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Corresponding author(s): Peng Zhang

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Reporting Summary

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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 experiments were programmed in MATLAB v2016b (The Math Works, Inc.) using the Psychophysics Toolbox v3.0.12.
Data analysis	MRI data were analyzed using AFNI v19.0.24 (https://afni.nimh.nih.gov/), FreeSurfer v6.0.0 (https://freesurfer.net/), ANTs v2.2.0 (https://stnava.github.io/ANTs/), neuropythy package v0.12.13, and the mripy package v0.7.1 developed in our lab (https://github.com/herrlich10/mripy). Effective connectivity of the fMRI data was analyzed with the DCM module of SPM12 (Version 7771). Decoding and clustering analyses were performed using scikit-learn v0.24.2 (https://scikit-learn.org/) and SciPy v1.7.1 (https://scipy.org/). Statistical analyses were conducted using Pingouin v0.5 (https://pingouin-stats.org/), seaborn v0.11.2 (https://seaborn.pydata.org/), JASP v0.14 (https://jasp-stats.org/), R v4.1 (https://www.r-project.org/), and home-built Python code. The mripy package, used in this study for high-resolution fMRI data processing, is available on Github (https://github.com/herrlich10/mripy).

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

Data to reproduce the main findings of this study can be downloaded from National Basic Science Data Center (https://www.scidb.cn/en/s/ZJVBza). Raw data can be requested by contacting the corresponding author P.Z. (zhangpeng@ibp.ac.cn).

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	We recruited participants of both genders (fourteen females and seventeen males in total) for our studies based on their self-reports. Sex or gender effects were not considered because this study focused on understanding the common mechanisms underlying all human beings.
Reporting on race, ethnicity, or other socially relevant groupings	Participants were not grouped by race or ethnicity in the design and analyses of this study.
Population characteristics	Sixteen healthy volunteers (seven females, aged 22–40 years) participated in Experiment 1. Fifteen healthy volunteers (seven females, aged 22–39 years) participated in Experiment 2. All observers had normal or corrected-to-normal vision.
Recruitment	Subjects were experienced psychophysical observers informally recruited from nearby labs based on availability and willingness to participate, without additional screening. Many of them had previous experience with binocular rivalry, but it was unlikely to bias the current results about the general neural mechanisms for the phenomenon.
Ethics oversight	Experimental protocols were approved by the Institutional Review Panel at the Institute of Biophysics, Chinese Academy of Sciences.

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

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

Life sciences study design

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

Sample size	Sample sizes were determined based on previous works in the literature and the expected effect sizes. Prior human fMRI studies on binocular rivalry typically employed small samples, both for cortical responses (e.g., n = 4 in Polonsky et al., 2000; Tong et al., 2001; n = 3 in Lee et al., 2005; n = 6 in Brascamp et al., 2015) and subcortical responses in the LGN (e.g., n = 4 in Haynes et al., 2005; n = 5 in Wunderlich et al., 2005; n = 3 in Yildirim et al., 2023). In comparison, our final sample sizes of 12 and 15 participants provide substantially greater power, particularly given the enhanced signal-to-noise ratio afforded by 7T fMRI.
Data exclusions	Three subjects were excluded in Experiment 1 due to lack of a clear OD pattern in V1, and one subject was excluded due to strong bias toward one eye. These conditions preclude further OD-specific analyses adopted in this study.
Replication	The reproducibility of ocular dominance columns/clusters identified in V1 (Extended Data Fig. 3d-j) and LGN (Figure 5a/b) were assessed and confirmed by scanning the same subject in different days, and by comparing results from odd and even runs for each individual (Extended Data Fig. 3c). The cortical depth dependent results in V1 were obtained using gradient echo EPI sequence (with T2* weighting and high sensitivity; Figure 2f) in the main experiment, and replicated (in a proof-of-concept case study) using a different pulse sequence (balanced SSFP, with more T2 weighting and better specificity; Figure 2j). The major findings in IPS, including eye-specific modulation during binocular rivalry (Figure 4c/d and Extended Data Fig. 7a) and delayed transition-related response in early visual areas relative to IPS (Figure 4f and Extended Data Fig. 7c) were successfully replicated between Exp.1 and Exp.2. We also showed individual results (Extended Data Fig. 3, 4, 5, 8) to facilitate inspection of replicability between different individuals.
Randomization	We used a within-subject design where all subjects were tested on the same set of experimental conditions, thus randomizing participants to different conditions was not necessary.

Blinding | All participants were exposed to the same experimental conditions. Thus blinding was not necessary.

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
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☐	☒ MRI-based neuroimaging

Plants

Seed stocks | *Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*

Novel plant genotypes | *Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*

Authentication | *Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*

Magnetic resonance imaging

Experimental design

Design type | The localizer task used block design, and the rivalry or replay tasks can be viewed as an event-related design where the events are endogenous.

Design specifications | In Experiment 1 and 2, 4-6 localizer runs were collected for each subject. Each run comprised 12 interleaved monocular stimulation blocks and 2 blank blocks at the beginning and end of the run. Each block lasted 24 s without inter-block interval. 4 rivalry and 4 replay runs, each lasted 256 s, were collected for each subject.

