

1 **Rapid cerebrovascular reactivity mapping:**

2 **Enabling vascular reactivity information to be routinely acquired**

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8 **Running Title:** Rapid cerebrovascular reactivity mapping

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21

22 **Abstract**

23

24 Cerebrovascular reactivity mapping (CVR), using magnetic resonance imaging (MRI)
25 and carbon dioxide as a stimulus, provides useful information on how cerebral blood
26 vessels react under stress. This information has proven to be useful in the study of
27 vascular disorders, dementia and healthy ageing. However, clinical adoption of this
28 form of CVR mapping has been hindered by relatively long scan durations of 7 to 12
29 minutes. By replacing the conventional block presentation of carbon dioxide enriched
30 air with a sinusoidally modulated stimulus, the aim of this study was to investigate
31 whether more clinically acceptable scan durations are possible. Firstly, the conventional
32 block protocol was compared with a sinusoidal protocol of the same duration of 7
33 minutes. Estimates of the magnitude of the CVR signal (CVR magnitude) and the
34 relative timing of the CVR response (CVR phase) were found to be in good agreement
35 between the stimulus protocols. Secondly, data from the sinusoidal protocol was
36 reanalysed using decreasing amounts of data in the range 1 to 6 minutes. The CVR
37 magnitude was found to tolerate this reduction in scan duration better than CVR phase.
38 However, these analyses indicate that scan durations in the range of 3 to 5 minutes
39 produce robust data.

40

- 41 Keywords: Cerebrovascular reactivity, magnetic resonance imaging, hypercapnia
42 challenge, BOLD.

43 **Introduction**

44

45 Whilst there are many clinical techniques to investigate cerebral physiology at rest,
46 methods to examine the brain during dynamic changes in demand are few in number.
47 Resting perfusion measurement techniques using Computed Tomography (CT) or
48 Magnetic Resonance Imaging (MRI) are able to confirm that the tissue is well supplied
49 at rest, but they do not provide information on how the vasculature will react during
50 increases in demand. By introducing a physiological challenge this aspect of
51 cerebrovascular health can be revealed. There are two main vasoactive challenges that
52 can be used to provide a stress test of the cerebral vasculature: acetazolamide and
53 carbon dioxide. Acetazolamide provides a large physiological challenge by maximally
54 dilating cerebral arterioles. However, its effects are relatively long lasting (~30 mins)
55 and it therefore has the potential to interfere with the accuracy of other diagnostic
56 measurements made in the same session. In contrast, carbon dioxide may have a weaker
57 vasodilatory effect, but it is rapidly cleared by the lungs enabling multiple short
58 repeated challenges to be performed without interfering with subsequent measurements.
59 When combined with an imaging modality this carbon dioxide stimulus, often termed a
60 hypercapnia challenge, enables cerebrovascular reactivity (CVR) to be mapped at the
61 tissue level. The most common imaging modality for this purpose is MRI.
62 Measurements have been performed using both Arterial Spin Labelling (ASL)¹ and

63 Blood Oxygenation Level Dependent (BOLD)² weighted techniques, each with their
64 own advantages and disadvantages. BOLD weighted imaging offers higher spatial and
65 temporal resolution and a higher signal to noise ratio (SNR) than ASL, whereas ASL
66 provides quantitative measurements of perfusion change and BOLD does not. In
67 practice BOLD weighted measurements are more commonly used due to their higher
68 sensitivity, more widespread availability and ease of analysis.

69 The information provided by CVR measurements has proven useful in a range
70 of applications. CVR mapping has perhaps made the biggest impact in the study of
71 vascular disorders of the brain. In patients with unilateral carotid stenosis it has been
72 used to show that CVR is reduced in both the affected and unaffected hemisphere³. In
73 Moyamoya patients, who share similar pathological narrowing of cerebral vessels,
74 BOLD based CVR has been shown to give comparable results with ASL based CVR¹.
75 CVR measurements have also been acquired in difficult patient populations such as in
76 subarachnoid haemorrhage⁴ or in rare conditions such as MELAS⁵ where in both cases
77 only limited biomarkers are available. CVR has also shown promise as a biomarker in
78 dementia and healthy ageing research. In Alzheimer's disease CVR has been shown to
79 be altered in patients with different variants of the APOE gene⁶. CVR has also been
80 used to investigate the effect of healthy ageing on brain haemodynamics⁷.

81 However, the clinical adoption of hypercapnia based CVR mapping has so far
82 been hindered by two main challenges: (i) relatively long scan times and (ii) long

83 patient preparation times. Clinical MRI examinations are typically split into discrete
84 diagnostic measurements of approximately 5 minutes in duration. However, currently
85 CVR examinations are between 7 and 12 minutes in duration, meaning that
86 compromises in diagnostic protocols must be made to accommodate such
87 measurements. Preparation of patients adds an additional time penalty that is dependent
88 on the means of gas administration and/or gas sampling. However, in this study we
89 concentrate on the question of reducing the duration of the CVR examination.

90 Typically, hypercapnic gas challenges are presented in blocks interleaved with a
91 baseline air breathing condition. One popular gas protocol used by researchers in
92 Toronto involves the use of two hypercapnic blocks of differing duration; an initial
93 short block followed by a second much longer block⁸. This protocol has also been used
94 to derive information about the relative timing of the CVR response using Transfer
95 Function Analysis (TFA)⁹. This timing information has been suggested to be reflective
96 of regional variations in blood arrival time¹⁰ or in the rate at which the CVR response
97 develops⁹. However, this block paradigm does not lend itself to easy scan time
98 reduction as it typically relies on long hypercapnic blocks to minimise the effect of
99 regional differences in vascular delays. Alternatively, in the limit of short blocks a
100 sinusoidally varying stimulus has several useful properties¹⁰. Firstly, accurate
101 synchronisation of the stimulus paradigm on a voxel by voxel basis is not required, as it
102 is merely modelled as a phase shift of a sinusoid at the frequency of the stimulus. In this

103 context the fitted amplitude of the sinusoid reflects CVR and the phase of the sinusoid
104 provides similar timing information to TFA. With respect to the aim of reducing scan
105 time, the sinusoidal stimulus protocol can be retrospectively reanalysed with fewer
106 stimulus cycles, or fractions of cycles, since it is not the duration of the stimulus that is
107 important but the stimulus frequency.

