Evaluating models of the ageing BOLD response

Henson, R.N.[1,2], Olszowy, W.[3,4], Tsvetanov, K.A.[5,6] , Yadav, P.S. [1], Cam-CAN[*] & Zeidman, P. [7]

[1] Medical Research Council Cognition and Brain Sciences Unit, University of Cambridge, UK
[2] Department of Psychiatry, University of Cambridge, UK
[3] Wolfson Brain Imaging Centre, Department of Clinical Neurosciences, University of Cambridge, UK
[4] Data Science Unit, Science and Research, dsm-firmenich AG, Kaiseraugst, Switzerland
[5] Department of Clinical Neurosciences, University of Cambridge, Cambridge CB2 0SP, UK
[6] Department of Psychology, University of Cambridge, Cambridge CB2 3EB, UK
[7] Wellcome Centre for Human Neuroimaging, University College London, UK
[*] list of authors at end of paper.

*Corresponding author:
Prof Richard Henson
Medical Research Council Cognition and Brain Sciences Unit
University of Cambridge
15 Chaucer Road
Cambridge CB2 7EF
United Kingdom
Telephone: +44 (0)1223 355 294

Email: rik.henson@mrc-cbu.cam.ac.uk

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Abstract

Neural activity cannot be directly observed using fMRI; rather it must be inferred from the
hemodynamic responses that neural activity causes. Solving this inverse problem is made possible
through the use of forward models, which generate predicted hemodynamic responses given
hypothesised underlying neural activity. Commonly-used hemodynamic models were developed to
explain data from healthy young participants; however studies of ageing and dementia are
increasingly shifting the focus towards elderly populations. We evaluated the validity of a range of
hemodynamic models across the healthy adult lifespan: from basis sets for the linear convolution
models commonly used to analyse fMRI studies, to more advanced models including nonlinear
fitting of a parameterised hemodynamic response function (HRF) and nonlinear fitting of a
biophysical generative model (hemodynamic modelling, HDM). Using an exceptionally large sample
of participants, and a sensorimotor task optimized for detecting the shape of the BOLD response to
brief stimulation, we first characterised the effects of age on descriptive features of the response
(e.g., peak amplitude and latency). We then compared these to features from more complex
nonlinear models, fit to four regions of interest engaged by the task, namely left auditory cortex,
bilateral visual cortex, left (contralateral) motor cortex and right (ipsilateral) motor cortex. Finally,
we validated the extent to which parameter estimates from these models have predictive validity, in
terms of how well they predict age in cross-validated multiple regression. We conclude that age-
related differences in the BOLD response can be captured effectively by models with three free
parameters. Furthermore, we show that biophysical models like the HDM have predictive validity
comparable to more common models, while additionally providing insights into underlying
mechanisms, which go beyond descriptive features like peak amplitude or latency, and include
estimation of nonlinear effects. Here, the HDM revealed that most of the effects of age on the BOLD
response could be explained by an increased rate of vasoactive signal decay and decreased transit
rate of blood, rather than changes in neural activity per se. However, in the absence of other types
of neural/hemodynamic data, unique interpretation of HDM parameters is difficult from fMRI data
alone, and some brain regions in some tasks (e.g, ipsilateral motor cortex) can show responses that
are more difficult to capture using current models.

Introduction

Functional magnetic resonance imaging (fMRI) is often used to infer changes in neural activity across
the brain as a function of a task or the individual being scanned. However, the Blood Oxygenation
Level Dependent (BOLD) signal measured in most fMRI experiments is a complex function of neural
activity, neurovascular coupling, blood flow, blood oxygenation and blood volume (Buxton et al.,
1998). Therefore, differences in the BOLD response across individuals can be caused by differences
in hemodynamics, rather than in neural activity per se. Here we focus on the effects of age, since it is
likely that age affects vascular factors as well as neural activity (Handwerker et al., 2012; Tsvetanov
et al., 2021; Wright & Wise, 2018). Indeed, neurovascular ageing is not only a confound in fMRI, but
an important process to assess alongside neural ageing (Abdelkarim et al., 2019; Tsvetanov et al.,
2021).

The most common way to model the BOLD impulse response to an experimental input (e.g., stimulus
or trial, assumed to cause a short burst of neural activity) is with a linear convolution model, in
which a delta function is convolved with a basis set of temporal functions, typically lasting 0-30s
post-stimulus. After convolution with multiple, sequential inputs in a typical fMRI experiment, each
convolved basis function forms a separate regressor within a general linear model (GLM). When
fitting the GLM to the fMRI timeseries from a voxel or region of interest (ROI), the weights
(parameter estimates) for each such function can be estimated using ordinary least squares

minimisation. There are multiple options for such basis sets (Henson, 2004), but a common one is
the Finite Impulse Response (FIR) basis set, which consists of multiple "top-hat" functions, e.g., 32
contiguous time bins of 1 s duration, spanning from 0 to 32 s post-stimulus (Figure 1).

Using such a flexible basis set (whether the FIR set in the time domain, or sinusoidal functions of
periodic frequencies in the Fourier domain), the first study to address age effects failed to find
differences in BOLD response shape between young versus older participants (D'Esposito et al.,
1999). However, like many studies, this study used relatively small groups (n=32 young and n=20
older), and the older volunteers may have been healthier than average for their age. Furthermore,
tests using such flexible basis sets may be less sensitive to subtle statistical differences in HRF shape.

Even though the BOLD response can vary across individuals and brain regions, it has a typical shape:
peaking around 5s and with an undershoot lasting 10-30s: often called the canonical hemodynamic
response function (HRF; see Figure 1 for an example). Thus a common approach is to assume this
canonical form, and allow for some variability around this by adding, e.g, its partial derivatives in
SPM's "informed basis set", or the first few singular vectors in FSL's data-driven FLOBS approach
(Woolrich et al., 2004; see Lindquist et al., 2009, for yet further models of HRF shape). Greater
sensitivity to ageing may be achieved by focusing on specific features of the HRF shape, such as the
latency of its peak. For example, Taoka et al. (1998) and Handwerker et al. (2007) found an age-
related delay in the time to peak, while Richter & Richter (2003) and Aizenstein et al. (2004) found
age-related reductions in the magnitude of the undershoot. By contrast, other studies have reported
no effect of age. For example, Ward et al. (2008) found no age effects on the HRF in contralateral
motor cortex during hand grips, while Grinband et al. (2017) found few effects of age on various HRF
features, and argued that those found previously could reflect age-related differences in neural
activity. Moreover, even if differences are found in the shape of the HRF (e.g, peak latency), relating
these to differences in underlying neural activity is far from simple, given that the mapping from
neural activity to BOLD response is nonlinear (see Discussion).

Again, the above studies involved relatively small samples. In the largest study of HRF shape of which
we are aware, West et al. (2019) compared a younger (n=74) and an older (n=173) group. They
found that HRFs differed between groups in auditory, visual and motor cortices, with increased time-
to-peak and decreased peak amplitude in older compared to younger adults. These groups are
actually a sub-set of the full set of n=645 participants used here. These participants come from the
CamCAN cohort (www.cam-can.org), approximately uniformly distributed across 18-88 years of age.
These participants were recruited using an opt-out procedure after contact from local surgeries,
making them more representative of healthy adults than most typical studies that use opt-in
recruiting via adverts (though the present participants are still biased towards people able to lie in
an MRI scanner for an hour, and towards those without physical or mental health problems). More
specifically, these data come from the CamCAN "sensorimotor" task, in which participants saw brief
trials consisting of bilateral visual checkerboards and/or auditory tones (Shafto et al., 2014).
Importantly, the time between trials (in terms of the stimulus onset asynchrony, SOA) was
deliberately optimised for detecting the shape of the HRF (assuming linear superposition of
overlapping responses), by using a 255-length "m-sequence" (Buračas & Boynton, 2002). Here we
extend the work of West et al. (2019) by examining the parametric effect of age across the whole
sample, and more importantly, by directly comparing different linear and nonlinear methods to
characterise age-related changes in the BOLD response.

This study addresses four objectives:

1. To characterise the effects of age on the BOLD response, using a model that makes minimal assumptions about the form of that response, at the cost of a large number of unconstrained parameters (a 32-parameter Finite Impulse Response model, FIR32) used as a basis set within the GLM.

2. To compare these effects of age against those inferred using a more parsimonious basis set with fewer parameters, which is statistically more efficient, but makes stronger assumptions: specifically, the 3-parameter, canonical or "informed" basis set used in the SPM software package (Can3).

3. To compare these linear fits to a potentially more flexible, 4-parameter model, in which the parameters refer to specific features of the BOLD response shape, such as latency and amplitude, and which are non-linearly fit to the trial-averaged FIR estimates (a Non-Linear Fitting approach, NLF4).

4. To go beyond the descriptive statistics provided by the models above, and fit a mechanistic, biophysical Hemodynamic Model (HDM) to the same data. This model explains the effects of ageing in terms of 3 biologically-meaningful parameters: neural efficacy, neurovascular signal decay rate and hemodynamic transit rate. A version of this HDM is widely used as part of the Dynamic Causal Modelling (DCM) framework used for connectivity analysis (Friston et al., 2003).

5. To test whether the models' parameters have real-world (predictive) validity. We did this by evaluating how well all the above models can predict the age of previously unseen participants, using cross-validation, and whether they relate to independent measures of vascular health and neural activity.

Methods

<u>Participants</u>

The N=645 participants were aged 18-88, fluent English speakers and in good physical and mental health based on the CamCAN cohort exclusion criteria, which excluded volunteers with a low Mini Mental State Examination score (<24), serious current medical or psychiatric problems or poor hearing or vision, and standard MRI contraindications (for more details, see Shafto et al., 2014). None showed evidence of neurodegeneration in their structural MRIs (though we cannot rule out sub-clinical effects of neural and/or vascular disease that increase with age). The study was conducted in compliance with the Helsinki Declaration. All participants gave written informed consent for the study and record linkage, as approved by the local ethics committee, Cambridgeshire 2 Research Ethics Committee (reference: 10/H0308/50). Nine participants were removed because they did not show a significant evoked response in at least one of the four ROIs (see ROI section below), leaving 636 participants, exactly half (318) of each sex.

<u>Paradigm</u>

Each trial consisted of two oval checkerboards containing a rectangular pattern presented either side of a central fixation cross (34 ms duration) and/or a simultaneously-onsetting binaural auditory tone (300 ms duration). The inter-stimulus interval was a blank screen containing only the fixation cross (to which participants were told to fixate throughout). The auditory tones were one of

three equiprobable frequencies (300 Hz, 600 Hz, or 1200 Hz). Frequency was not relevant to the task
or current hypotheses, so is collapsed here. The majority of the trials (120 of the 128) involved both
visual and auditory stimuli, which required a keypress with the right index finger; the remaining 8
randomly-intermixed "catch" trials had only visual (4 trials) or only auditory (4 trials) stimuli, and
participants were told to withhold their responses to such "unimodal" trials. The latter ensured that
participants needed to pay attention to both modalities in all trials. Visual acuity was corrected with
MRI-compatible glasses, while auditory presentation intensity was adjusted so that the tones were
audible for all participants.

