nature portfolio

Corresponding author(s): Benjamin I. Rapoport, M.D., Ph.D.

Last updated by author(s): Jul 31, 2025

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	Commercial and open-source software applications used for data collection and analysis are described in the Methods section: Recording Software and Data Pre-processing. The recording computers interface with either controller via a custom configuration of the Intan Technologies RHX Data Acquisition Software, which allows for real-time event-triggered averaging in addition to base functionality. Videos were recorded using a modified set of codes from DepthAI SDK.
Data analysis	Code that was used to analyze the data of this study, including preprocessing and visualizing the neural data, and training the machine learning models described herein, are publicly available on GitHub: https://github.com/precision-neuroscience/nbme2025. Algorithms were built using open-source deep learning frameworks, including PyTorch (https://pytorch.org) and TensorFlow (https://www.tensorflow.org). Commercial and open-source software applications used for data collection and analysis are described in the Methods section: Software Methods. Data processing is performed in C/C++, Python (3.10.14), and MATLAB (22.1-24.2), using community standard frameworks, including but not limited to Qt (6.3.2), CUDA (11.7), NumPy (1.26.4), SciPy (1.15.3), PyTorch (2.0.0), and Matplotlib (3.8.4). Machine learning model training is performed using PyTorch, accelerated by an NVIDIA RTX 4090. Machine learning model inference is performed using TorchScript, utilizing 12th generation Intel Core i7 processors. Real-time visualizations are implemented using the Qt framework. Video annotation was performed in Adobe Premier Pro 2023.

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

This study analyzed datasets containing high-resolution neural recordings from both large animals and human patients, along with clinical and demographics variables and deidentified imaging data from patients at West Virginia University. Example nonhuman neural recording datasets are publicly available in the following repository: https://github.com/precision-neuroscience/nbme2025. Reasonable requests for noncommercial research use of human electrophysiologic and other deidentified human clinical data will be considered and should be made to the corresponding author. Some restrictions apply to the availability of the data, due in part to patient confidentiality, and additional ethics review may be required.

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	Patients were screened for eligibility and were approached for consent to participate in the study without regard for sex or gender. Sex and self-reported gender were collected together with basic demographic patient data, but do not contribute to our findings and are not reported in this manuscript.
Reporting on race, ethnicity, or other socially relevant groupings	We did not collect such data on study participants as it was not considered pertinent to the study.
Population characteristics	Patients were screened for eligibility and were approached for consent to participate in the study without regard for sex or gender. Basic demographic covariates were collected but do not contribute to our findings and are not reported in this manuscript.
Recruitment	Patients presenting to the West Virginia University Department of Neurosurgery for treatment of malignant brain tumors were screened for eligibility and were approached for consent to participate in the study. All patients who met eligibility criteria during the recruitment period were approached for enrollment. Those who provided informed consent were enrolled in the study. Given the nature of this convenience sample, it is impossible to rule out that some degree of self-selection bias was present in the study sample. However, given the nature of the electrophysiologic data, the likelihood that this self-selection impacted the study results is judged by the authors to be very low.
Ethics oversight	West Virginia University Medical Center Institutional Review Board, Protocol Number 2207618749.

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	The minimum number of animals was used in each section of the preclinical work to ensure reproducibility and assess variability in triplicate or quadruplicate. This sample size was determined with a view toward ensuring reproducibility but without using unnecessarily many animals; formal statistical methods were not used to predetermine sample size given the nature of this work. The number of human patients enrolled was limited logistically by the duration of the study and the comparative rarity of malignant brain tumors in the population.
Data exclusions	No data were excluded.
Replication	The minimum number of animals was used in each section of the preclinical work to ensure reproducibility and assess variability in triplicate or quadruplicate. The number of human patients enrolled was limited logistically by the duration of the study and the comparative rarity of malignant brain tumors in the population. The reported observations in both animals and conclusions were replicated consistently.
Randomization	In the preclinical work, as described, testing was structured so that each animal provided its own control data. Randomization was not applicable to the human patients as this was effectively an observational study in that the investigators were not administering a treatment to the participants, so there was no intervention to randomize.

Blinding	Blinding was not possible overall due to the surgical nature of the studies and the intraoperative nature of data collection and real-time analysis.

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	Female Göttingen minipigs, age 10-11 months.
Wild animals	None.
Reporting on sex	All animals in the study were female.
Field-collected samples	None.
Ethics oversight	The study protocol was approved by the IACUC of DaVinci Biomedical Research Products, Inc.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	This was a feasibility study. Registration at ClinicalTrials.gov is not required for such studies.
Study protocol	The study was reviewed and approved by the West Virginia University Medical Center IRB (Protocol Number 2207618749). The protocol can be made available upon reasonable request.
Data collection	Clinical data were collected from March-August 2023 in the Neurosurgery Department at West Virginia University.
Outcomes	Primary outcomes included comparative measures of electrocorticographic signals obtained from standard electrode arrays relative to the novel electrode arrays (presence of physiologic signals, signal-to-noise measurements, and signal comparisons). Secondary outcomes included decodability of the obtained neural signals when correlating obtained signals with external stimuli or behavioral outputs such as sensory stimuli, motor movements, and speech. These were selected due to their clinical relevance.

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: MRI was not a part of the study design. However, MR images were obtained in the course of clinical care and surgical planning for the enrolled patients, according to the standard of care. Images were saved and used pre-, intra-, and postoperatively to confirm the anatomic sources of electrophysiologic recordings.

Design specifications: Clinical-standard gadolinium-contrast-enhanced, T1-weighted axial sequences.

Behavioral performance measures: None.

Acquisition

Imaging type(s): Clinical-standard gadolinium-contrast-enhanced, T1-weighted axial sequences.

Field strength: 1.5 Tesla

Sequence & imaging parameters: Clinical-standard gadolinium-contrast-enhanced, T1-weighted axial sequences.

Area of acquisition: Whole-brain.

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software: None.

Normalization: None.

Normalization template: None.

Noise and artifact removal: None.

Volume censoring: None.

Statistical modeling & inference

Model type and settings: None.

Effect(s) tested: None.

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

Statistic type for inference (See Eklund et al. 2016): None.

Correction: None.

Models & analysis

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