108 Therefore, the aim of this study was to develop a rapid CVR technique based on
109 a sinusoidal hypercapnic stimulus. Comparison was made with a commonly applied
110 block paradigm, which we term the Toronto protocol⁸. Both protocols produce estimates
111 of vascular reactivity and the timing of this reactivity, which to prevent ambiguity we
112 describe as CVR magnitude and CVR phase, respectively. Firstly, estimates of CVR
113 magnitude and CVR phase were compared for the Toronto and Sinusoid protocols with
114 the same scan duration. Secondly, the amount of data included in the analysis of the
115 Sinusoid protocol was progressively reduced to investigate how rapidly CVR
116 information can be acquired.

117

118 **Material and Methods**

119

120 Imaging

121 All imaging was performed on a Siemens Prisma 3T scanner (Siemens Healthineers,
122 Erlangen, Germany) using the body transmit coil and the vendors 32-channel receive

123 coil. This study was approved by the Medical Sciences Interdivisional Research Ethics
124 Committee (MS IDREC) subcommittee of the Central University Research Ethics
125 Committee (CUREC) at the University of Oxford (approval number: MSD-IDREC-C2-
126 2014-041). Research was conducted in accordance with the Good Clinical Practice
127 guidelines specified by the University of Oxford Clinical Trials and Research
128 Governance unit. Ten healthy volunteers (age range 19 – 21, 5 female) were recruited
129 and informed written consent obtained. Functional imaging consisted of BOLD-
130 weighted EPI images with the following pulse sequence parameters: repetition time
131 (TR) 2 s, echo time (TE) 30 ms, field of view (FOV) 220 mm × 220 mm, matrix 64 ×
132 64, slices 24, slice thickness 5 mm, slice gap 0.5 mm, flip angle 80°, GRAPPA 2. Each
133 functional scan had a duration of 7 mins, resulting in the acquisition of 210 imaging
134 volumes. A field map was acquired using a 2D Fast Low Angle Shot (FLASH) method
135 with the following parameters: TR 378 ms, TE1/TE2 4.92 ms / 7.38 ms, FOV of 220
136 mm × 220 mm, matrix 64 × 64, slices 24, slice thickness 4.5 mm, slice gap 0.45 mm,
137 flip angle 45°. Finally, a high resolution T₁-weighted structural image was acquired for
138 each subject using a 3D Magnetisation Prepared Rapid Acquisition Gradient Echo
139 (MPRAGE) pulse sequence¹¹ with the following parameters: TR 1.9s, TE 3.74 ms, FOV
140 174 mm × 192 mm × 192 mm, matrix 116 × 128 × 128, flip angle 8°, inversion time
141 (TI) 904 ms.

142 Details on how to access the imaging data that underlies this study can be found
143 in Appendix A.

144

145 Respiratory Stimulus

146 Hypercapnia challenges were delivered by a computer controlled gas blender
147 (RespirAct™ Gen 3, Thornhill Research Inc., Toronto, Canada) that implements a
148 prospective algorithm for the targeting of blood gases¹². Subjects were fitted with a
149 sequential gas delivery (SGD) breathing circuit, which was sealed to the face using
150 adhesive tape (Tegaderm, 3M Healthcare, St. Paul, Minnesota, USA) to prevent the
151 entrainment of room air. Subjects were then asked to sit comfortably outside the scanner
152 whilst the prospective algorithm was calibrated. The subject's specific resting end-tidal
153 carbon dioxide and oxygen partial pressures (PETCO₂ and PETO₂, respectively) were
154 first determined by averaging the first ten or so breaths into the breathing mask. The
155 calibration consisted of initiating a baseline targeted at the subject's specific resting
156 PETCO₂ and PETO₂. Initial estimates of the subject's VCO₂ and VO₂ (their resting
157 production/consumption of CO₂/O₂) based on height, weight and age were refined until
158 a constant baseline was achieved with minimal drift. A brief presentation of the
159 sinusoidal hypercapnic stimulus was then administered to the subject to prepare them
160 for the sensations they might encounter whilst in the scanner.

161 Gas stimulus protocols (Fig. 1a) were tailored to each subject's resting PETCO₂
162 and PETO₂ baselines. Modulations in PETCO₂ were targeted relative to baseline, whilst
163 PETO₂ was targeted to remain constant at baseline throughout. The Toronto gas protocol
164 consisted of two blocks of hypercapnia; one of 45 s duration and the other 120 s. The
165 former was preceded by a 60 s baseline and the latter by a 90 s baseline, with a final
166 baseline period of 105 s completing the 7 minute protocol¹³. The sinusoidal gas protocol
167 was composed of seven sinusoidal cycles, each with a period of 60 s. The amplitude
168 was set to vary from baseline PETCO₂ to 10 mmHg above baseline. In this
169 implementation, the prospective algorithm is very tolerant of increases in ventilation
170 rate compared with the baseline level during calibration, but not reductions in
171 ventilation. Therefore, subjects were coached to maintain their ventilation rate over the
172 scanner intercom should it be observed to have dropped below baseline levels.

173 During the presentation of each 7 minute stimulus protocol, imaging was
174 performed using the 7 minute BOLD-weighted EPI pulse sequence described above.
175 Synchronisation of the respiratory and imaging protocols was manually initiated.

176

177 Image Analysis

178 The basic image analysis pipeline is summarised in Fig. 1b. Imaging data from the two
179 stimulus protocols were first submitted to a common pre-processing stage including
180 motion correction¹⁴, fieldmap based EPI unwarping¹⁵, slice timing correction, removal

181 of non-brain tissue¹⁶ and spatial smoothing with a 5 mm FWHM kernel¹⁷. High pass
182 temporal filtering was also performed with cut-off values of 100 s and 200 s for the
183 Sinusoid and Toronto protocols, respectively. Images from the Toronto protocol were
184 registered to MNI space via the subject's structural image^{14,18}. This registration was
185 used to transform the MNI structural atlas¹⁹ and segmented structural images²⁰ to
186 functional space. Finally, the Sinusoid protocol images were registered to the Toronto
187 protocol images.

188 The FMRIB Expert Analysis Tool (FEAT) was used to perform model-based
189 multiple regression analysis²¹. Motion parameters were not included in this analysis. For
190 the Sinusoid protocol, the model was defined by sine and cosine terms with time periods
191 of 60 s (equivalent to 16.7 mHz). For the Toronto protocol, the model was defined by
192 the measured PETCO₂ change during the challenge experienced by each subject. This
193 PETCO₂ timecourse must first be synchronised with the associated BOLD signal
194 changes in the brain, due to intersubject differences in blood arrival time. This was
195 achieved by extracting the mean whole brain BOLD signal change, using the mask
196 generated during the brain extraction process, and finding the maximum cross-
197 correlation with the PETCO₂ data interpolated to the BOLD sampling frequency. High
198 pass temporal filtering with the same cut-off as the imaging data was then applied and
199 the temporal derivative included as an additional regressor.

