nature research

Corresponding author(s): Canan Dagdeviren

Last updated by author(s): Aug 9, 2020

Reporting Summary

Nature Research 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 Research 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	3D-DIC data collection was performed with open-source code, MultiDIC, in the MATLAB language, with the 2018b version. The real-time decoding algorithm was custom-written in Python 3.6 with use of the fastdtw Python library. Device-characterization electrical data were recorded in NI SignalExpress 2015. Mechanical tests performed on the Instron machine were recorded with BlueHill software. Code used for addressing and capturing images from the cameras for 3D-DIC is available at https://github.com/ConformableDecoders/PT-Grey-Image-Acquisition. Code used for 3D-DIC analysis is available at https://github.com/MultiDIC/MultiDIC. Code used for the data collection and analysis of real-time decoding of facial deformations is available at https://github.com/ConformableDecoders/cFaCES_RTD.
Data analysis	Custom code was written in MATLAB 2018b and Python 3.6 (using standard functions or libraries, such as numpy and matplotlib) to graph data from 3D-DIC and real-time decoding. Mechanical characterization and crystallography data were analyzed and graphed in Origin. Theoretical modeling and analysis was conducted in COMSOL Physics and MATLAB 2019.

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 Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

The data supporting the results in this study are available within the paper and its Supplementary Information. The raw patient data are available from the corresponding author, subject to approval from the Institutional Review Board of the Massachusetts Institute of Technology.

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	Eight identical cFaCESs were used to perform all experimental demonstrations to characterize the device performance and for use in in vivo tests (this is noted in Methods). Please see "Microfabrication process of a cFaCES" in Methods.
Data exclusions	No data were excluded.
Replication	All attempts at replication were successful.
Randomization	None. One device type was tested in the same human in vivo trial model.
Blinding	Data collection and analysis for each subject were performed by different researchers.

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
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Human epidermal keratinocytes (Sigma Aldrich, St. Louis, MO, USA).
Authentication	No cell-line authentication was pursued.
Mycoplasma contamination	The cells were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Human research participants

Policy information about studies involving human research participants

Population characteristics	ALS Subject 1: age 65, gender F, diagnosed with amyotrophic lateral sclerosis 3.5 years prior to testing ALS Subject 2: age 46, gender M, diagnosed with amyotrophic lateral sclerosis 2.5 years prior to testing Healthy Subject 1: age 38, gender M, no relevant health conditions Healthy Subject 2: age 21, gender F, no relevant health conditions Healthy Subject 3: age 22, gender F, no relevant health conditions Healthy Subject 4: age 33, gender F, no relevant health conditions Healthy Subject 5: age 34, gender M, no relevant health conditions
Recruitment	Subjects with mid-stage ALS were recruited via consultation with a medical doctor in the Greater Boston area. Healthy and ALS subjects were recruited to represent a variety of ages, genders and cultural backgrounds.
Ethics oversight	All procedures in the healthy and ALS subject tests were performed in accordance with the experimental protocol approved by the Committee on the Use of Humans as Experimental Subjects of the Massachusetts Institute of Technology (COUHES # 1809531633). The participants gave informed consent.

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