instantaneous phase
differences between adjacent vascular regions, a velocity response to respiratory challenges was
detected. Regarding the relationship to neurovascular coupling, the removal of the whole lag
structure, which can be considered as an optimized global-signal regression, resulted in a reduction

of signal variance, while preserving the fMRI response. Examination of the T2* and S_0, or non-BOLD,

components of the fMRI signal revealed that the lag structure is deoxyhemoglobin-dependent,

while paradoxically presenting a signal-magnitude reduction in the venous side of the cerebral

vasculature. These findings provide insight into the origin of BOLD sLFO, at least partly intrinsic to

the circulating blood.

1   Introduction

In functional magnetic resonance imaging (fMRI), there are two established physiological bases of

signal change: neuro-vascular coupling (NVC) and autoregulation. The former involves a local blood

flow increase at 30-70% which gives rise to 0.5-2% blood oxygenation level-dependent (BOLD) signal

increase with around 5-second delay (Buxton, 2013). This is the target phenomenon of fMRI as a

tool for brain mapping, due to its limited spatial extent mainly involving local arterioles (Hillman,

2014). In contrast, autoregulatory response in vessel diameter is found in a wide range of arteries

including internal carotid or middle cerebral arteries (Hoiland et al., 2016). Detection of a

compromised response in vascular disorders have been proven useful for clinical purpose (Murphy

et al., 2011). Importantly, there is no clear physiological distinction between these two phenomena

each involving multiple pathways (Willie et al., 2014). Their traces in the fMRI signal are also

uniformly postulated to reflect the increased cerebral blood flow and eventual dilution of deoxy-

hemoglobin (Hgb) in the postcapillary part of vasculature, with additional effect of local blood

volume increase (Kim & Ress, 2016).

In efforts to improve the efficiency of fMRI, studies have revealed various systemic physiological

components in BOLD signal fluctuations. Physiological parameters, such as cardiac pulsation (Chang

et al., 2009), blood pressure, and end-tidal CO_2 (Wise et al., 2004; Murphy et al., 2013), are

considered artifact sources. The contamination is expected to be emphasized in resting-state fMRI

(rs-fMRI), where signals are evaluated without trial averaging (Winder et al., 2017). However,

discrimination between neuronal and non-neuronal components has been a major challenge due to

the lack of validation techniques with comparable spatial and temporal precisions to those of fMRI.

Another source of difficulty is the fact that many neural and non-neural parameters are

intercorrelated in this low-frequency range (Murphy et al., 2013).

A focus of recent studies exploring this matter is the spontaneous BOLD low-frequency oscillation

(LFO, < 0.1 Hz) possibly encompassing multiple artifact sources (Zhu et al., 2015; Tong et al., 2017).

One well-known sLFO source would be the respiratory volume fluctuation involving a chemoreflex

loop (Birn et al., 2008). An sLFO in systemic blood pressure, known as the Traube–Hering–Mayer

wave, has been shown to originate from another autonomic loop (Guyton & Harris, 1951; Julien,

2006). Associated sLFOs in blood flow and velocity have been found (Killip, 1962; Fagrell et al.,

1977), and, later, transcranial Doppler ultrasonography and optical methods confirmed their traces

within the brain (Giller et al., 1999; Obrig et al., 2000). This optically detected sLFO was found in

both oxy- and deoxy-hemoglobin (Hb) with an interesting phase difference exclusively observed in
the brain (Rayshubskiy *et al.*, 2014; Tgavalekos *et al.*, 2016). sLFO was found even in
electroencephalographic recordings, for which arterial vasomotion was suggested as the origin
(Nikulin *et al.*, 2014), although it is unclear how the vasomotion accounts for the fMRI signal mainly
from the capillary bed.

As mentioned above, Hb-sLFO is postulated to be of systemic origin (Katura *et al.*, 2006; Tian *et al.*,
2011; Sassaroli *et al.*, 2012). Hence it was not surprising to find a correlation between the global
fMRI signal and extra-cerebral signals (NIRS or MRI), but the constant time shift across body/brain
parts was unexpected (Anderson *et al.*, 2011; Tong *et al.*, 2012). The demonstration of the similarity
between the low-frequency phase map and perfusion MRI in healthy participants was a milestone in
this direction, by presenting the perfusion time lag embedded in the BOLD signal (Tong *et al.*, 2017).
The resilient nature of the lag map against the fMRI task condition was shown, further supporting
its non-neuronal origin (Aso *et al.*, 2017a). In parallel, a number of clinical studies have established
the phase delays as a marker of cerebrovascular disorders (Amemiya *et al.*, 2013; Lv *et al.*, 2013;
Christen *et al.*, 2015; Ni *et al.*, 2017; Nishida *et al.*, 2018; Khalil *et al.*, 2018). Gross vascular anatomy
has been detected consistently in these studies, replicating the results from respiratory challenges
(Chang & Glover, 2009a; Blockley *et al.*, 2011), which importantly suggests an equivalence between
the sLFO and manipulated circulatory turbulences. Apart from patient data, a recent study involving
healthy participants revealed changes in venous drainage pattern with normal aging (Satow *et al.*,
2017). A body of evidence thus empirically supports the biological significance of the low-frequency
lag structure and its underlying principles.

The current analytical model of the BOLD lag structure assumes the presence of this signal variation
from the very early stages of cerebral perfusion (Tong *et al.*, 2018)(**Fig. 1A**). Such synchronized
variation should naturally affect the global mean signal and the model is hence related to the
unresolved fMRI global signal problem (Liu *et al.*, 2017; Power *et al.*, 2017). This view is not only
compatible with the occasional favorable effect of global signal regression (GSR) in task fMRI
(Aguirre *et al.*, 1998) but has led some scientists to propose the removal of the lag structure as an
approach for noise elimination (Erdoğan *et al.*, 2016; Amemiya *et al.*, 2016; Byrge & Kennedy, 2018).
Under this model, the elimination of the lag structure can be viewed as an optimized GSR (of the
low-frequency component) for each voxel group. Conversely, with the presence of the BOLD lag
structure, a simple GSR should retain a residual correlation between in-phase voxels that confounds
fMRI analyses (Taylor Webb *et al.*, 2013; Erdoğan *et al.*, 2016).

