Data Dictionary for the Brazilian Reproducibility Initiative

v1 – February 2025

1. Primary datasets

Gathered_data folder

EPM_data.csv – Contains experimental data for EPM experiments

Variables

EXP – Experiment code

LAB – Lab code

Animal_id – Code for the specific animal (as per data collection sheets)

Cage_id – Code for the specific cage (as per data collection sheets)

Litter_id – Code for the litter (for experiments with prenatal interventions only).

Batch_id – Code for the experimental batch

Group_Exp – Group identity (e.g. control, treated, vehicle), as described in the protocol/data collection sheet

Group – Identification of groups to be used in the main comparison

Recommend_exclusion – Whether the animal was excluded from the analysis by the lab or validation committee

All other columns: Specific outcomes for the EPM experiment (and other behavioral tests when applicable). Most experiments have data for numbers of entries and time spent in open and closed arms (Entries_OpenArms, Entries_ClosedArms, Time_OpenArms, Time_ClosedArms), while other outcomes only apply to specific experiments.

PCR_data.csv – Contains experimental data for PCR experiments

Variables

EXP – Experiment code

LAB – Lab code

Date of PCR – Date when PCR was performed

PlateID – ID for the plate (as per data collection sheets)

Experimental Unit LAB – ID corresponding to the experimental unit as defined by the lab.

Experimental Unit BRI – ID corresponding to the experimental unit as defined by the validation committee).

Animal ID – ID for the animal, as specified in the data collection sheets (animal experiments only).

CT Gene of Interest – Ct value for the gene of interest (for RT-qPCR experiments only).

CT Control Gene I – Ct value for the control gene, or for the first of two control genes (for RT-qPCR experiments only)

CT Control Gene II – Ct value for the second control gene (for RT-qPCR experiments with two control genes only)

Band Density Gene of Interest – Optical density for the band corresponding to the gene of interest (for conventional PCR experiments only).

Band Density Control Gene – Optical density for the band corresponding to the control gene (for conventional PCR experiments only).

Exclude? – Whether the sample should be excluded from the analysis (due to a recommendation by the lab or the validation committee).

Experimental Group – Full name of experimental/control group

Group – Designates control (Group1) or treated/intervention (Group2) groups.

Efficiency of primer pair of interest – PCR efficiency for gene of interest. Set to 2 when this was not calculated explicitly.

Efficiency of primer pair of control I – PCR efficiency for the first of two control genes. Set to 2 when this was not calculated explicitly.

Efficiency of primer pair of control II – PCR efficiency for the second control gene, if there was one. Set to 2 when this was not calculated explicitly.

MTT_data.csv – Contains experimental data for MTT experiments

Variables

LAB – Lab code

EXP – Experiment code

Date of MTT assay – Date when MTT assay was performed

Culture ID – ID for the culture (as per data collection sheets)

Plate ID – ID for the plate (as per data collection sheets)

Passage ID – ID for the passage (for cell line experiments only, as per data collection sheets)

Animal Pool ID – ID for the animal pool (for primary culture experiments, as per data collection sheets).

ID LAB – Experimental unit as defined by the lab.

Experimental Group – Full name of experimental/control group

Group – Designates control (Group1) or treated/intervention (Group2) groups.

Exclude? – Whether this sample should be excluded according to the lab or validation committee.

Optical density (a.u.) – Optical density (represents the outcome of the experiment, indicating the degree of MTT reduction).

EPM_meta.csv – Contains metadata for EPM experiments

Variables

LAB – Lab code

EXP – Experiment code

Grouping Variable Name – Indicates the column in EPM_data that should be used to define the experimental unit.

Primary outcome – Indicates the column in EPM_data that indicates the primary outcome of the experiment that will be used in the analysis.

Paired – Indicates whether analysis for the experiment is paired.

Group1_name – Indicates the full name of group 1 (control)

Group2_name – Indicates the full name of group 2 (treated/intervention)

Group3_name/Group4_name – Indicates the full name of other groups in experiments with additional groups beyond the primary comparison.

Outcome_name – Full description of the primary outcome.

Outcome_name_short – Short description of the primary outcome.

MTT_meta.csv – Contains metadata for MTT experiments

Variables

LAB – Lab code

EXP – Experiment code

Grouping Variable Name – Indicates the column in MTT_data that should be used to define the experimental unit in the primary analysis.

Grouping Variable Alternative – Indicates the column in MTT_data that should be used to define the experimental unit as defined by the lab, when this does not correspond to the one defined by the validation committee.

Paired – Indicates whether analysis for the experiment is paired.

Paired Summary – Indicates whether pairing should be included in the experimental summaries to calculate coefficients of variation. Applies when the original experiment has no error bar for controls.

Group1_name – Indicates the full name of group 1 (control)

Group2_name – Indicates the full name of group 2 (treated/intervention)

Outcome_name – Full description of the primary outcome.

PCR_meta.csv – Contains metadata for PCR experiments

Variables

LAB – Lab code

EXP – Experiment code

Paired – Indicates whether the primary analysis for the experiment is paired.

Paired Alternative – Indicates whether the analysis using the experimental unit as defined by the lab is paired.

Cycles – Number of PCR cycles in the experiment.

Primary outcome – Indicates the primary outcome of the experiment when data is analyzed in linear scale (for the main analysis, raw Ct values are used for RT-qPCR experiments and log-transformed relative optical density values are used for conventional PCR ones). This column also determines whether experiments are analyzed as conventional experiments (when filled as "Optical density (a.u.) or RT-qPCR ones (when filled as anything else).

Experimental Unit Column – Indicates the column in PCR_data that should be used to define the experimental unit in the primary analysis.

Experimental Unit Alternative – Indicates the column in PCR data that should be used to define the experimental unit as defined by the lab, when this does not correspond to the one defined by the validation committee.

Group1_name – Indicates the full name of group 1 (control)

Group2_name – Indicates the full name of group 2 (treated/intervention)

Outcome_name – Full description of the primary outcome.

Other_data folder

Inclusion_sets.xlsx – Contains data about each individual replication, including whether the replication was performed, whether it should be included in each of the various analysis sets, the results of replication assessments by the lab and validation committee, results from post-hoc power calculations and information about the replication teams.

Variables

EXP – Experiment code

LAB – Lab code

UNIT – Indicates whether the row concerns the replication with the experimental unit defined by the validation committee (BRI) or its version with the experimental unit defined by the lab (LABUNIT). When these diverge, different analyses will include one or the other. "INCLUDE" denotes inclusion, whereas non-included experiments are left blank.

Analysis_all_exps_lab_units – Indicates whether the experiment should be included in an analysis with all the experiments, using experimental units as defined by the lab "INCLUDE" denotes inclusion, whereas non-included experiments are left blank.

Analysis_included_by_lab – Indicates whether the experiment should be included in an analysis with all the experiments, using units as defined by the lab. "INCLUDE" denotes inclusion, whereas non-included experiments are left blank.

Analysis_primary – Indicates whether the experiment should be included in the primary analysis. "INCLUDE" denotes inclusion, while "MA ONLY" denotes inclusion in meta-analyses, but not as an independent experiment, due to insufficient sample size. Non-included experiments are left blank.

