

# Package ‘IalsaSynthesis’

October 1, 2015

**Title** Synthesizing Information Across Collaborating Research

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

**Version** 0.1.8

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**URL** <https://github.com/IALSA/IalsaSynthesis>, <http://www.ialsa.org/>

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

**Depends** R(>= 3.0.0),  
stats

**Imports** testit

**Suggests** devtools,  
knitr,  
readr,  
testthat (>= 0.9)

**License** GPL-2

**LazyData** TRUE

## R topics documented:

IalsaSynthesis-package . . . . .	2
extract . . . . .	3
validate . . . . .	4

<b>Index</b>	<b>6</b>
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IalsaSynthesis-package

*Synthesizing Information Across Collaborating Research*

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## 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)

**William Howard Beasley** –Assistant Professor of Research, **University of Oklahoma Health Sciences Center**, **Dept of Pediatrics**, Biomedical and Behavioral Methodology Core (**BBMC**)

**Andrey Koval** –Post Doc, **University of Victoria**, **Department of Psychology**

## 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)
```

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extract	<i>Extract the values within model output files.</i>
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## Description

Functions that extract the values within model output files.

## Usage

```
extract_scalar_string(regex, source)

extract_scalar_float(regex, source)

extract_output_filename(mplus_output, regex = ".+DATA: File = (.+);.*")

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

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

extract_scaling_correction(mplus_output,
  regex = "\\s+H0 Scaling Correction Factor\\s+([-\\d\\.]+)\\s+for MLR\\s+")

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

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

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

## Arguments

regex	Regular Expression pattern to capture and extract contents.
source	Text to run the regex against.
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_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.
```

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validate

*Functions that check the validity of values throughout the workflow.*

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## 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)
```

# Index

`extract`, [3](#)  
`extract_aic (extract)`, [3](#)  
`extract_bic (extract)`, [3](#)  
`extract_bic_adjusted (extract)`, [3](#)  
`extract_free_parameter_count (extract)`,  
[3](#)  
`extract_loglikelihood (extract)`, [3](#)  
`extract_output_filename (extract)`, [3](#)  
`extract_scalar_float (extract)`, [3](#)  
`extract_scalar_string (extract)`, [3](#)  
`extract_scaling_correction (extract)`, [3](#)  
  
`IalsaSynthesis-package`, [2](#)  
  
`validate`, [4](#)  
`validate_filename_output (validate)`, [4](#)