The fundamental and critical question remaining is the mechanism by which sLFO (or respiratory
maneuvers) creates the BOLD lag structure. The BOLD response to neural activity via NVC is a well-
documented passive process, involving the expansion of the intravascular compartment (Herman *et
al.*, 2009). A typical model of the BOLD signal change is described as follows (Hoge *et al.*, 1999):

$$102 \qquad \frac{\Delta BOLD}{BOLD_0} = M \left(1 - \left(\frac{CMRO_2}{CMRO_2|_0}\right)^{\beta} \left(\frac{CBV}{CBV_0}\right) \left(\frac{CBF}{CBF_0}\right)^{-\beta}\right) \qquad [1],$$

103 where $CMRO_2$ stands for the cerebral metabolic rate of oxygen in a voxel, CBV/CBF for cerebral

104 blood volume and flow, respectively. Beta is an exponent of the power-law describing the

105 relationship between T2* and deoxygenated Hb (deoxy-Hb) amount that only depends on $CMRO_2$

106 and CBF in a reciprocal manner, under the assumption of negligible inflow of deoxy-Hb. M is the

107 factor for the BOLD susceptibility effect defined as:

$$108 \qquad M \equiv TE \cdot B_0 \cdot CBV_0 \cdot [dHb]_{V0}^{\beta} \qquad [2],$$

109 where B_0 is the main magnetic field strength. Triggered by vasodilation of the arteriole, this effect is

110 diminished by an inflow of fresh blood, which increases the MR signal. This baseline BOLD effect has

111 been modelled in the formula for the off-resonance frequency shift as follows (Yablonskiy & Haacke,

112 1994; An & Lin, 2002):

$$113 \qquad \delta\omega = \gamma \cdot \frac{4}{3} \cdot \pi \cdot \Delta\chi_0 \cdot Hct \cdot OEF \cdot B_0 \qquad [3],$$

where γ is the gyromagnetic ratio (42.58 MHz/T), $\Delta\chi_0$ is the susceptibility difference between the

fully oxygenated and fully deoxygenated blood, and Hct is the hematocrit (volume fraction of

erythrocytes to the blood volume, typically around 40%). The oxygen extraction fraction (OEF)

represents the only source of deoxy-Hb, again, under the assumption of 100% oxygen saturation

(SaO_2) in the inflow. Variation of this base susceptibility can actually occur due to the local Hct and

SaO_2 changes and, in fact, has been shown to cause intersession variabilities (Cohen *et al.*, 2002;

Tuunanen & Kauppinen, 2006), but within-session fluctuations have rarely been considered

(Thomas *et al.*, 2000). For example, even at a constant Hb density and oxygen partial pressure, CO_2

fluctuation, a driving factor of vasomotion, alone can modify SaO_2 through pH changes (Collins et al.,

2015a). Although the assumption of constant base deoxy-Hb concentration may be sufficient for

modeling its dilution by NVC (Ogawa *et al.*, 1998), other effects might not be negligible in non-

neuronal fluctuations (**Fig. 1b**).

Fig. 1. Working model of the BOLD lag mapping. *A*, Schematic of the cerebral vascular tree presenting possible physiological models that account for the fMRI and NIRS observations. Each brain voxel has its lag (phase) of the spontaneous low frequency oscillation (sLFO) relative to the reference point, depicted in warm and cool colors. The inlet, center and outlet parts of the vasculature are determined purely by the temporal relationship and not by vessel types; all signals are supposed to originate from the capillary bed. Another schematic is inserted to illustrate the effect of the reference point selection in relation to the vascular path length, which accounts for the disagreement with other blood-tracking techniques. Below are shown three models with different physiological signal sources that are moving along the vasculature. While this axial inhomogeneity of the deoxy-hemoglobin (Hb) density may be linked with vasomotion (1), it can persist in the absence of vasomotion and flowmotion (2,3). The moving axial inhomogeneity would create a similar temporal profile with varying phase across regions. *B*, Dependence of the BOLD signal on inflow oxygen saturation (SaO2), a major determinant of deoxy-Hb concentration, at 3 T, TE = 30 ms. All other parameters were maintained constant at physiological values: oxygen extraction fraction = 45%, tissue blood volume fraction = 3%, and hematocrit = 40% (see Eqs. [1] and [2]).

In this exploratory study, we conducted three investigations to further advance our knowledge on
the BOLD lag structure and its underlying physiology. We first evaluated if changes in blood transit
velocity are embedded in the BOLD low-frequency phase to confirm its behavior as a virtual tracer
[a preliminary analysis of these data was presented previously as a poster (Aso *et al.*, 2017*b*)]. Next,
we investigated the effect of eliminating the lag structure from task-based fMRI, which has not
been tested yet. Finally, we used multi-echo imaging to assess the components of the BOLD signal
that determine the lag structure. One of the recent approaches toward fMRI denoising has focused
on S_0 fluctuation (signal at echo time = 0, which is the baseline MR signal from the fluid
compartments), as it is weakly associated with neural activity (Posse *et al.*, 1999; Wu *et al.*, 2012;
Kundu *et al.*, 2012; Yen *et al.*, 2017). In contrast, the total-Hb sLFO, detected by NIRS, is interpreted
as a local CBV change under the assumption of a constant Hct, which should also affect the non-
BOLD component via changes in plasma volume and inflow (Rostrup *et al.*, 2005). Again, the T2*
and S_0 components may contribute in a different manner than NVC to the BOLD lag structure that
have been overlooked in studies based on trial averaging. From the influences of three different
fMRI task paradigms, including a simple reaction-time visuomotor task, a short breath-holding task,
and a hyperventilation task on the neural and non-neural components of the fMRI signal, we sought
further validation of our hypothetical model of the BOLD lag structure.