200 From this analysis several outputs can be produced. Statistical maps were
201 generated and thresholded at the voxel level with a corrected voxel P threshold of 0.05.
202 The effect of the sine and cosine terms in the sinusoidal analysis were combined by
203 using an F-test, whereas for the Toronto analysis a single T-test was used. Maps of CVR
204 magnitude were calculated from the parameter estimates (PE) of the GLM analysis
205 using Eq. (1) for the Sinusoid protocol and Eq. (2) for the Toronto protocol, where S_{mean}
206 is the mean BOLD signal baseline and ΔP_{ETCO_2} is the change in end-tidal partial
207 pressure of CO_2 . Normalisation by ΔP_{ETCO_2} is included to control for difference in the
208 stimulus magnitude across subjects.

$$CVR_{sin}^{mag} = \frac{\sqrt{PE_{sin} + PE_{cos}}}{S_{mean} \Delta P_{ETCO_2}} \quad (1)$$

$$CVR_{tor}^{mag} = \frac{PE_{PETCO_2}}{S_{mean} \Delta P_{ETCO_2}} \quad (2)$$

209 Despite the use of a GLM analysis in this work, in contrast to the Fourier analysis used
210 previously¹⁰, it is still possible to calculate maps of CVR phase from the sinusoidal
211 protocol by using Eq. (3).

$$CVR_{sin}^{pha} = \tan^{-1} \frac{PE_{sin}}{PE_{cos}} \quad (3)$$

212 To provide CVR phase estimates that are comparable with the Toronto protocol, maps
213 were produced using the whole brain phase as a reference i.e. equivalent to the
214 synchronisation performed for the Toronto protocol. This was achieved by extracting a

215 whole brain BOLD signal timecourse and estimating the CVR phase using Eq. (3). This
216 global phase value was then subtracted from the CVR phase estimates from each voxel.

217 For the Toronto protocol Transfer Function Analysis (TFA)⁹ was used to
218 estimate CVR phase. Since this is a Fourier based method, and as such no standard tools
219 exist, it was implemented in MATLAB (Mathworks, Natick, MA, USA). The
220 normalised transfer function $H(f)$ is calculated by dividing the cross power spectral
221 density (CPSD) of the BOLD and PETCO₂ timecourses by the power spectral density
222 (PSD) of the BOLD timecourse. Both the BOLD and PETCO₂ timecourses were
223 demeaned prior to spectral analysis.

$$H(f) = \frac{CPSD_{BOLD, PETCO_2}(f)}{PSD_{BOLD}(f)} \quad (4)$$

224 CVR phase can be calculated from the real and imaginary parts of $H(f)$, denoted by
225 subscript r and i , at the frequency of interest. This was chosen to be 10 mHz, consistent
226 with previous work with the same stimulus protocol⁹.

$$CVR_{tor}^{pha} = \tan^{-1} \frac{H(f)_i}{H(f)_r} \quad (5)$$

227 The use of a GLM analysis also enables the errors in measurements of CVR
228 magnitude and CVR phase to be estimated. This can be achieved by propagating the
229 errors in the GLM parameter estimates and residuals through to the final CVR estimate.
230 The standard deviation in the CVR magnitude ($\sigma_{CVR_X^{mag}}$) can be calculated using Eq.

231 (6), where PE_X and $\sigma_{PE_X}^2$ are the parameter estimate and the variance in that estimate for
 232 protocol X and $\sigma_{S_{mean}}^2$ is the variance in the mean BOLD signal baseline.

$$\sigma_{CVR_X^{mag}} = \frac{PE_X}{S_{mean}} \sqrt{\frac{\sigma_{PE_X}^2}{PE_X^2} + \frac{\sigma_{S_{mean}}^2}{S_{mean}^2}} \quad (6)$$

233 Since the Sinusoid protocol uses a pair of parameter estimates to calculate CVR
 234 magnitude the variance in those estimates must first be combined using the equation
 235 below before application of Eq. (6), where $\sigma_{PE_{sin}}^2$ and $\sigma_{PE_{cos}}^2$ are the variance in the sine
 236 and cosine parameter estimates.

$$\sigma_{PE_{sin/cos}}^2 = \frac{PE_{sin}^2}{PE_{sin}^2 + PE_{cos}^2} \sigma_{PE_{sin}}^2 + \frac{PE_{cos}^2}{PE_{sin}^2 + PE_{cos}^2} \sigma_{PE_{cos}}^2 \quad (7)$$

237 However, the absolute error in CVR magnitude does not take into account the large
 238 differences in the scale of CVR magnitude particularly between grey and white matter.
 239 Under these conditions it is preferable to represent the standard deviation as a fraction
 240 of CVR magnitude by calculating the relative standard deviation (RSD).

$$RSD_{CVR_X^{mag}} = \frac{\sigma_{CVR_X^{mag}}}{CVR_X^{mag}} \quad (8)$$

241 Estimating the variance in the CVR phase measurement was only possible for the
 242 Sinusoid protocol due to the use of TFA in the Toronto protocol.

$$\sigma_{CVR_{sin}^{pha}} = \frac{1}{1 + PE_{sin}^2/PE_{cos}^2} \sqrt{\frac{\sigma_{PE_{sin}}^2}{PE_{cos}^2} + \frac{\sigma_{PE_{cos}}^2 PE_{sin}^2}{PE_{cos}^4}} \quad (9)$$

243 Details of how to access the code that was used to perform this analysis can be
244 found in Appendix A.

245

246 Stimulus performance

247

248 The normocapnic PETCO₂ (PETCO_{2,norm}) and the peak change in PETCO₂ (Δ PETCO₂)
249 were measured for each protocol and subject. First, the automated end-tidal picking
250 routine was manually inspected and corrected where necessary, using software provided
251 with the RespirAct, to ensure accurate PETCO₂ estimation. Linear regression was then
252 performed using a prototypical model of the stimulus (i.e. a boxcar temporally aligned
253 with the PETCO₂ data or sine/cosine pair at 16.7 mHz) and a constant term; the former
254 representing Δ PETCO₂ and the latter PETCO_{2,norm}.

