

## Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

### Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
- ☒ ☐ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided  
*Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
- ☐ ☒ A description of all covariates tested
- ☐ ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☒ ☐ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g.  $F$ ,  $t$ ,  $r$ ) with confidence intervals, effect sizes, degrees of freedom and  $P$  value noted  
*Give  $P$  values as exact values whenever suitable.*
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☒ ☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒ ☐ Estimates of effect sizes (e.g. Cohen's  $d$ , Pearson's  $r$ ), indicating how they were calculated

*Our web collection on [statistics for biologists](#) contains articles on many of the points above.*

### Software and code

Policy information about [availability of computer code](#)

Data collection The fMRI data is available via <https://zenodo.org/deposit/4423384>

Data analysis For the fMRI data analysis, SPM12 toolbox (Wellcome Department of Cognitive Neurology, Institute of Neurology, UCL, London, UK) running on matlab was used.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

### Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The fMRI data is available via <https://zenodo.org/deposit/4423384>

## Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☒ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

## Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	The manuscript describes a new robotic procedure and method to study hallucinations in different populations.
Research sample	The manuscript reuses the fMRI dataset from Bernasconi, Blondiaux et al., 2021 at <a href="https://zenodo.org/deposit/4423384">https://zenodo.org/deposit/4423384</a>
Sampling strategy	Not applicable
Data collection	No data were collected for this study. The manuscript reuses the fMRI dataset from Bernasconi, Blondiaux et al., 2021 at <a href="https://zenodo.org/deposit/4423384">https://zenodo.org/deposit/4423384</a>
Timing	Not applicable
Data exclusions	No data were excluded for the analysis
Non-participation	No participants dropped out.
Randomization	Participants were not allocated into experimental groups

## Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

### Materials & experimental systems

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

### Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input type="checkbox"/>	<input checked="" type="checkbox"/> MRI-based neuroimaging

## Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	The manuscript reuses the fMRI dataset from Bernasconi, Blondiaux et al., 2021 at <a href="https://zenodo.org/deposit/4423384">https://zenodo.org/deposit/4423384</a>
Recruitment	not applicable
Ethics oversight	The fMRI study was approved by the Cantonal Ethics Committee of Geneva (Commission Cantonale d'Ethique de la Recherche sur l'Être Humain - CCER)

Note that full information on the approval of the study protocol must also be provided in the manuscript.

## Magnetic resonance imaging

### Experimental design

Design type	task functional MRI and block design
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Design specifications	2 experimental blocks including two conditions (asynchronous and synchronous) of 30 sec with 20 sec rest (among those 0.5 sec and 1.5 sec are the "start" auditory cue and "stop" auditory cue). Each block lasts 12 min (8 repetition per conditions). The control tasks include one condition each (either robotic manipulation or robotic stimulation on the back) of 30 sec and also 20 sec of rest (including 0.5 sec and 1.5 sec are the "start" auditory cue and "stop" auditory cue). Those tasks lasted around 7 min (8 repetitions per condition).
Behavioral performance measures	The movement parameters of the front robot along the X and Z axis are recorded at a frequency of 100 Hz. Questionnaire data is also assessed after the scanning session.

## Acquisition

Imaging type(s)	functional and structural
Field strength	3T
Sequence & imaging parameters	Users can adapt this part as the robotic procedure does not depend on the MR sequence used. The data used in the current manuscript (Bernasconi, Blondiaux et al., 2021) uses the following sequences: - For the functional images, we used a whole brain echo-planar imaging (EPI) with the following parameters: 43 continuous slices, FOV=230mm, TR=2.5s, TE=30ms, flip angle=90°, in-plane resolution=2.5x2.5mm <sup>2</sup> , slice thickness=2.5mm. We used a 64-channel head-coil. The two experimental runs contained 320 volumes and the control conditions (in which there is only 8 repetitions per condition) included 160 volumes. - anatomical image was recorded using a T1-weighted MPRAGE sequence (TR=2.3s, TE=2.32 ms, Inversion time=900ms, flip angle=8°, 0.9mm isotropic voxels, 192 slices per slab and FOV=240mm).
Area of acquisition	whole brain
Diffusion MRI	<input type="checkbox"/> Used <input checked="" type="checkbox"/> Not used

## Preprocessing

Preprocessing software	Standard SPM12 preprocessing pipeline is applied to the images, which includes the following steps: first the functional images are corrected for slice timing and are spatially realigned. Then, the anatomical image is then co-registered with the mean functional image and segmented into grey matter, white matter and cerebro-spinal fluid (CSF) tissue. Finally, the anatomical and the functional images are normalized to the Montreal Neurological Institute (MNI) brain template. Functional images are then smoothed with a Gaussian kernel with full-width half-maximum of 6mm. The two experimental runs were filtered with a high-pass filter at 1/300 Hz to remove low frequency confounds, while the two control tasks were filtered with a high-pass filter at 1/100 Hz.
Normalization	Normalised
Normalization template	MNI template
Noise and artifact removal	Head motion is assessed based on framewise displacement (FD) calculation.
Volume censoring	Not applicable

## Statistical modeling & inference

Model type and settings	Mass univariate with fixed effects for the first and second level analysis
Effect(s) tested	Effect of interest: asynchronous condition > synchronous condition For the control conditions: motor task > baseline and touch task > baseline Conjunction analysis: asynchronous > [motor + touch] $\cap$ synchronous > [motor + touch]
Specify type of analysis:	<input checked="" type="checkbox"/> Whole brain <input type="checkbox"/> ROI-based <input type="checkbox"/> Both
Statistic type for inference (See <a href="#">Eklund et al. 2016</a> )	Cluster-wise P = 0.001
Correction	FWE-corrected threshold of P = 0.05

## Models & analysis

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Functional and/or effective connectivity
<input checked="" type="checkbox"/>	<input type="checkbox"/> Graph analysis
<input checked="" type="checkbox"/>	<input type="checkbox"/> Multivariate modeling or predictive analysis