Package: reskit (via r-universe)

May 20, 2026

Title Nice selection box of goodies for hobnobbing with NHP model results

Version 1.0.0

Description 'Wafer' goodbye to crumbly code, and dunk a sturdy reskit function in your data cuppa instead. We've clustered the cream of our results code here - it's a cracker!

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Encoding UTF-8

Roxygen list(markdown = TRUE)

Config/testthat/edition 3

Depends R (>= 4.5.0)

Imports azkit (>= 0.3.0), AzureStor, base64enc, cli, dplyr, forcats, ggbeeswarm, ggplot2, glue, gt, httr2, purrr, rlang, scales, snakecase, tidyr, tidyselect, yaml12, yyjsonr

Remotes The-Strategy-Unit/azkit

Suggests here, readr, testthat (>= 3.0.0), tibble, withr

Config/roxygen2/version 8.0.0

Config/pak/sysreqs
cmake make libicu-dev libuv1-dev libxml2-dev libssl-dev libnode-dev xz-utils libclang-dev

Repository https://the-strategy-unit.r-universe.dev

Date/Publication 2026-05-15 14:37:19 UTC

RemoteUrl https://github.com/The-Strategy-Unit/nhp_reskit

RemoteRef HEAD

RemoteSha effb6fe1f66ce11150fcbbdafa78ada71c03599a

Contents

`add_change_cols` *Add* `change` *and* `change_pct` *columns to a prepared results table*

Description

Add change and `change_pct` columns to a prepared results table

Usage

```
add_change_cols(tbl)
```

Arguments

`tbl`	A tibble of appropriately prepared results

Value

A tibble

`compile_change_factor_data` *Prepare data from the* `step_counts` *results table for display as charts*

Description

Prepare data from the `step_counts` results table for display as charts

Usage

```
compile_change_factor_data(
  results,
  measure,
  activity_type = c("ip", "op", "aae"),
  pods = NULL,
  sites = NULL,
  pod_lookup = get_principal_pods(),
  tpma_lookup = get_tpma_label_lookup(),
  include_baseline = TRUE
)
```

Arguments

`results`	A named list containing NHP results tables
`measure`	The measure to focus on for the output table. Valid values depend on which activity_type is selected
`activity_type`	string. One of "ip", "op", "aae". "ip" is the default.
`pods`	character vector. PoD labels to filter data to. The default value of `NULL` means no PoDs will be filtered out
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, pod and `pod_label`. This provides friendly labels for POD variables in the data. pod is the key column used for joining to data tables.
`tpma_lookup`	A tibble, or a function that returns a tibble, containing a column named `strategy` (used as a key for joining to the `step_counts` table) and a column named `tpma_label` that provides friendly labels for all TPMAs/strategies
`include_baseline`	Boolean. Whether to include baseline data

Value

A prepared tibble of step count changes for each included TPMA

`compile_detailed_activity_data` *Prepare data from the* `sex+age_group` *or* `sex+tretspef_grouped` *table*

Description

Prepare data from the `sex+age_group` or `sex+tretspef_grouped` table

Usage

```
compile_detailed_activity_data(
  results,
  measure,
  pod_lookup = get_detailed_pods(),
  tretspef_lookup = get_tretspef_lookup(),
  activity_type = c("ip", "op", "aae"),
  aggregation = c("age_group", "tretspef_grouped"),
  pods = NULL,
  sites = NULL
)
```

Arguments

`results`	A named list containing NHP results tables
`measure`	The measure to focus on for the output table. Valid values depend on which activity_type is selected
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`tretspef_lookup`	A tibble, or a function that returns a tibble, containing a code column (used as a key for joining to the tretspef table) and a `tretspef` column that provides friendly labels for specialties
`activity_type`	string. One of "ip", "op", "aae". "ip" is the default.
`aggregation`	string. One of "age_group" or "tretspef_grouped"
`pods`	character vector. PoD labels to filter data to. The default value of `NULL` means no PoDs will be filtered out
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data

---

`compile_distribution_plot_data` *Compile data to support the "activity distribution summary" tables*