The stimulus onset asynchrony (SOA) between trials was determined by a second-order m-
sequence (m = 2; Buračas & Boynton, 2002), in which half of the sequence elements were null
events. The minimal SOA was 2 s, with the null events serving only to produce SOAs that ranged
from 2 to 26 s (null events do not produce any change in stimulation when they occur). There was an
additional random jitter drawn from a uniform distribution of 0.1-0.3s before stimulus onset, which
meant that the effective sampling interval of the HRF across trials was 0.12s (Josephs & Henson,
1999). The total duration of the task was 8mins, 34secs (n=261 volumes).

<u>MRI data acquisition</u>

The MRI data were collected using a Siemens Trio 3T MRI Scanner system with a 32-channel
head coil. A T2*-weighted echo planar imaging (EPI) sequence was used to collect 261 volumes, each
containing 32 axial slices (acquired in descending order) with slice thickness of 3.7 mm and an
interslice gap of 20% (for whole-brain coverage including cerebellum; repetition time = 1970 ms;
echo time = 30 ms; flip angle = 78°; field of view = 192 mm x 192 mm; voxel size 3 x 3 x 4.44 mm).
Higher resolution (1 x 1 x 1 mm) T1- and T2-weighted structural images were also acquired to aid
registration across participants. For more details, see https://camcan-archive.mrc-
cbu.cam.ac.uk/dataaccess/pdfs/CAMCAN700_MR_params.pdf.

<u>MRI data preprocessing</u>

MRI preprocessing used the SPM12 software (Wellcome Centre for Human Neuroimaging;
https://www.fil.ion.ucl.ac.uk/spm), release 4537, implemented in the Automatic Analysis pipeline,
release 4.2 (Cusack et al., 2015). Preprocessing is described in (Taylor et al., 2017), but in brief,
structural images were rigid-body registered to a Montreal Neurological Institute (MNI) template
brain, bias corrected, segmented, and warped to match a gray matter template created from the
whole CamCAN Stage 2 sample using SPM's DARTEL toolbox. This template was subsequently affine
transformed to standard MNI space. The functional images were spatially realigned, interpolated in
time to the middle slice to correct for the different slice acquisition times, rigid-body coregistered to
the structural image, transformed to MNI space using the warps and affine transforms from the
structural image, and resliced to 3 mm x 3 mm x 3 mm voxels. An XML summary of preprocessing
can be found here: https://camcan-archive.mrc-
cbu.cam.ac.uk/dataaccess/ImagingScripts/mri_aa_release004_roistreams_v1_tasklist.xml.

<u>Single-participant (1st-level) models</u>

Two models were run, where neural activity was assumed to be: 1) locked to the onset of
each audiovisual stimulus or 2) locked to the subsequent key-press. We included unimodal trials for
the stimulus-locked model (since they still involved stimulation), but only included them for the
response-locked model if the participant incorrectly pressed the key.

GLMs for each participant were created and estimated in SPM release 7771[1] in Matlab
R2020b (https://www.mathworks.com). A single vector of delta functions at the onset of each trial
was convolved with each of the temporal basis functions (FIR or SPM's informed basis set; see
below) in a high-resolution space with 32 time-points every TR (resulting in a microtime resolution of
0.062s), and subsequently down-sampled at the middle point (to match the reference slice for the
slice-timing correction). Six additional regressors, representing the three rigid body translations and
the three rotations estimated in the realignment stage, were included to capture residual
movement-related artifacts, plus the timeseries extracted for WM and CSF compartments, to further
remove non-neural noise. Finally, the data were scaled to a grand mean of 100 over all voxels and
scans, and the model fit to the data in each voxel. The autocorrelation of the error was modelled
using a "first-order autoregressive plus white-noise" model, together with a set of cosines that were
used to high-pass filter both the model and the data at a frequency cutoff of 1/128 Hz. The GLM and
noise model were estimated using restricted maximum likelihood (ReML), and the resulting estimate
of error autocorrelation used to prewhiten both the model and the data. Finally, OLS was used to
estimate the model parameters for the whitened data.

Group model for FIR basis set

For the FIR basis set, the parameter estimate for each of the 32 x 1s time bins for each
participant was entered into a second-level GLM (equivalent to a repeated-measures ANOVA), as
well as a linear and a quadratic modulation by each FIR parameter by age (see Figure 2). Analyses
were restricted to a gray-matter mask, determined by thresholding the DARTEL template for voxels
with >50% proportion of gray-matter.

ROI definition

To maximise sensitivity to age, while not making assumptions about the shape of the BOLD
response, masks for each ROI were defined from an F-contrast in the second-level group FIR analysis
that spanned the (linear) effects of age.[2] For the left auditory cortex (lAC) and bilateral visual cortex
(bVC), these came from the stimulus-locked model, while for the left and right motor cortex (lMC
and rMC), these came from the response-locked model. The F-values were thresholded at F>5 to
define clusters of contiguous voxels[3]. This resulted in a mask of 280 and 182 voxels for lAC and bVC,
respectively, and 54 and 88 voxels for lMC and rMC, respectively.

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[1] except that orthogonalisation of regressors within each condition was switched off within
spm_fMRI_design.m (see https://github.com/RikHenson/AgeingHRF)

[2] The purpose of this study is to compare models of the effect of age on the HRF, so we want to define ROIs
that show strong age effects in the first place. Though performing this ROI selection from fits of the FIR model
biases the comparison of the FIR model with other models (as noted later), alternative definitions such as
defining ROIs on the average effect across participants would not identify the right motor cortex, because it
showed a particularly strong effect of age, while defining ROIs on anatomical criteria instead would be
problematic because the age effects could reflect functional boundaries not respected by anatomy. In other
words, our goal is not to identify (localise) brain regions that happen to show age effects in this paradigm, but
rather explain the nature of those effects (in terms of HRF shape or underlying physiological parameters)
wherever those age effects are strong.

[3] The degrees of freedom in this model are so high (>20,000) that nearly every active voxel survives correction
for multiple comparisons, hence the arbitrary threshold to define reasonably-sized ROIs.[4] Trial-locked FIR
effects that do not resemble a typical HRF are sometimes rejected as "non-hemodynamic", but in this case,
such an implicit model of the HRF would be better put explicitly into the GLM in the first place, e.g, by using a
more constrained basis set. Nonetheless, if the neural activity associated with a trial is sustained (more than a
second or so) and unknown in form, then a FIR basis set can be a useful "catch-all".

205   To allow for variability across participants in their most responsive voxels, we sub-selected
those voxels within the above masks that showed a significant F-contrast (at p<.05 uncorrected)
across time bins within each participant's first-level FIR models. Note that this entailed removing 9
participants with no voxels that survived this threshold. These 9 were roughly equally distributed
across age (22, 37, 41, 51, 52, 57, 64, 71, 80 years) and showed excessive motion artifacts in their
data (that rigid-body realignment could not correct). The median number of voxels across the
remaining participants that passed this threshold was 134, 77, 34 and 21 for lAC, bVC, lMC and rMC
respectively. Spearman correlations showed that this number did decrease significantly with age for
all ROIs, but we believe that matching the minimal signal-to-noise ratio across age is more important
than matching the number of voxels.

215   The fMRI timeseries for each ROI were then summarised in terms of the first temporal
216   component from a singular-value decomposition (SVD) across the voxels remaining from the above
217   F-contrast, using standard tools for ROI extraction in SPM. This entailed the high-pass filtering, pre-
218   whitening and correction for confounds described above during GLM estimation.

219   <u>HRF models</u>

220   For each ROI, we fit 4 types of model: two linear models (estimated using OLS) and two
nonlinear models (fit by gradient descent). The two linear models corresponded to 1) the 32 x 1s bin
FIR basis set described above (and used to define the ROIs) – henceforth the "FIR32" model – and 2)
SPM's informed basis set, consisting of a canonical HRF and two partial derivatives – henceforth the
"Can3" model. The two nonlinear models were based on shape-matching of the HRF using 4
parameters – the "NLF4" model – and a biophysical generative model with 3 parameters – the
"HDM3" model. These are detailed below.

227   *FIR32 model*

228   The "FIR32" model consisted of 32 top-hat temporal basis functions of 1s duration that captured the
229   first 32 seconds of post-stimulus time (Figure 1A). This FIR basis set is flexible, but can also capture
230   non-hemodynamic trial-locked effects (e.g, motion of the eyeballs during first time bin, in response
231   to a visual stimulus).[4] This approach is also called "selective averaging" (Dale & Buckner, 1997).

232   *Can3 model*

The canonical HRF used in SPM is a mixture of two gamma functions, one capturing the positive peak
around 5s and one capturing the negative undershoot peaking around 15s. The parameters of these
gamma functions were estimated from approximating the first singular vector of stimulus-locked
responses in a previous fMRI experiment (Friston et al., 1998). The second basis function in this
"informed" basis set is the temporal derivative of the canonical HRF, obtained by the finite
difference after shifting the onset of the canonical HRF by 1 second. The third basis function is the
dispersion derivative, obtained by the finite difference after increasing the dispersion of the gamma
function for the peak response by 1% (see Figure 1B).

241   *NLF4 model*

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[4] Trial-locked FIR effects that do not resemble a typical HRF are sometimes rejected as "non-hemodynamic",
but in this case, such an implicit model of the HRF would be better put explicitly into the GLM in the first place,
e.g, by using a more constrained basis set. Nonetheless, if the neural activity associated with a trial is sustained
(more than a second or so) and unknown in form, then a FIR basis set can be a useful "catch-all".

242   The NLF4 model refers to nonlinear fitting of a template HRF to each individual's FIR fit, using a first

243   order expansion with respect to amplitude and with respect to time (i.e., four parameters in total).

244   More precisely, the following model is fit:

245
$$\hat{Y}(t) = a_1 Y\left(\frac{t}{t_1} - t_0\right) + a_0$$

where vector Y is the template HRF, derived from the first singular vector from an SVD of the FIR

values across all participants, t is the post-stimulus time (PST), t_0 is the latency offset (constant

delay), t_1 is the latency scaling (cumulative delay), a_0 is the amplitude offset and a_1 is the amplitude

scaling – see Figure 1C. Thus for latency, t_0 moves the whole HRF forwards or backwards in time,

while t_1 extends the HRF in proportion to the time relative to trial onset. This model has greater

flexibility, e.g, in separating amplitude from different types of latency, than the above linear basis

sets. It is fit by maximising the correlation between (normalised) template and (normalised)

individual FIR. We have previously applied this approach to modelling the effect of age on the

latency of evoked MEG responses in the same task and participants (Price et al., 2017), and use the

same fitting procedure described there (gradient ascent on Pearson correlation). For similar

approaches to nonlinear HRF fitting, see Kruggel & Yves Von Cramon (1999).[5]

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[5] Note that, unlike the other 3 models, the NLF4 approach is fit to the FIR parameters (i.e, peristimulus time), rather than the original fMRI timeseries. One could take the best-fitting HRF shape from such nonlinear fitting of the FIR parameters, and insert it back into the first-level GLM for the fMRI timeseries, in order to estimate a single scaling (amplitude) parameter. This would enable inference to be performed on a single parameter, while allowing for variability in the HRF shape across ROIs and/or across participants. This has the potential to be more robust than re-inserting the FIR estimate of HRF shape for a given participant and ROI, if the latter is noisy, owing to the effective "regularisation" of the HRF by the average shape across participants and/or ROIs (similar to the formal hierarchical model used for HDM below). Nonetheless, care would be needed for regions like rMC that do not show a consistent HRF shape across participants (see Results).