Analysis_only_3_reps – Indicates whether the experiment should be included in an analysis considering only experiments with 3 replications. "INCLUDE" denotes inclusion, whereas non-included experiments are left blank.

Analysis_at_least_2_reps – Indicates whether the experiment should be included in an analysis considering only experiments with at least 2 replications. "INCLUDE" denotes inclusion, while "MA ONLY" denotes inclusion in meta-analyses, but not as an independent experiment, due to insufficient sample size. Non-included experiments are left blank.

Analysis_only_80_power_a_posteriori_T – Indicates whether the experiment should be included in an analysis considering only experiments with $\geq 80\%$ aggregate power in simulations using the *t* distribution using the number of experimental units for analysis. "INCLUDE" denotes inclusion, while "MA ONLY" denotes inclusion in meta-analyses, but not as an independent experiment, due to insufficient sample size. Non-included experiments are left blank.

Analysis_only_80_power_a_posteriori_Z – Indicates whether the experiment should be included in an analysis considering only experiments with $\geq 80\%$ power in simulations using the *z* distribution for analysis. "INCLUDE" denotes inclusion, while "MA ONLY" denotes inclusion in meta-analyses, but not as an independent experiment, due to insufficient sample size. Non-included experiments are left blank.

Analysis_only_80_power_a_posteriori_knha – Indicates whether the experiment should be included in an analysis considering only experiments with $\geq 80\%$ power in simulations using the *t* distribution using the number of replications (via the Knapp-Hartung approach) for analysis. "INCLUDE" denotes inclusion. Non-included experiments are left blank.

Done – Indicates whether the replication was performed.

Reason_for_not_done – If the replication was not performed, indicates why.

Q1_changes_from_preregistration – Indicates the degree of protocol deviation as rated by the lab (on a scale of 1 to 5) in step 1 of the debriefing process (see https://osf.io/xgth2).

Quest.1 – Considered valid? – Indicates whether the lab considered the replication valid in step 1 of the debriefing process.

Quest. 2 – Replication successful? – Indicates whether the lab considered the original result as successfully replicated in step 2 of the debriefing process.

Quest. 2 – Changes from original – Indicates the degree of protocol deviation compared to the original study as rated by the lab (on a scale of 1 to 5) in step 2 of the debriefing process.

Validation – Mean score - Indicates the degree of protocol deviation as rated by the validation committee (mean of 3 ratings on a scale of 1 to 5, see https://osf.io/e3fjg).

Validation – Decision - Indicates the validation committee's decision concerning inclusion of the experiment in the primary analysis. "Low sample size" indicates experiments in which the protocol was deemed acceptable, but the sample size was insufficient for inclusion.

Validation – Discussed? – Indicates whether the experiment was discussed by the validation committee to reach consensus.

Validation – Excluded by – For experiments excluded from the primary analysis, indicates the reason for exclusion (as a general category).

Validation – Reason for exclusion – For experiments excluded from the primary analysis, provides a more detailed reason for exclusion.

Post hoc power T – Post-hoc power calculated via simulations for the aggregate of valid replications, using the t distribution with the number of experimental units for analysis.

Post hoc power Z – Post-hoc power calculated via simulations for the aggregate of valid replications, using the z distribution for analysis.

Post hoc power knha – Post-hoc power calculated via simulations for the aggregate of valid replications, using the t distribution with the number of replications (Knapp-Hartung approach) for analysis.

n_protocol – Number of authors in the protocol team

mean_years_since_first_paper_protocol – Mean number of years since first publication for authors in the protocol team (authors with no publications count as 0).

mean_n_papers_protocol – Mean number of published papers in the Web of Science for authors in the protocol team.

mean_n_citations_protocol – Mean number of received citations in the Web of Science for authors in the protocol team.

n_data_collection – Number of authors in the data collection team

mean_years_since_first_paper_data_collection – Mean number of years since first publication for authors in the data collection team (authors with no publications count as 0).

mean_n_papers_data_collection – Mean number of published papers in the Web of Science for authors in the data collection team.

mean_n_citations_data_collection – Mean number of received citations in the Web of Science for authors in the protocol team.

n_all – Number of authors in the lab

mean_years_since_first_paper_all – Mean number of years since first publication for all authors in the lab (authors with no publications count as 0).

mean_n_papers_all – Mean number of published papers in the Web of Science for all authors in the lab.

mean_n_citations_all – Mean number of received citations in the Web of Science for all authors in the lab.

ruf_all – Folha University Ranking for the lab's institution.

Predictor-data.xlsx – Contains data from the original experiment, article, journal, authors and institution. Instructions for data extraction for this table are reported in https://osf.io/enjxy).

Variables

DOI – DOI of the original article from which the experiment was selected

EXP – Experiment code

Method – Experimental method (MTT, PCR or EPM)

Figure/Table – Describes the figure or table containing the experiment selected for replication and the groups being compared in the selected comparison.

Biological model – Biological model of the selected experiment (animal, cell line or primary culture).

Animal model (species) – Species used in the experiment (rat or mouse). Not applicable for cell line experiments.

Animal model (strain) – Rat or mouse strain used in the experiment. Not applicable for cell line experiments

Animal model (sex) – Sex of the animals used. Not applicable for cell line experiments.

Primary culture (cell type) – Cell type in primary culture (applicable for primary culture experiments only).

Cell culture model (cell line name) – Name of the cell line (applicable for cell line experiments only).

Statistical Test – Statistical test used in the original article, as described in the methods or figure legend.

y-axis – Dependent variable as mentioned in the y-axis of the figure (or table row)

Primary Outcome – Dependent variable as interpreted/abstracted by the Brazilian Reproducibility Initiative team.

Unit of analysis – Unit of analysis as described in the legend or methods ("not specified" when unclear).

Treatment – Intervention performed in the experimental group.

Control – Intervention performed in the control group.

Original p-value – P value of the original comparison, as reported in the original article.

N control – Sample size of the control group as reported in the original article. If no exact sample size was provided for the group, filled as NA.

N treated – Sample size of the control group as reported in the original article. If no exact sample size was provided for the group, filled as NA.

N (range for both groups) – Sample size of the groups when this was mentioned as a range covering multiple groups. If exact sample size was provided for each group, filled as NA.

Assumed Control Sample Size – Sample size for the control group assumed to estimate SDs for power calculations (corresponding to the upper bound of ranges). This may be different from the one used to estimate SDs for determining confidence intervals.

Assumed Treated Sample Size – Sample size for the treated group assumed to estimate SDs for power calculations (corresponding to the upper bound of ranges). This may be different from the one used to estimate SDs for determining confidence intervals.

Data processing – Contains any explanations available in the original article on how the primary outcome was calculated from the experimental measurements obtained, as described in the article text.

Cohen's d – Effect size of the original experiment in Cohen's d

P-value (calculated) – Calculated p value based on the extracted mean and standard deviation/SEM. P values were calculated using a Welch t test when both standard deviations were available or using a one-sample t test in the treated group when there was no variation in the control group (implying paired normalization).

