Standardising an infant fNIRS analysis pipeline to investigate neurodevelopment in global health

Chiara Bulgarelli[a*], Anna Blasi[a], Luca Pollonini[b], Sarah Lloyd-Fox[c], Laura Pirazzoli[d], Katherine L. Perdue[d], Charles A. Nelson[d], Clare E. Elwell[a]

[a] *Department of Medical Physics and Biomedical Engineering, University College London, Malet Street, London, WC1E7HY, United Kingdom*
[b] *Department of Engineering Technology, University of Houston, 4730 Calhoun Rd, Houston, TX 77004, United States*
[c] *Department of Psychology, University of Cambridge, Downing St, Cambridge, CB2 3EB, United Kingdom*
[d] *Boston Children's Hospital, Harvard Medical School, 1 Autumn Street, Boston, MA 02215, United States*
**Corresponding author e-mail address: c.bulgarelli@ucl.ac.uk*

Abstract: Data analysis methods for infant fNIRS data in global health are not standardised yet. This work proposes an analysis pipeline that improves the quality of the recovered HRF for use by other researchers in this field.

1. Introduction

Neuroimaging research in low- and middle- income countries (LMICs) has recently been focusing on finding early markers of compromised neurocognitive development [1,2]. These investigations can open a window into the very first years of life, which are known to be crucial for infant social and cognitive development [3]. Functional near-infrared spectroscopy (fNIRS) is proving to be an increasingly useful tool for global health studies given its suitability for use in resource poor settings [4]. However, these studies are not without challenges. For example, heat and humidity increase the participants' sweat during the testing sessions, negatively affecting the quality of the data and increasing the risk of movement of the headgear. Moreover, testing takes place in rooms not necessarily built for this purpose and which are often exposed to external noise. While some of these challenges can be overcome during the planning and data acquisition phases [for more details see 5], there is still a clear need for robust and standardised fNIRS data analysis methods which deal with a range of noise levels in the data. Studies recently published in this field deal with these issues using different analysis methods [for example see 2,6,7].

The current work proposes an analysis pipeline specifically designed for infant fNIRS data acquired in global health settings (Global, GBL), with the ultimate goal of making it available for other researchers in this field. We have tested the GBL pipeline on fNIRS data acquired in the Gambia from the Brain Imaging for Global Health (BRIGHT) Project at different age points over the first two years of life. We compared the performance of the GBL analysis pipeline with the one that has been used so far in the BRIGHT Project (Original, ORG). We hypothesise that the GBL pipeline performs better against motion artefacts and increases the signal-to-noise-ratio (SNR) of the recovered hemodynamic response (HRF) than the ORG pipeline.

2. Method

Data from 108 5-month-olds, 93 12-month-olds, 91 24-month-olds from the BRIGHT Project were used to assess the performance of the GBL pipeline. Data were collected from the temporal and inferior frontal brain regions, using the NTS optical imaging system (Gowerlabs Ltd.). At each time point, participants were presented with social and non-social videos and sounds in a block design task extensively used and validated in previous infant studies [8].The ORG and the GBL pipelines mainly differ on: i) the treatment of motion artefacts in the data: the ORG pipeline excludes sections with motion artefacts based on hard thresholds, whereas the GBL pipeline corrects motion using spline interpolation and wavelet [9]; ii) channel-pruning: the ORG pipeline excludes channels based on the coefficient of variation and frequency domain analysis, whereas the GBL pipeline additionally excludes channels with insufficient correlation between the two wavelengths (as measured by the scalp coupling index, SCI) and without a clear heart-rate peak (SCI and HR pruning) [10]. Infants were excluded from further analyses with both pipelines if they had poor headgear placement, defined by vertical or horizontal displacement of the optode over the preauricular point of more than 150 mm. Infants were also excluded if they had less than 3 valid trials per condition (based on off-line behavioural coding for compliance) and more than 40% of the channels excluded.

3. Results

To test the performance of both motion correction methods, we calculated the mean of the standard deviations (SD) of the recovered HRF of all the trials averaged across channels per each infant, assuming that variability within the same participant is a surrogate index of motion [7]. Fig 1 shows that the SD is consistently higher in the ORG pipeline than in the GBL pipeline across time points.

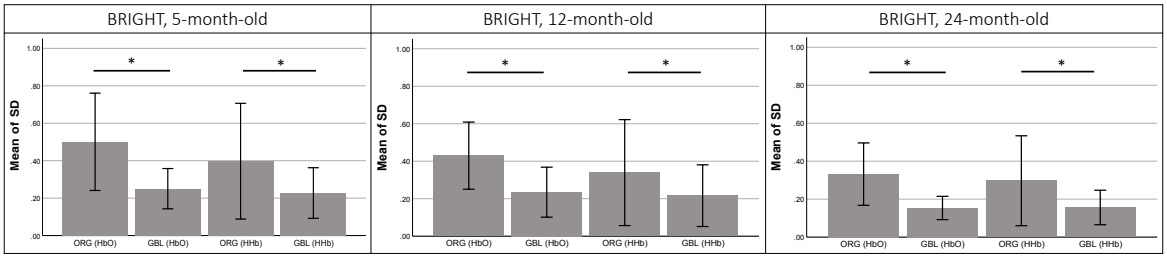

Fig. 1 Bar charts representing the mean of the SD of the recovered HRF of all the trials per each infant analysed with the ORG and GBL pipeline. Error bars are ± 1 SD, * marks significance at the paired t-tests.

As the HRFs recovered with the GBL pipeline after motion correction still showed some significant variability between infants, we introduced the SCI and HR pruning method in the analysis pipeline. The average SNR further increased when incorporating the SCI and HR pruning in the GBL pipeline (Table 1).

Table 1 SNR averaged across channels; average number of channels excluded per infant; and number of infants included in the analysis when using the ORG or the SCI and HR channel-pruning methods in the GBL pipeline.

	5 mo		**12 mo**		**24 mo**	
	ORG	**SCI+HR**	**ORG**	**SCI+HR**	**ORG**	**SCI+HR**
SNR	0.21	0.50	0.53	0.59	0.34	0.40
Average/Total channels	3.26/34	5.12/34	3.14/34	5.1/34	4.90/34	6.88/34
Infants included	52.77%	48.14%	59.13%	53.76%	70.32%	61.53%

4. Discussion

In this work we have tested the performance of the GBL pipeline, designed for infant fNIRS data collected in the context of global health studies. Compared to the ORG pipeline, the GBL pipeline showed a decreased SD of the recovered HRF and an increased SNR averaged across channels, within participant. These findings are consistent across ages. Channel-pruning with the SCI and HR method significantly increases the quality of the recovered HRFs, however it may have a negative impact on the size of the analysed dataset. This highlights the need for collecting data from large datasets, especially in settings where external factors impacting data quality are not as controllable. The SCI and HR method might have the potential to feedback data quality information during the testing phase, so that adjustments can be made before data collection starts.

In the near future, we aim to test the GBL pipeline on the fNIRS data collected in Bangladesh from the Bangladesh Early Adversity Neuroimaging (BEAN) Project. As the BEAN and the BRIGHT projects collected data at similar ages, with the same NIRS system, a very similar headgear and the same task, applying the GBL pipeline on the BEAN data would allow to unify analysis pipelines across the two sites. Further steps will also involve testing the GBL pipeline on synthetic data, to further confirm the robustness of this pipeline.

5. References

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