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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	No software was used for data collection.
Data analysis	fMRIPrep (v25.0.0), FreeSurfer (v7.3.2), huggingface (v0.24.1), mne (v.1.6.1), scipy (v1.12.0), torch (v2.2.0)

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 eye-tracking and fMRI dataset is available at https://openneuro.org/datasets/ds003974/versions/3.0.033. The listening fMRI dataset is available at https://openneuro.org/datasets/ds005345.

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	50 participants (25 females)
Reporting on race, ethnicity, or other socially relevant groupings	native English speakers
Population characteristics	mean age = 22.5 ± 4.1 years
Recruitment	All imaging and eye-tracking data were acquired at the Center for NMR Research at the Pennsylvania State University Hershey Medical Center in Hershey, Pennsylvania
Ethics oversight	Pennsylvania State University Institutional Review Board (CR00003867)

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

Behavioural & social sciences study design

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

Study description	The study involves participants reading articles in the fMRI scanner. The attention matrices of large language models for each sentence were regressed against the regressive eye saccade patterns. The data are qunatitative.
Research sample	The reading brain dataset (https://openneuro.org/datasets/ds003974/versions/3.0.033) involves a total of 52 participants.
Sampling strategy	Random sampling. No sample size calculation was performed. The sample size is larger than typical fMRI studies involve human subjects.
Data collection	All imaging data were acquired in 3 T Siemens Magnetom Prisma Fit scanner at the Center for NMR Research at the Pennsylvania State University Hershey Medical Center in Hershey, Pennsylvania. The researcher was blinded to experimental condition and/or the study hypothesis for this study.
Timing	April 2016 - April 2017
Data exclusions	One participant (sub-21) was excluded in eye-tracking analysis due to incomplete recording. Two participants (sub-21 and sub-52) were excluded in fMRI analysis due to fMRI preprocessing errors.
Non-participation	No participants dropped out/declined participation.
Randomization	The presentation order of the five texts was randomized across participants.

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 — Naturalistic reading

Design specifications — Participants read each article sentence-by-sentence in a self-paced manner, pressing a response button to advance to the next sentence.

Behavioral performance measures — At the end of each article, participants answered 10 multiple-choice questions to ensure their comprehension.

Acquisition

Imaging type(s) — functional

Field strength — 3T

Sequence & imaging parameters — The anatomical scans were acquired using a Magnetization Prepared RApid Gradient-Echo (MP-RAGE) pulse sequence with T1 weighted contrast (176 ascending sagittal slices with A/P phase encoding direction; voxel size = 1mm isotropic; FOV = 256 mm; TR = 1540 ms; TE = 2.34 ms; acquisition time = 216 s; flip angle = 9°; GRAPPA in- plane acceleration factor = 2; brain coverage is complete for cerebrum, cerebellum and brain stem). The functional scans were acquired using T2* weighted echo planar sequence images (30 interleaved axial slices with A/P phase encoding direction; voxel size = 3 mm × 3mm × 4 mm; FOV = 240 mm; TR = 400 ms; TE = 30 ms; acquisition time varied on the speed of self-paced reading, maximal 5.1 minutes per run; multiband acceleration factor for parallel slice acquisition = 6; flip angle = 35°; where the brain coverage missed the top of the parietal lobe and the lower end of the cerebellum). A pair of spin echo sequence images with A/P and P/A phase encoding direction (30 axial interleaved slices; voxel size=3mm× 3mm× 4mm; FOV=240mm; TR=3000ms; TE=51.2 ms; flip angle = 90°) were collected to calculate distortion correction for the multiband sequences (Glasser et al., 2013).

Area of acquisition — whole-brain

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	fMRIPrep (v25.0.0)
Normalization	Final resampling to MNI space and fsaverage5 surface was performed in a single interpolation step using antsApplyTransforms and mri_vol2surf.
Normalization template	MNI152, fsaverage5 surface
Noise and artifact removal	field inhomogeneity artefacts correction
Volume censoring	Volumes exceeding FD>0.5 mm or standardized DVARS>1.5 were flagged as motion outliers. All transforms were applied in a single interpolation step using antsApplyTransforms with Lanczos interpolation.

Statistical modeling & inference

Model type and settings	We performed ridge regressions using the attention matrix at each layer from each LLM to predict each voxel's BOLD vector in the whole brain for each subject.
Effect(s) tested	Significant correlation coefficients.

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

Statistic type for inference (See Eklund et al. 2016)	cluster-wise: Clusters were formed from statistics corresponding to a p-value less than 0.05, and only clusters spanning a minimum of 50 vertices were included in the analysis
Correction	FDR corrections

Models & analysis

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

Multivariate modeling and predictive analysis	We performed ridge regressions using the attention matrix at each layer from each LLM to predict each voxel's BOLD vector in the whole brain for each subject. We then tested whether the trained ridge regression model can predict test BOLD signals.