Quality of reporting index, from gaps in original protocol – Quality of reporting index, representing the percentage of key methodological information reported in the original article's description of the experimental methods, as described in https://osf.io/9rnuj

Randomization – Whether random allocation of units among experimental groups was reported for the original experiment ("yes(experiment)"), for other experiments in the article ("yes(any)") or not reported ("no/not reported").

Blinded conduct of experiment – Whether the experimenter performing the experimental procedures was blinded in any step of the experimental procedures before outcome assessment.

Blinding – Whether blinding for outcome assessment was reported for the selected experiment ("yes(experiment)"), for other experiments in the article ("yes(any)") or not ("no/not reported"). When outcome assessment for the selected experiment was automated and blinding was not applicable, this was filled as "automated (experiment)".

Sample size calculation – Whether a sample size calculation was reported for the selected experiment ("yes(experiment)"), for other experiments in the article ("yes(any)") or not ("no/not reported").

Inclusion/exclusion criteria – Whether inclusion/exclusion criteria or exclusion of specific experimental units was reported for the selected experiment ("yes(experiment)"), for other experiments in the article ("yes(any)") or not ("no/not reported").

Year of online publication – Year of online publication of the original article.

Journal – Journal of publication of the original article.

Journal Area – Area(s) of the Journal in the 2020 Journal Citation Reports

Number of citations (first 2 years) – Citations received by the article (as registered by the Web of Science) in the year of publication and 2 subsequent years.

Normalized impact factor – Impact factor of the journal in the year of publication (as extracted from the Journal Citation Report of that year) divided by the median impact factor for the field. If the journal belongs to multiple fields, the mean of the median impact factors of these fields was used. Not available for journals not mentioned in the JCR.

Last authors' academic age – Number of years since first publication in the Web of Science for the last author in the author list.

Number of papers 5 years before publishing the article – Number of articles by the last author in the year of publication of the article and in the 5 previous years, as extracted from the Web of Science.

Institution of the last author – Institution of affiliation of the last author in the author list.

Position in the Folha Ranking (current) – Position of the institution in the 2019 Folha University Ranking (https://ruf.folha.uol.com.br/2019/).

Geographical Region – Geographical Region of Brazil in which the institution is located (N, NE, S, SE, CE).

Institution type – Type of institution (i.e. public university, private university, research institute).

Extracted Data from Original Experiments.xslx – Contains numerical data from the original experiment.

Variables

Prediction Markets ID – Study number as included in the Brazilian Reproducibility Initiative prediction survey and markets.

EXP – Experiment code in the Brazilian Reproducibility Initiative

Selected Figure/Table – Describes the figure or table containing the experiment selected for replication and the groups being compared in the selected comparison.

Original Article DOI – DOI of the original article from which the experiment was selected

Method – Experimental method (MTT, PCR or EPM)

Statistical Test – Statistical test used in the original article, as described in the methods or figure legend.

Data Processing – Contains any explanations available in the original article on how the primary outcome was calculated from the experimental measurements obtained, as interpreted by the Initiative's coordinating team.

Original p-value – P value of the original comparison, as mentioned in the original article.

Control Mean – Mean of the control group, as extracted from text, figure or table.

Treated Mean – Mean of the treated group, as extracted from text, figure or table.

Error Type – Nature of the error bar in the figure, or number after ± in text or table (SEM or SD)

Control Error – Value of the control group error measure in the figure (whether SEM or SD). If 0, paired normalization was inferred.

Treated Error – Value of the treated group error measure in the figure (whether SEM or SD)

Reported Control Sample Size – Sample size of the control group as described in the original article. If no exact sample size was provided, filled as NA.

Reported Treated Sample Size – Sample size of the control group as described in the original article. If no exact sample size was provided, filled as NA.

Sample size (range for both groups) – Sample size of the groups when this was mentioned as a range covering multiple groups. When exact sample size was provided for each group, filled as NA.

Assumed Control Sample Size – Sample size for the control group assumed to estimate SDs for power calculations (corresponding to the upper bound of ranges).

Assumed Treated Sample Size – Sample size for the treated group assumed to estimate SDs for power calculations (corresponding to the upper bound of ranges).

Control Sample Size for DFs – Sample size for the control group assumed to estimate SDs and degrees of freedoms for determining confidence intervals and coefficients of variation for the analyses of replications (corresponding to the midpoint of ranges).

Treated Sample Size for DFs – Sample size for the control group assumed to estimate SDs and degrees of freedoms for determining confidence intervals and coefficients of variation for the analyses of replications (corresponding to the midpoint of ranges).

SD Estimate – Data on the basis of which the standard deviation was calculated (reported SD, reported SEM and N or reported SEM and range for N – in the latter case, the SD estimate is based on an assumption about the sample size and may be overestimated).

Assumed Test for Sample Size Calculation – Test used as the basis for sample size calculation (Two-sample t test with unequal variances or One-sample t test)

Estimated Sample Size for 95% Power – Sample size needed to achieve 95% power according to the power calculation

Sample Size for Replication – Sample size calculated to achieve desired power in each individual replication

Replication-criteria-dict.xlsx – Contains short and long names for variables used to define replication success, to be used in figures and tables generated by code.

Variables

Metric – Variable name as used in the code.

MetricLongName – Long description for variable.

Metric ShortName – Short description of variable.

<u>Subjective assessment of reproducibility</u> – Contains answers from the second debriefing questionnaire, compiled by Google Forms and concerning subjective judgments of results reproducibility (see https://osf.io/xgth2 and https://osf.io/xue5k). Both the form and answers were in Portuguese.

Variables

Código do Laboratório – Lab code.

Código do Experimento – Experiment code.

Na opinião do laboratório, os resultados do experimento original foram replicados com sucesso? – Whether the lab feels the original experimental results were successfully replicated. "Sim" means "Yes", "Não" means "No".

Justificativa: Sucesso – Justification for the previous response (in Portuguese).

Justificativa: Email – Additional justification provided by e-mail for the response about replication success. Labs for which justification did not seem to match the answer (implying that the question may have been misunderstood) were contacted by e-mail to confirm their responses).

Caso tenha considerado que o resultado original não foi replicado com sucesso, quais vocês julgam ser os motivos mais prováveis para essa falha de replicação? – Most likely reasons for replication failure, if the lab considered the original were not successfully replicated (in Portuguese).

Na opinião do laboratório, quão relevantes foram as diferenças e adaptações entre o protocolo do experimento original e o da replicação? – How relevant were the differences between the original protocol and the replication protocol in the lab's opinion (on a scale of 1 to 5).

Justificativa: Diferenças – Justification for the previous response (in Portuguese).