2 Materials and methods

2.1 Subjects and experimental procedures

Twenty-one healthy subjects (eight women, 19–26 years of age) participated in Experiment 1; one
subject was excluded from the analysis because of abrupt head motion, which prevented BOLD lag
mapping (see Data processing). The remaining 20 participants performed the sparse visuomotor
and 10-s breath-holding tasks, but the hyperventilation task was only performed by 18 participants,
as it was introduced after the first two participants had concluded their participation. Another 21
participants were recruited for Experiment 2, involving multi-echo acquisition, all of whom
performed the above three tasks but with an 18-s version of the breath-holding task. To avoid
vigilance level fluctuations, all MRI sessions were scheduled in the morning and the participants
were encouraged to sleep well the previous night.

The protocol for this study was approved by the internal ethics review board of Kyoto university.
The subjects provided written informed consent in advance, according to the Declaration of Helsinki,
for the analysis of anonymized MRI scans and simultaneously acquired physiological data.

2.2 Image acquisition

A Tim-Trio 3-Tesla scanner (Siemens, Erlangen, Germany) with a 32-channel phased-array head coil
was used for MRI acquisition. For Experiment 1, T2*-weighted echo-planar images were acquired
using multiband gradient-echo echo-planar imaging (EPI) (Feinberg *et al.*, 2010) with the following

parameters to cover the entire cerebrum: 64 × 64 pixels, interleaved 35 slices, 192-mm field of view
(FOV), 3.5-mm slice thickness, repetition time (TR)/echo time (TE) = 500/35 ms, flip angle = 40°, and
multiband factor of five. Three 9-min runs (1,080 volumes) were acquired for each of the three task
conditions. The same pulse sequence program was used in Experiment 2 but with multi-echo
settings: TE1 = 7.76 ms and TE2 = 25.82 ms for the first six subjects and TE1 = 11.2 ms and TE2 =
32.78 ms for the remaining 15 subjects. A smaller multiband factor of two was selected to allow for
the short TE in combination with a parallel imaging using GRAPPA. Other acquisition parameters
were: TR = 1,300 ms, flip angle = 65°; interleaved 36 slices, FOV = 256 × 192 mm^2, 64 × 48 matrix,
3.5-mm slice thickness. Three 7-min (323 TRs) runs were acquired. Seven subjects in Experiment 2
underwent two additional runs with a shorter TR of 700 ms and a flip angle of 45° to examine the
sensitivity of the respiration-related signal component to inflow modulation. At the end of every
experimental session, a 3D MPRAGE T1-weighted image was acquired for obtaining anatomical
information (Aso *et al.*, 2017*a*). A dual-echo gradient-echo dataset for B0 field mapping was also
acquired after the BOLD scan in the same orientation.

2.3   Task conditions

Throughout the experimental session, task instructions were presented via an LCD monitor inside
the scanner room, viewed through a mirror. Beat-to-beat fluctuations in the mean arterial pressure
and heart rate were obtained via a non-invasive MR-compatible device (Caretaker, BIOPAC Systems,
Inc., Goleta, CA, USA). Careful instructions were provided to the participants on how to avoid
motion, especially during the respiratory challenges.

2.3.1 Sparse visuomotor task

A simple visuomotor task with a varying intertrial interval of 6 to 24 s was performed during the first
run. Subjects were instructed to press a button with their right index finger as soon as the computer
screen changed from "Please hold still" to "Press the button." The screen returned to "Please hold
still" at the button press or after 3 s, if the participant had not pressed the button.

2.3.2 Breath-holding task

To minimize head motion induced by the tasks, the two respiratory challenges were adapted to be
less strenuous than in earlier studies. In Experiment 1, the breath-holding task was cued by a "Hold
your breath" instruction on the screen, at which point the subjects were asked to immediately hold
their breath, irrespective of the respiration phase. The holding periods lasted for 10 s and were
separated by 90-s intervals. This short duration was selected to minimize strain that can cause body
movements, while evoking a detectable autoregulatory response (Murphy *et al.*, 2011). In
Experiment 2, a longer holding period of 18 s after a brief inhalation for 2 s was used to evoke a
more pronounced vasodilation.

2.3.3 Hyperventilation task

The hyperventilation task involved paced breathing at 1/5 Hz for 25 s, separated by a 30-s rest. Each 5-s cycle began with the screen presenting "Please inhale" for 1.5 s, followed by "Please exhale slowly," lasting 3.5 s. Subjects were instructed to breathe as deeply as possible, while avoiding head movement. A short inspiration period was selected to suppress motion by minimizing movements in the thoracic cage and spine.

2.4 Data processing

For image processing, SPM12 (Wellcome Department of Cognitive Neurology, London, United Kingdom) and FSL5 (FMRIB Software Library, www.fmrib.ox.ac.uk/fsl) (Smith *et al.*, 2004) were used in combination with in-house MATLAB scripts. Off-resonance geometric distortions in the EPI data were corrected using FUGUE/FSL with B0 field maps. After inter-scan slice-timing correction, head motion was compensated by 3D motion correction and data repair (Mazaika *et al.*, 2009). The repairing procedure aimed to remove motion-related signal dropout and involved searching for time points satisfying two stringent criteria: (1) global signal change between consecutive volumes exceeding 1% and (2) head displacement exceeding a Euclidian distance of ±1 mm or ±1° rotation per TR. The affected time points were replaced with linearly interpolated values, but this procedure was required in only six of the 41 participants. The data were further cleaned by regressing out 24 head motion-related parameters. Unlike in previous studies, the six rigid-body parameter timeseries were not directly used because of the possible contamination of the motion parameters with the global signal when the subjects were immobile (Freire & Mangin, 2001). We used the first temporal derivatives of the motion parameters, their shifted versions by 1 TR, and the squares of those 12 timeseries (Satterthwaite *et al.*, 2013). Images were spatially normalized to the template space using the T1-weighted anatomical image and resliced to a 4-mm isotropic voxel size to achieve a high voxel temporal signal-to-noise ratio.

