Package: psyinfr (via r-universe)

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Type Package

Title R functions as an infrastructure for psychological research

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`add_jpaQmd` *Add jpaQmd*

Description

Add jpaQmd

Usage

```
add_jpaQmd()
```

Examples

```
# add_jpaQmd()
```

`add_paperQmd` *Add paperQmd*

Description

Add paperQmd

Usage

```
add_paperQmd()
```

Examples

```
# add_paperQmd()
```

print.jatos_data *Print a summary of the object returned by readJatos()*

Description

Print a summary of the object returned by readJatos()

Usage

```
## S3 method for class 'jatos_data'
print(x, ...)
```

Arguments

x	object of class jatos_data
...	ignored

readJatos *Read JATOS/jsPsych results and tidy them for analysis in R*

Description

Reads a JATOS results file (the text file exported from JATOS, in which each line holds the jsPsych data of one component result) collected with cbat4r::jatosify()-style tasks, and reshapes it into analysis-ready data frames.

Three representations are produced:

- trials: one row per jsPsych trial. All scalar trial fields (rt, trial_type, trial_index, time_elapsed, ...) become columns; nested fields (e.g. question_order) are collapsed with sep, and deeper structures are kept as JSON text.
- long: one row per response item (participant x task x trial x item). response objects such as {"mood_1":1,"mood_2":0} are unnested into item/value pairs, with a numeric copy in value_num.
- wide: one row per participant, one column per response item, which is the format usually wanted for statistical analysis.

Besides the line-delimited text export, a whole-file JSON array and the JATOS "JSON with metadata" export are also accepted; in the latter case the surrounding JATOS metadata (worker id, study result id, ...) is carried along in columns prefixed with jatos_.

Usage

```
readJatos(
  file,
  format = c("all", "trials", "long", "wide"),
  id_col = "workerID",
  task_col = "taskName",
  response_col = "response",
  item_cols = character(),
  index_col = NULL,
  extra_cols = character(),
  prefix = c("auto", "always", "never"),
  sep = "|",
  drop_cols = character(),
  encoding = "UTF-8"
)
```

Arguments

file	Path to a JATOS results file (e.g. "jatos_results_data_20260809054431.txt").
format	One of "all" (default, returns a list of the three data frames), "trials", "long" or "wide" (returns that data frame only).
id_col	Name of the trial field identifying a participant. Default "workerID". If absent, JATOS metadata or the result number is used.
task_col	Name of the trial field identifying a task/component. Default "taskName". If absent, the result number is used.
response_col	Name of the trial field holding the response. Default "response".
item_cols	Character vector of further trial fields to treat as response items, in addition to response_col. Useful for tasks that store their answers in custom fields, e.g. item_cols = c("aspect_text", "selected_adjectives"). Each field becomes an item named after the field.
index_col	Name of a trial field that numbers repeated items (e.g. "aspect_number"). When given, long gets an index column and the wide columns are suffixed with it (aspect_text_1, aspect_text_2, ...). If an indexed item occurs more than once for a participant, the last value is kept (it reflects corrections made by going back).
extra_cols	Character vector of trial columns to carry into wide (one value per participant, the first non-missing one). For instance extra_cols = "id" picks up a completion code stored in the trial.
prefix	How to name the columns of wide: "auto" (default) prefixes the task name only when an item name is ambiguous (used by more than one task, or named like response_col), "always" always prefixes, "never" never does.
sep	Separator used when collapsing a vector-valued field into one string. Default "|".
drop_cols	Trial columns to drop from trials; nothing is dropped by default. Set e.g. drop_cols = "stimulus" to discard long HTML strings.
encoding	Encoding of file. Default "UTF-8".

Value

A list of data frames (`trials`, `long`, `wide`) of class `jatos_data`, or a single data frame if `format` is not `"all"`.

Examples

```
# d <- readJatos("jatos_results_data_20260809054431.txt")
# head(d$wide)
# readJatos("jatos_results_data_20260809054431.txt",
#           format = "wide", extra_cols = "id")
# # a task storing answers in custom fields, one set per aspect
# readJatos("jatos_results_data_20261008071223.txt",
#           item_cols = c("aspect_text", "selected_adjectives"),
#           index_col = "aspect_number",
#           extra_cols = c("id", "completion_type"))
```

---

render_elnjp_pdf *render function for Japanese e-labnotebook in PDF*

Description

render function for Japanese e-labnotebook in PDF

Usage

```
render_elnjp_pdf(Rmd_file)
```

Arguments

`Rmd_file`	file name of R Markdown file

---

render_manuscript *Render a Quarto Manuscripts project into all of its formats*

Description

Runs `quarto render` in the manuscript project, which produces the website (`_manuscript/index.html`) **and** the PDF (`_manuscript/paper.pdf`).

The Render button of RStudio runs `quarto preview`, and a preview renders only the first format of the project (the website), leaving the PDF to be built when its download link is clicked. Use this function when the PDF should be built every time.

When the render succeeds, `_manuscript/index.html` is opened in the browser.