Authorship_list.xslx

Variable

lab – LAB code

author – Name of the author

authorship_protocol_design – Experiments in which the author was involved in protocol design.

authorship_data_collection – Experiments in which the author was involved in data collection

affiliation – Author affiliation

orcid – ORCiD of the author.

lattes – Link to author profile in CV Lattes (Brazil's national academic CV system).

conflicts_of_interest – Whether the author reported conflicts of interest.

highest_degree – Highest academic degree received by the author ("Ensino Médio", high school, "Graduação", undergraduate degree, "Mestrado", MsC, "Doutorado", PhD).

highest_degree_year_conclusion – Year in which the abovementioned degree was received.

h_index – h index of the author (in May-December 2024) according to the Web of Science (or Scopus if no profile in the Web of Science was found.

n_papers – Number of articles published by the author in May-June 2024 according to the Web of Science (or Scopus if no profile in the Web of Science was found.

n_citations – Number of citations received by the author in May-June 2024 according to the Web of Science (or Scopus if no profile in the Web of Science was found.

year_first_paper – Year of first publication by the author in May-June 2024 according to the Web of Science (or Scopus if no profile in the Web of Science was found.

acronym – Acronym for the university/institution in which the lab was located.

geographic_region – Brazilian geographic region of the institution ("Sul", South, "Sudeste", Southeast, "Centro-Oeste", Central-West, "Nordeste", Northeast, "Norte", North).

ruf2023 – Folha University Ranking (https://ruf.folha.uol.com.br/) for the university (filled as "NA" for labs located in non-university institutions).

font_wos – Author profile in the Web of Science. Filled with NA if no profile was found.

algorithm – Whether researcher profile in the Web of Science was algorithmically generated ("Yes") or manually claimed ("No").

Intermediate_steps.xlsx – contains data on labs that registered for participation, were included in the project and contributed data. These data are in different tabs of the spreadsheet.

"Registered" Tab – includes all registrations to participate in the project.

Variables

author – Person who registered the lab in the Initiative (usually the lab coordinator).

state – Brazilian state in which the lab is located.

geographic_region – Brazilian geographic region in which the lab is located ("Sul", South, "Sudeste", Southeast, "Centro-Oeste", Central-West, "Nordeste", Northeast, "Norte", North).

"Included" Tab – includes all labs that had protocols assigned to them.

Variables

lab – Lab code.

author – Person who registered the lab in the Initiative (usually the lab coordinator).

state – Brazilian state in which the lab is located.

geographic_region – Brazilian geographic region in which the lab is located ("Sul", South, "Sudeste", Southeast, "Centro-Oeste", Central-West, "Nordeste", Northeast, "Norte", North).

"Concluded" Tab – includes all labs that contributed at least one data point to the project.

Variables

lab – Lab code.

author – Person who registered the lab in the Initiative (usually the lab coordinator).

state – Brazilian state in which the lab is located.

geographic_region – Brazilian geographic region in which the lab is located ("Sul", South, "Sudeste", Southeast, "Centro-Oeste", Central-West, "Nordeste", Northeast, "Norte", North).

Coordinating team assessment of difficulties.xlsx – contains assessment of the relative importance of project difficulties/challenges by the coordinating team. Originally filled in Portuguese, translated English version available at https://osf.io/q76vj.

Variables

Categoria – General category of the project difficulty/challenge.

Dificuldade – Project difficulty/challenge being rated.

Exemplo/explicação – Explanation of the project difficulty, eventually including specific examples.

Nota Bruna – Rating of the difficulty/challenge's impact on the project (on a scale of 1 to 10) by rater #1 (Bruna Valério Gomes).

Nota Clarissa – Rating of the difficulty/challenge's impact on the project (on a scale of 1 to 10) by rater #2 (Clarissa Carneiro).

Nota Kleber – Rating of the difficulty/challenge's impact on the project (on a scale of 1 to 10) by rater #3 (Kleber Neves).

Nota Mari – Rating of the difficulty/challenge's impact on the project (on a scale of 1 to 10) by rater #4 (Mariana Abreu).

Nota Olavo – Rating of the difficulty/challenge's impact on the project (on a scale of 1 to 10) by rater #5 (Olavo Amaral).

Nota Pedro – Rating of the difficulty/challenge's impact on the project (on a scale of 1 to 10) by rater #6 (Pedro Tan).

Soma_um – Sum of ratings for the difficulty/challenge's impact of the project for the six raters.

Nota Bruna – Rating of the difficulty/challenge's priority for discussion in a publication (on a scale of 1 to 10) by rater #1 (Bruna Valério Gomes).

Nota Clarissa – Rating of the difficulty/challenge's priority for discussion in a publication (on a scale of 1 to 10) by rater #2 (Clarissa Carneiro).

Nota Kleber – Rating of the difficulty/challenge's priority for discussion in a publication (on a scale of 1 to 10) by rater #3 (Kleber Neves).

Nota Mari – Rating of the difficulty/challenge's priority for discussion in a publication (on a scale of 1 to 10) by rater #4 (Mariana Abreu).

Nota Olavo – Rating of the difficulty/challenge's priority for discussion in a publication (on a scale of 1 to 10) by rater #5 (Olavo Amaral).

Nota Pedro – Rating of the difficulty/challenge's priority for discussion in a publication (on a scale of 1 to 10) by rater #6 (Pedro Tan).

Soma_dois – Sum of ratings for the difficulty/challenge's priority for discussion in a publication for the six raters.

Manuscript Figure Correspondence.xlsx – contains the correspondence between figures and tables generated by the code and their numbering in the manuscript, in order to generate the _manuscript_figures_and_tables folder in the output.

Variables

type – states whether item is a table or figure.

manuscript_name – number of the table or figure in the manuscript.

code_generated_filename – file in the output corresponding to the table/figure number.

observations – marks figures that are not generated by code or are generated by a separate script.

Pred_data_survey.csv – Contains summarized data from each experiment extracted from the prediction survey for use in the predictor analysis. Primary data for the survey at the individual participant level is available at https://doi.org/10.7910/DVN/2RLSMG.

Variables

EXP – Experiment code in the Brazilian Reproducibility Initiative

Survey – Replication – Mean predicted probability of replication success for the experiment (expressed as percentage)

Survey – Effect size – Mean predicted effect size for the replication (expressed as percentage of the original)

Survey – Challenge – Mean score attributed to how technically challenging the replication experiment will be (on a scale of 0 to 100, obtained from a Likert scale varying from "Very simple" to "Very challenging").

Other_data/self-assessment folder

Avaliação_subjetiva_final.xlsx - contains the same data as "Subjective assessment of reproducibility.xlsx", with responses to the survey distributed as Step 2 of debriefing (see https://osf.io/xgth2), with the addition of the tabs "**Taxonomia**" (describing the taxonomy used to categorize justifications for reproducibility assessment), **"Classificações"** (containing classified answers by individual rates) and **"resolvidas"** with resolved discrepancies. Only the variables in the latter tab (which are the ones used in the analysis) will be described here. Both the form and answers were in Portuguese.

Variables

Código do Laboratório – Lab code.

Código do Experimento – Experiment code.

replicou – Answer to the question "Were the results of the original experiment successfully replicated?". Only two options were available: 'Sim' (Yes) and 'Nao' (No).

Justificativa – Answer to the question "Explain the aspects considered in your reasoning to define whether the replication was successful or not". This was a free text response and was later codified into categories (see 'Categoria1:3').

Justificativa-email – In a few cases, the answer given in the previous question was unclear or referring to the replication of methods instead of results, as was expected. These labs were contacted by e-mail to amend their responses, which are included within this column.

Avaliador(1:2) – Identification of the coordinating team members who coded the responses given in 'Justificativa' and 'Justificativa-email'.

