

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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	Data was produced in our own laboratory (total mercury and mercury isotope results).
Data analysis	Statistical analyses were done using R version 4.2.3. One-way analysis of variance (ANOVA) was performed to determine differences in Hg stable isotope signatures between sites and species. Prior to the ANOVA, a Shapiro-Wilk test was conducted to test for normality of data, and a Brown-Forsythe test was undertaken to test for equal variances between groups. A Welch ANOVA test was applied due to unequal variances identified for some groups, and a Games-Howell post hoc test was used to assess individual group differences (using R-package 'rstatix 0.7.1'). Temporal trends in Hg stable isotope signatures were evaluated using the Mann-Kendall and Theil-Sen's slope analysis on subadult ringed seals (≤ 4 years) and polar bears (males ≤ 5 years; females ≤ 4 years) (using R-packages 'Kendall 2.2.1' and 'mblm 0.12.1'). Differences were regarded significant at $p < 0.05$.

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](#)

All data presented in this paper are provided as a Source Data file.

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

Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

Ecological, evolutionary & environmental sciences study design

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

Study description

The study is based on analyses of polar bear, ringed seals, shorthorn sculpin, arctic char, and glaucous gull specimens collected in Greenland during 1983-2023; since 1994 in association with deliveries to the Arctic Monitoring and Assessment Programme (AMAP). More detailed information on sampling year(s) for each sample type is provided in Extended Data Table 1. Although it is not currently used for Hg monitoring, glaucous gull was included in our study to represent seabirds. The locations of the sampling sites are shown in Fig. 1a. The AMAP sampling sites with approximate coordinates are Ittoqqortoormiit (70.29°N, 21.58°W), Qaanaaq (77.28°N, 69.15°W), Qeqertarsuaq (69.15°N, 53.32°W), and Isortoq (60.54°N, 47.33°W). A thorough description of the programme is given in AMAP (2021). Furthermore, peat was sampled at palsas in Zackenberg and Qeqertarsuaq. A palsa is a typical feature of a permafrost-affected landscape and is common in poorly drained lowlands in Greenland. Palsas are mounds that contain lenses of segregation ice and represent continuous peat formation and formation of ice in the core due to capillary water undergoing slow freezing. Palsa formation and collapse is a dynamic feature. Two complete (non-collapsing) palsas were sampled: one east of the Zackenberg River and north of Zackenberg Research Station (74°29'05"N; 20°33'58"W) in Northeast Greenland with a height of ca. 1 m and one in Blæsedalen east of Qeqertarsuaq on Disko Island (69°16'05"N; 53°28'06"W) in West Greenland with a height of ca. 0.7 m. The Zackenberg palsa was sampled in September 2012 and the Disko palsa in August 2022. Both palsas were fully covered by vegetation dominated by mosses and grasses. Roots occurred at both locations throughout the top 25 cm but dominated the top 5 cm. A nearby

palsa in the Zackenberg area has been dated based on microfossils to 2623 ± 123 BP (14C AMS) at 0.5 m depth. The samples were collected from the litter layer and the active layer comprising the top 25 cm. From the permafrost table, a steel pipe was hammered down into the soil with 10 cm depth increments, after which the sample was carefully collected from the pipe before sampling the next 10 cm. The samples were stored in plastic bags and kept frozen (below -6°C). Prior to analyses, the samples were taken out of the freezer and the outer 0.5 to 1 cm cut off with a ceramic knife and discarded. The samples were subsequently cut into slices using a ceramic knife and put into plastic bags for further processing.

Research sample

We applied polar bear, ringed seals, shorthorn sculpin, arctic char, and glaucous gull tissue samples. All the species are selected as key monitoring species the frame work of AMAP (the Arctic Monitoring and Assessment Programme under the Arctic Council) to represent different environments and higher trophic level species most exposed to Hg pollution. To study sources and environmental processes, we focused on muscle tissue from the specimens due to minimal Hg isotope fractionation (as it consists of nearly 100% MeHg). To study internal fractionation, we additionally used liver tissue for all species, and for polar bears also hair and kidney. Temporal trends in Hg isotopes were studied during 1983-2024 using muscle tissue from subadult individuals of ringed seals (both males and females up to 4 years) and polar bears (males up to 5 years and females up to 4 years). The selection of subadult individuals were done to identify changes in Hg characteristics faster (as old individuals is likely to contain Hg accumulated during their longer lifespan) and to normalize for potential differences related to age. Finally peat core samples from Central West Greenland and Northeast Greenland was collected to assess temporal variation in Hg deposition characteristics over a longer time span than the biota samples.