255

256 Comparison between Toronto and Sinusoid protocols

257 Investigations were made to compare the sensitivity and equivalence of the two
258 protocols. Firstly, the number of statistically significant voxels that passed the corrected
259 voxel level threshold ($p < 0.05$) were counted for each subject and protocol. In order to
260 control for potential differences in subject motion between protocols the mean motion
261 as calculated during the motion correction step was extracted¹⁴. Mean motion represents
262 the mean-root-mean square displacement between adjacent time points and has been

263 shown to be associated with reduced temporal signal to noise ratio (SNR) in fMRI
264 experiments²². It is important that the effective temporal SNR is fairly constant across
265 protocols in order to isolate the effect of different stimulus paradigm rather than
266 difference in noise characteristics.

267 Next the equivalence of the CVR estimates produced by the Toronto and
268 Sinusoid protocols was explored. Cortical ROIs were taken from the co-registered MNI
269 atlas and further refined using a grey matter mask (grey matter segmentation partial
270 volume estimate thresholded at 0.5). The mean and standard deviation of CVR
271 magnitude and phase values extracted from these ROIs were calculated for each subject.
272 Systematic differences between the estimates of CVR magnitude and phase from each
273 of the protocols were assessed by fitting a simple model: linear slope and intercept.

274

275 Effect of reducing Sinusoid protocol scan duration

276 The effect of reducing the amount of data used to measure the CVR parameters using
277 the Sinusoid protocol was explored. This was achieved by truncating the data set at scan
278 durations between 1 minute (30 volumes) and 6 minutes (150 volumes) in steps of 1
279 minute (30 volumes). The full analysis, including pre-processing and GLM analysis,
280 was performed for each truncated dataset, and maps of CVR magnitude and phase were
281 generated. High pass temporal filtering at 100 s was disabled for the 1 minute scan
282 duration.

283 The impact of scan time reduction was investigated at the level of whole brain
284 grey matter. An ROI was generated based on voxels in the Toronto protocol that met the
285 statistical threshold and was then refined using a grey matter mask (grey matter
286 segmentation partial volume estimate thresholded at 0.5). The mean and standard
287 deviation of the CVR magnitude and phase values in this ROI were calculated for each
288 scan duration and subject. In addition, the number of statistically significant voxels
289 from the GLM analysis were calculated for each scan duration and subject. These
290 results were subjected to a two-way ANOVA test to investigate the null hypothesis that
291 the group mean values were equal. In the case that the group mean values were found to
292 be significantly different, pairwise comparison was performed using the Tukey-Kramer
293 method (honest significance difference test) to consider which pairs of group means
294 were significantly different. The Tukey-Kramer method controls for multiple
295 comparisons by correcting for the family wise error rate. In this sense it is less
296 conservative than multiple T-tests with Bonferroni correction.

297

298 **Results**

299

300 Both stimulus protocols yielded reliable and accurate respiratory challenges. Table 1
301 details this performance by listing the baseline $PETCO_2$ and stimulus induced $\Delta PETCO_2$.
302 Although within the accuracy of the end-tidal gas targeting system, on average baseline

303 PETCO₂ was 0.9 mmHg higher and Δ PETCO₂ was 0.7 mmHg lower for the Toronto
304 protocol compared with the Sinusoid protocol. Paired two tailed T-tests showed that
305 these differences were significant at $p < 0.001$ and $p < 0.01$, respectively. Although the
306 target of 10 mmHg PETCO₂ change was not attained, all subjects experienced similar
307 PETCO₂ changes within a standard deviation of 1.2 mmHg.

308 In order to compare the sensitivity of the two protocols the number of voxels
309 that passed the voxel level statistical threshold were counted. Table 2 displays these
310 results for the full 7 minute data sets, as well as two examples of the truncated Sinusoid
311 protocol data. The mean motion is also tabulated here to demonstrate the impact of
312 motion on the statistical maps. Mean motion is fairly consistent between protocols and
313 truncated data sets, with one exception. Subject 10 shows considerably higher mean
314 motion for the full Sinusoid protocol compared with the Toronto protocol or truncated
315 data sets. Further investigation revealed large translations in the last two stimulus
316 cycles. Since this would lead to a varying error contribution in the GLM analysis across
317 truncated data sets, this subject was excluded from further analysis. For the remaining
318 subjects, a paired two-tailed T-test showed that the number of statistically significant
319 voxels was insignificantly different between the Toronto and Sinusoid protocols
320 ($p=0.36$).

321 Examples of the main outputs of the analysis are displayed for both protocols in
322 Fig. 2, consisting of unthresholded Z-statistic maps, CVR magnitude, CVR magnitude

323 RSD, CVR phase and CVR phase standard deviation (SD). Both protocols can be seen
324 to produce qualitatively similar results. A reduced Z-statistic value is observed in the
325 Sinusoid protocol compared with the Toronto protocol (Fig. 2a/e). However, similar
326 grey matter to white matter contrast is observed across CVR magnitude (Fig. 2b/f) and
327 phase (Fig. 2d/h) maps. Similarly estimates of the error in these parameters demonstrate
328 increased variance in white matter compared with grey matter. To investigate the
329 quantitative equivalence of the protocols Fig. 3 plots cortical ROI estimates of CVR
330 magnitude (Fig. 3a) and CVR phase (Fig. 3b) from both methods. Both CVR
331 parameters are significantly correlated across protocols; CVR magnitude $p < 0.001$ and
332 CVR phase $p < 0.05$. Linear regression across the nine remaining subjects produced a
333 slope of 0.97 ± 0.05 for CVR magnitude and 0.34 ± 0.15 for CVR phase. Per subject
334 estimates of the slope reveal that the group mean is not significantly different from
335 unity for CVR magnitude ($p = 0.98$, Fig. 3c) or for CVR phase ($p = 0.13$).