2.4.1 Lag mapping

A recursive technique was used (Aso *et al.*, 2017*a*) after temporal bandpass filtering at 0.008–0.07 Hz to ensure that the phase was uniquely determined within the cross-correlation range. Whereas lag was tracked up to 7 s for most analyses, it was limited to 4 s in both directions, upstream and downstream, for the calculation of the relative BOLD transit time (rBTT, see below). This shorter tracking range allowed a higher cutoff frequency (0.12 Hz) to preserve the high-frequency component in the velocity change profiles.

The global mean signal was used to select the initial seed that defined the reference phase (lag = 0). First, voxels presenting a cross-correlogram peak at 0 with the global signal were determined. The time course averaged over this set of voxels served as the initial reference. In each step of the recursive procedure towards up- and downstream, a cross-correlogram was calculated between the timeseries obtained from the previous seed voxels and every undetermined voxel to find a set of

voxels with a peak at ± 0.5 s, which then served as the new seed. This tracking part retained some
voxels without any lag values because cross-correlogram peaks < 0.3 were not used (Tong et al.,
2017). These voxels were later filled one by one with average phases from voxels with similar time
courses at correlation coefficients > 0.3. There were single isolated holes even after this procedure,
which were filled by linear interpolation, using the six neighbors. There is a concern that this
threshold of correlation coefficient is too low to claim significant correlation. However, the
recursive tracking involves finding the cross-correlogram peak precisely at ±0.5 s, which conveys
different information from its height. Besides, a majority of earlier works, empirically supporting
biological significance of this phenomenon, involved no thresholding. When the threshold
correlation-coefficient was increased to 0.6, most brain voxels required the hole-filling procedure,
but we still obtained similar lag maps (by between-voxel intra-class correlation ICC(2,1) > 0.4) in 16
out of 20 subjects.

267 2.4.2 fMRI analysis on "cleaned" BOLD datasets

Individual BOLD data from Experiment 1, after the above pre-processing steps including the motion
parameter regression, served as the reference or "raw" dataset. GSR with low-pass filtered global
signal, normal GSR, global scaling implemented in SPM12, and removal of the perfusion lag
structure ("deperfusioning") were compared with the raw dataset.

The GSR involves regression by the global signal and extracting the residuals in each voxel. In
deperfusioning, instead of the uniform regressor, a corresponding timeseries was used for each
voxel group by the lag value ("dynamic" GSR) (Erdoğan et al., 2016). For global scaling, the raw
dataset was entered into the same SPM pipeline, except for the option of internally dividing each
volume by its global mean signal instead of the constant session mean. The normal GSR and global
scaling thus affected all frequency ranges, whereas the filtered GSR and deperfusioning removed
only the low-frequency components.

Random effects analysis (Friston et al., 2002) was used to evaluate the effect of these procedures
on the fMRI results from the standard analysis framework. For the visuomotor task, the neural
response to each trial was modeled as an event of 0.5-s duration. For the hyperventilation condition,
a boxcar with 25-s duration modeled the activation related to volitional respiratory control.
Similarly, both the onset and offset timing of breath holding were used to model the time-locked
neural activity. The canonical hemodynamic response function was convolved to the model
timeseries to create the regressors of interest. All activation maps were thresholded at p = 0.05
after correcting for multiple comparisons, using family-wise error across the whole brain (Poline et
al., 1997).

288 2.4.3 Relative BOLD transit time

289 **Fig. 3A** illustrates the method. This analysis was performed on data from Experiment 1, acquired at
290 a short TR of 0.5 s. The lag structure consisted of a lag map and the set of timeseries averaged over

the voxels with the same phase. This structure represents the propagation of the sLFO phase along the vessels. The phase is expected to move across adjacent regions of the vascular tree every 0.5 s, the lag tracking step, on average. However, if there is variation in propagation velocity, there would be deviation of the instantaneous phase difference from 0.5. Here, the phase difference is supposed to reflect the time the blood requires to cross the boundary between the neighboring voxel groups.

Based on this supposition, the phase difference fluctuation was calculated from each of the 16 pairs of seeds corresponding to lags of -4 to +4 s at 0.5-s intervals. Because of the broad frequency range of the fluctuations of interest, we chose smooth sliding window algorithm (window length = 30 s, Kaiser window with a parameter beta of 4) instead of analytic methods (e.g., Hilbert transform). The region timeseries were resampled to a 0.02-s resolution to capture minute phase difference fluctuation (4%) from 0.5 s. Instantaneous phase differences from each pair of seeds were averaged over respiratory task events and divided by 0.5 to obtain the time course of the rBTT. The rBTTs from the 16 pairs of neighboring regions were then averaged to obtain the regional or global rBTT. According to this model, the inverse of the rBTT corresponded to the instantaneous velocity (relative to the baseline average velocity), as the rBTT should reflect the average time the required to traverse fixed distances.

2.4.4 Multi-echo combination

For Experiment 2, involving multi-echo acquisition, S_0 and T2* datasets were created by a simple estimation used in earlier works (Posse *et al.*, 1999; Yen *et al.*, 2017). We assumed a single compartment monoexponential decay of the MR signal as follows:

$$S(TE) = S_0 \; exp(-TE/T_2^*) \qquad [4],$$

where T2* and S_0 were calculated for each TR as follows (Kundu et al., 2012; Posse et al., 1999):

$$T_2^* = (TE2 - TE1)/\ln(S_1/S_2) \qquad [5] \text{ and}$$

$$S_0 = S_1^{TE2/(TE2-TE1)}/S_2^{TE1/(TE2-TE1)} \qquad [6],$$

where S_1 and S_2 are the acquired signals at TE1 and TE2, respectively. Negative values or T2* exceeding 100 ms were considered as noise and were ignored. All four datasets (S_0, S_1, S_2 or BOLD, and T2*) were entered into the same analysis pipeline used for Experiment 1 but taking the different TR of 1.3 s into account. The following analyses were performed on a resampled time course at a TR of 0.5 s.