Figure 1. HRF models: (A) linear Finite Impulse Response basis set with 32 x 1s bins (FIR32); (B) an "informed" linear basis set with a canonical HRF (blue), its temporal derivative (red) and dispersion derivative (yellow) (Can3); (C) nonlinear fitting of average empirical HRF for a given ROI (here lAC) using amplitude and latency offsets and scalings (NLF4); (D) nonlinear hemodynamic modelling using differential equations with three free parameters (in red) (HDM3).

HDM3 model

This nonlinear model is a biophysical, generative model based on differential equations that can be
integrated to produce HRFs, as a function of biologically relevant parameters (e.g, vasodilatory time
constants), rather than parameters that simply describe the shape of the HRF (as in NLF4 above). We
used a well-established hemodynamic model (Friston et al., 2000; Stephan et al., 2007; Havlicek et
al., 2015) with some updates to the parameters. The form of the model is explained in detail in
Appendix 5 of Zeidman et al. (2019), and it is shown schematically in Figure 1D. To briefly reprise,
there are four hidden states: vasoactive signal s, regional cerebral blood flow f_{in}, venous volume v
and deoxyhemoglobin q. Their dynamics are governed by the following equations:

$$\dot{f}_{in} = s \tag{1}$$

$$\dot{s} = \beta z(t) - \kappa s - \gamma(f_{in} - 1) \tag{2}$$

$$\tau_h \dot{v} = f_{in}(t) - f_{out}(v, t) \tag{3}$$

$$\tau_h \dot{q} = f_{in}(t) \frac{1 - (1 - E_0)^{\frac{1}{f_{in}(t)}}}{E_0} - \frac{f_{out}(v, t) q(t)}{v(t)} \tag{4}$$

$$y = 100 \cdot V_0 \left(k_1(1 - q) + k_2 \left(1 - \frac{q}{v}\right) + k_3(1 - v) \right) \tag{5}$$

$$k_1 = 4.3 \cdot \vartheta_0 \cdot E_0 \cdot T_E \tag{6}$$
$$k_2 = \epsilon_h \cdot r_0 \cdot E_0 \cdot T_E \tag{7}$$
$$k_3 = 1 - \epsilon_h \tag{8}$$

Equations 1-2 model the vasoactive signal s, which induces blood flow f_{in} in response to neural
activity $z(t) \in \{0,1\}$ with neural efficacy parameter β. This part of the model subsumes a variety of
neurovascular coupling mechanisms, such as nitric oxide signalling. The decay of the vasoactive
signal is governed by rate parameter κ, while rate parameter γ provides autoregulatory feedback[6].
Together these equations form a coupled oscillator.

Equations 3-4 model the cerebral blood volume v relative to the blood volume at steady state, as
well as the proportion of deoxyhemoglobin relative to rest, q. These equations correspond to the
balloon model of Buxton et al. (1998), where parameter $1/\tau_h$ is the rate of blood flow through the
vessel, and parameter E_0 is the resting oxygen extraction fraction. The blood outflow from the
vascular compartment is $f_{out}(v, t) = v(t)^{1/\alpha}$, in which Grubb's exponent α relates cerebral blood
flow (CBF) and cerebral blood volume (CBV).

Finally, Equations 5-8 model the generation of the fMRI BOLD signal (Obata et al., 2004, Stephan et
al., 2007). Parameter V_0 is the resting blood volume fraction, ϑ_0 is the frequency offset at the outer
surface of magnetised vessel, r_0 is the slope of intravascular relaxation rate against O_2, T_E is the echo
time and ϵ_h is the ratio of intra-vascular to extra-vascular components of the gradient echo signal.

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[6] The autoregulatory feedback parameter may not have a direct physiological correlate at the vascular level.
Indeed, it has been proposed that neurovascular coupling can be modelled as a purely feedforward system, in
conjunction with inhibitory neural activity (Havlicek et al., 2015). In the absence of a neural model, the
purpose of the feedback parameter here is simply to enable damped oscillatory dynamics on a physiologically
plausible timescale. See Appendix 5 of Zeidman et al. (2019) for details.

In the present HDM3 model, we allowed three parameters to be estimated from the data: 1) neural
efficacy parameter, β (as a proxy for neural activity), 2) rate of decay of vasoactive signal, κ and 3)
transit rate of blood flow, $1/\tau_h$. The remaining parameters were fixed based on empirical priors (see
Supplementary Material).

To fit the HDM, we used https://github.com/pzeidman/HDM-toolbox, which requires the SPM
software package (https://www.fil.ion.ucl.ac.uk/spm/software). The model was fit using the
standard Bayesian model fitting scheme in the SPM software, called Variational Laplace (Friston et
al., 2007). For participant i with timeseries Y_i, this returns a multivariate normal probability density
over the parameters, $P(\theta_i|Y_i)\sim N(\mu_i,\Sigma_i)$. The estimated values of the parameters μ_i were those
that maximised the log-evidence for the model, as approximated by the free energy $F_i \approx \ln P(Y_i)$.

While this scheme provides parameter estimates for individual participants, μ_i, it also yields the
estimated covariance of the parameters Σ_i. To convey both μ_i and Σ_i to the group level, we used the
Parametric Empirical Bayes (PEB) framework in SPM (Friston et al., 2016, Zeidman et al., 2019). This
is a Bayesian hierarchical linear regression model applied to the estimated parameters of all
participants' models (see Supplementary Material for more details). We then tested the evidence for
the presence versus absence of each covariate (mean and effect of age) on each hemodynamic
parameter using Bayesian Model Reduction (BMR, Friston et al., 2018), which iteratively prunes
mixtures of group-level parameters from the PEB model, where doing so does not reduce the free
energy.

<u>Temporal resolution</u>

In terms of temporal resolution (which determines the PST resolution in Figure 4 and latency
resolution in Figure 6), the choice of the FIR bin width of 1s was deemed as a reasonable trade-off
between bin-width and number of samples per bin (and this sub-TR sampling is only possible
because of the jitter described above; Josephs & Henson, 1999). The Can3 basis functions were
simulated at the resolution of 0.062s (TR/32), as stated in the "Single-participant (1st-level) models"
section above. Even though the NLF model is fit to the FIR, and so has the same 1s resolution, the
latency scaling is estimated via interpolation, so can have higher resolution. Finally, the HDM model
was simulated at its default resolution of 0.375s (a higher resolution of 0.062s did not affect results).

<u>Nonlinearities as a function of SOA</u>

Nonlinearities are known to exist for SOAs below around 10s. A key feature of the HDM3 model is
that, as a non-linear model of hemodynamics, it explicitly captures these nonlinearities, which can
then be visualised using a mathematical device called a Volterra expansion (Friston et al., 2000). This
expresses the relationship between the output of the system (the HRF) and the input of the system
(the stimulus) as the weighted sum of *Volterra kernels*. A first-order Volterra kernel is the modelled
HRF in response to a brief stimulus, and a second-order Volterra kernel is the nonlinear change in
the HRF as a function of time elapsed since the previous stimulus. (Crucially, the second order
kernels can only be estimated in the context of an experimental design that samples nonlinearities,
through the use of variable SOAs, as here.) These kernels are shown and discussed in Supplementary
Figure S8.

Of the total variance in the BOLD timeseries explained by the two Volterra kernels, the proportion
explained by the second-order kernel ranged from 4.5% to 29% across ROIs (i.e, the first-order
kernel explaining the remaining 95.5% to 71%). Thus nonlinearities as a function of SOA were
relatively small, though not insignificant, which needs to be kept in mind when interpreting the
results of the other three models that assume linearity. Nonetheless, the proportion of this second-

order variance that related to age (linear and/or quadratic) only ranged from 1% to 12% across ROIs,
suggesting that this nonlinearity is unlikely to dramatically affect age-related conclusions drawn from
the linear models.

Results

<u>Whole-brain analyses</u>

Separate analyses were performed to identify BOLD responses time-locked to stimulus
presentation in sensory cortices, and BOLD responses time-locked to button presses in motor
cortices.[7] For each analysis, the parameter estimates for each basis function (time bin) from the
FIR32 GLM were entered into a second-level group model across participants to estimate the mean,
linear and quadratic effect of age for each basis function.

An F-test across the mean values from the stimulus-locked analysis showed many voxels that
responded (relative to interstimulus baseline), the most significant of which were in bilateral
auditory and visual cortices (Figure 2A).[8] Left (contralateral) motor cortex showed a significant mean
effect in the response-locked analysis. All three regions showed a linear effect of age, with additional
linear effects seen in right (ipsilateral) motor cortex (Figure 2B), as well as supplementary motor
cortex (not analysed further). No voxels showed strong quadratic effects of age.

The stimulus-locked, mean FIR estimates from the peak of the left auditory cortex cluster
showed a typical BOLD impulse response, peaking around 4-5s and with a more sustained
undershoot (Figure 2C, top). Interestingly, the estimates for the effect of age on each time bin
(Figure 2C, bottom) showed a profile that resembled a temporal derivative of the mean response,
such that the BOLD response became more delayed with age (which can be visualised by adding the
bottom plot in Figure 2C to the top plot). Similar results were found for the visual and left motor
clusters (not shown, but see later).[9]

The response-locked mean FIR for the rMC (Figure 2D, top), however, was not typical, and it
was the effect of age (Figure 2D, bottom) that appeared more like a typical HRF. This pattern can be
explained when plotting the HRF by age in the next section, where it becomes apparent that the
young showed a negative BOLD response that disappeared with age (see also Mayhew et al., 2022;
Tak et al., 2021).

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[7] Statistical parametric maps for the stimulus-locked and response-locked group FIR models were similar, as
would be expected since the median across participants of their median reaction time (RT) across trials was
282ms (range = 182ms - 679ms), which is short relative to the time-constants of the BOLD response.
Nonetheless, this variability in RTs (across both trials and participants) is important for latency analyses below.
[8] The degrees of freedom in this model are so high (>20,000) that nearly every active voxel would survive
correction for multiple comparisons, so the statistical and extent thresholds were chosen simply to obtain
reasonably-sized ROIs.
[9] Note that the slight "sawtooth" modulation across alternating FIR bins (particularly apparent in tail of HRFs)
reflects the differential sampling across the run owing to the non-integer ratio of bin-width relative to TR, such
that even-numbered bins tended to be sampled from trials later in the run than odd-numbered bins.