Categoria(1:3) – Up to 3 categories were selected for each response, included within these 3 columns. The order of the categories are arbitrary and do not reflect the original text. A detailed description of each category is given in sheet 'Taxonomia' of the same file.

Observações – Free text field for general observations from the coding procedure.

Dificuldades Experimentais (Responses) - manual edit.xlsx – contains the responses to the survey distributed as Step 3 of debriefing (see https://osf.io/xgth2) and categorization of relevant text fields. Both the form and answers were in Portuguese.

Variables

Quem está preenchendo o formulário? – Identification of the person(s) filling in the survey.

LAB – Lab code

EXP – Experiment code

score_agree – Answer to the question "Does the laboratory agree with the score given by the validation committee to the protocol deviations?". Only two options were available: 'Sim' (Yes) and 'Nao' (No).

Caso não concorde, justifique sua resposta – Answer to the question "If you don't agree, justify your answer". This was a free text response and was not categorized for analysis.

decision_agree - Answer to the question "Does the laboratory agree with the validation committee's decision on the inclusion/exclusion of the experiment?". Only two options were available: 'Sim' (Yes) and 'Nao' (No).

Quais as principais razões para os desvios encontrados no protocolo? - Answer to the question "What are the main reasons for the deviations found in the protocol?". This was a free text response and was later codified into categories (see 'reasons_cat').

reasons_cat – Categorization of the responses given to the question "What are the main reasons for the deviations found in the protocol?". Each category is identified by a number alone or a combination of number and letter, separated by a semi-colon within each cell. Categories are detailed at https://osf.io/5gjb7.

6_outros – In case the category 'other' was used, this column includes a summarized description of the reason given for the protocol deviations.

preventable - Answer to the question "Could some of these deviations have been prevented?". Only two options were available: 'Sim' (Yes) and 'Nao' (No).

preventable_how - Answer to the question "If so, explain how.", referring to the previous question. This was a free text response and was not categorized for analysis.

would_change - Answer to the question "If you were to carry out this replication experiment again, would you change anything about the protocol that was pre-registered?". Only two options were available: 'Sim' (Yes) and 'Nao' (No).

change_what - Answer to the question "If so, what?", referring to the previous question. This was a free text response and was not categorized for analysis.

Observações adicionais - Free text space for additional comments that had not been addressed in previous questions. These responses were not categorized for analysis.

Avaliação Geral Individual (Responses) - manual edit.xlsx – contains the responses to the project evaluation survey (see https://osf.io/nfr6y) and categorization of relevant text fields.

Variables

Timestamp – Original timestamp of survey submission.

ID – Unique numeric identifier randomly assigned to each response to allow for intra-responder analysis.

Qual o seu cargo/função no laboratório durante a realização do projeto? - Answer to the question "What is your position/function in the laboratory during the project?". Response options were: undergraduate student ('Aluno de Iniciação Científica'), MSc student ('Mestrando'), PhD student ('Doutorando'), postdoc ('Pós-doutorando'), professor/researcher ('Professor / Pesquisador'), lab technician ('Técnico de Laboratório'), other (in which case they were asked to describe their position/function).

Qual a sua avaliação sobre a experiência da Iniciativa Brasileira de Reprodutibilidade? - Answer to the question "What is your assessment of the experience of the Brazilian

Reproducibility Initiative?". Response options were integers between 1 ('very negative') to 5 ('very positive').

Como você avalia seu entendimento sobre os objetivos e metodologia do projeto como um todo? - Answer to the question "How do you assess your understanding of the project's objectives and methodology as a whole?". Response options were integers between 1 ('none') to 5 ('complete').

Como você avalia o engajamento do seu laboratório nas tarefas que lhe foram designadas? - Answer to the question "How do you rate your laboratory's engagement in the tasks assigned to it?". Response options were integers between 1 ('low') to 5 ('high').

Como você avalia o engajamento do seu laboratório no projeto, para além das tarefas específicas que foram designadas? - Answer to the question "How do you assess your lab's engagement in the project, beyond the specific tasks that were assigned?". Response options were integers between 1 ('low') to 5 ('high').

Qual foi a sua participação individual no projeto? - Answer to the question "What was your individual participation in the project?". Respondents could select multiple options from: preparing protocols ('Elaboração de protocolos'), carrying out experiments ('Realização de experimentos'), data analysis ('Análise de dados'), filling out forms ('Preenchimento de formulários'), communicating with the organizing committee ('Comunicação com a comissão organizadora'), other (in which case they were asked to name the activity).

Qual a sua avaliação sobre o seu engajamento individual com o projeto? - Answer to the question "What is your assessment of your individual engagement with the project?". Response options were integers between 1 ('low') to 5 ('high').

De que outras atividades da Iniciativa você participou durante a realização do projeto? - Answer to the question "What other activities of the Initiative did you participate in while carrying out the project?". Respondents could select multiple options from: General meetings ('Reuniões gerais'), Webinars ('Webinários'), Laboratory meetings with the organizing committee ('euniões do laboratório com a comissão organizadora'), Validation committee ('Comissão de validação'), Spin-off projects ('Projetos spin-off'), other (in which case they were asked to name the activity).

Qual a sua avaliação sobre o trabalho da equipe coordenadora da Iniciativa em relação a: [Apresentação do projeto] – Answer to the question "What is your assessment of the job done by the Initiative's coordinating team concerning: (a) presentation of the project". Response options were integers between 1 ('very negative') to 5 ('very positive').

Qual a sua avaliação sobre o trabalho da equipe coordenadora da Iniciativa em relação a: [Agilidade na comunicação] - Answer to the question "What is your assessment of the job done by the Initiative's coordinating team concerning: (b) agility in communication". Response options were integers between 1 ('very negative') to 5 ('very positive').

Qual a sua avaliação sobre o trabalho da equipe coordenadora da Iniciativa em relação a: [Clareza nas orientações] - Answer to the question "What is your assessment

of the job done by the Initiative's coordinating team concerning: (c) clarity of guidelines". Response options were integers between 1 ('very negative') to 5 ('very positive').

Qual a sua avaliação sobre o trabalho da equipe coordenadora da Iniciativa em relação a: [Material de apoio disponibilizado] - Answer to the question "What is your assessment of the job done by the Initiative's coordinating team concerning: (d) supporting material". Response options were integers between 1 ('very negative') to 5 ('very positive').

Qual a sua avaliação sobre o trabalho da equipe coordenadora da Iniciativa em relação a: [Disponibilidade para auxílio aos laboratórios] - Answer to the question "What is your assessment of the job done by the Initiative's coordinating team concerning: (e) availability in assisting laboratories". Response options were integers between 1 ('very negative') to 5 ('very positive').

Qual a sua avaliação sobre o trabalho da equipe coordenadora da Iniciativa em relação a: [Transparência nas decisões tomadas] - Answer to the question "What is your assessment of the job done by the Initiative's coordinating team concerning: (f) transparency in decisions". Response options were integers between 1 ('very negative') to 5 ('very positive').

Como você avalia a carga de trabalho do projeto em relação à sua expectativa inicial? - Answer to the question "How do you assess the project workload compared to your initial expectation?". Response options were integers between 1 ('Well below expectation') to 5 ('Well above expectation').