Sampling strategy

The biota samples were collected within the frame work of AMAP during the past four decades. Sites were selected to represent different regions in Greenland, and are characterized as remote sites with minimal local Hg contamination sources. Samples were collected mainly the local subsistence hunters in Greenland following local ethics and legislation. All samples obtained from polar bears were exported/import under the international IUCN CITES regulations. The sample sizes for the AMAP collections been determined based on numerous past assessments of pollutants in Greenland to cover the natural variability both spatially and temporally, while also taking available funding into account. In this study, we selected all individuals of ringed seals and polar bears from the recent years to study spatial variations, environmental processes and internal Hg isotope fractionation, while for the time-trend analyses (1983-2024) of ringed seals and polar bears, we focused on subadult individuals to ensure that the Hg measured have been bio-accumulated recently (within max. 4-5 years) prior to the collections and therefore minimizing the influence of animal age in the time-trend analyses. Peat samples were collected in association with research activities at Center for Permafrost (CENPERM) at University of Copenhagen and the two peat profiles in the study were selected as representative to the sites. The sample sizes selected show significant differences for Hg isotopes, both spatially and temporally as well as between species/tissues, and we therefore consider them appropriate for the purpose of the study, although we will certainly expand our studies in the coming years to include more samples, sample types and sites.

Data collection

The total Hg and Hg isotope data was produced at the Trace Metal and Isotope Geochemistry Laboratory at Department of Ecoscience, Aarhus University (<https://ecos.au.dk/en/researchconsultancy/research-facilities/metal-isotope-geochemistry-lab>). Total Hg was measured using an Agilent 7900 ICP-MS instrument by Sandra Drewes Fabricius. Hg isotopes were measured using a Thermo Neptune Plus MC-ICP-MS instrument by Jens S ndergaard as described in detail in the methods section.

Timing and spatial scale

Collection of biota samples were done in Greenland in the period 1983-2024 in connection with the Greenland AMAP Core program and was conducted approximately every 2-3 years. The timespan between collections is chosen for mainly economical reasons and because it is considered sufficient to identify long-term contaminant time trends in the region. The specific years of collections are shown in the figures and supplied in the Data Source file. The sampling sites cover South Greenland (Isortoq), Central West Greenland (Qeqertarsuaq), Northwest Greenland (Qaanaaq), and East Greenland (Ittoqqortoormiit). Peat core samples from two established research sites/stations in Central West Greenland (Qeqertarsuaq) and Northeast Greenland (Zackenberg) were collected in 2022 and 2012 and included in the study to evaluate long-term trends across these regions.

Data exclusions

No data was excluded.

Reproducibility

To ensure reproducibility, we regularly measured blank samples and the certified reference material (CRM) NIST 8610 (at least for every 6 samples) in connection with the Hg isotope analyses to ensure minimal carry-over as well as high accuracy and precision (confirming that the instrument was running stable). CRMs with matrix similar or close to the samples were also included in the digestions and the total Hg analyses to ensure 100% digestion of the samples. During the Hg isotope analyses, we evaluated signal intensities after dilution of the samples to ensure all Hg in the digestion solution was reduced in the cold vapour unit and measured for Hg isotopes. Finally, we measured many of the samples as duplicates (i.e. as two different subsamples) to further confirm good instrumental performance as well as homogeneity of the samples.

Randomization

The collected biota samples reflects specimens collected by mainly local subsistence hunters in Greenland. We have no knowledge of how random these collections are to the total population at the sites. For some part of the study (the temporal trend study), we specifically selected subadult individuals of polar bears and ringed seals to identify any changes in Hg accumulation in these species faster and to normalize for potential age effects.

Blinding

This is not considered relevant for this study. The only selection of samples we did was based on age characterization (subadult individuals) determined based on age determination in teeth.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions

The samplings were conducted during the summer period (May-September) throughout Greenland with climates spanning from sub-Arctic to high-Arctic.

Location	The locations of the sampling sites are shown in Fig. 1a. The AMAP sampling sites with approximate coordinates are Ittoqqortoormiit (70.29°N, 21.58°W), Qaanaaq (77.28°N, 69.15°W), Qeqertarsuaq (69.15°N, 53.32°W), and Isortoq (60.54°N, 47.33°W). The peat sampling sites are Zackenberg (74°29'05"N; 20°33'58"W) and Qeqertarsuaq on Disko Island (69°16'05"N; 53°28'06"W).
Access & import/export	Specimen samples were collected by mainly local subsistence hunters in Greenland as part of the Greenland AMAP programme following local ethics and legislation incl. CITES permitting. All samples obtained from polar bears were under the international IUCN CITES regulations legally exported from Greenland (295/2000, 61/2001, 69/2001, 66/2003, 156/2004, 23/2005, 17/2006, 08GL0706599, 09GL0805839, 10GL0806166, 10GL0805167, 42 10GL0806333, 10GL0806334, 11GL1003311, 12GL1003376, 13GL1003418, 14GL1003515, 15GL1166847, 16GL1167015, 17GL1167116, 18GL1717224, 19GL1717365, 20GL1717427) to Denmark (IM 0813-642/01, IM 0312-080/01, IM 1116-901/04, IM 1116-954/05, IM 0316-613/06, IM 0811-266/06, IM 0711-993/08, IM 0630-137/09, IM 0611288/10, IM 0611-290/10, IM 1223-856/10, IM 1223-855/10, IM 1214-596/11, IM 1199-728/12, IM 0826-378/13, IM 1202-211714, IM 1222-060/15, IM 1202-580/16, IM 0818-549/17, IM 0928-712/18, IM0816-496/19, DK2020-0017113-01).
Disturbance	The study is not considered to have caused significant disturbance.

