

Package ‘assertHE’

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Title Visualisation and Verification of Health Economic Decision Models

Version 1.0.0

Description Designed to help health economic modellers when building and reviewing models. The visualisation functions allow users to more easily review the network of functions in a project, and get lay summaries of them. The asserts included are intended to check for common errors, thereby freeing up time for modellers to focus on tests specific to the individual model in development or review. For more details see Smith and colleagues (2024)<[doi:10.12688/wellcomeopenres.23180.1](https://doi.org/10.12688/wellcomeopenres.23180.1)>.

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URL <https://dark-peak-analytics.github.io/assertHE/>,
<https://github.com/dark-peak-analytics/assertHE>

BugReports <https://github.com/dark-peak-analytics/assertHE/issues>

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Author Robert Smith [aut, cre, cph] (<<https://orcid.org/0000-0003-0245-3217>>),
Wael Mohammed [aut] (<<https://orcid.org/0000-0003-0370-4903>>),
Jack Smith [aut],
Oliver Dolin [aut] (<<https://orcid.org/0000-0003-0766-1277>>),
Dark Peak Analytics Ltd [cph, fnd]

Maintainer Robert Smith <rsmith@darkpeakanalytics.com>

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Details

If the input expression `x` is not an atomic value, symbol, or an environment pointer, the function breaks it up into a list of components. It also handles expressions of the form `foo$bar` by splitting them up, keeping only the relevant parts for parsing.

If `x` is a list of expressions, the function recursively parses each expression until they can no longer be listed, filtering out atomic values in the process.

If `x` is not listable (e.g. a function), it is deparsed into a character string.

Value

A character string or a list of parsed components, depending on the input expression.

assertHE_example	<i>Get path to assertHE example</i>
------------------	-------------------------------------

Description

assertHE comes bundled with a number of sample files in its `inst/extdata` directory. This function make them easy to access

Usage

```
assertHE_example(file = NULL)
```

Arguments

`file` Name of file. If NULL, the example files will be listed.

Value

If `file` is NULL, returns a character vector containing the names of all files and directories available in the package's directory (`extdata`). If `file` specifies the name of an existing example file, returns a character vector of length one containing the full path to that file. Stops with an error if the specified file does not exist within the example directory.

Examples

```
assertHE_example()  
assertHE_example("example_scripts/example_tricky_functions.R")
```

check_init	<i>Check and initialize a vector</i>
------------	--------------------------------------

Description

This function checks a given vector for several conditions, including values being within the range 0 to 1 inclusive and the sum of values being equal to 1. If the vector is named, the function checks all elements have names and no names are duplicates.

Usage

```
check_init(x)
```

Arguments

x A numeric vector with named elements.

Value

If successful there is no message, otherwise, it issues warnings with informative messages for each failed condition.

Examples

```
x <- setNames(object = c(0.2, 0.3, 0.4, 0.1), nm = letters[1:4])
check_init(x) # x is a valid input, no warnings issued

x <- setNames(c(0.2, 0.3, 0.4, 0.1), nm = c("H", NA, "NA", "D"))
check_init(x) # Should issue a warning about missing names

x <- c(-2, 0.3, 0.4, 0.1)
check_init(x) # Should issue a warning about a value below 0 and about not summing to 1
```

check_markov_trace	<i>Check Markov Trace</i>
--------------------	---------------------------

Description

This function checks the properties of a markov trace conform to expectations. That it is: numeric, values are between 0 and 1 with all rows summing to 1. Also allows users to check that the dead state is monotonically decreasing (if provided)

Usage

```
check_markov_trace(
  m_TR,
  dead_state = NULL,
  confirm_ok = FALSE,
  stop_if_not = FALSE
)
```

Arguments

m_TR	The markov trace to be checked.
dead_state	character vector length 1 denoting dead state (e.g. "D")
confirm_ok	if OK, return a message confirming all checks passed.
stop_if_not	return error messages. The default (FALSE) returns warnings.

Value

A message indicating whether the matrix passed all the checks or an error message if any check failed.