336 An example of the effect of reducing scan duration is displayed in Fig. 4. Two
337 examples of the truncated Sinusoid protocol (5 minutes and 3 minutes) are presented
338 alongside the full 7 minute acquisition. Values of the Z-statistic can be seen to reduce
339 with the amount of data included in the analysis (Fig. 4a-c). CVR magnitude maps look
340 qualitatively very similar across scan durations (Fig. 4d-f), whilst CVR phase maps
341 show some small differences when only 3 minutes of data are used (Fig. 4g-i). This is
342 further explored across all subjects in Fig. 5. The group mean of the mean CVR

343 magnitude across the ROI (Fig. 5a) was seen to increase slightly with reduced scan
344 time. A two-way ANOVA test showed that not all group means were equal ($p<0.001$),
345 but a paired multiple comparisons analysis showed that only the 1 minute duration was
346 significantly different ($p<0.001$) to the full data set. A similar increase was observed for
347 the group mean standard deviation of the CVR magnitude (Fig. 5b). Again group means
348 were not all equal ($p<0.001$) and only the 1 minute duration was significantly different
349 ($p<0.001$) to the full data set. The group mean of the mean CVR phase displayed little
350 variation (Fig. 5c) and was not significant ($p=0.99$). The group mean of the standard
351 deviation of the CVR phase showed the largest increase with time reduction (Fig. 5d).
352 The group means were significantly different ($p<0.001$) and the 1 minute ($p<0.001$) and
353 2 minute ($p<0.01$) scan durations were significantly different to the full data set. The
354 group mean number of statistically significant voxels (Fig. 5e) reduced with scan time
355 and were significantly different ($p<0.001$). Pairwise comparison revealed significant
356 differences between the 1, 2 and 3 minute durations ($p<0.001$) and the full data set.
357 Finally, for comparison Fig. 5f scales the group means of the standard deviation of the
358 CVR magnitude and phase to the full data set, demonstrating a larger effect of scan time
359 reduction on CVR phase than CVR magnitude.

360

361 **Discussion**

362

363 CVR mapping using MRI is a promising clinical tool for stress testing cerebral blood
364 vessels. However, there are several aspects of current CVR mapping techniques that
365 limit their clinical application. In this study we concentrated on minimising the scan
366 duration in order to improve the compatibility of this technique with clinical workflows.
367 By utilising a sinusoidally modulated hypercapnia challenge we were able to
368 retrospectively examine the effect of reducing the scan duration. In turn we were able to
369 demonstrate that good quality CVR maps can be acquired in around 3 minutes, rather
370 than the more typical 7 minutes. Furthermore, we demonstrated that CVR maps
371 generated using this sinusoidal stimulus are equivalent to the more conventional block
372 paradigm.

373

374 Stimulus performance

375 Gas stimulus protocols were tailored to each subject's individual baseline PETCO₂. This
376 baseline was maintained within 1 mmHg between the protocols, but was statistically
377 significantly different none the less. Since the vascular response to carbon dioxide is
378 sigmoidal in form²³ it is possible that the two protocols were performed on different
379 parts of the sigmoid curve. However, in practice maintaining baseline PETCO₂ to a
380 higher accuracy than 1 mmHg is challenging. Both stimulus protocols elicited PETCO₂
381 changes of the order of 7 mmHg, which should place the vascular response within the
382 linear regime of the sigmoidal vascular response²³. A statistically significant difference

383 in ΔPETCO_2 was observed, although well within the accuracy of the gas delivery system
384 at 0.7 mmHg. Unfortunately, subject tolerance of both stimulus protocols was not
385 recorded. However, none of the subjects reported discomfort from either stimulus
386 protocol.

387

388 Comparison between Toronto and Sinusoid protocols

389 Before discussing the results of the protocol comparison it is useful to consider the
390 advantages and disadvantages of the two stimulus protocols. As a more conventional
391 block paradigm, the Toronto protocol is an easier stimulus to implement. However,
392 synchronisation of the measured PETCO_2 experienced by the subject with the BOLD
393 data is critical to the accurate estimation of magnitude of the CVR change. Whilst this is
394 practical when synchronising with the whole brain average BOLD signal, the presence
395 of local variations in vascular delays opens up the possibility of the underestimation of
396 CVR magnitude, or the measurement of spurious negative signal changes⁹. This can be
397 mitigated by the use of long blocks of hypercapnia, but therefore limits how short the
398 total acquisition can be. In contrast sinusoidal stimuli have seen only limited
399 application²⁴. To be clinically practical, computer controlled gas delivery is desirable,
400 although a manual implementation has also been demonstrated²⁵. In the previous
401 implementation a Fourier analysis approach was used based on in-house analysis
402 software¹⁰. However, in this study we reframe the analysis in order to use free and

403 widely available fMRI analysis tools¹⁵. One of the inherent advantages of the Sinusoid
404 protocol is its insensitivity to local vascular delays. This is due to the fact that any
405 sinusoid with arbitrary amplitude and phase can be represented by the sum of a sine and
406 a cosine with different amplitudes. In this context only the frequency of the stimulus is
407 important, rather than the timing. This enables the short time-period stimuli used in this
408 work, which would otherwise result in underestimates, or artefactual negative values, of
409 CVR magnitude. Finally, simple sine and cosine functions were used as regressors in
410 the GLM analysis, rather than the measured PETCO₂ timecourse. Despite this, the
411 number of statistically significant voxels (Table 2) was not significantly different to the
412 Toronto protocol across the group. This approach simplifies the analysis as the PETCO₂
413 data does not need to be transferred to the analysis computer and synchronised with the
414 BOLD data.

415 Maps of CVR magnitude were found to have qualitatively similar features (Fig.
416 2b/f). Furthermore, quantitative analysis comparing regional estimates of CVR
417 magnitude at the level of the cerebral lobes demonstrated significant correlation
418 between protocols (Fig. 3a) and equivalence of the absolute values (Fig. 3c). By
419 utilising estimates of the variance in the parameter estimates and the residuals from the
420 GLM analysis it was possible to evaluate the standard deviation of the CVR magnitude
421 measurement. By presenting this as the relative standard deviation (RSD), with respect
422 to the mean, the large degree of heterogeneity in CVR magnitude is controlled,

423 revealing more noisy estimates in white matter (Fig. 2c/g). However, the standard
424 deviation in CVR magnitude, as estimated using Eq. (6), should be viewed with caution
425 as it relies on the variance in S_{mean} from the residuals. The residuals include
426 contributions from motion and physiological noise that aren't included in the GLM
427 model. Therefore, large amounts of motion will result in larger values of RSD, in effect
428 being categorised as noise.

429 Maps of CVR phase also showed clear similarities between methods (Fig. 2d/h).
430 Quantitative analysis showed that the protocols were significantly correlated (Fig. 3b).
431 However, the slope between the protocols varied in the range -0.63 to 1.44 and was
432 trending towards being significantly different to unity (the value expected for
433 equivalence). This disparity may be due to the properties of phase, particularly the
434 incorrect unwrapping of phase values close to $\pm 2\pi$. It is also possible that CVR phase
435 behaves differently between the protocols given the large difference in stimulus
436 duration between the Toronto (45–120 s above baseline PETCO_2) and the Sinusoid
437 protocol (30 s above baseline PETCO_2 in each 60 s cycle). Maps of the standard
438 deviation of the CVR phase measurement were estimated for the Sinusoid protocol by
439 propagating the errors in the parameter estimates (Fig. 2i). RSD was not used because
440 of the relative nature of phase i.e. the reference phase is arbitrary. It is not possible to
441 estimate the standard deviation of the Toronto CVR phase due to the use of TFA,
442 although an analysis of the effects of noise was included in the original paper⁹.