Quais os principais aprendizados obtidos por você com o projeto? - Answer to the question "What are the main lessons learned from the project?". This was a free text response and was later codified into categories (see 'Aprendizados_cat').

Aprendizados-cat - Categorization of the responses given to the question "What are the main lessons learned from the project?". Each category is identified by a number alone or a combination of number and letter, separated by a semi-colon within each cell. Explanation of categories are detailed at https://osf.io/5gjb7.

Aprendizados-cat-outros - In case the category 'other' was used, this column includes a summarized description of the reason given for the protocol deviations.

Quais as principais dificuldades encontradas pelo laboratório ao longo do projeto? - Answer to the question "What are the main difficulties found by the laboratory throughout the project?". This was a free text response and was later codified into categories (see 'Dificuldades_cat').

Dificuldades-cat - Categorization of the responses given to the question "What are the main difficulties found by the laboratory throughout the project?". Each category is identified by a number alone or a combination of number and letter, separated by a semi-colon within each cell. Explanation of categories are detailed at **https://osf.io/5gjb7**.

Dificuldades-cat-outros - In case the category 'other' was used, this column includes a summarized description of the reason given for the protocol deviations.

Você acha que algo deveria ter sido feito de forma diferente na organização do projeto pela comissão organizadora? Se sim, o quê? - Answer to the question "Do you think

anything should have been done differently in the organization of the project by the organizing committee? If so, what?". This was a free text response and was not categorized for analysis.

Você acha que algo deveria ter sido feito de forma diferente por seu laboratório em sua participação no projeto? Se sim, o quê? - Answer to the question "Do you think anything should have been done differently by your lab in its participation in the project? If so, what?". This was a free text response and was not categorized for analysis.

Você estaria disponível para uma entrevista de 15-20 minutos com a equipe coordenadora para coletar suas impressões sobre o processo da Iniciativa? - Answer to the question "Would you be available for a 15 to 20-minute interview with the coordinating team to gather your impressions of the Initiative process?". Only two options were available: 'Sim' (Yes) and 'Nao' (No). Descriptions of the follow up interviews are available at https://osf.io/nfr6y.

other-data/survey-data folder

BRI Study number and experimental code correspondence.csv - links study numbers used in the survey of beliefs (1-20 for each technique) with experimental codes used in the rest of the BRI. It also contains the study DOI.

Variables

Code – Experiment code in the Brazilian Reproducibility Initiative.

Technique – Experimental method.

Study – Experiment code in the prediction survey.

DOI – DOI for the article from which the experiment originated.

BRI_summarized_surveys_combined.csv – Contains the same data for the prediction survey present in Pred_Data_Survey.csv, with some additional information, and is used to generate figures of survey results. Primary data for the survey at the individual participant level is available at https://doi.org/10.7910/DVN/2RLSMG.

Technique – Experimental method

Study – Study code in the survey.

Code – BRI experiment code.

Replication_probability – Mean predicted probability of replication success for the experiment (expressed as percentage).

Replication_rel_effect_size – Mean predicted effect size for the replication (expressed as percentage of the original).

Difficulty – Mean score attributed to how technically challenging the replication experiment will be (on a scale of 0 to 100, obtained from a Likert scale varying from "Very simple" to "Very challenging").

DOI – Study DOI.

2. Intermediate datasets (generated by code based on primary data)

Other-data folder

Original Experiments Statistical Summaries.tsv – Contains the same primary data from the original experiments as "Extracted data from original experiments", along with additional calculated variables (generated by code based on the original variables and used to analyze replication success).

Additional calculated variables

Control SD – Standard deviation of the control group to be used for the analysis when calculating confidence intervals and coefficients of variation. Based on the average estimate of sample size (Control Sample Size for DFs) when SEM and a range for sample size are provided.

Treated SD – Standard deviation of the treated group to be used for the analysis when calculating confidence intervals and coefficients of variation. Based on the average estimate of sample size (Control Sample Size for DFs) when SEM and a range for sample size are provided.

Delta – Difference between the means of both groups.

Pooled SD – Pooled standard deviation for both groups.

Treated Mean (Relative to Control) – Mean of the treated group expressed as percentage of the control group mean.

Delta (Relative to Control) – Difference between groups expressed as percentage of the control group mean.

Control SD (Relative to Control) – Standard deviation of the control group expressed as percentage of the control group mean.

Treated SD (Relative to Control) – Standard deviation of the treated group expressed as percentage of the control group mean.

Pooled SD (Relative to Control) – Pooled standard deviation expressed as percentage of the control group mean.

degrees_of_freedom – Degrees of freedom used for analysis of the individual experiment using the t distribiution. Calculated on the basis of standard deviations and sample sizes for each group, as described in https://psyteachr.github.io/handyworkbook/between-subjects-welchs-t-test.html.

output folder

Replication Rate Aggregate.tsv and **Replication Rate Aggregate – without Method.tsv** – Contain a summary of replication rates using multiple inclusion sets, criteria and analysis methods. "Replication Rate Aggregate" also provides results broken down by method, while the "-without Method" file only provides aggregate results for all methods. These tables are used to generate specification curves.

Variables

Inclusion_Set – The set of experiments used for analysis.

Level – Whether the analysis refers to the aggregate of replications for each experiment (set of replications) or to individual replications.

MA_Dist – Distribution used for analysis (z, t (using the number of experimental units) or knha (a t distribution using the Knapp-Hartung approach to calculate degrees of freedom).

Metric – Criterion used to assess replication success.

MetricShortName – Textual description of the criterion.

IsPercentage – A check to assess that all rates in fact represent percentages.

Method – The method to which the replication rate refers to. "ALL_PCR" refers to all experiments with PCR ones aggregated in log scale, while "ALL_ALTPCR" refers to all experiments with PCR ones aggregated in linear scale.

Value – Replication rate for the particular set of experiments, analysis method, criterion and method.

N – Total number of experiments/replications analyzed for the particular set of experiments, analysis method, criterion and method.

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Successful – Absolute number of successful experiments - for the particular set of experiments, analysis method, criterion and method.

Experiment Numbers Overview – wide.tsv – Contains the total number of experiments that were planned, completed and validated, along with reasons for lack of completion or validation.

Variables

Status – Whether the row refer to the number of planned experiments, those that were done or those that were not done.

Validation – Validation status of performed experimetns.

Reason – Reason for lack of completion or validation of experiments.

n – Number of experiments in that particular category.

output subfolders

Replication Assessment by Experiment.tsv – Contains numerical data from the aggregate replications of each experiment. Data included in this table is contingent to the specific set of replications being analyzed (as defined by the "inclusion_sets" spreadsheet).