Examples

```
v_hs_names <- c("H", "S", "D")
n_hs <- length(v_hs_names)
n_t <- 10

m_TR <- matrix(data = NA,
               nrow = n_t,
               ncol = n_hs,
               dimnames = list(NULL, v_hs_names))

m_TR[, "H"] <- seq(1, 0, length.out = n_t)
m_TR[, "S"] <- seq(0, 0.5, length.out = n_t)
m_TR[, "D"] <- 1 - m_TR[, "H"] - m_TR[, "S"]
check_markov_trace(m_TR = m_TR, dead_state = "D", confirm_ok = TRUE)

# the following results in an error because the trace has infeasible values
m_TR[10, "D"] <- 0
m_TR[9, "S"] <- 1
try(check_markov_trace(m_TR = m_TR, stop_if_not = TRUE, dead_state = "D", confirm_ok = TRUE))
```

Description

This function checks the properties of a transition probability array with 2 or three dimensions conform to standard expectations. That it is that each slice is: square, numeric, values are between 0 and 1 with all rows summing to 1. If a dead state is provided, it checks that the dead state -> dead state probability in each slice is equal to 1.

Usage

```
check_trans_prob_array(a_P, dead_state = NULL, stop_if_not = FALSE)
```

Arguments

`a_P` The transition probability array to be checked.
`dead_state` character vector length 1 denoting dead state (e.g. "D")
`stop_if_not` return error messages. The default (FALSE) returns warnings.

Value

A message indicating whether the array passed all the checks or a warning/error message if any check failed.

Examples

```
v_hs_names <- c("H", "S", "D")
n_hs <- length(v_hs_names)
a_P <- array(
  data = 0,
  dim = c(n_hs, n_hs, 1000),
  dimnames = list(v_hs_names, v_hs_names, 1:1000)
)
a_P["H", "S", ] <- 0.3
a_P["H", "D", ] <- 0.01
a_P["S", "D", ] <- 0.1
a_P["S", "H", ] <- 0.5

for(x in 1:1000){
  diag(a_P[, ,x]) <- 1 - rowSums(a_P[, ,x])
}

check_trans_prob_array(a_P = a_P, stop_if_not = FALSE)
# introduce error
a_P["H", "S", 1:10] <- 0

try(check_trans_prob_array(a_P = a_P, stop_if_not = FALSE))
```

check_trans_prob_mat *Check Transition Probability Matrix*

Description

This function checks the properties of a transition probability matrix conform to standard expectations. That it is: square, numeric, values are between 0 and 1 with all rows summing to 1. If a dead state is provided, it checks that the dead state -> dead state probability is 1.

Usage

```
check_trans_prob_mat(
  m_P,
  dead_state = NULL,
  confirm_ok = FALSE,
  stop_if_not = FALSE
)
```

Arguments

m_P	The transition probability matrix to be checked.
dead_state	character vector length 1 denoting dead state (e.g. "D")
confirm_ok	if OK, return a message confirming all checks passed.
stop_if_not	return error messages. The default (FALSE) returns warnings.

Value

A message indicating whether the matrix passed all the checks or a warning/error message if any check failed.

Examples

```
v_hs_names <- c("H", "S", "D")
n_hs <- length(v_hs_names)
m_P <- matrix(data = 0, nrow = n_hs, ncol = n_hs,
              dimnames = list(v_hs_names, v_hs_names))
m_P["H", "S"] <- 0.3
m_P["H", "D"] <- 0.01
m_P["S", "D"] <- 0.1
m_P["S", "H"] <- 0.5
diag(m_P) <- (1 - rowSums(m_P))
check_trans_prob_mat(m_P)

# introduce error
m_P["H", "S"] <- 0.2
try(check_trans_prob_mat(m_P, confirm_ok = TRUE, stop_if_not = TRUE))
```

create_prompt	<i>Create a prompt for a LLM</i>
---------------	----------------------------------

Description

Uses the function arguments and function body as inputs to create a prompt for the LLM.