The interaction between the signal component and vascular anatomy was examined by extracting
the signal timeseries from the inlet, center, and outlet parts of the vascular tree, based on the
individual lag map created from the BOLD (i.e., at TE2) dataset. By exploiting the longer lag tracking
range (± 7 s) than the one used in the rBTT analysis in Experiment 1, the center region in this
analysis covered a wider range (± 2.5 s). Using the JMP12 Software (SAS Institute, Cary, NC), the
magnitude and phase of the regional signals were analyzed by repeated-measures ANOVA followed
by post hoc analysis, using Tukey's honestly significant difference (HSD) test. Statistical significance
was assumed for $p < 0.05$. Additional analyses were performed to examine the origins of the signal
components, including a region-of-interest analysis and an SPM analysis of respiration phase-
related small S_0 fluctuation.

3   Results

336 The average root mean square of head motion measured as the framewise displacement, i.e., the
337 shift in the position of the brain in one volume compared to the previous volume, was 0.039 ± 0.007
338 mm (mean ± standard deviation over subject) for Experiment 1, with a maximum displacement of
339 0.37 ± 0.18 mm, and 0.034 ± 0.015 mm for Experiment 2, with a maximum of 0.24 ± 0.12 mm (Van
340 Dijk et al., 2012).

Fig. 2. Representative spatial and temporal profiles of the BOLD lag structure. (A) Lag map created by tracking the BOLD low-frequency oscillation (LFO) phase up to 7 s toward both up- and downstream. Group average map shows the gross vascular anatomy with the early phase (positive values) distributed in the middle cerebral artery territories. The individual map provides more detailed information. (B) Seed time courses updated at each step (0.5 s) of the recursive lag tracking procedure, representing the temporal aspect of the lag structure. The warm-colored traces with advanced phase originate from the voxels with the same colors in the lag map, corresponding to the inlet or arterial side of the vasculature. A gradual change in the temporal profile is noted on top of the slow component, which is stable across regions. The white vertical lines indicate the timing of the visuomotor task, whose NVC was modeled by the hemodynamic response function (dark gray trace). The detected LFO was poorly correlated with the task-related fluctuation of neuronal origin (see main text).

Fig. 2A shows the average and an individual BOLD lag map during the sparse visuomotor task. Warm colors indicate a positive travel time from those voxels to the phase of the global LFO, signifying that the voxels are considered "upstream." Most brain voxels fell into the -4 to +4 s range (mean ± SD, 93.8 ± 2.9%). The recursively defined seed time courses are shown in **Fig. 2B** with warm colors indicating averaged timeseries from the upstream voxels. This time course of the lag structure was poorly correlated with the visuomotor task (white vertical lines) or the evoked NVC response (trace in dark gray), supporting non-neuronal origin of the sLFO. This was confirmed by the correlation coefficient between the global mean signal and the modeled response that was not significantly different from zero (0.0265 ± 0.140, mean and SD over 20 participants), although still slightly positive in some subjects and its regression affected the activation maps (see section 3.2). In addition to the constant phase shift across regions, the lag structure time courses presented minute fluctuations of the phase difference (i.e., the temporal relationship between the lines) over time.

3.1 Flow velocity information in the instantaneous phase

A transient change in propagation velocity of the low-frequency phase, obtained as the inverse of the global rBTT, was found in response to the respiratory challenges. **Fig. 3B** shows the stacked histograms of distribution of instantaneous phase difference measured by the moving window analysis. This instantaneous phase difference (in s) is interpreted as the time the blood required to move over a unit distance that requires 0.5 s on average. The time courses are presented in **Fig. 3C**. After approximately 10 s of delay, increase and decrease of the BOLD signal was found during breath holding and hyperventilation, respectively (arrows). This delay in the autoregulatory BOLD response is consistent with earlier work (Murphy *et al.*, 2011).

Fig. 3. Measurement of relative bold transit time (rBTT). (A) Schematic illustration of the analysis. For each pair of voxel groups representing neighboring regions of the vascular tree, the two average timeseries were fed into a moving window analysis of instantaneous phase difference. (B) Time point histograms of the instantaneous phase difference averaged over 16 pairs of neighboring regions in the lag structure. Twenty subjects are stacked. Deviation of the phase difference from 0.5 s reflects a fluctuation of the flow velocity, although the slight shift of the peak is observed in the breath hold data presumably due to the effect of windowing. (C) Response to the respiratory challenges of the physiological recordings, the raw BOLD signal, and inverse of the rBTT that can be interpreted as relative velocity. Thin arrows indicate the autoregulatory response of the raw BOLD signal. The five cycles of volitional breathing for hyperventilation are indicated with yellow bands representing the inspiration phase. Shaded areas indicate the 95% confidence interval of the mean across subjects.

The temporal profile of the instantaneous velocity (green curves) was roughly in phase with the global BOLD response but had different onset and peak timings, indicating the different physiological bases. To evaluate the relationship of this phenomenon with the vascular structure,

the inlet, center, and outlet regions were separately analyzed (**Fig. 4**). In both respiratory challenges,
there was a clear asymmetry over the vasculature, with pronounced velocity responses in the inlet
region. Despite similar BOLD response profiles, the velocity response was not clearly found in the
outlet region.

Fig. 4. Autoregulatory responses to respiratory challenges in the three vascular regions, using
the same conventions as in **Fig. 3**. The inlet (arterial side), center, and outlet (venous side) of the
parenchymal vasculature were defined for each subject, using the lag map created from the
session data per se. The relative changes in propagation velocity were detected as the inverse of
instantaneous transit time deviation from 0.5 s (rBTT), since the lag mapping was performed at
0.5-s steps. The BOLD signal time courses present different peak latencies for the three regions
(broken lines are aligned to the center region peak), directly reflecting the lag structure, but with
similar profiles, ruling out its effects on the rBTT measurement. Shaded regions represent the
95% confidence intervals (N = 20).

