

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

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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 tasks inside the MR scanner were implemented by Psychtoolbox in Matlab.

Data analysis Imaging data analysis were carried out using SPM12, CONN, PhysIO toolbox in Matlab. Machine learning models were developed using scikit-learn in Python. Statistical test was performed by SciPy in Python and lme4 in R.

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](#)

Processes generated in this study will be deposited in the repository found at the following link: <https://github.com/mokazuma/AuditoryRewardBrain>. The data that support the findings of this study are available from the corresponding author upon reasonable request. The pre-processed data used for figure generation are available in the accompanying Source Data File.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research.](#)

Reporting on sex and gender	Sex and gender were not considered in the design. Sex was self-reported by experiment participants. Gender information was not collected. These variables were not considered in our analyses because they were beyond the scope of the current study.
Population characteristics	In the final sample of 38 participants in Experiment 1, there were 24 males and 14 females aged between 20 and 25 years ($M = 21.8$, $SD = 1.4$). The sample of 11 participants in Experiment 2, there were 9 males and 2 females aged between 20 and 25 years ($M = 21.9$, $SD = 1.6$). All participants had normal hearing and normal or corrected-to-normal vision. From BMRQ (Barcelona Music Reward Questionnaire) scores, we confirmed that the participants did not include strong musical anhedonia.
Recruitment	Participants were recruited using the participant database of the Center for Information and Neural Networks (CiNet). Participants tended to be undergraduate or Master's students at Kansai area and reflected the demographics of the local student population.
Ethics oversight	The study was approved by the human ethics research committee of the National Institute of Information and Communications Technology (NICT).

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	For Experiment 1, a target sample size was determined according to similar previous studies predicting behavior from resting-state functional connectivity ($N = 35$, Spisak et al., 2020) and from brain fluctuations immediately before task ($N = 43$, Chew et al., 2019). In addition, we verified that the sample size was appropriate using learning curve analysis. Sample size for Experiment 2 was determined based on the expected prediction accuracy provided by nested cross-validation.
Data exclusions	In Experiment 1, four participants were removed because they did not report any chills or tears responses during the experiment. One participant was removed due to having an abnormality of autonomic nervous system activity. In Experiment 2, one participant was excluded due to misunderstanding online emotion ratings.
Replication	The presented results are replicable given the program codes deposited at public repositories, as listed above. A remarkable reproducibility on new datasets is expected as the predictive model trained in Experiment 1 turned out to generalize well to the independent validation Experiment 2 conducted with different scanner.
Randomization	Only one group of participants was tested and thus participants were not assigned to experimental groups.
Blinding	No group assignment took place, blinding was therefore 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
<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 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

Magnetic resonance imaging

Experimental design

Design type	Resting fMRI, Task fMRI with event-related design
Design specifications	Participants performed a music listening task, preceded by short time resting-state recording. 8 songs were presented in 2 run of 4 songs. Across participants, a run lasted in average 24.9 minutes in Experiment 1 and 28.1 minutes in Experiment 2.
Behavioral performance measures	In the scanner, we recorded the onset and duration of button presses during the task imaging sessions (not performance-related).

Acquisition

Imaging type(s)	fMRI
Field strength	3T
Sequence & imaging parameters	In Experiment 1, data were acquired using a 3T Siemens Trio scanner equipped with a 32-channel head coil. We recorded two experimental runs corresponding to the two blocks of trials in the main experimental task. Functional volumes were acquired using a T2*-weighted gradient echo, EPI sequence (62 interleaved slices, gap: 0.3 mm, voxel size: 3 × 3 × 3 mm, matrix size: 64 × 64, FOV: 192 mm, TE: 30 ms, TR: 2000 ms, flip angle: 75°, multiband factor: 2). In Experiment 2, neuroimaging data were acquired on a 3T Siemens Prisma scanner with a 64-channel head coil. Functional volumes were acquired with the same parameters as experiment 1.
Area of acquisition	whole-brain
Diffusion MRI	<input type="checkbox"/> Used <input checked="" type="checkbox"/> Not used

Preprocessing

Preprocessing software	Preprocessing was performed using SPM12, CONN, and PhysIO toolbox.
Normalization	Functional images were co-registered to the structural image and warped to the Montreal Neurological Institute template.
Normalization template	Montreal Neurological Institute template
Noise and artifact removal	The common nuisance variables were regressed out, including the subject-specific white matter mask and the cerebrospinal fluid signal mask (five PCA parameters, CompCor), 12 movement regressors (six head motion parameters and their first-order temporal derivatives), and spike regressors for excessive movements. Physiological noise regressors were also included as the nuisance variables. PhysIO toolbox was used to calculate HR and RR variables, including cardiac response function, respiratory response function, and RETROICOR at the same temporal resolution as the fMRI time series. The linear trends of time courses were removed, and band-pass filtering (0.008–0.09 Hz) was applied to the time series of each voxel to reduce the effect of low-frequency drifts and high-frequency physiological noise.
Volume censoring	The first five volumes were excluded from all analyses to allow for scanner calibration. ART-based scrubbing was marked as outliers and subsequently censored.

Statistical modeling & inference

Model type and settings	Connectome-based predictive modeling
Effect(s) tested	We examined whether functional connectivity derived from resting-state immediately before task can predict self-report emotion duration, physiological responses, and bold activities during task.
Specify type of analysis:	<input type="checkbox"/> Whole brain <input checked="" type="checkbox"/> ROI-based <input type="checkbox"/> Both
Anatomical location(s)	For resting fMRI, Regions of Interested were setted by the Seitzman atlas (NeuroImage, 2020). For task fMRI, all Regions of Interested were demarcated using the Automated Anatomical Labeling atlas 3.1

(except cerebellum).

Statistic type for inference
(See [Eklund et al. 2016](#))

We used functional connectivity measures in the current study. We were not interested in clusters from task-based activations.

Correction

We performed false-discovery rate correction.

Models & analysis

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

Functional and/or effective connectivity

Partial correlation

Multivariate modeling and predictive analysis

We used LASSO (least absolute shrinkage and selection operator) regression and evaluated the performance of the models with two metrics: correlation between predicted and observed scores, and coefficient of determinations.