Usage

```
create_prompt(foo_arguments, foo_body, foo_name, foo_desc, foo_title)
```

Arguments

foo_arguments	the arguments to the function
foo_body	the body of the function
foo_name	function name
foo_desc	function description
foo_title	function title

Value

a single prompt in the form of a character string

Examples

```
create_prompt(  
  foo_arguments = LETTERS[1:3],  
  foo_body = "D <- A+B+C; return(D)",  
  foo_name = "calculate_QALYs",  
  foo_desc = "This function calcs QALYs",  
  foo_title = "Calculate the QALYs")
```

define_app_server	<i>Create Shiny app server logic</i>
-------------------	--------------------------------------

Description

Create Shiny app server logic

Usage

```
define_app_server(network_object, project_path, foo_path)
```

Arguments

network_object visNetwork object to be displayed in the shiny app
 project_path Path to the project directory
 foo_path path to the function folder

Value

Shiny app server logic

define_app_ui *Create Shiny app UI*

Description

Create Shiny app UI

Usage

```
define_app_ui(network_title)
```

Arguments

network_title Character string representing the title of the network to be displayed above the network.

Value

Shiny app user interface

extract_function_name *Extract function name from a string*

Description

Extract function name from a long string. This works by identifying "function(" in the string and then finding the operand before and splitting on that before keeping the character there.

Usage

```
extract_function_name(string)
```

Arguments

string A string containing a function definition, this must contain the word 'function'

Value

A string containing the function name

Examples

```
extract_function_name("better_name <- function(x){\n more code} asfdas <- function(x){}")
extract_function_name("better_name <- function(x){\n more code}")
```

find_files

find_files

Description

Find files based upon regular expression searching IMPORTANT - a Directory is NOT a file. (for most instances of file systems)

Usage

```
find_files(
  file_regx = ".R",
  path = ".",
  recursive = TRUE,
  exclude_files = NULL,
  exclude_dirs = NULL
)
```

Arguments

```
file_regx      = ".*" - a regular expression for files to source
path           = "." - a path to search
recursive      = TRUE - recurse into subdirectories
exclude_files  = NULL - regx for files to exclude
exclude_dirs   = NULL - regx for directories to exclude
```

Value

list of files

Examples

```
find_files(file_regx = ".*", ## any file name
  path = ".*", # the current directory and all subdirectories
  recursive = FALSE, # don't recurse
  exclude_files = ".*utility.*", # exclude "utility" anywhere in basename
  exclude_dirs = "\\<tmp\\>|/tmp/|/tmp\\>|\\<tmp/" # exclude any directory named "tmp", or subdirs
)
```

find_folder_function_definitions

Creates summary of R files in folder with functions defined within and locations.

Description

Applies find_function_definitions to each file in a folder and aggregate results

Usage

```
find_folder_function_definitions(  
  foo_folder = ".",  
  f_excl = NULL,  
  d_excl = NULL  
)
```

Arguments

foo_folder A folder to apply find_function_definitions to each script in.
f_excl A regular expression for files to NOT process (basename)
d_excl A regular expression for directories to NOT process (dirname)

Value

A dataframe containing a column for function string and a column for function location.

Examples

```
# Skip listed files "somefile.R", and "another_file.R"  
folder_path <- assertHE_example("example_project")  
find_folder_function_definitions(  
  foo_folder = folder_path,  
  f_excl = "\\b(somefile\\.R|another_file\\.R)\\b"  
)
```

find_function_calls_in_file

Find all function calls in file

Description

Searches through a file for function calls using SYMBOL_FUNCTION_CALL

Usage

```
find_function_calls_in_file(  
  relative_path = NULL,  
  foo_strings,  
  filter_for_test_that = FALSE  
)
```

Arguments

`relative_path` path of file to search in

`foo_strings` string vector of function names to search for

`filter_for_test_that` whether to filter for only functions used after the call to `test_that`. Default `FALSE`.

Value

a dataframe with the columns 'foo' for function name and 'location' which gives the file in which the function is called with the line in which the function is called appended.