3.2 Effect of deperfusioning on the detection of NVC

Removal of the whole lag structure exhibited unique effects on the fMRI analysis. While the mean
and standard deviation images from the individual activation maps showed similar spatial
distribution, all procedures reduced the sensitivity compared to the Raw dataset where only the
motion-related variances were removed (**Fig. 5**). However, after the deperfusioning procedure,
primary motor cortex activation was successfully detected by decreased interindividual variances

(black circles). The effect of these procedures was not uniform between the respiratory challenges
(**Fig. 6**), but some interpretable clusters were selectively captured by the "deperfusioned" signals
despite the reduced cluster number. For example, the so-called laryngeal motor cortices were
detected at the onset and offset of the 10-s breath-holding (Kumar *et al.*, 2016). In the
hyperventilation condition, bilateral recruitment of the putamen was noted. This is consistent with
reports using optimized acquisition techniques (Dresel *et al.*, 2005; Pattinson *et al.*, 2009),
supported by anatomical (Simonyan & Jürgens, 2003), as well as electrophysiological (Radna &
MacLean, 1981) studies. A premotor peak found at coordinates [+56, 0, 40] was also very close to
the reported activation site for volitional respiration (McKay *et al.*, 2008).

Fig. 5. Effect of the denoising procedures on the detection of neurovascular coupling during the
visuomotor task. Mean and standard deviation maps from 20 individual activation maps
(contrast images) illustrate the spurious negative responses by the global-signal based methods
(white circle) and the reduced between-subject variation by the lag structure removal or
deperfusioning (black circle). Activation maps were thresholded at p = 0.05, corrected for FWE
of multiple comparisons over the entire brain, and zoomed in to show the "hand-knob" of the
left primary sensorimotor cortex. FWE, family-wise error corrected.

Fig. 6. SPM results of the respiratory challenges. Color panels show un-thresholded t map slices at the height of the laryngeal motor cortex (z = 35) (Kumar et al., 2016), revealing spurious negative responses (cool colors) after global signal removal but not after the deperfusioning procedure. In the hyperventilation condition, the "deperfusioned" data revealed clusters in the bilateral putamen and premotor cortex (white circle), consistently with the findings of earlier reports.

Voxel histograms from the group SPMs showed clear leftward shifts by the global signal removal, indicating spurious deactivations (**Fig. 7**). The correlation of the neuronal response with the global signal (or the extracted sLFO) was near zero, as described above, but it varied across subjects and

tended to be positive. This trace of NVC may have created the spurious deactivation after
regression. Notably, this effect was very weak after deperfusioning across all three conditions
(green plots), despite a large amount of variance removed by the procedure. This finding is in
agreement with the results of earlier work on resting-state fMRI (Erdoğan *et al.*, 2016).

Fig. 7. Effect of preprocessing on group SPMs. Removal of the lag structure or deperfusioning
resulted in greatest reduction of the signal variance under all three tasks (left panels).
Nevertheless, the spurious negative task responses were attenuated in comparison to the
removal of global fluctuation (middle and right panels). Error bars indicate the standard
deviation. The vertical broken line in the histogram indicates the statistical height threshold of p
= 0.05, corrected for multiple comparisons by family-wise error rate. GSR, global signal
regression.

3.3   MR signal components of the lag structure

455 As depicted in **Figure 8**, the percent signal change of the sLFO, or the lag structure amplitude,
456 revealed a clear T2*-dependence with a significant reduction of amplitude in the outlet, i.e., the
457 venous side of gross vasculature (post hoc Tukey's HSD between T2* signals from the inlet and

458   outlet regions, following a repeated-measures ANOVA). This finding replicates a previous
459   observation in the raw BOLD signal (Aso *et al.*, 2017*a*).

Each error bar is constructed using a 95% confidence interval of the mean.

Fig. 8. Standard deviation of the percent signal change as a measure of sLFO magnitude. No
main effect of vascular region was observed by repeated-measures ANOVA, but the T2*
magnitude was significantly different between the inlet and outlet or arterial and venous sides
($p < 0.05$, Tukey HSD). The short-TE image was not included in the ANOVA to avoid data
redundancy.

In lag maps from the three T2*-weighted images, we noted some effect of the respiratory
challenges, but the gross cerebral vascular structure was preserved across tasks; the periventricular
regions and major venous sinuses were uniformly found downstream (i.e., with negative arrival
time) of the global signal phase, while the cortical territory of the middle cerebral arteries
presented earlier arrival (**Fig. 9A**). Only the S_0 image presented a different lag structure, which was
confirmed by the image similarity (**Fig. 9A**, right panels).

Temporal analysis of the signal components revealed significant main effects of both region [F
$(2,532) = 16.877$, $p < 10^{-6}$] and T2* weighting [F $(2,532) = 280.786$, $p < 10^{-6}$] (**Supp. Fig. 1A**). The S_0
timeseries failed to show a correlation with the T2*-weighted signals, but the z-value in the inlet,
i.e., the arterial side, differed significantly from other regions ($p < 0.05$, Tukey's HSD). A region
effect was also found for phase relationships (**Supp. Fig. 1B**). Again, the main effects for both region
[F $(2,532) = 27.548$, $p < 10^{-6}$] and T2* weighting [F $(2,532) = 44.679$, $p < 10^{-6}$], as well as their
interaction [F $(4,532) = 24.902$, $p < 10^{-6}$], were significant. The phase of the TE1 signal, which is less
T2*-weighted than is BOLD, gradually advanced, finally showing a phase lead in the outlet region,
further supporting an interaction between the signal components and vascular regions. These signal

phase dissociations within regions are displayed in **Supp. Fig. 1C**. Significant differences among the three T2*-weighted signals were also found after the post-hoc test ($p < 0.05$). The signal-region interaction was evident in the signal response to the respiratory challenges shown in **Fig. 9B**. The traces contain higher frequency components, which were eliminated for lag mapping. In contrast to the changes in T2* responses for both phase and magnitude, the S_0 component was stable across vascular regions.

Fig. 9. Analysis of signal components and the lag structure. *A*, S_0 and T2* signals were interpolated based on multi-echo acquisition at short and typical echo times for BOLD fMRI. The lag map created from the S_0 image shows a unique structure but fails to reflect the arterial and venous structures that are consistently found in the BOLD lag map. Using the T2*-weighted signals, the lag map changes upon respiratory challenges, which should primarily reflect the modification of the perfusion pattern; however, an interaction with the signal component is not excluded. The right panels show intraclass correlation coefficients as a quantitative measure of within-subject image similarity with the BOLD lag map, with error bars indicating 95% confidence intervals. *B*, Temporal profiles from the three vascular regions indicate absence of region effect in the S_0 signal, suggesting a globally uniform mechanism underlying the S_0 response.