Description

Compile data to support the "activity distribution summary" tables

Usage

```
compile_distribution_plot_data(
  results,
  measure,
  activity_type = c("ip", "op", "aae"),
  pods = NULL,
  pod_lookup = get_detailed_pods(),
  sites = NULL
)
```

Arguments

`results`	A named list containing NHP results tables
`measure`	The measure to focus on for the output table. Valid values depend on which activity_type is selected
`activity_type`	string. One of "ip", "op", "aae". "ip" is the default.
`pods`	character vector. PoD labels to filter data to. The default value of `NULL` means no PoDs will be filtered out
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data

Value

A tibble

`compile_distribution_summary_data`

Compile data to support the "activity distribution summary" tables

---

Description

Compile data to support the "activity distribution summary" tables

Usage

```
compile_distribution_summary_data(
  results,
  value_type = c("median", "principal"),
  pod_lookup = get_detailed_pods(),
  sites = NULL
)
```

Arguments

`results`	A named list containing NHP results tables
`value_type`	string Either "median" or "principal"
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data

Value

A tibble

`compile_indiv_change_factor_data`

Prepare data from `step_counts` *results table for display as charts*

Description

Prepare data from `step_counts` results table for display as charts

Usage

```
compile_indiv_change_factor_data(
  results,
  measure,
  activity_type = c("ip", "op", "aae"),
  pods = NULL,
  sites = NULL,
  pod_lookup = get_principal_pods(),
  tpma_lookup = get_tpma_label_lookup(),
  sort_by = c("value", "tpma_label")
)
```

Arguments

`results`	A named list containing NHP results tables
`measure`	The measure to focus on for the output table. Valid values depend on which activity_type is selected
`activity_type`	string. One of "ip", "op", "aae". "ip" is the default.
`pods`	character vector. PoD labels to filter data to. The default value of `NULL` means no PoDs will be filtered out
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`tpma_lookup`	A tibble, or a function that returns a tibble, containing a column named `strategy` (used as a key for joining to the `step_counts` table) and a column named `tpma_label` that provides friendly labels for all TPMAs/strategies
`sort_by`	string, one of "value" or "tpma_label". The former sorts the output table by the value of the change, the latter alphabetically by the TPMA label

Value

A prepared tibble of projected negative changes in activity, by TPMA

`compile_principal_los_data` *Prepare data from tretspef+los_group results for displaying as summary table*

Description

Prepare data from tretspef+los_group results for displaying as summary table

Usage

```
compile_principal_los_data(
  results,
  measure,
  pod_lookup = get_principal_pods(),
  sites = NULL
)
```

Arguments

`results`	A named list containing NHP results tables
`measure`	Either "admissions" or "beddays". The measure to focus on for the output table
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data

Value

A filtered and sorted tibble of principal projections of results, by point of delivery and grouped length of stay

---

`compile_principal_pod_data` *Prepare data from default results table for displaying as summary table*

Description

Prepare data from default results table for displaying as summary table

Usage

```
compile_principal_pod_data(
  results,
  pod_lookup = get_principal_pods(),
  sites = NULL
)
```

Arguments

`results`	A named list containing NHP results tables
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data

Value

A filtered and sorted tibble of principal projections of results, by activity type and point of delivery (PoD)

`export_detailed_activity_data` *Prepare a site-level summary of detailed activity results by PoD and LoS*

Description

Intended to be used to create a table to be exported to .csv/.xlsx

Usage

```
export_detailed_activity_data(
  results,
  pod_lookup = get_detailed_pods(),
  tretspef_lookup = get_tretspef_lookup(),
  aggregation = c("age_group", "tretspef_grouped"),
  sites = NULL
)
```

Arguments

`results`	A named list containing NHP results tables
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`tretspef_lookup`	A tibble, or a function that returns a tibble, containing a `code` column (used as a key for joining to the tretspef table) and a `tretspef` column that provides friendly labels for specialties
`aggregation`	string. One of "age_group" or "tretspef_grouped"
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data

Value

A tibble

`export_distribution_summary_data` *Prepare a site-level summary of activity distribution summary data*

Description

Intended to be used to create a table to be exported to .csv/.xlsx

Usage

```
export_distribution_summary_data(
  results,
  pod_lookup = get_detailed_pods(),
  sites = NULL
)
```