Examples

```
file_path <- assertHE_example("example_project/tests/testthat/test-calculate_costs.R")  
find_function_calls_in_file(  
  relative_path = file_path,  
  foo_strings = "calculate_costs"  
)
```

find_function_calls_in_folder

Find specific function calls in a folder

Description

Runs `find_function_calls_in_file` on all files in a folder, and combined results into a single dataframe

Usage

```
find_function_calls_in_folder(  
  test_folder,  
  foo_strings,  
  filter_for_test_that = FALSE  
)
```

Arguments

test_folder folder containing all tests
 foo_strings string vector of function names to search for
 filter_for_test_that
 whether to filter for only functions used after the call to test_that. Default FALSE.

Value

dataframe with two columns. 'foo' contains function names, location contains the location of the tests for each function (file and line number).

Examples

```
folder_path <- assertHE_example("example_project/tests/testthat")
find_function_calls_in_folder(
  foo_strings = c("calculate_costs", "calculate_QALYs",
    "create_Markov_trace", "FOO_WITH_NO_TESTS"),
  test_folder = folder_path
)
```

find_function_definitions

Parses an R source file, returns function names defined within.

Description

Using `utils::getParseData()`, searches for function definitions by matching the `FUNCTION` keyword (i.e. "function") with it's associated `SYMBOL` (i.e the function name)

Usage

```
find_function_definitions(filename)
```

Arguments

filename A string containing a path to an R source file

Value

A dataframe with interesting information

Examples

```
file_path <- assertHE_example("example_scripts/example_tricky_functions.R")
find_function_definitions(filename = file_path)
```

`find_next_vector_element`*Find the next element of the vector after a value*

Description

Find the next element of the vector after a value

Usage

```
find_next_vector_element(value, vector, LTE = FALSE)
```

Arguments

value	A value of numeric values
vector	A vector of numeric values
LTE	a boolean to determine collection on "greater than or equal"

Value

The next element of the vector after the value

Examples

```
find_next_vector_element(value = 5, vector = 1:10)
find_next_vector_element(value = 5, vector = 1:4)
find_next_vector_element(value = 5, vector = 1:5, LTE = FALSE)
find_next_vector_element(value = 5, vector = 1:5, LTE = TRUE)
```

`find_previous_vector_element`*Find the previous element of the vector before a value*

Description

Find the previous element of the vector before a value

Usage

```
find_previous_vector_element(value, vector, LTE = FALSE)
```

Arguments

value	A value of numeric values
vector	A vector of numeric values
LTE	a boolean to determine collection on "less than" or "less than equal"

Value

The previous element of the vector before the value

Examples

```
find_previous_vector_element(value = 5, vector = 1:10)
find_previous_vector_element(value = 5, vector = 6:10)
find_previous_vector_element(value = 5, vector = 5:10, LTE = FALSE)
find_previous_vector_element(value = 5, vector = 5:10, LTE = TRUE)
```

get_active_functions *get all active functions that exist in the global environment*

Description

get all active functions that exist in the global environment

Usage

```
get_active_functions(packages = "assertHE")
```

Arguments

packages a vector containing the names of packages to include in the search

Value

a vector containing the names of all active functions in the global environment

get_fileCheersClassifications
Get cheers classification tags from a given file

Description

For a provided filepath, identify the cheers classification tags and the function names that follow them.

Usage

```
get_fileCheersClassifications(
  filename,
  cheers_pattern,
  function_pattern = "(\\s|=|-)function\\"
)
```


Arguments

- filename A string containing the filepath to the file to be checked
- cheers_pattern A string containing the roxygen tag for cheers which is used as an identifier
- function_pattern A string containing the pattern to identify functions

Value

A list containing the cheers tags and the function names that follow them

See Also

Other cheers: [get_folderCheersClassifications\(\)](#)

get_folderCheersClassifications
Get cheers classification tags from a given folder

Description

For a provided folder path, identify the cheers classification tags and the function names that follow them.