Variables

EXP – Experiment code. PCR has results for PCR experiments analyzed by aggregating log-scale relative expression values (e.g. ΔCT), while ALTPCR has results for the same experiments analyzed by aggregating linearized values (e.g. $2^{-\Delta\Delta CT}$).

original_es – Original effect size (expressed as the natural logarithm of the ratio between treated and control means)

original_ci_lower – Lower bound of the 95% confidence interval of the original effect size.

original_ci_upper – Upper bound of the 95% confidence interval of the original effect size.

n_completed_reps – Number of completed replications with n > 1 in the analysis set that generated the spreadsheet.

replication_es – Aggregate replication effect size for the experiment (expressed as the natural logarithm of the ratio between treated and control means). Corresponds to the random-effects meta-analysis estimate (rema_es) when more than one replication is available, or to the effect size of a single experiment when only one is available.

rema_es – Effect size estimate from a random-effects meta-analysis of the available replications (expressed as the natural logarithm of the ratio between treated and control means). Only applicable for experiments with multiple replications.

rema_pi_lower – Lower bound of the 95% prediction interval of the effect size estimate from a random-effects meta-analysis of the available replications. Only applicable for experiments with multiple replications.

rema_pi_upper – Upper bound of the 95% prediction interval of the effect size estimate from a random-effects meta-analysis of the available replications. Only applicable for experiments with multiple replications.

rema_pvalue – p value of a significance test (based on the t or z distribution, depending on analysis options) of a random-effects meta-analysis of the available replications. Only applicable for experiments with multiple replications.

rema_I2 – Heterogeneity in a random-effects meta-analysis for the replication, measured as I^2. Only applicable for experiments with multiple replications.

rema_tau2 – Heterogeneity in a random-effects meta-analysis for the replication, measured as τ^2. Only applicable for experiments with multiple replications.

rema_Qp – Cochran's Q in a test for residual heterogeneity (see https://wviechtb.github.io/metafor/reference/rma.uni.html#test-for-residual-heterogeneity).

fema_es – Effect size estimate from a fixed-effects meta-analysis of the available replications (expressed as the natural logarithm of the ratio between treated and control means). Only applicable for experiments with multiple replications.

fema_ci_lower – Lower bound of the 95% confidence interval of the effect size estimate from a fixed-effects meta-analysis of the available replications. Only applicable for experiments with multiple replications.

fema_ci_upper – Upper bound of the 95% confidence interval of the effect size estimate from a fixed-effects meta-analysis of the available replications. Only applicable for experiments with multiple replications.

fema_pvalue – (based on the t or z distribution, depending on analysis options) for the fixed-effect meta-analysis estimate of the available replications. Only applicable for experiments with multiple replications.

t_score_FEMA – t score (i.e. effect estimate divided by the standard error) for the comparison between groups in the fixed-effects meta-analysis. Only applicable for experiments with multiple replications. The sign corresponds to the direction of the original effect: positive t scores indicate effects in the same direction as the original, while negative t scores indicate effects in the opposite direction.

t_score_mean – mean of the t scores for the comparisons between groups in each replication. The sign corresponds to the direction of the original effect: positive t scores indicate effects in the same direction as the original, while negative t scores indicate effects in the opposite direction.

t_score – t score used for the experiment in the predictor analysis, corresponding to t_score_FEMA when a meta-analysis is available, or to the t score of a single replication when only one is available.

corrected_sign_original_es – absolute value of the original effect size (original_es), corresponding to the natural logarithm of the ratio between the higher and lower mean between both groups (and thus always positive).

corrected_sign_replication_es – replication effect size (replication_es), expressed as natural logarithm of the ratio of means, considering the direction of the original effect: effects in the same direction as the original are positive, while effects in the opposite direction are negative.

log_es_ratio – difference between the original (original_es) and replication (replication_es) effect sizes, both expressed as natural logarithms.

es_ratio – exponentiated version of log_es_ratio, corresponding to the ratio between the ratios of means in the original and replication experiments.

original_cv – coefficient of variation in the original experiment, calculated as the pooled SD divided by the mean of both group means.

replication_cv – mean coefficient of variation in the replications for a particular experiment, calculated as the pooled SD divided by the mean of both group means. For PCR experiments, only provides meaningful results for the ALTPCR version, as coefficients

of variation only makes sense for ratio scale variables (which is not the case for ΔCt values).

mean_abs_diff_reps – mean of the absolute differences between the effect sizes of individual replications (in natural logarithmic scale). Represents the mean of 3 pairs when 3 replications are available, a single difference when two are available, and is not applicable when there is only one replication.

mean_abs_diff_reps_orig – mean of the absolute differences between the effect size of each individual replication and the original effect size (in natural logarithmic scale). Is considered not applicable when a single replication is available as it is used for paired comparisons with the mean difference between replications (mean_abs_diff_reps).

significant_reps – Number of replications with p<0.05 in the same direction in a t test between groups (two-sample or one-sample, depending on whether the original was paired).

n_voting_reps – Number of replications with independently valid results (i.e. with a priori power of at least 80% to detect the original difference).

subjective_sucess_reps – Number of replications considered successful by the replicating team.

Replication Assessment by Replication.tsv – Contains numerical data from the individual replications. Data in this table is contingent to the specific set of replications being analyzed (as defined by the "inclusion_sets" spreadsheet).

Variables

LAB – Lab code.

EXP – Experiment code. PCR has results for PCR experiments analyzed by aggregating log-scale relative expression values (e.g. ΔCT), while ALTPCR has results for the same experiments analyzed by aggregating linearized values (e.g. $2^{-\Delta\Delta CT}$).

original_es – Original effect size (expressed as the natural logarithm of the ratio between treated and control means).

original_ci_lower – Lower bound of the 95% confidence interval of the original effect size.

original_ci_upper – Upper bound of the 95% confidence interval of the original effect size.

replication_es – Effect size for the individual replication (expressed as the natural logarithm of the ratio between treated and control means).

ci_lower – Lower bound of the 95% confidence interval of the replication effect size.

ci_upper – Upper bound of the 95% confidence interval of the replication effect size.

log_es_ratio_individual – difference between the original_es and replication_es for the individual replication, both expressed as natural logarithms.

es_ratio_individual – exponentiated version of log_es_ratio_individual, corresponding to the ratio between the ratios of means in the original and replication experiment.

p value – p value of a two-tailed t or z test (depending on analysis options) for the individual replication.

t_score_individual – t score used for the experiment in the predictor analysis. The sign corresponds to the direction of the original effect: positive t scores indicate effects in the same direction as the original, while negative t score indicate effects in the opposite direction.

t_pvalue – p value obtained in a two-sample Welch t test (for non-paired original experiments) or in a one-sample t test (for paired original experiments).

original_cv – coefficient of variation in the original experiment, calculated as the pooled SD divided by the mean of both group means.

replication_cv –coefficient of variation in the replication, calculated as the pooled SD divided by the mean of both group means. For PCR experiments, only provides meaningful results for the ALTPCR version, as coefficients of variation only makes sense for ratio scale variables (which is not the case for ΔCt values).

subjective_success – whether the replication was considered successful (true) or unsuccessful (false) according to the replication team

ma_only – whether the experiment has insufficient sample size and should only count for meta-analysis (true) or should be counted individually (false)

Replication Success by Experiment.tsv – Contains categorical data on replication success for the dichotomous criteria used to evaluate the aggregate of replications for each experiment.

Variables

EXP – Experiment code

REP_Orig_in_REMA_PI – Whether the original effect is within the 95% prediction interval of a random-effects meta-analysis of the replications.