Behavioral performance measures | Mean rivalry interval was 7.13 s for Exp.1 and 7.85 s for Exp.2. No significant difference was found for different eyes or colors (see Extended Data Fig. 1 for mean dominance duration and its confidence interval for each eye and color).

Acquisition

Imaging type(s) | functional, structural

Field strength | 7 Tesla

Sequence & imaging parameters | In Experiment 1, T2*w BOLD signals from the occipital and parietal cortices were acquired with a 2D GE-EPI sequence (0.8 mm isotropic voxels, 31 oblique-coronal slices, FOV = 128×128 mm, TE = 23 ms, TR = 2000 ms, nominal flip angle = 80°, bandwidth = 1157 Hz/pixel, partial Fourier = 6/8, GRAPPA = 3). One subject was also scanned with a 2D passband balanced SSFP sequence to acquire T2w BOLD signals (voxel size 0.5 × 0.5 × 1.5 mm, 2 oblique-coronal slices, FOV = 96 × 96 mm, volume acquisition time = 2400 ms for localizer and 1600 ms for rivalry/replay, TR = 5.64 ms, TE = 2.82 ms, nominal flip angle = 29° or 30°, bandwidth = 521 Hz/pix, no in-plane acceleration for localizer and GRAPPA = 2 for rivalry/replay). 3D passband bSSFP sequence (0.8-mm isotropic voxels, 10 oblique-coronal slices, FOV = 102 × 102 mm, volume acquisition time = 6 s, TR = 5.54 ms, TE = 2.77 ms, nominal flip angle = 15°, bandwidth = 471 Hz/pix, partial Fourier = 7/8 in both phase and slice direction, GRAPPA = 2) was also used in a separate localizer session to evaluate the robustness of V1 ODC pattern.
The same 2D GE-EPI sequence was used, albeit with different parameters in Experiment 2 (1.2 mm isotropic voxels, FOV = 180×180 mm, TE = 22 ms, flip angle = 78°, bandwidth = 1587 Hz/pix, GRAPPA = 2. 62 oblique-transversal slices were acquired for 8 of 15 subjects with a multi-band factor of 2. 31 slices were acquired for the rest of subjects without

multi-band acquisition). EPI volumes with reversed phase encoding and readout directions were also acquired for susceptibility distortion correction.
For all Experiments, T1w anatomical volumes were acquired using a MP2RAGE sequence (0.7 mm isotropic voxels, FOV = 224×224 mm, 256 sagittal slices, TE = 3.05 ms, TR = 4000 ms, TI1 = 750 ms, flip angle = 4°, TI2 = 2500 ms, flip angle = 5°, bandwidth = 240 Hz/pix, partial Fourier = 7/8, GRAPPA = 3).

Area of acquisition

In Exp.1, 31 oblique-coronal slices were placed at the back of the brain to simultaneously cover both V1 (calcarine sulcus) and the parietal cortex (intraparietal sulcus). For the bSSFP experiment, two coronal slices (0.5 mm in-plane resolution and 3 mm total thickness) were carefully prescribed to be perpendicular to the calcarine sulcus in one hemisphere, where the ODCs went approximately parallel with the orientation of elongated 'pencil' voxels (Fig. 2h, Extended Data Fig. 3g), so that cortical layers and OD columns can be simultaneously resolved in-plane.
In Exp.2, 62 oblique-transversal slices were acquired for 8 of 15 subjects, covering most of the cortex except for the bottom of the temporal lobe. For the rest of subjects, 31 slices with AP orientation were acquired (without multi-band acceleration) to maximize SNR in the subcortical regions.

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software

MRI data were preprocessed using AFNI (v19.0.24), FreeSurfer (v6.0.0), ANTs (v2.2.0), and the mripy package developed in our lab (https://github.com/herrlich10/mripy). EPI volumes were corrected for slice timing, susceptibility distortion (blip-up/down method), head motion (6 parameters rigid body), and rescaled to percent signal change. To minimize the loss of spatial resolution, all spatial transformations were combined and applied in a single interpolation step (sinc method), in which the data were also up-sampled by a factor of 2. The anatomical volumes were segmented and reconstructed into surfaces using the default FreeSurfer pipeline (recon-all with -hires option for submillimeter T1 volumes). The surfaces were visual inspected and manually edited, mainly to remove dura mater and sinuses from the gray matter. The T1 volume and the surface were aligned to the mean of preprocessed EPI images (cost function: lpc). Relative cortical depth (0-1) for each voxel was estimated using an equivolume method (mripy_compute_depth.ipy in mripy). To match the up-sampled volume grid and alleviate the vertex-missing problem during surface-to-volume projection, high density surface meshes were created (mripy_create_hd_mesh.ipy).

Normalization

The fMRI data were analyzed in the native space of individual subjects to exploit the submillimeter spatial resolution. The ODC pattern in V1 is unique for each subject and defies spatial normalization.

Normalization template

The data were not normalized.

Noise and artifact removal

Motion correction parameters were included as regressors of no interest in the GLM analysis.