Usage

```
get_folderCheersClassifications(path, cheers_pattern, path_ignore = "tests/")
```

Arguments

- path A string containing the filepath to the folder to be checked
- cheers_pattern A string containing the roxygen tag for cheers which is used as an identifier
- path_ignore A string containing the pattern to identify files to ignore

Value

A list containing the cheers tags and the function names that follow them

See Also

Other cheers: [get_fileCheersClassifications\(\)](#)

get_foo_coverage *Get coverage by function*

Description

Get coverage by function

Usage

```
get_foo_coverage(foo_folder, test_folder)
```

Arguments

foo_folder folder containing functions
test_folder folder containing tests

Value

a dataframe with a column for functions and a column for coverage

Examples

```
# Example takes more than 5 seconds to run
if(require(testthat)) {
  folder_path1 <- assertHE_example("example_project/R")
  folder_path2 <- assertHE_example("example_project/tests/testthat")
  get_foo_coverage(
    foo_folder = folder_path1,
    test_folder = folder_path2
  )
}
```

get_function_data *Retrieve Function data to a list*

Description

This function retrieves data about the arguments and body of a specified function.

Usage

```
get_function_data(foo_name, envir = environment())
```

Arguments

- foo_name The name of the function to retrieve data from.
- envir The environment in which to look for the function.

Value

A list with elements for 'arguments' and 'body' of the specified function.

get_function_line *Extract function line in file path*

Description

Extract function line in file path

Usage

```
get_function_line(file_location)
```

Arguments

- file_location Character scalar specifying the path of a file.

Value

A numeric scalar

get_function_path *Remove artefacts from file path*

Description

Remove artefacts from file path

Usage

```
get_function_path(file_location, project_path)
```

Arguments

- file_location Character scalar specifying the path of a file.
- project_path Character scalar specifying the path of the project.

Value

A character scalar

get_isolated_foo *Get Isolated Functions*

Description

Get Isolated Functions

Usage

```
get_isolated_foo(df_edges)
```

Arguments

df_edges A dataframe with two columns ("from" and "to") representing the dependencies.

Value

A vector of isolated function names.

get_roxygen_description
Get Title and Description from Parsed List

Description

This function extracts the title and description from a parsed list.

Usage

```
get_roxygen_description(parsed_list)
```

Arguments

parsed_list A list containing parsed elements.

Value

A list containing the title and description.

Examples

```
parsed_list <- list(list(tag = "title", val = "Sample Title"),  
                  list(tag = "description", val = "This is a sample description."))  
get_roxygen_description(parsed_list)
```

`get_roxygen_description_from_foo`*Get roxygen title and description from function*

Description

Get roxygen title and description from function

Usage

```
get_roxygen_description_from_foo(foo_name)
```

Arguments

`foo_name` function for which want description

Value

text containing description

`identify_dependencies` *Identify Dependencies*

Description

Identify dependencies between functions.

Usage

```
identify_dependencies(v_unique_foo, pkg_env = environment())
```

Arguments

`v_unique_foo` Vector of unique function strings.

`pkg_env` The package environment where the functions are defined (e.g. global).

Value

A dataframe with two columns ("from" and "to") representing the dependencies.

locate_funcs	<i>locate_funcs</i>
--------------	---------------------

Description

locates the lines which define a function within a single file

Usage

```
locate_funcs(file)
```

Arguments

file = a connection object or a character string path to a file.

Value

Returns a data frame with the following columns: func_num: The ID of the function - monotonic increasing from 1. func_start: The line number (within the file) of the function start. func_end: The line number of the function end.

make_closable_tab	<i>Create closable shiny tab</i>
-------------------	----------------------------------

Description

Create closable shiny tab

Usage

```
make_closable_tab(tab_name, content_output_Id, output_type = "text")
```

Arguments

tab_name Character scalar representing the name or title of the shiny tab.

content_output_Id Character scalar representing the id of the shiny tab.

output_type Character scalar specifying the type of rendered output. Default is "text" and can also accept "HTML".

Value

A tab that can be passed to shiny::tabsetPanel()

plotNetwork	<i>Plot Network</i>
-------------	---------------------

Description

Visualize a network plot using the visNetwork package.

