nature portfolio

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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	Study 1: movisensXS, version 0.6.3658 (movisens GmbH, Germany, https://xs.movisens.com); Geocoder software 1.0 (movisens GmbH, Germany,www.movisens.com) Study 2: movisensXS, version 1.5-INDICATE (movisens GmbH, Germany, https://xs.movisens.com)
Data analysis	SAS software version 9.4, SAS Institute Inc., Cary, NC, USA; CONN-toolbox v.19c (http://web.mit.edu/swg/software.htm); SPM12 (www.fil.ion.ucl.ac.uk/spm); DataAnalyzer, version 1.6.12129 (movisens GmbH, Germany, www.movisens.com); MATLAB version 9.8 (R2020a), The MathWorks, Inc., Natick, Massachusetts, USA

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 data that support the findings of this study are available from the corresponding author upon reasonable request. The Figures 1, 2 and eFigure 1 have associated raw data. The custom code used for the analyses of this study is available from the corresponding author upon reasonable request.

For the neuroimaging analysis we used a 100 regions 7 networks parcellation atlas21: https://github.com/ThomasYeoLab/CBIG/tree/master/stable_projects/brain_parcellation/Schaefer2018_LocalGlobal/Parcellations/MNI

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	sex
Reporting on race, ethnicity, or other socially relevant groupings	nationality
Population characteristics	We studied a community-based cohort of 317 healthy young adults aged 18 to 28 years (57.09 % females) for 7 days in everyday life (study 1). We further studied a replication sample (study 2) of 30 healthy adults aged 18 to 63 years (50% females) for 6 months in everyday life during the COVID-19 pandemic in Germany.
Recruitment	Study 1: Based on a two-stage proportionally layered procedure (stratified by age, sex, and nationality), participants were randomly selected from population registries at the Psychiatric-Epidemiological Center at the Central Institute of Mental Health (CIMH; Mannheim, Germany) between September 2014 and October 2018. To the best of our knowledge, there was no self-selection bias. Study 2: Participants were recruited from the local community by advertisement between December 2019 and July 2022.
Ethics oversight	The Medical Faculty Mannheim (medical ethics committee II) at the Ruprecht-Karls-University in Heidelberg approved both studies.

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	In this cohort study using accelerometry, electronic diaries and neuroimaging in a community-based sample of 317 young adults, we show that people felt worse when lacking social contact, but less so when engaging in physical activity.
Research sample	Since we were interested in resilience mechanisms for mental health we studied a community-based cohort of 317 healthy young adults aged 18 to 28 years (57.09 % females), recruited from September 2014 to November 2018, for 7 days in everyday life. According to our sampling strategy we consider the sample to be representative.
Sampling strategy	Based on a two-stage proportionally layered procedure (stratified by age, sex, and nationality), participants were randomly selected from population registries at the Psychiatric-Epidemiological Center at the Central Institute of Mental Health (CIMH; Mannheim, Germany) between September 2014 and October 2018. To the best of our knowledge, there was no self-selection bias.
Data collection	Study 1: Participants wore a triaxial accelerometers (Move II or Move III; movisens GmbH, Germany) for 7 consecutive days during waking hours on the right hip. Study 2: Participants wore a triaxial accelerometers (Move 4; movisens GmbH, Germany) on their non-dominant wrist.

	Besides the researcher, research assistants were present during data collection, but not aware of the specific research question.
Timing	Study 1: Participants were recruited from September 2014 to November 2018, for 7 days in everyday life. Study 2: Participants were recruited from December 2019 to July 2022, for 6 months in everyday life during the COVID-19 pandemic in Germany.
Data exclusions	Following established procedures, we excluded participants if the following criteria applied: (i) severe technical problems with the accelerometer such as a prematurely terminated measurement (N = 28), (ii) e-diary compliance below 30% (N = 2), or (iii) missing questionnaire data (N = 9). The final sample consisted of 317 healthy participants (57.09 % females) with a mean age of 23.08 years (SD = 2.83).
Non-participation	No participants dropped out/declined participation.
Randomization	Randomization was not relevant because we conducted an observational and no intervention study.

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	Resting-state (duration: 6:52 minutes, 206 whole-brain scans).
Design specifications	Participants were instructed to relax, not engage in any particular mental activity during the scan and to keep their eyes open, while a gray background with a fixation cross was presented.
Behavioral performance measures	During resting-state fMRI measurements participants do not perform any behavioral tasks.

Acquisition

Imaging type(s)	functional magnetic resonance imaging
Field strength	3 Tesla
Sequence & imaging parameters	Functional data were acquired with an echo-planar-imaging sequence with the following parameters: echo time (TE) 30 ms, 28 oblique slices oer volume, 4 mm slice thickness, 1 mm slice distance, repetition time (TR) 2000 ms, 80° flip angle,

192 mm field of view (FOV) and 64 x 64 matrix.

Area of acquisition: whole-brain

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software: SPM12 (www.fil.ion.ucl.ac.uk/spm); CONN-toolbox v.19c (http://web.mit.edu/swg/software.htm).

Normalization: Direct normalization to the MNI template (T1-weighted).

Normalization template: Montreal Neurological Institute (MNI) space with resampling to 2 × 2 × 2 mm voxels.

Noise and artifact removal: CompCor approach (White Matter and CSF ROIs, 6 motion parameters + 6 first-order temporal derivatives).

Volume censoring: Scrubbing of movement-related outlier scans with a framewise displacement > 0.9 mm or global BOLD signal changes > 5 standard deviations.

Statistical modeling & inference

Model type and settings: The extraction of resting-state functional connectivity values does not require any statistical model.

Effect(s) tested: n/a

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

Anatomical location(s): All nodes of the default mode network (specifically, regions 38 – 50 and 90 – 100 of the atlas) as defined by the Schaefer-Yeo 100 regions parcellation.

Statistic type for inference: n/a

(See Eklund et al. 2016)

Correction: n/a

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: Functional connectivity was calculated by computing pairwise Pearson correlations between the time series of two DMN regions of interest as defined by the Schaefer-Yeo 100 regions parcellation.