443

444 Effect of reducing Sinusoid protocol scan duration

445 Rather than acquire multiple scans with different durations, the same 7 minute protocol
446 was truncated to investigate the effect of reducing scan duration. From a qualitative
447 perspective, whilst the values of the Z-statistic are reduced with decreasing scan
448 duration, there appears to be relatively little effect on maps of CVR magnitude at scan
449 durations of 3 or 5 minutes, and only small differences in the 3 minute CVR phase map
450 (Fig. 4). Quantitative analysis confirmed that the number of above threshold voxels in
451 the Z-statistic maps was significantly different in the 1, 2 and 3 minute scan durations
452 when compared with the full data set. Furthermore, the results in Fig. 5e are consistent
453 with the expected reduction in sensitivity demonstrated for fMRI analysis²⁶. CVR
454 magnitude was only minimally affected, consistent with the qualitative assessment
455 above, with only the 1 minute scan duration found to be significantly different to the
456 full data set for both the mean and standard deviation across the ROI. Estimates of CVR
457 phase appear to be more strongly affected by scan time reduction. Whilst the mean over
458 the ROI was not significantly different as a function of scan duration, the standard
459 deviation was significantly different for the 1 and 2 minute durations. This increased
460 sensitivity of CVR phase to scan time reduction, relative to CVR magnitude, was
461 highlighted by normalising Fig. 5b and Fig. 5d to their 7 minute values. The standard
462 deviation of CVR phase over the ROI clearly increases much more rapidly for CVR

463 phase than CVR magnitude, necessitating longer scan duration where CVR phase is a
464 priority. In summary, the results would suggest that scan time could be reduced to be in
465 the range of 3 to 5 minutes with minimal effect on the resulting maps of CVR.

466

467 Limitations and future work

468 In the current implementation of this technique, long patient preparation times remain
469 the largest barrier to clinical adoption. Whilst it was not the aim of this study to tackle
470 this problem, it does deserve further consideration. To maintain a constant PETCO₂
471 baseline with minimal drift using the prospective end-tidal gas targeting system used in
472 this study, the system must be calibrated to each individual. In our hands this process
473 takes about 30 minutes, including application of the mask, although it may be shorter
474 for more experienced users. However, there is a great deal of scope for time reduction
475 by automating this calibration step, which will likely be implemented in future hardware
476 developments. In the short term, using the current hardware, it should still be possible to
477 realise shorter patient preparation times, albeit at the expense of a small amount of
478 PETCO₂ baseline drift. As noted above, the gas targeting system provides an initial setup
479 based on the height, weight and age of the subject. The calibration process enables this
480 setup to be refined. However, the initial estimate results in only small amounts of drift
481 in many cases. Small amounts of drift are removed by the high-pass temporal filter and
482 will not affect estimates of CVR so long as the vasculature remains in the linear regime

483 of the sigmoidal vascular response. Further work is required to investigate this
484 approach.

485

486 **Conclusions**

487

488 In this study we have demonstrated that a sinusoidal hypercapnia stimulus provides
489 equivalent information about CVR to a conventional block paradigm. Furthermore, we
490 have shown that the scan duration of the Sinusoid protocol can be drastically reduced
491 with only a small effect on the resulting CVR maps. This development should enable
492 scan durations between 3 and 5 minutes and has the potential to enable more
493 widespread clinical adoption.

494

495 **Appendix A. Supplementary data**

496

497 The raw data that underpins this work can be accessed via the Oxford Research Archive
498 repository, doi: <https://doi.org/10.5287/bodleian:Xk48adQAO>. Furthermore, the code to
499 perform the analyses on these data can be accessed via the Zenodo repository, doi:
500 <http://doi.org/10.5281/zenodo.203128>.

501

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503

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507

508 **Declaration of conflicting interests**

509

510 The author(s) declared no potential conflicts of interest with respect to the research,
511 authorship, and/or publication of this article.

512

513 **Author's contributions**

514

515 NPB and DPB designed the study. NPB, JWH and DPB performed the research. NPB
516 analysed the data. NPB, JWH and DPB wrote the paper.

517

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589 fMRI temporal signal to noise ratio and necessary scan duration. *Neuroimage*
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- 591

592 **Tables**

593

594 Table 1 – Respiratory stimulus performance across protocols as defined by baseline

595 normocapnic PETCO₂ (PETCO_{2,norm}) and the change in PETCO₂ due to the stimulus

596 (Δ PETCO₂).

Subject ID	Toronto protocol		Sinusoid protocol	
	PETCO _{2,norm}	Δ PETCO ₂	PETCO _{2,norm}	Δ PETCO ₂
01	38.6	7.0	37.8	7.9
02	37.9	7.1	37.1	8.0
03	43.1	6.2	41.9	6.9
04	43.8	5.0	42.2	5.9
05	40.4	7.4	39.5	7.5
06	31.0	6.0	29.9	6.6
07	41.2	5.3	40.5	6.2
08	40.6	7.9	40.0	8.0
09	38.7	8.0	38.5	8.5
10	38.7	7.7	37.4	9.7
Mean	39.4	6.8	38.5	7.5
SD	3.5	1.1	3.5	1.2

597

598 Table 2 – Number of voxels above the voxel level statistical threshold for the 7 minute
 599 datasets of each protocol and the Sinusoid protocol truncated at 5 minutes and 3
 600 minutes. The mean motion, defined as average root mean square displacement between
 601 adjacent time points, for each data set is presented alongside voxel count to highlight
 602 the effect of subject motion.