Volume censoring

A volume would be censored if the derivative of head motion parameters has a Euclidean norm greater than 0.3.

Statistical modeling & inference

Model type and settings

For the eye-preference localizer, mass univariate regression analysis was conducted at the first-level using the Block4 HRF in AFNI. Slow drift in the signal was modeled using Legendre polynomials of an automatically determined order (3dDeconvolve -polort 'A'). Head motion parameters were included as nuisance regressors. Temporal autocorrelation was accounted for using a ARMA(1,1) model (3dREMLfit). At the second level, subject was treated as a random effect, and experimental manipulation (rivalry vs replay) and different layers or ROIs as fixed effects. For rivalry and replay condition, both event-related averaging and deconvolution analysis (3dDeconvolve with CSPLINzero model in AFNI) were used.

Effect(s) tested

For eye-specific response modulation, the main dependent variable is the difference in BOLD response when the subjects report seeing the left eye image vs seeing the right eye image. For synchrony across visual field, the dependent variable is the width of r-value distribution for moment-to-moment correlation between V1 activation pattern and its ODC map. The main effect of interest is rivalry vs replay, and cortical layers (deep, middle, superficial). Repeated measures ANOVA was used for hypothesis testing, followed by paired t-tests.

Specify type of analysis: ☐ Whole brain ☒ ROI-based ☐ Both

Anatomical location(s)

In Experiment 1, V1 ROIs were manually drawn on the cortical surface to select regions with a clear and roughly balanced pattern of ODCs (see Extended Data Fig. 3a for the OD patterns and ROIs of all subjects). Vertices with significant ocular bias (LE-RE contrast abs(t) > 2) and visual response (LE+RE t > 2) were then projected to the volume space to select voxels in a column-wise manner. IPS was defined as the union of IPS0 to IPS5 in Wang15 atlas (Wang et al., 2015), whose masks were generated using the neuropythy package (Benson et al., 2018). pIPS and aIPS was defined as IPS0-2 and IPS3-5, respectively.
In Experiment 2, anatomical mask for each LGN was manually delineated in the T1w volume, and two clusters of voxels with significant ocular bias (LE-RE abs(t) > 2; for a few LGNs the threshold was relaxed to 1.5 or 1) were identified for each LGN (Extended Data Fig. 8 shows the ocular biased clusters for all subjects). V1 voxels with significant ocular bias (LE-RE abs(t) > 2) and positive visual response (LE+RE > 0) were included for ROI analysis.

Statistic type for inference

(See Eklund et al. 2016)

We performed ROI-based analyses and ROIs were selected using independent functional localizers and anatomical information.

Correction | Holm correction were used for multiple comparisons across ROIs and conditions when needed.

Models & analysis

n/a	Involved in the study
☐	☒ Functional and/or effective connectivity
☒	☐ Graph analysis
☐	☒ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Effective connectivity of the fMRI data was analyzed with the DCM module of SPM12 (Version 7771). Multivariate decoding timeseries from V1, V2, and IPS were used as VOI inputs. The model (Fig. 4e inset) had two inputs: the eye-of-origin of the currently perceived stimulus (high for LE and low for RE) was defined as a driving input to V1 in the replay condition, while all brain areas (V1/V2/IPS) could receive such an eye-specific driving input during rivalry. Fixed connections were defined between and within all brain areas, and the between-areas connections were allowed to be modulated by the 2nd input during binocular rivalry. Both inputs were mean-centered. A bilinear, single state, deterministic model with default parameters was used. At the first level, the full DCM for each subject was estimated using all data from rivalry and replay runs concatenated together. At the second level, we used the parametric empirical Bayes method to perform Bayesian model reduction, Bayesian model average, and make inferences about the connectivity strength. Default parameters and priors were used during model fitting.

Multivariate modeling and predictive analysis

To obtain a single real number that best predicts which eye is stimulated based on the activation pattern in a given ROI, a set of linear weights can be learned by training a linear classifier (we used linear support vector machines from the scikit-learn package with default hyper-parameters) on ocular bias localizer data to predict which eye was stimulated on a TR-by-TR basis, and the multivariate response patterns from other conditions can then be linearly projected using the optimal weights into a 1D timeseries that reflects the distance to the decision boundary at each moment. This decoding timeseries is the multivariate differential response, and can be used to compute an event-related average response.
For feature selection, voxels with above-threshold visual response (omnibus $F > 1$, L+R $t > 1$, L+R beta < 5) and ocular bias (200 most biased voxels (2x up-sampled) in both ends of the L-R t distribution, with positive monocular response, e.g., LE > 0 for LE-biased voxels) in the GLM results of ocular bias localizer were selected. Results were similar across a reasonable range of thresholds. The ideal response timecourse for the localizer was created by convolving the HRF ("GAM" with default parameters in AFNI) with boxcar functions indicating LE or RE blocks, and then taking their difference. Volumes at the flat part of the block responses (absolute value of the ideal response > 0.75 * maximum) were selected for training, whereas all volumes from the rivalry/replay runs were used at test time for generating the multivariate differential response. Each sample (feature vector) was normalized to have unitary Euclidean norm before training or testing.