Arguments

`results`	A named list containing NHP results tables
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data

Value

A tibble

`export_principal_cf_data` *Prepare a site-level summary table of change_factor results*

Description

Intended to be used to create a table to be exported to .csv/.xlsx

Usage

```
export_principal_cf_data(
  results,
  sites = NULL,
  pod_lookup = get_principal_pods(),
  tpma_lookup = get_tpma_label_lookup()
)
```

Arguments

`results`	A named list containing NHP results tables
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`tpma_lookup`	A tibble, or a function that returns a tibble, containing a column named `strategy` (used as a key for joining to the `step_counts` table) and a column named `tpma_label` that provides friendly labels for all TPMAs/strategies

Value

A tibble

`export_principal_los_data` *Prepare a site-level summary of main projection results by PoD and LoS*

Description

Intended to be used to create a table to be exported to .csv/.xlsx

Usage

```
export_principal_los_data(
  results,
  pod_lookup = get_principal_pods(),
  sites = NULL
)
```

Arguments

`results`	A named list containing NHP results tables
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data

Value

A tibble

`export_principal_pod_data` *Prepare a site-level summary of main projection results*

Description

Intended to be used to create a table to be exported to .csv/.xlsx

Usage

```
export_principal_pod_data(
  results,
  pod_lookup = get_principal_pods(),
  sites = NULL
)
```

Arguments

`results`	A named list containing NHP results tables
`pod_lookup`	A tibble, or a function that returns a tibble, containing columns named `activity_type_label`, `pod` and `pod_label`. This provides friendly labels for POD variables in the data. `pod` is the key column used for joining to data tables.
`sites`	Either `NULL` (the default) or a vector of site codes to filter to. `NULL` means don't filter; include all sites present in the data

Value

A tibble

`get_detailed_pods` *Prepare a lookup table with activity type labels and PoD labels for each PoD*

Description

This function condenses all A&E activity to a single category - compare `get_detailed_pods()` which *keeps* all A&E categories

Usage

```
get_detailed_pods(use_local = FALSE)

get_principal_pods(use_local = FALSE)
```

Arguments

`use_local`	logical. Whether to use a local file (internal to the reskit package) or attempt to pull the lookup file from GitHub. Default is `FALSE`, meaning it will use the GitHub route. If you want to always use a local file (for example, for fully offline working), you can set the `reskit.local.lookups` option to `TRUE` using `options(reskit.local.lookups = TRUE)` or `withr::with_options()`

Value

A tibble

A tibble

`get_results_dir_path` *Return a path to a specific results directory*

Description

Provides some logic and checks to assist the user in locating a valid directory from which to read in NHP results data

Usage

```
get_results_dir_path(
  container,
  path,
  version,
  scheme,
  scenario = NULL,
  dttm_stamp = NULL
)
```

Arguments

`container`	An Azure container.
`path`	string. The path to the directory within the container, where the desired results data is stored
`version`	string. The NHP model version in the format "v3.6", or "dev"
`scheme`	string. The code/name of the NHP scheme. May be "national" etc
`scenario`	string. If `NULL`, the default, and only a single scenario is available within the particular combination of `version` and `scheme`, this single path will be followed. However if multiple scenarios are available, an error will be thrown. The user may avert this by simply supplying an existent scenario name

`dttm_stamp`	string. If `NULL` (the default) and only a single model run directory is available within the particular combination of `version` `scheme` and `scenario`, this path will be returned. If `NULL`, and multiple model runs are found, an error will be thrown. Alternatively, the date-time stamp of the desired model run can be supplied. This is expected to be in the format 'YYYYMMDD_HHMMSS', and must of course match a subdirectory of the selected 'scenario' directory, else an error will be thrown. A third alternative is to supply the string `"max"`, which will return the path to the most recent model run, where multiple runs are found

Value

A path to an Azure blob storage directory, as a string

`get_tpma_label_lookup` *Get a lookup of TPMA labels*

Description

Currently reads from a fixed location within the package.

Usage

```
get_tpma_label_lookup()
```

Value

A 2-column tibble, with columns `strategy` and `tpma_label`

`get_tretspef_lookup` *Get a lookup of tretspef codes to descriptions*

Description

Currently reads from a fixed location within the package.