Usage

```
plotNetwork(
  df_edges,
  from_col = "from",
  to_col = "to",
  df_summary,
  df_coverage,
  color_no_test = c(background = "#fad1d0", border = "#9c0000", highlight = "#9c0000"),
  color_with_test = c(background = "#e6ffe6", border = "#65a765", highlight = "#65a765"),
  color_mod_coverage = c(background = "#FFD580", border = "#E49B0F", highlight =
    "#E49B0F"),
  moderate_coverage_range = c(0.2, 0.8),
  show_in_shiny = FALSE,
  network_title = NULL,
  scale_node_size_by_degree = FALSE
)
```

Arguments

df_edges	A data frame containing columns "from" and "to" representing the edges of the network.
from_col	Name of the column in df_edges representing the source nodes.
to_col	Name of the column in df_edges representing the target nodes.
df_summary	A summary dataframe containing the information about each function.
df_coverage	a summary dataframe with function names and test coverages
color_no_test	named vector with hexcodes for background, border and highlight
color_with_test	named vector with hexcodes for background, border and highlight
color_mod_coverage	named vector with hexcodes for background, border and highlight where coverage moderate
moderate_coverage_range	vector of two values giving range defined as moderate coverage.
show_in_shiny	logical scalar indicating whether to prepare/deploy the network using a built in shiny app. Default is FALSE.
network_title	title of the network plot.
scale_node_size_by_degree	Scale the node size by the degree centrality of the node.

Value

A visNetwork object representing the network plot.

plot_PSA_stability *Plot cumulative mean Probabilistic Sensitivity Analysis results*

Description

This function plots the cumulative mean of incremental net monetary benefit (INMB), incremental cost-effectiveness ratio (ICER), incremental costs, or incremental effects for different strategies compared to a specified comparator.

Usage

```
plot_PSA_stability(
  m_eff,
  m_cost,
  lambda,
  currency_symbol = "$",
  v_strategy_labels = NULL,
  v_strategy_colors = NULL,
  comparator = NULL,
  output = "inmb",
  include_reference_line = TRUE,
  log_x = FALSE
)
```

Arguments

m_eff	Numeric matrix of effects for different strategies.
m_cost	Numeric matrix of costs for different strategies.
lambda	Numeric value specifying the willingness-to-pay threshold for ICER.
currency_symbol	String specifying the currency symbol for y-axis labels.
v_strategy_labels	Named vector of strategy labels e.g. c("A" = "Strategy A").
v_strategy_colors	Named vector of strategy colors e.g. c("A" = "#665BA6").
comparator	Column name representing the comparator strategy (e.g. "A").
output	String specifying the type of plot, limited to: "inmb", "icer", "costs", or "effects".
include_reference_line	Logical indicating whether to include a reference line.
log_x	Logical indicating whether to use a logarithmic scale on the x-axis.

Value

A ggplot object representing the cumulative mean PSA stability plot.

Examples

```
# create example matrices
n_psa <- 10000

m_eff <- matrix(data = runif(n = n_psa * 4, min = 0, max = 1),
               nrow = n_psa,
               ncol = 4,
               dimnames = list(NULL, paste0("Strategy ", c("A", "B", "C", "D"))))

m_cost <- matrix(data = runif(n = n_psa * 4, min = 5000, max = 20000),
                 nrow = n_psa,
                 ncol = 4,
                 dimnames = list(NULL, paste0("Strategy ", c("A", "B", "C", "D"))))

v_strategy_colors <- setNames(object = grDevices::palette.colors(n = ncol(m_eff)),
                              nm = colnames(m_eff))

plot_PSA_stability(m_eff = m_eff,
                  m_cost = m_cost,
                  lambda = 20000,
                  currency_symbol = "\u0024",
                  v_strategy_labels = colnames(m_eff),
                  v_strategy_colors = v_strategy_colors,
                  comparator = colnames(m_eff)[1],
                  output = "inmb",
                  include_reference_line = TRUE,
                  log_x = FALSE)
```

processNodes

Process Nodes

Description

Process unique nodes from a dataframe of edges.

Usage

```
processNodes(df_edges, from_col = "from", to_col = "to")
```

Arguments

df_edges	A data frame containing columns "from" and "to" representing the edges of the network.
from_col	Name of the column in df_edges representing the source nodes.
to_col	Name of the column in df_edges representing the target nodes.

Value

A data frame of unique nodes with labels.

return_message	<i>Extract the content from the output of the LLM</i>
----------------	---

Description

Extracts content and prints the number of tokens used as a message.