REP_REMA_in_Orig_CI – Whether the aggregate replication effect size is within the 95% confidence interval of the original effect.

REP_FEMA_SSS_Orig – Whether the fixed-effect size meta-analysis of the available replications is significant at p <0.05 in the same direction as the original effect (using a t or z distribution according to the analysis option).

REP_Voting – Whether most (>50%) replications are significant in a two-sample Welch t test (for non-paired original experiments) or in a one-sample t test (for paired original experiments).

REP_Voting_WithTies – Whether at least half of replications are significant in a two-sample Welch t test (for non-paired original experiments) or in a one-sample t test (for paired original experiments).

REP_Subjective – Whether most (>50%) replications were considered successful by the replicating lab.

REP_Subjective_WithTies – Whether at least half of replications were considered successful by the replicating lab.

REP_Most_Criteria – Whether the experiment was successfully replicated by at least half of the preregistered criteria (REP_Orig_in_REMA_PI, REP_REMA_in_Orig_CI, REP_FEMA_SSS_Orig, REP_Voting_WithTies, REP_Subjective_WithTies).

SignalErrorAll – Whether a fixed meta-analysis of the available replications is significant at $p < 0.05$ in the opposite direction as the original effect size.

es_ratio – exponentiated version of log_es_ratio, corresponding to the ratio between the ratios of means in both experiments.

log_es_ratio – difference between original_es and replication_es, both expressed as natural logarithms.

t_score_mean – mean of the t scores for the comparisons between groups in each replication.

t_score_FEMA – t score for the comparison between groups in the fixed-effects meta-analysis. Only applicable for experiments with multiple replications. The sign corresponds to the direction of the original effect: positive t scores indicate effects in the same direction as the original, while negative t score indicate effects in the opposite direction.

t_score – t score used for the predictor analysis, corresponding to t_score_FEMA when a meta-analysis is available, or to the t score of a single replication when only one is available. The sign corresponds to the direction of the original effect: positive t scores indicate effects in the same direction as the original, while negative t score indicate effects in the opposite direction.

OriginalES – Original effect size (expressed as the natural logarithm of the ratio between the higher and lower mean between both groups, and thus always positive). Corresponds to corrected_sign_original_es in the Replication Assessment by Experiment table.

OriginalCV – coefficient of variation in the original experiment.

mean_abs_diff_reps – mean of the absolute differences between the effect sizes of individual replications (in natural logarithmic scale). Represents the mean of 3 pairs when 3 replications is available, a single difference when two are available, and is not applicable when there is only one replication.

mean_abs_diff_reps_orig – mean of the absolute differences between the effect size of each individual replication and the original effect size (in natural logarithmic scale). Is considered not applicable when a single replication is available because it is used for paired comparisons with the mean difference between replications (mean_abs_diff_reps).

Replication Success by Replication.tsv – Contains categorical data on replication success for each dichotomous criteria used for individual replications.

LAB – Lab code.

EXP – Experiment code.

REP_Individual_Rep_in_Orig_CI – Whether the individual replication effect size is within the 95% confidence interval of the original effect.

REP_Individual_SSS – Whether the replication is significant at p <0.05 in the same direction as the original effect (using a t or z test as defined by the analysis option).

REP_Individual_IndivSubjective – Whether the individual replication was considered successful by the replicating lab.

Significant_Individual - Whether the replication is significant at p <0.05, irrespective of direction.

SignalErrorAll_Individual – Whether a replication has a significant effect in the opposite direction as the original (true) or not (false). All replications are applicable.

es_ratio_individual – exponentiated version of log_es_ratio_individual, corresponding to the ratio between the ratios of means in both experiments.

log_es_ratio_individual – difference between the original_es and replication_es, both expressed as natural logarithms.

t_score_individual – t score for the individual replication.

OriginalES_Individual – Original effect size (expressed as the natural logarithm of the ratio between the treated and control means).

OriginalCV_Individual – coefficient of variation in the original experiment.

Replication Rate Summary.tsv – Contains aggregated values for the whole output for the variables in the "Replication Success by Experiment" (first 18 rows) and "Replication Success by Replication" tables (last 10 rows). Cells express fractions or absolute numbers of "TRUE" entries for categorical variables, or mean values for quantitative variables.

Value_ALL_PCR – Rate of "TRUE" (for categorical variables) /mean value (for quantitative variables) for all experiments (using the main PCR analysis with log values).

Value_ALL_ALTPCR – Rate of "TRUE" (for categorical variables) /mean value (for quantitative variables) for all experiments (using the alternative PCR analysis with linearized values).

Value_MTT – Rate of "TRUE" (for categorical variables) /mean value (for quantitative variables) for MTT experiments (first 18 rows)/replications (last 10 rows).

Value_PCR – Rate of "TRUE" (for categorical variables) /mean value (for quantitative variables) for PCR experiments (first 18 rows)/replications (last 10 rows) analyzed with log values.

Value_ALTPCR – Rate of "TRUE" (for categorical variables) /mean value (for quantitative variables) for PCR experiments (first 18 rows)/replications (last 10 rows) analyzed with linearized values.

Value_EPM – Rate of "TRUE" (for categorical variables) /mean value (for quantitative variables) for EPM experiments (first 18 rows)/replications (last 10 rows).

N_ALL_PCR – Total number of experiments (first 18 rows)/replications (last 10 rows).

N_ALL_ALTPCR – Total number of experiments (first 18 rows)/replications (last 10 rows).

N_MTT – Total number of MTT experiments (first 18 rows)/replications (last 10 rows).

N_PCR – Total number of PCR experiments (first 18 rows)/replications (last 10 rows).

N_ALTPCR – Total number of PCR experiments (first 18 rows)/replications (last 10 rows).

N_EPM – Total number of EPM experiments (first 18 rows)/replications (last 10 rows).

successful_ALL_PCR – Total number of successfully replicated experiments (first 18 rows)/replications (last 10 rows) or signal errors, using the main PCR analysis with log values. Not applicable for quantitative variables.

successful_ALL_ALTPCR – Total number of successfully replicated experiments (first 18 rows)/replications (last 10 rows) or signal errors, using the alternative PCR analysis with linearized values. Not applicable for quantitative variables.

successful_MTT – Number of successfully replicated MTT experiments (first 18 rows)/replications (last 10 rows) or signal errors. Not applicable for quantitative variables.

successful_PCR – Number of successfully replicated PCR experiments (first 18 rows)/replications (last 10 rows) or signal errors, using the main PCR analysis with log values. Not applicable for quantitative variables.

successful_ALTPCR – Number of successfully replicated PCR experiments (first 18 rows)/replications (last 10 rows) or signal errors, using the alternative PCR analysis with linearized values. Not applicable for quantitative variables.

successful_EPM – Number of successfully replicated EPM experiments (first 18 rows)/replications (last 10 rows) or signal errors. Not applicable for quantitative variables.

MetricLongName – Long description of the row metric. For metrics with NA, see descriptions in the data dictionary for the "Replication Success" tables.

MetricShortName – Brief description of the row metric. For metrics with NA, see descriptions in the data dictionary for the "Replication Success" tables.