Figure 2. Panels A and B show maximal intensity projections (MIPs) of statistical parametric maps (SPMs) of F-contrast for (A) the mean effect across participants, locked to audio-visual stimulation (thresholded for 50 contiguous voxels with F>80), and (B) the (linear) effect of age, locked to the right finger press (thresholded for 50 contiguous voxels with F>5). The clusters corresponding to the four functional ROIs analysed below (lAC, bVC, lMC and rMC) are labelled on the sagittal, coronal and transverse sections, along with the F-contrast and the design matrix (bottom right). Panels C and D show the mean of each FIR parameter (upper plot) and effect of age on each parameter (lower plot) for the peak voxel from the (C) lAC ROI [-39 -33 +12] and (D) rMC ROI [+36 -21 +51]. Note that the scale of the y-axis is in arbitrary units and differs across plots; for % signal change, see Figure 4. Red bars show 90% confidence interval.

The clusters showing linear age effects were used to define four functional ROIs: lAC, bVC,
lMC and rMC (see Methods). FIR models were then re-fit to the first temporal component of a
singular value decomposition of each voxel's BOLD timeseries for each ROI. The first 16s of these ROI
FIR responses are shown for each participant as heatmaps in the top row of Figure 3, and averaged
within age tertiles as plots in the top row of Figure 4.

The effect of age for stimulus-locked responses in lAC and bVC is a reduction in amplitude
(of both peak and undershoot), and an increase in dispersion (e.g., delay in centre of mass of the
response). Indeed, the undershoot almost vanishes for the oldest participants. For response-locked
data, the lMC shows a similar increase in dispersion, but smaller age-related decrease in amplitude.
The rMC however shows a quite different response that is almost triphasic, with a smaller peak but
larger undershoot in young people (explaining the mean and age effects in Figure 2D). Note also that
there is some variability in HRF shape across ROIs (see Supplementary Figure S3).

Figure 3. HRFs shown as heatmaps for each ROI (columns) and model (rows). The y-axis represents each participant, sorted by age, while the x-axis represents post-stimulus time (PST), truncated at 16s for easier visualisation. The fits were smoothed across participants with a 5-participant running average. lAC = left auditory cortex, bVC = bilateral visual cortex, lMC = left (contralateral) motor cortex, rMC = right (ipsilateral) motor cortex. The lAC and bVC data are from the stimulus-locked model; lMC and rMC are from the response-locked model.

Figure 4. Average HRFs within age tertiles (18-44, 44-66 and 66-88 years) for each ROI (columns) and model (rows). Y = young; M = mid-life; L = late-life. The dotted lines in rows 2-4 are the (replotted) FIR estimates (i.e. same as top row) for reference. Note y-axis scale different across ROIs but matched across models. See Figure 3 legend for more details.

Features of FIR32 fits

One could extract a number of features (i.e., descriptive statistics) from the FIR fits to each
participant. As an example, we defined the peak amplitude and peak latency from the FIR time bin
with the maximal absolute value within the first 16s.

For peak amplitude, Spearman rank correlations showed significant decreases in peak
amplitude with age for lAC, bVC and lMC, but a significant increase in peak amplitude for rMC (top
row of Figure 5).

Figure 5. Amplitude estimates for each ROI (columns) and model (rows), plotted for each participant as a function of age. Amplitude is defined as the maximum absolute value of the fit within the first 16s, except for the NLF4 model, where the amplitude scaling parameter is plotted instead (since it is designed to capture amplitude without defining a peak). The R and p-value for Spearman rank correlations with age are shown in legend. See Figure 3 legend for more details.

For peak latency (top row of Figure 6), there is clearly limited resolution (given the FIR bin

size) and there are many potential outliers (even when truncated at a maximum of 16s).

Nonetheless, Spearman rank correlations showed small but significant effects of age in increasing

peak latency for lAC and lMC. Peak latency decreased with age in rMC, though this likely reflects the

difficulty of defining the peak for the more complex response shape in this ROI (cf. the latency

parameters from NLF model below).

Figure 6. Latency estimates for each ROI (columns) and model (rows), plotted for each participant as a function of age. Latency is determined by the time of the maximum absolute value of the fit (peak) within the first 16s, except for the NLF4 model, where the absolute value of the latency scaling parameter is plotted instead (since it is designed to capture latency without defining a peak). See Figure 5 legend for more details.

We also examined the root-mean squared error (RMSE) of the residuals across the original
BOLD timeseries (top row of Supplementary Figure S4a). Note there is some statistical circularity for
the FIR model, since the same model was used to define the ROIs in the first place, but its inclusion
here at least provides a lower bound on the residuals, albeit biased, with which to compare the
other models. Not surprisingly therefore, the FIR32 model had least error in fitting the original
timeseries, though also likely because it had the most degrees of freedom (i.e, most flexibility). This
error then increased numerically from the Can3 to NLF4 to HDM3 models.

The bottom row of Supplementary Figure S4a shows the RMSE across trial-averaged, post-
stimulus time, namely the fit of the Can3, NLF4 and HDM3 models to the FIR fit. In this case, the
NLF4 model had least error (except in rMC), followed by the Can3 model and then HDM3.

Note however that a better test of the models than the above RMSE metric is to apply cross-
validation, in order to adjust for differences in model flexibility, as is done later. More importantly,
Supplementary Figure S4b plots the residuals (from original timeseries) as a function of age. The
residual error increased with age for all models and in all ROIs except bVC, as did the variability
across participants. This suggests that a subset of older participants have more (non-stimulus-
locked) noise remaining in their fMRI data (e.g, residual effects of head motion) and/or demonstrate
more trial-to-trial variability in their HRF.

Can3 fits and HRF features

The second row of Figures 3-4 shows the fits of the Can3 basis set (see Methods), while the
second row of Figures 5-6 shows its estimates of peak amplitude and peak latency derived from the
reconstructed HRF for each participant. Figure 4 shows that the Can3 basis set is accurate in
capturing variation in the BOLD response shape across age tertiles and across ROIs (closely following
the FIR estimates in dotted lines). One potential limitation of the Can3 set is the inability to decouple
the amplitude of the peak and that of the subsequent undershoot (see, for example, lAC and bVC
where the magnitude of the undershoot is slightly over-estimated).[10]

The correlations of peak amplitude and peak latency with age were stronger for the Can3 fits
than the FIR fits for lAC, bVC and lMC (cf. first and second rows of Figures 5-6). This suggests that the
Can3 basis set is more sensitive to effects of age on features of the HRF shape (as would be expected
when the peak amplitude and latency are effectively derived from a weighted sum of many time
bins, rather than a single time bin in case of the FIR). For rMC however, Can3 no longer showed a
significant increase in peak amplitude with age, and showed a smaller negative correlation for peak
latency (cf. the NLF4 model considered next). Indeed, there is clearly a bimodal distribution of peak
latencies from the Can3 model, reflecting whether the peak or undershoot has greater absolute
displacement from zero.

NLF4 fits and HRF features

The third row of Figures 3-4 shows the fits of the NLF4 model (see Methods), while the third
row of Figures 5-6 shows its estimates of amplitude and latency. This model does not appear to fit all
ages as well as the Can3 model, particularly effects of age on the undershoot, and particularly in the
rMC. The latter is understandable from the fact that the average across participants (or first singular

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[10] We did try a fifth model in which the gamma function for the peak and the gamma function for the
undershoot were separate basis functions (along with their temporal derivatives, i.e. 4 basis functions in total),
but this model did not perform as well (e.g., in the cross-validated prediction of age reported later). Also note
that, according to the HDM model, the peak and undershoot are highly coupled, since they are part of the
same damped oscillation in response to a brief burst of neural activity.

temporal component) for the rMC may not correspond to the typical "template" HRF required by
this approach.

Note that the purpose of the NLF4 model is to estimate amplitude and latency directly,
rather than derive them post hoc from the peak of the fitted responses, so the third row in Figure 5
reflects the NLF4 amplitude scaling parameter and the third row in Figure 6 reflects the NLF4 latency
scaling parameter. Indeed, this model distinguishes two types of amplitude and latency – an offset
(shift) and a scaling (stretch) – see Methods. The advantage of the NLF4 model can be seen in the
generally stronger correlations of amplitude and latency with age. For lAC and bVC for example, the
amplitude scaling parameter shows a more negative effect of age than does the peak amplitude
estimated from fits of the FIR32 or Can3 basis sets, while the latency scaling parameter shows a
more positive effect of age. This is because the NLF4 model explicitly separates the amplitude from
the latency. For rMC, the NLF4 model recovers a significant positive effect of age on amplitude, but
no longer produces a significant negative effect of age on latency, most likely because it eschews the
need to define the peak of a more complex evoked response shape (cf. issue of peak and undershoot
for Can3 model above).

HDM3 fits and its parameters

Whereas the NLF4 model is designed to fit features of the BOLD response shape (specifically
amplitude and latency), the final model considered here is a biologically-plausible generative model
of how that response is caused. While the full HDM potentially has multiple free parameters (see
Supplementary Material), we focus on an HDM3 version, in which we fixed several parameters to
their prior expected value, leaving three free parameters: neural efficacy, neurovascular decay rate
and hemodynamic transit rate.

The bottom row of Figures 3-4 shows the fits of the HDM3 model, while the bottom row of
Figures 5-6 shows estimates of amplitude and latency from the HDM3 fit. The HDM3 model does
reasonably well for all ROIs, though appears to peak earlier than the FIR model, and struggles to
capture age effects in rMC.

The three free parameters of the HDM3 model are shown as a function of age in Figure 7.
Neural efficacy (top row) showed a small negative effect of age in lAC and bVC (but not lMC), but a
positive effect of age in rMC. Neurovascular decay rate (second row) showed strong positive effects
of age in all ROIs. The hemodynamic transit rate (bottom row) showed strong negative effects of age
in lAC, bVC and lMC, but not rMC. Indeed, in rMC, there were many participants for whom the
default transit rate of 1.02 was sufficient (likewise for the default neurovascular decay rate of 0.64).

Figure 7. HDM3 parameters (rows) for each ROI (column) plotted for each participant as a function of age. The R and p-value for Spearman rank correlations with age are shown. Parameter estimates for decay and transit rates are after transforming the posterior expected values from their log-values back into original units of Hz (see Supplementary Material).

Furthermore, we can incorporate the HDM results into a hierarchical linear model, in order to
regularise the parameter estimates across participants, using SPM's PEB framework (see Methods).
More specifically, we fit a group-level model that included a constant term (average parameter value
across participants) and a linear age effect (slope of parameter change with age). We then used BMR
to prune parameters that are not needed in order to maximise the model evidence for this group-
level model. This analysis takes into account the posterior covariance between parameters,
effectively dropping parameters whose effects can be accommodated by another parameter (while
maintaining similar model evidence).

The results of PEB-BMR on the linear effect of age on each parameter are shown in Figure 8 (results
for the mean across participants are shown in Supplementary Figure S5). After PEB-BMR, the
posterior expectation for the neural efficacy parameter remained close to its prior (0) in lAC, bVC
and lMC, i.e., there was no need for age to moderate neural efficacy. Only in rMC was there a need
to increase neural efficacy with age. By contrast, neurovascular decay rate showed an increase with
age across all ROIs, while hemodynamic transit rate showed a decrease with age in lAC, bVC and
lMC.