Usage

```
return_message(API_response, verbose = TRUE)
```

Arguments

API_response	response from the LLM API
verbose	whether to include the message for the number of token's used

Value

A single string summary of the content of the LLM response

run_shiny_app	<i>Run a Shiny app to host a network visualization</i>
---------------	--

Description

Run a Shiny app to host a network visualization

Usage

```
run_shiny_app(
  uiFunction = define_app_ui,
  serverFunction = define_app_server,
  network_object,
  network_title = "Function Network",
  project_path,
  foo_path
)
```

Arguments

uiFunction	Function defining shiny user-interface
serverFunction	Function defining shiny server logic
network_object	visNetwork object to be displayed in the shiny app
network_title	Title to be displayed in hte app above the title
project_path	Path to the project directory
foo_path	Path to the function folder

Value

A shiny app

source_funcs	<i>source_funcs</i>
--------------	---------------------

Description

Sources *only* the functions discovered in an R file.

Usage

```
source_funcs(file, env)
```

Arguments

file	a connection object or a character string path to a file.
env	the environment in which to source the functions.

Value

No return value, called for side effects.

IMPORTANT !!!

Sourcing *this* file is a mistake - may result in infinite recursion.

source_lines	<i>source_lines</i>
--------------	---------------------

Description

Sources specified lines within a single file.

Usage

```
source_lines(file, lines, env)
```

Arguments

file	a connection object or a character string path to a file.
lines	A vector of integers specifying the lines to be sourced.
env	the environment in which to source the lines.

Value

No return value, called for side effects.

IMPORTANT !!!

Sourcing *this* file is a mistake - may result in infinite recursion.

summarise_function_from_arguments_and_body	<i>Summarise a function from its arguments and body</i>
--	---

Description

Summarise a function using a LLM via API and retrieve the result

Usage

```
summarise_function_from_arguments_and_body(
  foo_name,
  foo_arguments,
  foo_body,
  foo_title,
  foo_desc,
  model_name = "gpt-3.5-turbo-0125",
  llm_api_url = Sys.getenv("LLM_API_URL"),
  llm_api_key = Sys.getenv("LLM_API_KEY")
)
```

Arguments

foo_name	function name
foo_arguments	vector of arguments
foo_body	single character containing the unparsed body
foo_title	function title
foo_desc	function description
model_name	name of the LLM to use (default gpt-3.5-turbo-0125)
llm_api_url	url to the API for the LLM
llm_api_key	key for the API for the LLM

Value

response from LLM containing all pertinent information & tokens used

Examples

```
## Not run:
tmp <- summarise_function_from_arguments_and_body(
  foo_arguments = LETTERS[1:3],
  foo_body = "D <- A+B+C; return(D)",
  model_name = "gpt-3.5-turbo-0125",
  llm_api_url = Sys.getenv("LLM_API_URL"),
  llm_api_key = Sys.getenv("LLM_API_KEY"),
  foo_desc = "add three numbers, these numbers relate to the number of apples on three trees",
  foo_title = "apple adder",
  foo_name = "apple_add"
)
htr::content(tmp)

## End(Not run)
```

summarise_function_with_LLM

Summarize a function using a Large Language Model

Description

This function summarizes another function using a Language Model.

Usage

```
summarise_function_with_LLM(
  foo_name,
  llm_api_url = Sys.getenv("LLM_API_URL"),
  llm_api_key = Sys.getenv("LLM_API_KEY"),
  envir = environment()
)
```

Arguments

foo_name	function name
llm_api_url	url to the API for the LLM
llm_api_key	key for the API for the LLM
envir	The environment in which to look for the function.

Value

A character string with a summary of the function based on its arguments and body.

Examples

```
## Not run:
summarise_function_with_LLM(foo_name = "get_active_functions",
                           llm_api_url = Sys.getenv("LLM_API_URL"),
                           llm_api_key = Sys.getenv("LLM_API_KEY"),
                           envir = rlang::ns_env("assertHE"))

## End(Not run)
```

summarise_model	<i>Summarise the model functions in a single folder.</i>
-----------------	--

Description

Summarise the model functions in a single folder.