Usage

```
render_manuscript(project_dir = ".", preview = FALSE, open = TRUE)
```

Arguments

project_dir	Directory of the manuscript project (the folder holding _quarto.yml). Default ".".
preview	If TRUE, quarto preview --render all is run instead, so that all formats are rendered and the preview server is started. Default FALSE.
open	If TRUE (default), _manuscript/index.html is opened in the browser after a successful render. Ignored when preview = TRUE, because the preview server opens a browser by itself.

Value

The exit status of the quarto command, invisibly.

Examples

```
# render_manuscript()
# render_manuscript("manuscript")
```

---

researchIn *start research with new Japanese e-labnotebook*

Description

start research with new Japanese e-labnotebook

Usage

```
researchIn(rc = TRUE)
```

Arguments

rc	If you are using Research Compendium of senshuRmd, you can create a e-labnotebook file in the "labnote" directory from the current directory. In that case, please set rc to TURE.

Examples

```
# researchIn()
```

researchOut *upload Japanese e-labnotebook to GitHub*

Description

upload Japanese e-labnotebook to GitHub

Usage

```
researchOut(rc = TRUE)
```

Arguments

rc	If you are using Research Compendium of senshuRmd, you can create a e-labnotebook file in the "labnote" directory from the current directory. In that case, please set rc to TURE.

Examples

```
# researchOut()
```

runHighLoad *run high load computing and psuh to GitHub*

Description

run high load computing and psuh to GitHub

Usage

```
runHighLoad(r_file)
```

Arguments

r_file	set r file to run

Examples

```
# runHighLoad(r_file)
```

runParallelR *run r files using parallel*

Description

run r files using parallel

Usage

```
runParallelR(r_files)
```

Arguments

r_files	set vector of r files

senshu_thesis *R Markdown output formats Template for thesis at Department of Psychology, Senshu University*

Description

R Markdown output formats Template for thesis at Department of Psychology, Senshu University

Usage

```
senshu_thesis(Rmd_file, Bib_file)
```

Arguments

Rmd_file	file name of R Markdown file
Bib_file	file name of Bib file

`set_manuscript` *Set up a Quarto Manuscripts project with the senshuQmd template*

Description

Creates a Quarto manuscript project (`project: type: manuscript`) whose article is `paper.qmd` taken from the senshuQmd template (https://github.com/ykunisato/senshuQmd), together with two notebooks, `notebooks/Analysis_01.qmd` and `notebooks/Data_collection.qmd`.

The layout created is:

```
<project>/
  _quarto.yml
  paper.qmd            article (senshuQmd template)
  bibliography.bib
  figures/
  _extensions/senshu/  senshu-pdf format
  notebooks/
    Analysis_01.qmd
    Data_collection.qmd
  data/
    jatos_results_data_demo.txt
```

`Data_collection.qmd` holds an example of building an online survey with **cbat4r** (`set_ic()`, `set_qnr()`, `set_cc()`, `jatosify()`) in an R chunk, and `Analysis_01.qmd` an analysis skeleton that reads the demo data in `data/` with `readJatos()`, so that the project renders as it is.

Usage

```
set_manuscript(
  project_name = "manuscript",
  output_dir = ".",
  add_root_dir = TRUE,
  overwrite = FALSE,
  open = rstudioapi::isAvailable(),
  branch = "main"
)
```

Arguments

`project_name`	Name of the manuscript project. Default `"manuscript"`. Used as the folder name when `add_root_dir = TRUE`.
`output_dir`	Where the project is created. Default `"."`.
`add_root_dir`	If `TRUE` (default), a `project_name` folder is created inside `output_dir` and the files are placed there. If `FALSE`, the files are placed directly in `output_dir`.
`overwrite`	If `TRUE`, existing files are overwritten. Default `FALSE`, which stops when `paper.qmd` or `_quarto.yml` already exists.

open	If TRUE (default in RStudio), paper.qmd is opened.
branch	Branch of the senshuQmd repository to download. Default "main".

Value

The path of the created project, invisibly.

Examples

```
# set_manuscript()
# set_manuscript("paper2026", output_dir = "paper")
```

---

set_rc *Research Compendium of Department of Psychology, Senshu University*

Description

Research Compendium of Department of Psychology, Senshu University

Usage

```
set_rc()
```

Examples

```
# set_rc()
```

---

setGitSlack *run high load computing and psuh to GitHub*

Description

run high load computing and psuh to GitHub

Usage

```
setGitSlack(
  git_name,
  git_email,
  slack_token = "FALSE",
  slack_channel = "#general"
)
```

Arguments

git_name	set user name of GitHub
git_email	set e-mail of GitHub
slack_token	set slack API token
slack_channel	set channel name of slack

Examples

```
# setGitSlack(user_name_github, email_github, slack_token, slack_channel, slack_username)
```

---

up2osf *upload Japanese e-labnotebook to OSF*

Description

upload Japanese e-labnotebook to OSF

Usage

```
up2osf(eln_osf = TRUE, rc_osf = TRUE)
```

Arguments

eln_osf	URL of pdf directory in OSF
rc_osf	If you are using Research Compendium of senshuRmd, you can create a e-labnotebook file in the "labnote" directory from the current directory. In that case, please set rc to TURE.

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