Note that while these Bayesian results were generally consistent with the Spearman correlations of
each parameter with age in Figure 7, at least for the decay and transit parameters, the PEB-BMR
results question the significant negative Spearman correlations of neural efficacy with age in lAC and
bVC. This is because the PEB-BMR approach takes into account the posterior covariance among
parameters, which was ignored by the correlation analyses above, which were done independently
on each parameter. The presence of correlation between the posterior estimates of the neural
efficacy parameter estimates and those of the other two "vascular" parameters means that not all
are needed to simultaneously capture the effects of age on the BOLD response.

Figure 8. Results of PEB BMR on HDM parameters for each ROI for the linear effect of age across participants. Grey bars show posterior expectation with 90% credible interval in pink; missing bars are parameters that BMR has removed as unnecessary (in terms of maximising evidence for PEB model). For decay and transit parameters, units are log deviations.

Cross-validated Prediction of Age

We tested how well each of the four models could predict participants' chronological age based on
their parameter estimates, combined across all four ROIs, using multiple linear regression and leave-

one-out cross-validation.[11] The top panel of Figure 9 shows that all models did a reasonable job of
prediction, with the Can3 model explaining the most (44%) variance in age, and the NLF4 model
explaining the least (25%).

The bottom panel of Figure 9 shows the absolute error in those predictions. Sign tests showed that
the Can3 model did significantly better (smaller median error) than the FIR32 model, despite the fact
that the FIR32 model had smaller RMSE when fitting individual timeseries data (see Supplementary
Figures S4a and S4b). This is likely because the much greater number of parameters in the FIR32
model results in over-fitting (i.e, capturing some noise in individual fits), such that their estimates do
not generalise well to data from other individuals. The NLF4 model was significantly worse than the
FIR32 model, suggesting that its parameters were failing to capture some important aspects of
ageing. The HDM3 model did not differ significantly from the FIR32 model, which is reassuring for
this model, though it did not perform as well as the Can3 model.

For comparison, Supplementary Figure S6 shows the age prediction error for the Can3 model, when
fitting the canonical HRF only, or adding its temporal derivative, or adding both its temporal and its
dispersion derivatives. This suggests that all three basis functions are needed.

Supplementary Figure S7 shows the age prediction error for four versions of the HDM model (the
HDM3 used here, plus versions with 4, 5 and 6 free parameters). The HDM3 model did better than
the more complex models with more parameters (indeed, performed significantly better than the
HDM4 model). This is why we focused on the HDM3 model here.

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[11] We did try adding second-order expansions of HDM parameters (including interaction terms), as well as
more advanced ML techniques (such as gradient boosting), but these did not show better cross-validated
prediction than standard (unregularised) multiple regression (indeed, SHAP analyses showed linear terms are
sufficient).

Figure 9. Results of cross-validated prediction of age for each model, using all parameters across all ROIs. Top panel shows the Pearson correlation between actual and predicted age. Bottom panel shows boxplots of absolute error, where each grey line corresponds to one participant. An asterisk means that a two-tailed sign-test revealed significantly different error than from the FIR32 model. The average across ROIs of the median error was 9.98 years (FIR32), 9.20 years (Can3), 11.90 years (NLF4) and 10.33 years (HDM3), respectively.

External validation of HDM3 parameters

Finally, we sought external validation of the HDM3 parameters. In previous work (King et al., 2023),
we estimated three latent vascular factors (LVFs) from six potential measures of vascular health in
the CamCAN dataset. These factors corresponded roughly to total blood pressure (LVF1), pulse
pressure (LVF2) and heart rate variability (LVF3), shown to be associated to cerebrovascular health

measures in the CamCAN cohort (Fuhrmann et al., 2019; Tsvetanov et al., 2021). N=625 of the
present participants had valid data for these LVFs.

A priori, the LVF1 and LVF2 factors that related to blood pressure would seem most likely to relate to
the hemodynamic transit rate parameter of the HDM model. Nonetheless, to test for any possible
relationship between the three vascular factors and three HDM3 parameters, we performed nine
mediation analyses (using the Matlab toolbox available here:
https://github.com/canlab/MediationToolbox; Shrout & Bolger, 2002), testing whether each LVF
mediated the effect of age on each HDM3 parameter.[12] The HDM3 parameters were taken before
PEB-BMR (see above), and averaged across the four ROIs for each participant, in order to reduce
multiple comparisons and potentially obtain a more accurate estimate for each participant,
assuming that the true vascular parameters are similar across brain regions within the same person.

The only mediation test that survived Bonferroni correction for nine tests was that of the first LVF
(LVF1) on the HDM3 transit parameter. In this model, age was positively related to LVF1 (total blood
pressure; a-path=0.34, T=8.97), and negatively related to mean transit rate (c-path without LVF1
present=-0.27, T=-6.90), both as expected. Somewhat surprisingly, LVF1 was positively related to
transit rate (b-path=0.15, T=3.64), such that higher total blood pressure was associated with faster
transit, whereas one might expect age-related chronic vascular alterations, such as atherosclerosis,
to lead both higher BP and lower CBF (slower transit times). In any case, the relationship between
age and transit rate became more negative with the inclusion of the LVF1 mediator (c'-path=-0.32),
producing the significant mediation effect (ab-path=0.05, T=3.36, p<.001). While interpretation of
this mediation may be complex (see Discussion), the fact that the only analysis to reveal a
relationship between age, vascular health and HDM parameters involved the expected transit rate
HDM parameter and one of the two expected LVFs related to blood pressure, supports the validity of
the above age-related changes on HDM parameters.

We also performed mediation analyses relating the HDM parameters to an independent measure of
neural activity in the same participants performing the same task in MEG (see Price et al., 2017, for
details). We took the mean evoked responses estimated from source-reconstruction of planar
gradiometer data from N=586 of the present participants, and summarised these responses in terms
of their energy (sum-of-squares of values from 0 - 400ms post stimulus- or response-onset, after
mean-correction for a pre-onset baseline period of 100ms).

A priori, we would expect this MEG measure of neural activity to mediate the effect of age on the
neural efficacy parameter of the HDM3 model, but not the other two vascular parameters. In this
case, we ran mediation analyses separately for each ROI, since the HDM neural efficacy parameter
showed different effects of age in the rMC compared to other ROIs. Thus, we ran all twelve possible
mediation analyses (three HDM3 parameters and four ROIs). None of these analyses showed a
significant mediation effect, even at p<.05 uncorrected (and even in rMC). Thus we could not
independently validate the HDM neural parameter with these MEG data, though we note that the
energy of first 400ms of the evoked response is unlikely to capture all neural activity detectable by
fMRI (see Discussion).

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[12] One could also enter such independent measures as additional covariates in the PEB model (as could higher-order polynomial expansions of age, in case there are nonlinear effects of age on the HDM parameters). However, given the high correlation of these vascular/neural factors with age, here we sought instead to test whether such measures mediated the age effects that we already found.

Discussion

We compared the ability of four models to capture age-related changes in the BOLD response to
brief audiovisual stimuli and key presses, using a large (N=645) and representative dataset
containing individuals uniformly distributed across the adult lifespan, and an fMRI paradigm
optimised to estimate the shape of the HRF.

Whole-brain analysis using the first model – the "FIR32" model with 32 temporal basis functions
capturing the HRF every 2s – revealed strong effects of age in many brain regions, particularly
bilateral visual, auditory and motor cortices. The predominant effects of increased age were to
reduce the amplitude of the BOLD response and to shift its centre of mass later in time.

Focusing on four of these ROIs, we compared the FIR fit to a more parsimonious linear model using a
canonical HRF and two of its partial derivatives ("Can3" model), as well as two nonlinear models. In
terms of capturing features of the HRF such as peak amplitude and peak latency, the Can3 model
showed stronger effects of age than the FIR32 model. However, a nonlinear model in which 4
parameters were fit to the FIR estimates ("NLF4" model, comprising zero- and first-order expansions
of amplitude and post-stimulus time) showed even stronger effects of age in most ROIs, suggesting
better de-coupling of amplitude and latency.

However, it is unclear whether such HRF features are informative with respect to the underlying
neural activity, which is normally what fMRI is used to infer. Indeed, the mapping from neural
activity to BOLD response is nonlinear, depending on vascular and hemodynamic parameters that
are also likely to change with age. Only the fourth model, based on prior work on biophysical,
generative hemodynamic modelling (Buxton et al., 1998; Friston et al., 2000), attempted to estimate
such neural and vascular parameters separately. When allowing three of these parameters to vary
(neural efficacy, neurovascular decay rate and hemodynamic transit rate), this "HDM3" model
suggested that the majority of age-effects on the BOLD response arise from vascular/hemodynamic
differences. Indeed, only one ROI – right motor cortex (rMC) – showed an effect of age on HDM3's
neural parameter, and this actually reflected increased neural activity in this ipsilateral motor region
with age (see below for further discussion about this particular region).

We compared all four models in terms of the accuracy with which the age of a new participant could
be predicted from parameters fit to the remaining participants, i.e., their out-of-sample cross-
validated performance. Given that the models are typically fit using different statistical frameworks
(ordinary least squares, gradient ascent and Variational Bayes), the cross-validated performance was
useful as a common basis for comparing all the models' sensitivity to ageing. Comparison of the
average (absolute) prediction error for 1, 2 and 3 basis functions in the Can3 model (Supplementary
Figure S6), and of the four versions of the HDM model with 3-6 parameters (Supplementary Figure
S7), confirmed the value of this approach. When applied to the four main models considered here,
age prediction was better for the Can3 model than FIR32 model, suggesting that the greater
flexibility of the latter resulted in over-fitting. Age prediction for the NLF4 model, on the other hand,
was worse than the FIR32 model, suggesting that it cannot capture all types of age-related variance.
The HDM3 model was comparable to the FIR32 model, suggesting that it is doing a reasonable job, in
addition to providing more physiologically-meaningful parameters.

Finally, we sought external validation of the HDM parameters using independent data about vascular
health (abstracted from blood pressure, BMI and ECG measures) and neural activity (from an
analysis of evoked MEG responses by the same participants in the same task). While our MEG
measure did not provide evidence of mediating the effect of age on the HDM3 neural parameter,

one of our independent vascular factors did show evidence of mediating the effect of age on the
HDM3 hemodynamic transit time, which provides some validation for the HDM3 model.