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

Antibodies

Antibodies used	Describe all antibodies used in the study; as applicable, provide supplier name, catalog number, clone name, and lot number.
Validation	Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer's website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	State the source of each cell line used and the sex of all primary cell lines and cells derived from human participants or vertebrate models.
Authentication	Describe the authentication procedures for each cell line used OR declare that none of the cell lines used were authenticated.
Mycoplasma contamination	Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	Name any commonly misidentified cell lines used in the study and provide a rationale for their use.

Palaeontology and Archaeology

Specimen provenance	Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.
Specimen deposition	Indicate where the specimens have been deposited to permit free access by other researchers.
Dating methods	If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are

provided.

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight

Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.

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

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

For laboratory animals, report species, strain and age OR state that the study did not involve laboratory animals.

Wild animals

Specimens of polar bears, ringed seals, glaucous gull, shorthorn sculpin, and arctic char were collected in Greenland, mainly by local subsistence hunters, and following local ethics and legislation.

Reporting on sex

Reporting on sex-specific differences was beyond scope of the paper.

Field-collected samples

Samples were stored at -20 degrees C the Specimen Sample Bank at Aarhus University (for biota) and at Center for Permafrost at University of Copenhagen (for peat cores).

Ethics oversight

No specific ethical requirements since collections were done by local subsistence hunters in Greenland following local ethics and practices.

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

Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.

Study protocol

Note where the full trial protocol can be accessed OR if not available, explain why.

Data collection

Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.

Outcomes

Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No Yes

- | | | |
|--------------------------|--------------------------|----------------------------|
| ☐ | ☐ | Public health |
| ☐ | ☐ | National security |
| ☐ | ☐ | Crops and/or livestock |
| ☐ | ☐ | Ecosystems |
| ☐ | ☐ | Any other significant area |

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☐	☐
☐	☐
☐	☐
☐	☐
☐	☐
☐	☐
☐	☐
☐	☐
☐	☐

☐ Demonstrate how to render a vaccine ineffective
☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☐ Increase transmissibility of a pathogen
☐ Alter the host range of a pathogen
☐ Enable evasion of diagnostic/detection modalities
☐ Enable the weaponization of a biological agent or toxin
☐ Any other potentially harmful combination of experiments and agents

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, mosaicism, off-target gene editing) were examined.

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links May remain private before publication.	For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.
Files in database submission	Provide a list of all files available in the database submission.
Genome browser session (e.g. UCSC)	Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.

Methodology

Replicates	Describe the experimental replicates, specifying number, type and replicate agreement.
Sequencing depth	Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.
Antibodies	Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.
Peak calling parameters	Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.
Data quality	Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.
Software	Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.

Flow Cytometry

Plots

Confirm that:

- ☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☐ All plots are contour plots with outliers or pseudocolor plots.
- ☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	<i>Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.</i>
Instrument	<i>Identify the instrument used for data collection, specifying make and model number.</i>
Software	<i>Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.</i>
Cell population abundance	<i>Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.</i>
Gating strategy	<i>Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.</i>

- ☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type	<i>Indicate task or resting state; event-related or block design.</i>
Design specifications	<i>Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.</i>
Behavioral performance measures	<i>State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).</i>

Acquisition

Imaging type(s)	<i>Specify: functional, structural, diffusion, perfusion.</i>
Field strength	<i>Specify in Tesla</i>
Sequence & imaging parameters	<i>Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.</i>
Area of acquisition	<i>State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.</i>
Diffusion MRI	☐ Used ☐ Not used

Preprocessing

Preprocessing software	<i>Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).</i>
Normalization	<i>If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.</i>
Normalization template	<i>Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.</i>
Noise and artifact removal	<i>Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).</i>

Volume censoring

Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.

Statistical modeling & inference

Model type and settings

Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).

Effect(s) tested

Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.

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

Statistic type for inference

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

(See [Eklund et al. 2016](#))

Correction

Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).

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

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

Graph analysis

Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).

Multivariate modeling and predictive analysis

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.