Usage

```
summarise_model(
  project_path = ".",
  foo_folder = "R",
  exclude_files = NULL,
  exclude_dirs = NULL,
  test_folder = NULL,
  output_format = "dataframe"
)
```

Arguments

project_path	path to the project folder, if not provided, will use current working directory.
foo_folder	path to folder containing all functions for the model
exclude_files	A regular expression for files to NOT process (basename)
exclude_dirs	A regular expression for directories to NOT process (dirname)
test_folder	folder containing all tests
output_format	output format to use, defaults to dataframe, options include latex and word.

Value

dataframe with three columns. 'foo_string' contains function names, 'foo_location' contains the location of the function definitions, 'test_location' contains the locations of tests for each function (both file and line number).

Examples

```
project_path <- assertHE_example("example_project")
foo_folder <- "R"
test_folder <- "tests/testthat"

summarise_model(
  project_path = project_path,
  foo_folder = foo_folder,
  test_folder = test_folder
)

summarise_model(
  project_path = project_path,
  foo_folder = foo_folder,
  test_folder = NULL
)
```

visualise_project	<i>Visualize Project</i>
-------------------	--------------------------

Description

Visualize the dependencies between functions in a project using a network plot.

Usage

```
visualise_project(
  project_path,
  foo_path = "R",
  test_path = NULL,
  exclude_files = NULL,
  exclude_dirs = NULL,
  run_coverage = FALSE,
  color_no_test = c(background = "#fad1d0", border = "#9c0000", highlight = "#9c0000"),
  color_with_test = c(background = "#e6ffe6", border = "#65a765", highlight = "#65a765"),
  color_mod_coverage = c(background = "#FFD580", border = "#E49B0F", highlight =
    "#E49B0F"),
  moderate_coverage_range = c(0.2, 0.8),
  print_isolated_foo = FALSE,
  show_in_shiny = FALSE,
  network_title = "Function Network",
```

```

    scale_node_size_by_degree = TRUE
  )

```

Arguments

project_path	Path to the project folder.
foo_path	Path to the folder containing foo functions.
test_path	Path to the folder containing test functions.
exclude_files	A regular expression for files to NOT process (basename)
exclude_dirs	A regular expression for directories to NOT process (dirname)
run_coverage	Boolean determining whether to run coverage assessment
color_no_test	named vector with hexcodes for background, border and highlight
color_with_test	named vector with hexcodes for background, border and highlight
color_mod_coverage	named vector with hexcodes for background, border and highlight where coverage moderate
moderate_coverage_range	vector of two values giving range defined as moderate coverage.
print_isolated_foo	Print the isolated functions to the console (default false)
show_in_shiny	logical scalar indicating whether to prepare/deploy the network using a built in shiny app. Default is FALSE.
network_title	title of the network plot.
scale_node_size_by_degree	Scale the node size by the degree centrality of the node.

Value

A visNetwork object representing the network plot of function dependencies.

Examples

```

# Example takes more than 5 seconds to run
# Visualize project dependencies in HTML
if(require(testthat)) {
  folder_path <- assertHE_example("example_project")
  visualise_project(
    project_path = folder_path,
    foo_path = "R",
    test_path = "tests/testthat",
    run_coverage = TRUE
  )
}

# Visualize project dependencies in shiny
if(interactive()) {

```



```
visualise_project(  
  project_path = folder_path,  
  foo_path = "R",  
  test_path = "tests/testthat",  
  run_coverage = TRUE,  
  show_in_shiny = TRUE  
)  
}
```

wrap_string*Wrap a string to lines of a specified width*

Description

This function takes an input string and wraps it to lines of a specified width, breaking the string at word boundaries.

Usage

```
wrap_string(input_string, width = 80)
```

Arguments

input_string The input string to be wrapped.
width The maximum width of each line. Default is 80 characters.

Value

A character vector where each element represents a line of the wrapped string.

Examples

```
input_string <- "This is a long string that needs to be wrapped to fit within  
                  a specified width."  
wrapped_lines <- wrap_string(input_string, width = 30)  
cat(wrapped_lines, sep = "\n")
```

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