Studying Ageing with fMRI

If one just wants to detect (e.g, localise in the brain) the effects of age on the BOLD response, rather
than interpret those effects in terms of neuronal versus vascular influences, then the present results
demonstrate that SPM's canonical basis set, Can3, is best. It outperformed the FIR32 model in its
cross-validated ability to predict age, and will offer greater statistical power by virtue of using fewer
degrees of freedom.[13]

However, if one wishes to interpret age effects on the BOLD response in terms of neural activity,
then such linear basis functions are not sufficient. For this, a biophysically-plausible generative
model is needed. Although its performance was worse than the Can3 model, cross-validated age-
prediction performance of the HDM3 model was comparable to the FIR32 model. Importantly, if the
HDM3 model correctly distinguishes neural and hemodynamic contributions to the BOLD response,
then the present results have important potential implications for previous fMRI studies that have
interpreted age-related differences in the BOLD response in terms of differences in neural activity (at
least in sensorimotor tasks like the present one). This is because the present HDM3 results suggest
that most age effects on the BOLD response arise from vascular factors instead. This is consistent
with recent work combining BOLD fMRI with glucose PET (Stiernman et al., 2023), which showed
that effects of age on the BOLD response (during a working memory task) were not accompanied by
effects of age on glucose metabolism. Indeed, we found that age need not affect neural efficacy in
early visual, auditory and contralateral motor regions, at least when using a Bayesian approach to
prune away parameters whose effects are close to zero or well captured by the other parameters.
This is consistent with a previous study (Tsvetanov et al., 2015) that adjusted activations in the
present task by empirical estimates of vascular reactivity from an independent resting-state fMRI
dataset, called Resting-State Fluctuation Amplitudes (RSFA). That study also found dramatically
attenuated effects of age on visual, auditory and contralateral motor BOLD responses, once they
were scaled by RSFA. Interestingly, that study also found that the BOLD increases with age in rMC
remained after RSFA scaling, again consistent with the present HDM3 results in suggesting a neural
origin for age effects in ipsilateral motor responses.

The positive effect of age on the vasodilatory decay parameter of the HDM3 model in all ROIs
suggests that vasodilatory signals decay faster in older people. This seems plausible, and may reflect
changes in the efficacy of neurovascular coupling. Increasing this decay rate reduces the peak
response and attenuates the post-peak undershoot (Supplementary Figure S1). Meanwhile, the
negative effect of age on the hemodynamic transit rate parameter in most ROIs (except rMC)
suggests that blood flow is reduced (i.e., longer transit times) in older people. This also seems
plausible; cerebral blood flow decreases 0.3-0.5% per year in healthy ageing (Graff et al., 2023).
Decreasing this hemodynamic transit rate delays the HRF (Supplementary Figure S1).

The HDM3 finding that age increases the neurovascular decay rate is also consistent with a previous
study that used DCM to examine resting-state connectivity in the CamCAN dataset (Tsvetanov et al.,
2016), in which there was a significant positive effect in three of the four resting-state networks.
That study also found the same negative effect of age on the hemodynamic transit rate, though it

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[13] The more constrained nature of the Can3 basis set also prevents false detection of trial-locked effects that are implausible as hemodynamic responses, such as "activity" in the eyeballs for the first FIR time bin only, which reflects stimulus-driven eye-motion instead.

was only significant in one resting-state network. Nonetheless, that study used a different neural
model (based on a 1/f neural power spectrum in the resting-state, rather than the brief burst of
neural activity in response to a stimulus assumed here) and a different formalisation of the HDM (in
which the ratio of intra-vascular to extra-vascular components of the signal, ϵ_h, was also estimated;
see Supplementary Material). Moreover, it examined different (higher-order) brain regions. These
converging findings for the effects of age on the BOLD response are reassuring.

Note that we are not claiming that there are absolutely no age-related differences in neural activity
in the present sensorimotor task, particularly given that we have previously shown age-related
delays in evoked responses measured by MEG on the same participants in the same task (Price et al.,
2017). Indeed, we used the same NLF4 model in that study to demonstrate that age increased the
latency offset (shift) in visual evoked responses and the latency scaling (stretch) in auditory evoked
responses. However, these latency differences were small (approximately 20ms offset and 20%
scaling), and so unlikely to have much effect on the HRF, given that the HRF integrates over several
seconds of neural activity. Thus we are claiming that age may not affect the type of neural activity
that can be detected by fMRI, at least within the present ROIs and type of task. In other words, we
are claiming that our HDM3 results demonstrate that neurovascular and vascular changes are
sufficient to explain age effects on the BOLD response in the ROIs and task considered here. By
extension, the onus is on researchers who wish to use BOLD fMRI to infer about effects of age on
neural activity to first rule out age-related vascular effects.

<u>Linear Basis Sets and HRF Features</u>

While the Can3 basis set showed best cross-validated prediction of age, the partial derivatives of the
canonical HRF are important to capture this variability (Supplementary Figure S6). Thus, studies of
ageing that use only a single canonical HRF are likely to miss age-related differences in the HRF. Such
studies need to ensure that parameter estimates for the derivatives are also taken forward to any
group-level (2nd-level) analyses (or else combined to estimate a shape-independent effect size, e.g.,
Calhoun et al., 2004; Cignetti et al., 2016). The additional flexibility provided by the partial
derivatives is also important to capture variability across brain regions (Supplementary Figure S3).

Supplementary Figure S3 also shows that the canonical HRF used in SPM is more dispersed than the
BOLD responses estimated here. One reason for this could be that the canonical HRF was derived
from studies in which the data were not slice-time corrected (Friston et al., 1998, 2000), so there
was likely to be a delay (around TR/2 on average, typically corresponding to 1-1.5s), relative to
stimulus onset, in the activated brain regions. Here we were careful to synchronise the GLM with the
reference slice, ensuring no such delay. Another reason is that only a small number of participants
were used in those studies, who may not have been representative, whereas the HRFs in
Supplementary Figure 3 are averaged across a larger range of adults, spanning the whole adult
lifespan. In case it is helpful, we have added a "revised" canonical HRF (and its partial derivatives) to
the github page associated with this paper, in which the parameters of its two gamma functions are
estimated by fitting the average FIR across participants and across the lAC, bVC and lMC ROIs.
However, while this canonical form may be more appropriate for the average, healthy adult aged
between 18 and 88 than SPM's current one, the main point of the present study is to show how age
changes the HRF, so ideally researchers would use age-appropriate HRFs for their analyses. By also
providing the FIR fit for all current participants on the github page, researchers can define their own
canonical HRF matched to the ages of their own sample (at least for the 4 ROIs considered here; or
indeed download the raw data and estimate an FIR fit for any set of voxels).

Beyond localisation, it is unclear whether there are effects of age on the shape of the HRF that can
be directly interpreted (at least without a biophysical model). There may be information about the
latency of neural activity in the latency of BOLD responses, but this seems most likely for latency
differences between two or more conditions (e.g. types of stimuli), found within the same brain
region and same individual tested within the same session. In such situations, one can reasonably
assume that hemodynamic variables are constant, so any differences are neural in origin. In this
case, temporally-extended basis sets like the Can3 can better estimate latencies than individual FIR
time bins, which are more prone to noise, though the present results show that non-linear fitting of
models that explicitly parametrise different types of latency (e.g, offset and scaling, like in the NLF4
model) leads to even higher sensitivity. Even so, reverse inferences about the latency of neural
activity from latency of the BOLD response are complicated due to convolution (e.g, a difference in
peak latency of the HRF can arise from differences in the duration rather than onset of neural
activity, Henson et al., 2002), not to mention potential nonlinearities in the neural-BOLD mapping.
Most importantly however, for the study of ageing, or other individual/group differences, it seems
unlikely that differences between individuals in the latency (or indeed amplitude) of their BOLD
responses could ever be uniquely attributed to differences in neural activity, at least in the absence
of a validated biophysical model or independent data about hemodynamic differences.

Conversely, it is important to remember that any individual differences in the HRF (e.g. as a function
of age) cannot be uniquely attributed to hemodynamic factors, unless one knows that neural activity
is invariant across individuals (or can estimate that activity separately, e.g. with a biophysical model).
This point was made by Grinband et al. (2017) in the context of ageing. We believe that our
paradigm minimised factors that could cause age-related differences in neural activity (compared to
some previous paradigms) because our trial-based design entailed very brief, simple, meaningless
stimuli (<=300ms) that required minimal processing. While older people are generally slower to
react in such tasks, we accommodated this delay (for analysis of motor cortices) by locking analysis
to the keypress rather than the stimulus, which should allow for age-related variability in execution
time at least (though differences could remain in motor force and other kinematic variables).
However, our task did involve long and variable SOAs, in order to maximise the ability of fMRI to
estimate HRF shape (Josephs & Henson, 1999), so it is possible that age-related differences in
sustained attention existed that modulated neural activity (Grinband et al., 2017). But this is exactly
why more sophisticated models like the HDM are needed (in the absence of independent measures
of neural/hemodynamic factors), to try to separate effects of age on neurodynamics and
hemodynamics.

<u>Caveats with HDM</u>

Though the present HDM3 model offers the potential to separate neural and vascular contributions
to the BOLD impulse response, this is subject to several assumptions, as detailed in the
Supplementary Material. We fixed several parameters of the full HDM to their prior expected values,
whereas in reality they may also have changed with age. The reason for fixing some of them is that
the effects of several parameters on the BOLD response are very similar, so they are difficult to
disentangle in the absence of independent data (e.g, about blood flow or blood volume). This is
reflected in high posterior covariances between some parameters when fitting a 6-parameter HDM
(Supplementary Figure S2), and the fact that freeing up more than 3 HDM parameters did not
significantly improve cross-validated age prediction (Supplementary Figure S7). Thus, interpretation
of some of the age effects that we found with the HDM3 model could be wrong, mandating follow-
up studies that complement the BOLD response with other measurement modalities.

For example, regarding the neural efficacy parameter, its effects on the scaling of HRF are very
similar to those of the venous blood volume fraction (V_0), and V_0 is known to change with age.
Nonetheless, since V_0 must be positive, it cannot be solely responsible for the negative BOLD peak
we found in rMC. The effects of the neural efficacy parameter can also be similar to those of the
resting oxygen extraction fraction E_0 (Supplementary Figure S1), resulting in a high negative
correlation in their parameter estimates (Supplementary Figure S2). However, we argue in the
Supplementary Material that effects of age on oxygen extraction fraction are unlikely to be
detectable in the BOLD signal measured here. The effects of the neural efficacy parameter are also
related to vessel stiffness parameter α (Grubb et al., 1974), though in this case, they tend to have
opposite effects on the HRF amplitude (inducing positive correlation in their parameter estimates).
Nonetheless, our application of PEB to the HDM3 model resulted in no effects of age on neural
efficacy β in any ROI except rMC, and the latter is unlikely to be explained by parameters such as
blood volume fraction, oxygen extraction or vessel stiffness, because the effects of age on these are
unlikely to differ dramatically across cortical regions, particularly across contralateral ROIs like lMC
and rMC.

Likewise, the effects of age that we did find on neurovascular decay rate and hemodyamic transit
rate could also be attributed to effects of age on other HDM parameters that we fixed, particularly
the neurovascular feedback parameter, whose effects on the latency of the HRF are similar to those
of the hemodynamic transit rate (Supplementary Figure S1). To properly decouple these HDM
parameters, one would need independent measurements of blood flow, oxygenation, vasodilatory
signal and neural activity, to simultaneously constrain their values, for example using Arterial Spin
Labelling (ASL) fMRI for blood flow, or Vascular Space Occupancy (VASO) fMRI for blood volume.

