

Package ‘IalsaSynthesis’

April 15, 2021

Title Synthesizing Information Across Collaborating Research

Description Synthesizes information across collaborating research. Created specifically for Integrative Analysis of Longitudinal Studies of Aging (IALSA).

Version 0.2.0

URL <https://github.com/IALSA/IalsaSynthesis>, <https://www.maelstrom-research.org/mica/network/ialsa#/>

BugReports <https://github.com/IALSA/IalsaSynthesis/issues>

Depends R(>= 3.0.0)

Imports testit

Suggests devtools,
knitr,
readr,
testthat (>= 2.0)

License GPL-2

Encoding UTF-8

RoxygenNote 7.1.1

Config/testthat/edition 3

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IalsaSynthesis-package

Synthesizing Information Across Collaborating Research

Description

Synthesizing information across collaborating research. Created for **Integrative Analysis of Longitudinal Studies of Aging** (IALSA).

Note

The release version will be available through [CRAN](#). The most recent development version is available through [GitHub](#). Please see the installation examples below.

If you're having trouble with the package, please install the development version. If this doesn't solve your problem, please create a [new issue](#), or email Will or Andrey.

Author(s)

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References

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Examples

```
## Not run:
# Install/update IalsaSynthesis with the release version from CRAN.
install.packages('IalsaSynthesis')

# Install/update IalsaSynthesis with the development version from GitHub
#install.packages('devtools') #Uncomment if `devtools` isn't installed already.
devtools::install_github('IALSA/IalsaSynthesis')

## End(Not run)
```

extract

Extract the values within model output files.

Description

Functions that extract the values within model output files.

Usage

```
extract_scalar_string(regex, source)

extract_scalar_float(regex, source)

extract_named_wald(parameter_name, mplus_output)

extract_output_filename(mplus_output, regex = "\\bDATA:\\s+File = (.+);.*")

extract_free_parameter_count(
  mplus_output,
  regex = "\\bNumber of Free Parameters\\s+(\\d{1,})\\b"
```

```

)

extract_loglikelihood(
  mplus_output,
  regex = "\\bLoglikelihood\\s+H0 Value\\s+([-\\d\\.]+)\\b"
)

extract_scaling_correction(
  mplus_output,
  regex = "\\bH0 Scaling Correction Factor\\s+([-\\d\\.]+)\\s+for MLR\\b"
)

extract_aic(
  mplus_output,
  regex = "\\bAkaike \\(AIC\\)\\s+([-\\d\\.]+)\\b"
)

extract_bic(
  mplus_output,
  regex = "\\bBayesian \\(BIC\\)\\s+([-\\d\\.]+)\\b"
)

extract_bic_adjusted(
  mplus_output,
  regex = "\\bSample-Size Adjusted BIC\\s+([-\\d\\.]+)\\b"
)

```

Arguments

regex	Regular Expression pattern to capture and extract contents.
source	Text to run the regex against.
parameter_name	Variable name in Mplus output to extract.
mplus_output	Text containing model output. This should be the text read from the file (not a file path).

Value

A numeric value corresponding to the desired quantity.

Functions

- `extract_scalar_float`: Generalizable function to return a single numeric value.
- `extract_named_wald`: Determine the estimate, standard error, z-score, and two-tailed p-value of an estimate (ie, the results of a Wald test).
- `extract_output_filename`: Determine the path of the Mplus output file.
- `extract_free_parameter_count`: Determine the number of free parameters for the model estimation.
- `extract_loglikelihood`: Determine the log likelihood for the model estimation.
- `extract_scaling_correction`: Determine the H0 Scaling Correction Factor for the model estimation.
- `extract_aic`: Determine the AIC for the model estimation.

- `extract_bic`: Determine the BIC for the model estimation.
- `extract_bic_adjusted`: Determine the Sample-Size Adjusted BIC for the model estimation.

Author(s)

Will Beasley

Examples

```
library(IalsaSynthesis) #Load the package into the current R session.
```

validate

Functions that check the validity of values throughout the workflow.

Description

These functions help identify mistakes in formatting before the create difficult-to-diagnose problems later.

Usage

```
validate_filename_output(
  filename,
  path,
  file_extension_expected = "out",
  underscore_count_expected = 4L
)
```

Arguments

<code>filename</code>	The name of the file to be validated.
<code>path</code>	The location of the file to be validated.
<code>file_extension_expected</code>	The extension of the file. This defaults to "out", which corresponds to Mplus output.
<code>underscore_count_expected</code>	The number of underscores required in the name (not currently used).

Value

An invisible TRUE value if the filename is valid. Otherwise, an error is thrown.

Author(s)

Will Beasley

Examples

```
library(IalsaSynthesis) #Load the package into the current R session.
## Not run:
path <- "./studies/eas"
good_name <- "u1_male_aehplus_muscle_noCog_hand_noCogSpec.out"
validate_filename_output(good_name, path)

bad_name <- "missing_something.outtttt"
validate_filename_output(bad_name, path)

## End(Not run)
```

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