To further investigate the signal origin, we extracted the response in the motor/premotor area activation peak, where NVC was expected to dominate (**Supp. Fig. 2A**). For this analysis, the group activation map from Experiment 1 was used to define the regions-of-interest in order to avoid bias. We found high-frequency components dominating the S_0 responses in comparison to the responses from larger regions shown in **Figure 9B**. During hyperventilation, it presented respiratory phase-related fluctuations, with a signal decrease initiated by inhalation and followed by a positive deflection during exhalation. The T2* signal also exhibited small fluctuations but with a different phase, possibly dominated by the NVC component.

We conducted an additional analysis for this fast respiration-related non-BOLD component. The spatial distribution of this response is shown in **Supp. Fig. 2B**. Interestingly, there was a clear anterior-posterior segmentation of response polarity, with the posterior regions presenting the opposite phase of this fast S_0 deflection by respiratory maneuver. Some additional symmetrical structures were found in deep-brain regions, near the deep middle cerebral and inferior ventricular veins, implying a unique vascular involvement. Importantly, this spatial pattern was not that of a typical motion artifacts that can accompany volitional respiration in spite of the careful instruction.

Finally, **Supp. Fig. 2C** shows the data from a subset of participants, obtained using a different TR/flip-angle setting to manipulate the inflow effect. The T2* response was smaller than that shown in the panel **2A**, presumably due to the short TR. The different TR also contributed to the rich high-frequency components by the fast sampling rate. The slow S_0 change was also diminished, but the respiration-related fast component was relatively preserved suggesting absence of a strong inflow effect.

4 Discussion

The principal findings of this study are summarized as follows. First, based on the instantaneous phase difference within the BOLD lag structure, we observed a trace of blood flow velocity change

selectively in the inlet region of the vasculature. Next, the complete elimination of the lag structure

reduced interindividual variance and spurious deactivation, supporting our hypothesis that NVC

could be observed more specifically by this deperfusioning procedure. Finally, the lag structures in

the S_0 (or non-BOLD) component did not correlate with that from T2*, either spatially or temporally.

We also found a vascular region-dependent change in the T2* LFO, with a decreased amplitude in

the venous side, in contrast to the S_0 response that remained constant in both amplitude and phase.

The S_0 component exhibited a unique brain region-dependent response to the respiratory phase,

suggesting that certain perfusion parameters are specifically contributing to this component, but

not the perfusion lag. Overall, the BOLD low-frequency phase behaved as a deoxy Hb-based virtual

contrast agent in the present data, leaving a global, but separable noise component for the fMRI

analysis.

The observation that the velocity on the arterial side exhibits changes alongside respiratory

variations is consistent with the findings of previous reports using transcranial Doppler

ultrasonography (Malatino *et al.*, 1992; Poulin *et al.*, 1996). During the initial whole-brain CBV

increase in response to autoregulatory vasodilation, a sole increase in the inflow should first occur

to meet the volume demand. It is reasonable that this effect is absent in the outlet, i.e., the venous

side of the gross vasculature, as observed in the current study. The low-frequency phase hence

appears to directly reflect the perfusion.

This result is compatible with the model that the BOLD lag structure is derived from an axial non-

uniformity in the vessels, already present in the inflow (Tong *et al.*, 2018). The diminished

magnitude observed in the outlet side of the vasculature also suggests a distinct mechanism of the

lag structure, other than CBF increase which creates a larger response in the draining vessels (Krings

et al., 1999). It is unclear what proportion of this axial variation is systemic, i.e., originating from the

autonomic loops, mediated by peripheral baro- or chemoreceptors. At least, even if the neural

activity is contributing to this component creating the sLFO, the resulting lag structure would be

mainly of vascular origin. In this work, we focused on non-neuronal mechanisms to account for the

BOLD lag structure to the extent possible, in the hope that it may ultimately help achieve a better

understanding and modeling of the fMRI signal.

4.1   Source of BOLD LFO signals

Previous studies on sLFO have reported that both Hb species fluctuate, but with varying phase

difference that is selectively found in the brain (Obrig *et al.*, 2000; Rayshubskiy *et al.*, 2014;

Tgavalekos *et al.*, 2016). The observed fluctuations of total Hb density have been linked to CBV

changes (Boas & Dale, 2005; Kennerley *et al.*, 2005; Kim & Ogawa, 2012), but interpretations for

that of deoxy-Hb have rarely been provided. Only one series of studies by Fantini and others directly

addressed the possible axial variation of blood content including oxygen saturation (Fantini, 2014).

In support of the conventional theory, Rayshubskiy and colleagues reported, in their human

intraoperative study, slow Hb oscillation correlated with vasomotion in the superficial arteries
(Rayshubskiy *et al.*, 2014). However, it remains unclear whether an equivalent vasomotion exists in
the non-arterial vessels to fully account for the observed lag structure. It is hence worth considering
other sources of deoxy-Hb variation. The concept of vasomotion stems from an active diameter
change in the precapillary vessels, driving local velocity fluctuations, termed "flowmotion"
(Intaglietta, 1990). This flowmotion can reportedly accompany the fluctuation of local Hct that
should directly affect deoxy-Hb density (Fagrell *et al.*, 1980; Hudetz *et al.*, 1999). Another possible
source for the deoxy-Hb fluctuations is a change in SaO2 that ranges from 94–98% in the artery
(Intaglietta *et al.*, 1996; Collins *et al.*, 2015). For example, the respiration-related BOLD signal
component is supposed to be mediated by blood CO_2 level and pH, which also shift the oxygen
dissociation curve (Birn *et al.*, 2006; Chang & Glover, 2009*a*). These parameters are considered to
fluctuate in the blood as part of the autonomic loop, possibly driving vasomotion, at least in part,
which persists even after denervation (Morita *et al.*, 1995). As mentioned above, the phase
difference between the two Hb species remains to be elucidated (Sassaroli *et al.*, 2012), but this
observation itself substantiates an unstable deoxy-Hb supply in brain tissues. Besides, such a signal
component would have escaped detection in NVC studies using trial averaging.