Here we made a preliminary attempt to validate the HDM parameters against other, independent
data from CamCAN, using mediation analysis. We did find that the effect of age on the HDM transit
rate parameter was significantly mediated by a previous cardiovascular factor related to total blood
pressure (systolic plus diastolic). A relationship between hemodynamic transit and blood pressure
would appear to make sense. Nonetheless, we note that this mediation took the form of a
"suppressor effect", whereby the negative relationship between age and transit rate became more
negative in the presence of the cardiovascular mediator. One interpretation of this is that increases
in blood pressure compensate for age-related reductions in transit rate (given the positive
relationship between the cardiovascular factor and transit rate). Whatever the interpretation, this
highly significant mediation provides some construct validity to the HDM model.

We did not find any relationship between any of the HDM parameters and the amplitude of early,
evoked MEG responses from the same participants performing the same task. One might have
expected a mediation of age effects on the HDM neural efficacy parameter, but given that the BOLD
response integrates over several seconds of neural activity, it is possible that this short-lived evoked
amplitude measure is not sufficient. Future work could examine the effects of age on the power
spectrum of neural responses (evoked and induced), for example to see if BOLD amplitude relates to
a shift in power towards higher frequencies (Kilner et al., 2005).

Thus in summary, we are not claiming that the HDM3 model used here is the best or most accurate
model. Rather our aim is to illustrate how biophysical models like the HDM could be used in principle
to better interpret effects of age on the BOLD impulse response, e.g. in separating neural and
vascular components. Indeed, we expect future studies to continue to improve the HDM as an
explanation for the genesis of BOLD fMRI, and to extend the model to integrate complementary
imaging modalities. To illustrate, Havlicek et al. (2015, 2017) proposed improvements to the form of
the HDM model to better explain transient features of the BOLD response, and extended it to

explain functional ASL measurements. Thus while the present work supports the face validity and
predictive validity of HDM, further support for its construct validity will require independent
measurement of several of its variables, beyond the final BOLD response. For example, EEG/MEG
can provide independent measurements of neural activity from the same people doing the same
task, while other types of fMRI contrast, which depend on blood flow or blood volume, could be
acquired concurrently.

Other caveats

There are other caveats with the general approach adopted here. Firstly, while our paradigm
(specifically the m-sequence distribution of SOAs) was optimised to estimate the shape of the HRF,
this is under linear convolution assumptions. Nonlinearities have been shown for SOAs below
around 10s (Friston et al, 2000), which we replicated here from the HDM3 model (see Methods).
Furthermore, we showed significant effects of age on the second-order Volterra kernel
(Supplementary Figure 8). However, the proportion of variance explained by the second-order
kernel was relatively small, and the proportion of this variance related to age was even smaller. Thus
we think it unlikely that many of the present inferences about age effects were confounded by
nonlinearities as a function of SOA. Nonetheless, this remains possible, and there are other types of
nonlinearities, such as nonlinearities in the BOLD response as a function of stimulus duration or
magnitude, which are typically bigger than nonlinearities as a function of the SOAs (Birn et al., 2001).
While stimulus duration was fixed here, it remains possible that the duration of induced neural
activity differed with age. We have no way to test this, other than to note that reaction times (RTs)
did not differ much with age in the present task, by design, because it was unspeeded.

Secondly, we identified voxels within ROIs that showed a significant effect (at $p<.05$ uncorrected) of
stimulus/response-locked activity versus baseline. The number of such voxels did decrease with age.
While the number of voxels does not necessarily bias estimates of the average across voxels, it is
possible that the range of cortical areas sampled, and hence HRF shapes, differed for younger versus
older people. Future studies could perform more detailed analyses of individual voxels, possibly
better functionally-aligned across participants (than with the present anatomical normalisation),
whose HRF shapes might vary, for example, in the contribution of draining veins.

Ipsilateral motor cortex

Finally, the BOLD response in rMC is noteworthy in its difference from the other ROIs: it showed a
negative and delayed BOLD response versus baseline in young people, which became more positive
with age (see also (Mayhew et al., 2022; Ward et al., 2008; Tak et al., 2021; Knights et al., 2021, or
Mattay & Weinberger, 1999, for review). Indeed, the HRFs in rMC were the hardest to fit,
particularly for the HDM3 model. There may be several reasons for this. For example, it has been
suggested that the motor cortex ipsilateral to the effector is inhibited by the contralateral motor
cortex, but that this inhibition decreases with age, explaining the increase in neural efficacy with age
disclosed by the HDM3 model. Such activity in inhibitory interneurons may have metabolic
consequences (hemodynamics) that differ from those assumed by the HDM for excitatory activity
(Vazquez et al., 2018). Indeed, the neural component of the HDM could be augmented by
distinguishing excitatory and inhibitory cell populations, as was proposed for DCM (Marreiros et al.,
2008). Furthermore, the neural activity in ipsilateral motor cortex in such tasks could be more
delayed/dispersed than the brief burst assumed by all models used here. Ipsilateral motor cortex
would therefore be an interesting region to explore more closely in terms of its neurodynamics and
hemodynamics.

Summary

Age has strong effects on the form of the HRF, as shown using all four models we tested, and this
should be taken into account when analysing fMRI data. The model one would select for a study
depends on its aims. Where the priority is regional localisation, our results demonstrate that the
three parameter Can3 model works well. It is parsimonious, has similar sensitivity to ageing effects
as the other models we compared, and has best predictive validity. However, when interpreting
differences between individuals that have been localised this way, such as due to their age, caution
should be exercised before interpreting those differences in terms of neural differences (rather than
vascular ones). By contrast, where the aim is to ask mechanistic questions about the underlying
causes of ageing effects, there is an opportunity to deploy physiological models such as the HDM. As
illustrated here, these kinds of models can generate mechanistic hypotheses, which could then be
tested with other modalities that can provide direct measures of neural activity, blood perfusion, or
blood volume. Thus, with the appropriate model and data, we can go beyond descriptive statistics
such as time-to-peak or peak amplitude, and ask mechanistic questions about the genesis of the
BOLD response and its dysfunction in ageing.

Data and Code Availability

The raw functional and structural images and their preprocessed versions are available from https://camcan-archive.mrc-cbu.cam.ac.uk/dataaccess. All Matlab code for extracting data from ROIs and fitting the models above is available in https://github.com/RikHenson/AgeingHRF.

Author contributions

Designed research: R.N.H. Performed research: R.N.H., W.O. & P.Z. Analysed data: R.N.H., W.O. & P.Z. Writing—original draft: R.N.H. & P.Z. Writing – review & editing: R.N.H., W.O., K.A.T. & P.Z.

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Declaration of Competing Interests

The authors declare no competing interests.

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*Cam-CAN corporate author

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Supplementary Material for Evaluating models of the ageing BOLD response
Henson, R.N., Olszowy, W., Tsvetanov, K.A., Yadav, P.S., Cam-CAN & Zeidman, P.

Further details about Haemodynamic modelling (HDM)

Equations 1-8 in the main paper summarise the HDM. Here we expand on its estimation, priors and parameter effects.

Within the model, latent or hidden variables are divided into two types: *states,* which change over time, and *parameters*, which are constant. Only the parameters are estimated from the data, using a Bayesian modelling scheme (Variational Laplace), and the parameters determine the evolution of the states over time.

For the main HDM3 model in the paper, we allowed three parameters to be free: one to capture the magnitude of neural activity, β; one to capture neurovascular effects, namely the rate of decay of vasoactive signal, κ; and one to capture vascular effects, namely the transit rate of blood flow, $1/\tau_h$. The remaining parameters were fixed at their default priors, for reasons expanded below.

- An important vascular parameter is vessel stiffness (the windkessel effect), which is characterised by Grubb's exponent α (Grubb et al., 1974). In the range estimated here, increasing α primarily decreases the amplitude of the BOLD response (as well as delay its peak somewhat; see Supplementary Figure S1). Thus its primary effect on the HRF is inversely related to that of the neural efficacy parameter, β, resulting in a positive correlation between their parameter estimates (see Supplementary Figure S2; in general, parameters whose effects are negatively correlated tend to have estimates that are positively correlated, and vice versa). Therefore, we decided to fix the value of α here at 0.33 in the HDM3 model, consistent with previous studies (Friston et al., 2000) (though allowed it to vary in the HDM4 model below). This value of 0.33 is consistent with previous human and animal studies, in which values for α typically range between 0.2 and 0.4 (as reviewed by Leung et al., 2008). Nonetheless, this parameter is likely to change with age. In rats, α has been found to drop from around 0.35 in young individuals (4-5 months) to around 0.25 in very old age (40-41 months) (Dubeau et al., 2011). Thus, it should be kept in mind that some effects of age, particular on the neural parameter β, could also be accounted for by differences in vessel stiffness. Then again, our finding using the HDM3 model that there are no effects of age on neural efficacy β in any ROI except rMC, is unlikely to be explained by α, because vessel stiffness is unlikely to differ dramatically between contralateral ROIs like lMC and rMC (see Discussion of main paper).

- The neurovascular parameter γ is the rate constant controlling the feedback from blood flow. Together with the decay parameter κ, the two produce a damped oscillation of the vasodilatory signal. However the primary effect of decreasing γ is to delay the HRF, which is similar to the primary effect of decreasing the haemodynamic transit rate $1/\tau_h$ (Supplementary Figure S1), resulting in a high negative correlation between them (Supplementary Figure S2). For the HDM3 model, we therefore fixed γ here based on its prior expected value of 0.41Hz from Friston et al. (2000) (though allowed it to vary in the HDM5 model below). This does mean, however, that changes in neurovascular feedback could also reflect changes in haemodynamic transit rate.

- Resting oxygen extraction fraction E_0 refers to the percentage of the oxygen removed from the blood by tissue during its passage through the capillary network, and is typically assigned a fixed value (40%) in the HDM model (Friston et al., 2000). The effect of E_0 on the magnitude of the HRF is complex: it can produce an initial negative dip with high values, but at least for values below 40%, increases in E_0 tend to increase the amplitude of the peak of the HRF (Supplementary Figure S1). This can explain why the present empirical estimates of E_0 had a high negative correlation with estimates of the neural efficacy parameter, β (Supplementary Figure S2). While evidence suggests that E_0 increases by about 0.1% per year of adult life (Peng et al., 2014; Leenders et al., 1990), simulations of such changes of up to 7% around the prior of 40% (given the 70 year span in the current sample) showed little effect on the HRF. Therefore we decided to keep E_0 fixed at 40% in the HDM3 model (though allowed it to vary in the HDM6 model below).