Subject ID	Toronto protocol		Sinusoid protocol					
	7 mins		7 mins		5 mins		3 mins	
	# voxels	Motion	# voxels	Motion	# voxels	Motion	# voxels	Motion
01	18995	0.11	17089	0.10	14735	0.10	10345	0.11
02	15650	0.13	17054	0.10	15969	0.10	15380	0.11
03	17820	0.14	15104	0.15	14221	0.14	13695	0.13
04	9590	0.20	10174	0.20	8736	0.20	5013	0.19
05	16828	0.09	17185	0.09	15764	0.09	13941	0.09
06	5090	0.27	7106	0.29	6895	0.29	4785	0.22
07	15507	0.20	14643	0.24	12490	0.22	12081	0.21
08	19356	0.23	12400	0.30	10986	0.32	8070	0.34
09	19333	0.08	19507	0.12	17852	0.12	15109	0.10
10	19630	0.19	6767	0.40	15776	0.21	12890	0.22

Mean	15780	0.16	13703	0.20	13343	0.18	11131	0.17
SD	4814	0.06	4437	0.11	3509	0.08	3945	0.08

603

604 **Figures**

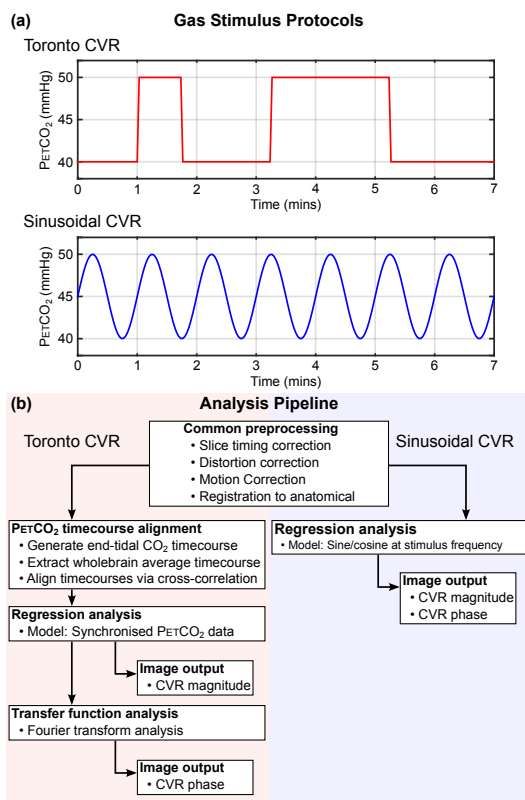
605

606 Figure 1 – Data analysis pipeline for Toronto and Sinusoid protocols. It is important for

607 the end-tidal CO₂ regressor to be well-aligned with the BOLD data in the Toronto

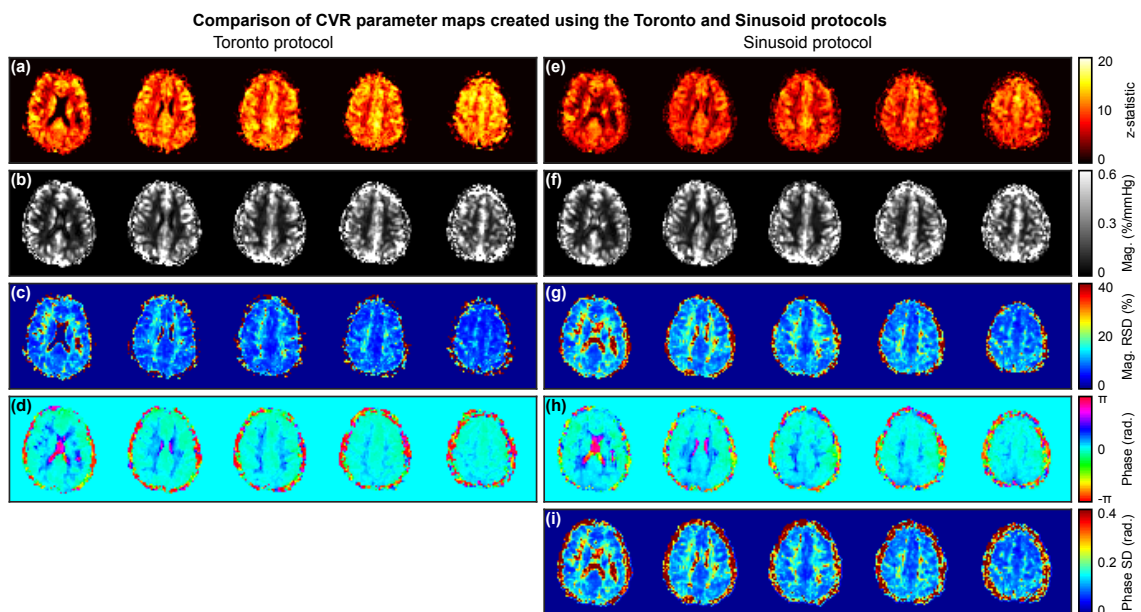
608 protocol to avoid underestimating changes in CVR Magnitude. The Sinusoid protocol

609 analysis is inherently insensitive to such time delays and does not require this step.