A signal origin intrinsic to the flowing blood may, as suggested by Tong and colleagues, thus explain
the constant phase difference among signals from different body parts (Tong *et al.*, 2012, 2017). In
the literature, an axial variation of the Hct in the brain has indeed been suggested, in relation to
both NVC (Kleinschmidt *et al.*, 1996; Siegel *et al.*, 2003; Chen & Pike, 2009) and sLFOs (Fagrell *et al.*,
1980; Mayhew *et al.*, 1996). Furthermore, the reduction in T2* LFO amplitude in the venous side
can be explained by the high tissue deoxy-Hb density, which probably diminishes the proportional
effect of intrinsic deoxy-Hb fluctuations, unless the oxygen consumption is completely coupled to
this variation. Importantly, temporal dispersion alone would not fully account for the amplitude
reduction, as it was only found in the venous side, despite the fact that the lag structure was
tracked both up- and downstream from the global phase. These results provide good contrast with
the stable S_0 response, reflecting its insensitivity to oxygen saturation. Although it would be too
challenging to incorporate complex rheological parameters, a reconsideration of the constant
deoxy-Hb assumption may help improve the BOLD signal modelling.

In the hyperventilation condition, we observed a fast response to each ventilation cycle,
accompanying blood pressure change. Although the effect of respiratory movement cannot be fully
excluded, the spatial pattern in **Supplementary Figure 2B** is not that of a typical motion artifact
centered on the brain surface (Krings *et al.*, 2001). In healthy subjects, inhalation increases systemic
venous return through decreased intrathoracic pressure, causing elevation of the cardiac output
with some delay. In contrast, exhalation is considered to cause CBV increase through elevated
cerebral venous pressure. To our knowledge, the timing order of these events has not been studied
at the precision of the current data, and further studies are needed to determine the source of this
S_0 fluctuation (Yen *et al.*, 2017). The only available clue is the spatial distribution, such as the

interesting anterior-posterior segmentation (resembling the unique "S_0 lag structure" in **Fig. 9a**) or
the symmetrical pattern in the deep brain structures. At least, some mechanical effect of the
respiratory act on the fluid dynamics likely exists, causing this spatially-heterogeneous S_0 deflection.

4.2   Lag structure as noise

Based on the assumption that the global signal fluctuation is the sum of all variations by NVC, its
elimination by GSR has been considered to negatively bias the results (Caballero-Gaudes & Reynolds,
2017). However, as noted by Aguirre and others, there are cases where GSR yields interpretable
results even in the absence of global motion artifacts (Aguirre *et al.*, 1998). The rise in popularity of
rs-fMRI since 2005 has led to this issue resurfacing in a different form. A variation in GSR, in which
the timeseries extracted from a set of regions-of-interest (whole brain, white matter, and
cerebrospinal fluid) are removed, has become a *de facto* standard. It is indeed computationally
closer to our deperfusioning in that the regional phase difference is somehow tolerated. However,
because this practice lacked strong theoretical background (Chang *et al.*, 2009; Liu *et al.*, 2017),
currently, the identification and elimination of bodily movements and physiological noise are more
widely recommended. There are various approaches to this end, such as simultaneous physiological
measurements (Chang & Glover, 2009*b*), as well as data-driven methods that only use fMRI data
(Smith *et al.*, 2013). To date, however, objective criteria for distinguishing neural activity from noise
components remains an issue (Salimi-Khorshidi *et al.*, 2014).

In the present study, the lag structure was treated as a broadly-distributed structured noise for
fMRI. Indeed, it can be substantially eliminated by sophisticated denoising techniques (Aso *et al.*,
2017*a*). However, the specificity of lag mapping in isolating information on a purely vascular origin
remains, however, unclear. For example, measurement of velocity changes critically depends on a
recursive lag-tracking method, which incorporates the gradual change in LFO over regions (Tong &
Frederick, 2014). Adaptation for changes in the waveform that may arise from different paths of the
blood is not only theoretically plausible, but was demonstrated to increase the reproducibility of the
lag (Aso *et al.*, 2017*a*). However, as the changes in waveform reflect any fluctuation originating
either from the vascular anatomy or NVC, removing the whole lag structure may lead to type II
errors in the fMRI results. The favorable impacts of the deperfusioning procedure that we observed
on the fMRI results are clearly insufficient to prove the advantage of this technique and require
further confirmation.

Importantly, the detection of the lag structure itself is dependent on data quality and affected by
body movements. This would be the case when a significant head movement results in a
synchronized deflection that exceeds the LFO amplitude, thus obscuring the phase variation.
However, it can be also questioned if the correlational structure of neural activity is reliably
detected from such motion-contaminated data. In general, NVC should have a limited spatial extent
and signal magnitude without time-locked averaging (Power *et al.*, 2012). In turn, successful

tracking of a lag structure may even be considered as evidence of "clean" data. Thus, the
elimination of this identified lag structure can be a relatively straightforward approach to reduce
structured physiological noise (Caballero-Gaudes & Reynolds, 2017).

In conclusion, by investigating various aspects of the BOLD sLFO, we compiled supporting evidence
for a component intrinsic to flowing blood that has been a focus of interest in earlier works (Tong *et*
al., 2017). To establish a framework by which the fMRI signal can be fully modeled, more detailed
characterization of the lag structure as part of the "global noise" is needed (Glasser *et al.*, 2018).

5   Conflict of Interest

643 *The authors declare that the research was conducted in the absence of any commercial or financial*
644 *relationships that could be construed as a potential conflict of interest.*

6   Author Contributions

646 All authors provided approval of the final version of the manuscript to be published. TA contributed
647 to concept and design of this research, data analysis and interpretation, and drafting of the
648 manuscript. SU contributed to data acquisition and drafting of the manuscript. SU, HF, and TM
649 contributed to data interpretation and review of the final draft.

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9   Data Availability Statement

657 The datasets analyzed for this study can be provided upon request.

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