- Venous blood volume fraction V_0 is the proportion of tissue occupied by venous blood, and is also typically assigned a fixed value (4%) in the HDM model (Friston et al., 2000). For grey matter containing small vessels, V_0 is generally taken to be in the range 1-4% (Buxton et al., 1998; Havlicek et al., 2015; Hua et al., 2019). Leenders et al. (1990) investigated effects of ageing on V_0, and found it decreases by around 0.05% per year of adult life: from 6.48% for 18 year olds to 3.25% for 88 year olds. Because V_0 simply scales the BOLD response (see Eq. 5), it is perfectly correlated with the neural efficacy β, i.e., one cannot estimate both V_0 and β using fMRI data alone. Here we chose to estimate β instead, but it should be kept in mind that any effects of ageing on β could be accounted for by V_0 (though again, our finding of a negative BOLD response in rMC cannot be explained soley by V_0, since V_0 is always positive).

- We adjusted the values of parameters ϵ_h, r_0 and ϑ_0 to correspond to the MRI field strength for the CamCAN data, where $B_0 = 3T$. In previous implementations of this model, the ratio of intra-vascular to extra-vascular signal, ϵ_h, was estimated from the data, reflecting uncertainty about its value in the literature (Stephan et al., 2007). Here, we decided to fix its value for stability, as large values of ϵ_h can induce phase transitions that give rise to unrealistic BOLD responses. Following Havlicek et al., 2015, we used the expected value of $\epsilon_h = 0.44$, based on the ranges of T2* relaxation rates (for further detail, see the MATLAB script *Heinzle_epsilon_derivation.m* in the HDM Toolbox, https://github.com/pzeidman/HDM-toolbox). We set the value of $r_0 = 110s^{-1}$ and $\vartheta_0 = 28.265B_0 = 31.27s^{-1}$, following Heinzle et al. (2016), who drew on the results of Uludag et al. (2009).

Supplementary Figure S1. Each plot shows the predicted BOLD response under different values of a parameter, indicated by the title. The central parameter value (producing the dotted line) reflects the prior expectation; the dark solid line and light solid line reflect smaller or larger values respectively (the values of all parameters other than the one varied in a plot were fixed at their prior expectation, except neural efficacy, β, which was set to 0.2).

Supplementary Figure S2. The mean across participants of the posterior correlation between HDM parameters after fitting a 6-parameter HDM model (HDM6) to the data in the paper. Apart from rMC, note that the other ROIs have a large positive correlation between neural efficacy β and vascular stiffness α, and large negative correlations between neurovascular feedback γ and haemodynamic transit rate $1/\tau_h$, and between oxygen extraction E_0 and β.

A summary of the prior expected value and variance for the three free parameters in the main HDM3 model used in the paper are shown in Supplementary Table 1. Note that, in order to enforce positivity constraints on two of these parameters, new parameters l_κ and l_{τ_h} are introduced, which are log versions of decay rate κ and transit rate, $1/\tau_h$, respectively. The scaling values of 0.64 and 1.02 are taken from (Friston et al., 2000). The neural efficacy parameter β is not constrained to be positive so is untransformed.

Additionally, in order to enforce positivity constraints on the states f_{in}, v and q, each variable is log-transformed, requiring the equations to be supplemented as follows:

$$\frac{d \ln f_{in}}{dt} = \frac{\dot{f}_{in}}{f_{in}} \tag{9}$$

$$\frac{d \ln v}{dt} = \frac{\dot{v}}{v} \tag{10}$$

$$\frac{d \ln q}{dt} = \frac{\dot{q}}{q} \tag{11}$$

Supplementary Table 1: Free parameters of HDM3 model

Model	Parameter	Compartment	Prior expectation	Prior variance	Parameterisation
HDM3	β	Neural	0	1	-
HDM3	l_κ	Neurovascular (CBF)	0	1/32	$\kappa = 0.64 s^{-1} \cdot \exp(l_k)$
HDM3	l_{τ_h}	Vascular (CBV)	0	1/32	$\frac{1}{\tau_h} = 1.02 s^{-1} \cdot \exp(l_{\tau_h})$

The HDM models with 4, 5 and 6 free parameters (used later in Sup Mat) included the values in Supplementary Table 1, plus the one or more of rows of Supplementary Table 2.

Supplementary Table 2: Additional free parameters of HDM4, HDM5 and HDM6 models

Model	Parameter	Compartment	Prior expectation	Prior variance	Parameterisation
HDM4	l_α	Vascular	0	1/32	$\alpha = 0.33 \cdot \exp(l_\alpha)$
HDM5	l_γ	Neurovascular	0	1/32	$\gamma = 0.41 s^{-1} \cdot \exp(l_\gamma)$
HDM6	l_{E_0}	Vascular	0	1/32	$E_0 = 0.40 \cdot \exp(l_{E_0})$

Group-level model using Parametric Empirical Bayes (PEB)

For the PEB estimation of a group-level model (Zeidman et al., 2019), parameter estimates from all n participants are concatenated into a vector of random variables, $\theta^{(1)} = (\theta_1, \theta_2 \dots \theta_n)$. Between-participant effects were then modelled using a general linear model:

$$\theta^{(1)} = X\theta^{(2)} + \epsilon \tag{12}$$

The design matrix X included regressors for the effect of each of two covariates (mean over participants and age) on each of $P = 3$ haemodynamic parameters ($\beta, l_\kappa, l_{\tau_h}$). This design matrix can be written formally as:

$$X = X_B \otimes I_P \tag{13}$$

where between-participants design matrix X_B contained two columns: a column of ones (to model the average haemodynamic parameters over participants) and the z-scored age of each participant. This was replicated over the three parameters by taking the Kronecker tensor product $\otimes$ with the identity matrix of dimension P.

Unexplained between-participants variability ϵ was modelled using a covariance component model, with a separate I.I.D. precision component for each of the three haemodynamic parameters, allowing each type of parameter to have a separate level of between-participants variability.

The parameters $\theta^{(2)}$ and free energy F of the PEB model were estimated using standard routines in the SPM software. We then tested the evidence for the presence versus absence of each covariate on each haemodynamic parameter using an automated procedure. This was an automatic search that iteratively pruned mixtures of group-level parameters $\theta^{(2)}$ from the PEB model, where doing so did not reduce the free energy. This was performed using an analytic approach called Bayesian Model Reduction (Friston et al., 2016).

Supplementary Figure S3. Mean across all participants of the FIR fits for lAC, bVC and lMC (solid lines), along with SPM's canonical HRF (dotted line). The rMC is not shown because it varied so much with age (see main text). Peak amplitude is matched by scaling by the maximum positive value. The lAC and bVC data are from the stimulus-locked model, while lMC is from the response-locked model.

SPM's canonical HRF is more dispersed than the FIR fits (delayed peak and undershoot). This may not have been noticed before because early studies generating this canonical shape (Friston et al., 2000) did not allow for slice-timing delays. So a delay of TR/2 (typically ~1s) could partly explain this mismatch. Here we did correct the data for different slice-times and were careful to synchronise the GLM (for FIR32 and Can3 basis sets) with the reference slice used for slice-timing. Grinwald et al. (2017) still observed deviations despite slice-timing, though ones that derivatives should be able to accommodate.

Supplementary Figure S4a. Boxplots (of log) of Root of Mean of Squared Error (RMSE) across scans (top row) or across FIR bins (bottom row) for each ROI and model. Note there is statistical circularity for the FIR model, since the same model was used to define the ROIs in the first place, but its inclusion here at least provides a lower bound, albeit biased, with which to compare the other models. Note also that there can be no RMSE for the FIR32 model in bottom row, and in the top row, the RMSE across scans for the NLF model was calculated by re-inserting the participant- and ROI-specific fitted HRF into each participant's first-level GLM (hence only 1 effective degree of freedom). The lAC and bVC data are from the stimulus-locked model, while lMC and rMC are from the response-locked model. Note that these measures of model fit ignore differences in model complexity, and so are not as good for generalisation to new data as the cross-validated error in Figure 9.

Supplementary Figure S4b. Square-root of Mean of Squared residuals (RMSE) across scans for each model and for each ROI, as a function of participant's age, together with Spearman correlation R- and p-values. The lAC and bVC data are from the stimulus-locked model, while lMC and rMC are from the response-locked model. Note that the RMSE for the NLF model was calculated by re-inserting the participant- and ROI-specific fitted HRF into each participant's first-level GLM (hence only 1 effective degree of freedom).

Supplementary Figure S5. Results of PEB BMR on HDM parameters for each ROI for the mean across participants, in terms of deviation of each parameter from its prior expectation. Grey bars show posterior expectation with 90% credible interval in pink; missing bars are parameters that BMR has removed as unnecessary (in terms of maximising evidence for PEB model). For decay and transit parameters, units are log deviations.

Supplementary Figure S6. Cross-validated absolute error in predicting age, using Can model parameters combined across all ROIs, as the number of basis functions increases, from canonical HRF only (Can1), to adding its temporal derivative (Can2) and then also its dispersion derivative (Can3). Each grey line corresponds to one participant. Superimposed on these lines are boxplots together with outliers (red crosses). An asterisk means that a sign-test revealed significantly better prediction than the simplest (Can1) model. The median error was 12.2 years (Can1), 10.0 years (Can2) and 9.2 years (Can3).

Supplementary Figure S7. Cross-validated absolute error in predicting age, using the HDM model parameters combined across all ROIs, as the number of parameters increased. The HDM3 model is as in main paper; an HDM4 model with the additional vessel stiffness parameter α; an HDM5 model with the additional neurovascular feedback parameter γ; an HDM6 model with the additional oxygen extraction fraction E_0. Each grey line corresponds to one participant. Superimposed on these lines are boxplots together with outliers (red crosses). An asterisk means that a sign-test revealed significantly different prediction than the simplest (HDM3) model. The average across ROIs of the median error was 10.3 years (HDM3), 10.8 years (HDM4), 10.6 years (HDM5) and 10.5 years (HDM6). Note this is using the parameter estimates before application of PEB.

Supplementary Figure S8. Second-order Volterra kernels for each ROI from the HDM3 model, capturing nonlinear effects of time between trial onsets (SOA; plotted on both axes). The top row shows the mean across participants, while the bottom row shows the effect of age. Note that in order to see effects (e.g, in rMC), the grayscale is optimised for each ROI and kernel separately (units are arbitrary).

The dark region in the top row indicates under-additivity (saturation) for SOAs below ~6s in all ROIs, while the white region shows super-additivity for SOAs from ~6s to ~10s, replicating previous findings from Friston et al. (1998). The maximal saturation varied for SOAs 2.6s-3.8s across ROIs, and was highly significant in all ROIs ($T(636) > 19.6$, $p < 1e-16$, though uncorrected for multiple comparisons).

The bottom row shows that the under-additivity below ~6s, as well as the super-additivity between 6-10s, is attenuated with age in all ROIs except rMC, where they are augmented with age. Taking the SOAs with the maximal effect in the top row (which does not bias the orthogonal age effect), the age-related effect was significant for all ROIs, two-tailed $T(636) > 2.52$, $p < .05$.

The percentage of variance from the two kernels that was explained by the second-order kernel had a median value across participants of 29.2%, 15.6%, 23.9% and 4.5% for lAC, bVC, lMC and rMC respectively. The proportion of that second-order variance related to age (linear and/or quadratic) was 12.1%, 6.1%, 4.5% and 1.3% respectively.

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