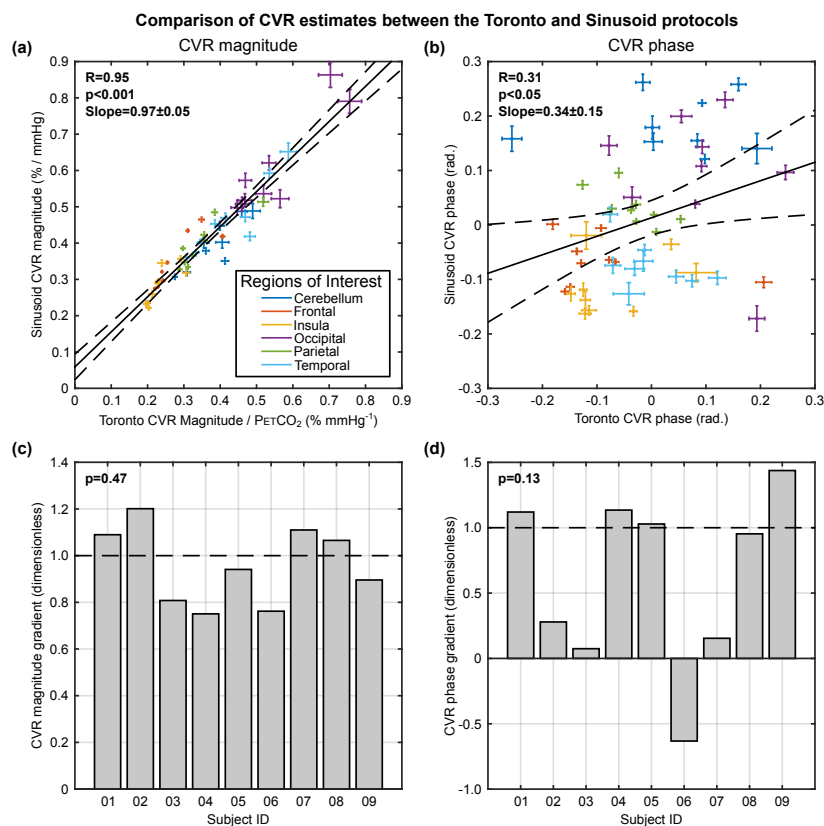
610

611 Figure 2 – Example CVR maps from a single subject (Subject 01). A subset of five
612 contiguous slices are displayed superior to the lateral ventricles. Maps (a)-(d) were
613 produced using the Toronto protocol and (e)-(i) using the Sinusoid protocol. Maps were
614 generated to display (a/e) statistical correlation with the CO₂ stimulus (Z-statistic), (b/f)
615 CVR magnitude (normalised by the change in PETCO₂), (c/g) relative standard
616 deviation (RSD) of the CVR magnitude estimate, (d/h) CVR phase and (i) standard
617 deviation of the CVR phase estimate. Note: It is not possible to generate maps of the
618 error in CVR phase for the Toronto protocol.



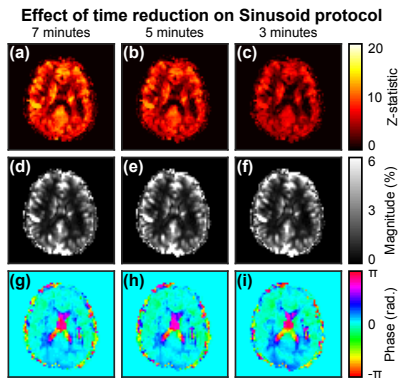
619

620 Figure 3 – Estimates of (a) CVR magnitude and (b) CVR phase were compared on the
621 basis of cortical regions of interest at the level of the cerebral lobes. Both measurements
622 were found to be significantly correlated across protocols. To assess the equivalence of
623 the two protocols a simple linear model was fitted for each subject. The mean and
624 standard deviation of the slope was found to be 0.96 ± 0.17 and 0.62 ± 0.68 for (c) the
625 CVR magnitude and (d) the CVR phase, respectively. Neither were found to be
626 significantly different to unity, indicating that estimates from the protocols are
627 equivalent.



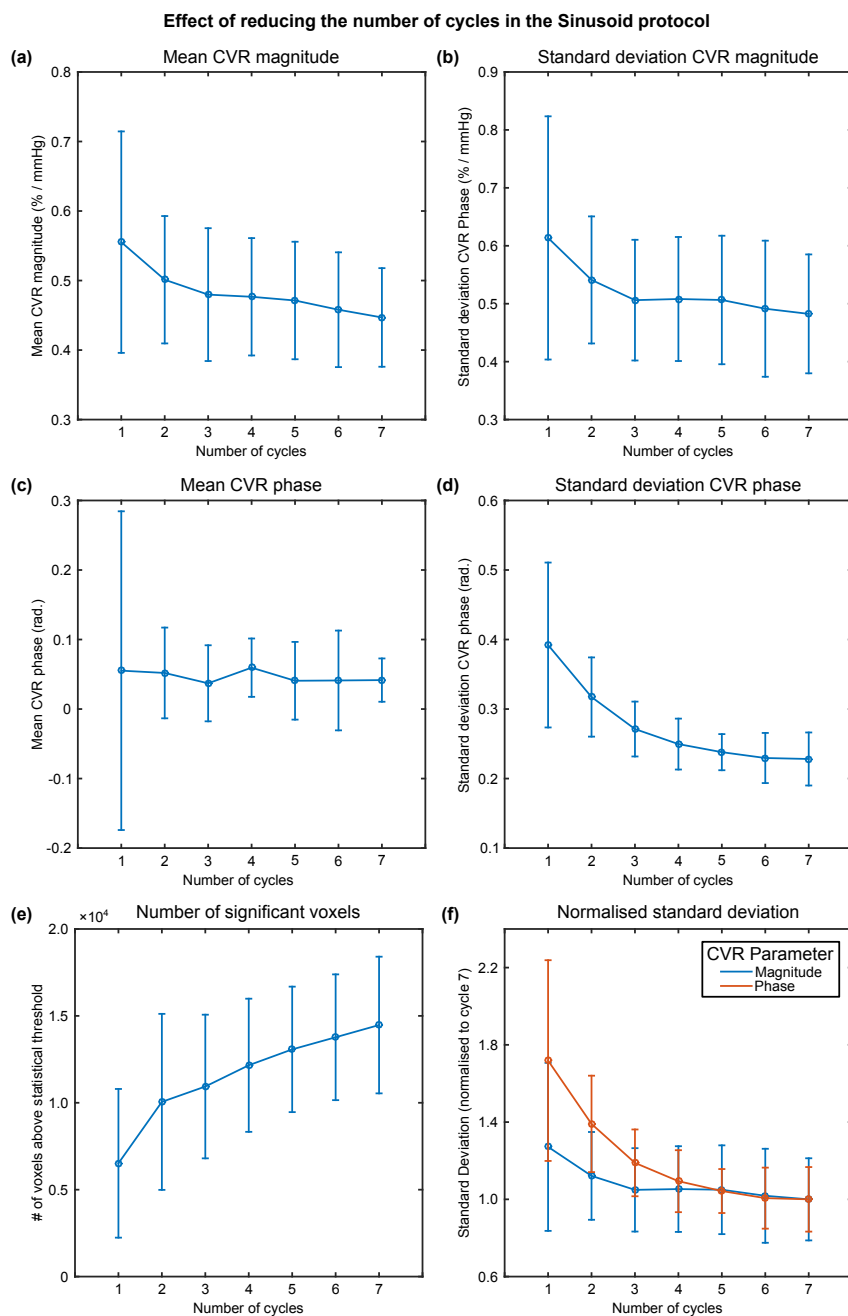
628

629 Figure 4 – Example single slice of CVR maps from the Sinusoid protocol as scan
630 duration is reduced (Subject 01) for (a)-(c) statistical correlation, (d)-(f) CVR magnitude
631 and (g)-(i) CVR phase.



632

633 Figure 5 - Analysis of the effect of reducing the scan duration of the Sinusoid protocol
634 for (a/b) CVR magnitude, (c/d) CVR phase and (e) the number of voxels above the
635 voxel level statistical threshold. Analysis was performed for a grey matter region of
636 interest (ROI) where the mean and standard deviation of the estimates within the ROI
637 were calculated. The standard deviation of the CVR magnitude and phase are compared
638 directly (f) by normalising to the 7 minute scan duration.
639



640

641