Usage

```
get_tretspef_lookup()
```

Value

A 2-column tibble with columns `code` and `tretspef`

`get_trust_sites` *From any results table, get list of all site codes for this scheme*

Description

The "default" table is recommended

Usage

```
get_trust_sites(res_tbl, col = "sitetret")
```

Arguments

`res_tbl`	A tibble from the results list
`col`	string The name of the column containing site codes. `sitetret` by default

Value

A character vector

`make_beeswarm_distrib_plot` *Generate a "beeswarm" chart showing the distribution of model run values*

Description

Generate a "beeswarm" chart showing the distribution of model run values

Usage

```
make_beeswarm_distrib_plot(distrib_plot_data, show_zero = FALSE)
```

Arguments

`distrib_plot_data`	data frame. As produced by compile_distribution_plot_data
`show_zero`	Boolean. Whether to extend the chart to show a zero value, for context.

`make_cumulative_distrib_plot` *Generate a cumulative distribution function (ecdf) chart of model run values*

Description

Generate a cumulative distribution function (ecdf) chart of model run values

Usage

```
make_cumulative_distrib_plot(distrib_plot_data, show_zero = FALSE)
```

Arguments

`distrib_plot_data`	data frame. As produced by compile_distribution_plot_data
`show_zero`	Boolean. Whether to extend the chart to show a zero value, for context.

`make_detailed_activity_table` *Create a gt table with data from compile_detailed_activity_data()*

Description

Create a gt table with data from compile_detailed_activity_data()

Usage

```
make_detailed_activity_table(detailed_activity_data, final_year)
```

Arguments

`detailed_activity_data`	A suitable tibble
`final_year`	string. The horizon year eg "2042/43"

Value

A gt table

`make_distribution_summary_table` *Create a gt table with data from compile_distribution_summary_data()*

Description

Create a gt table with data from compile_distribution_summary_data()

Usage

```
make_distribution_summary_table(distr_summary_data)
```

Arguments

`distr_summary_data`	A suitable tibble

Value

A gt table

`make_individual_cf_plot` *Generate bar charts by change factor at individual TPMA level*

Description

Generate bar charts by change factor at individual TPMA level

Usage

```
make_individual_cf_plot(indiv_change_factor_data)
```

Arguments

`indiv_change_factor_data`	data frame. As produced by compile_indiv_change_factor_data

---

`make_overall_cf_plot` *Generate overall change factor ("waterfall") chart*

Description

Generate overall change factor ("waterfall") chart

Usage

```
make_overall_cf_plot(principal_change_factor_data)
```

Arguments

`principal_change_factor_data`	data frame. As produced by compile_change_factor_data

`make_principal_los_table` *Create a gt table with data from compile_principal_los_data*

Description

Create a gt table with data from compile_principal_los_data

Usage

```
make_principal_los_table(principal_los_data)
```

Arguments

`principal_los_data`	A suitable tibble

Value

A gt table

`make_principal_pod_table`

Create a gt table with data from compile_principal_pod_data

Description

Create a gt table with data from compile_principal_pod_data

Usage

```
make_principal_pod_table(principal_pod_data)
```

Arguments

`principal_pod_data`	A suitable tibble

Value

A gt table

`read_results_parquet_files`

Read a selection of (or all) parquet files in an Azure directory

---

Description

Read a selection of (or all) parquet files in an Azure directory

Usage

```
read_results_parquet_files(container, path, tables = NULL)
```

Arguments

`container`	An Azure container.
`path`	string. Path to an Azure directory of results data. Potentially produced by get_results_dir_path
`tables`	character vector. `NULL`, the default, results in all available parquet files in the `path` folder being read in. If you wish only to read in a subset of the files, specify their names here, without the ".parquet" file extension

Value

A named list of tibbles

Examples

```
## Not run:
  data <- azkit::get_container("data_container") |>
    read_results_parquet_files("data/dev/national/test", "acuity")

  data_list <- azkit::get_container("data_container") |>
    get_results_dir_path("files", version = "v4.0", scheme = "national") |>
    read_results_parquet_files()

## End(Not run)
```

`shim_results` *Wrangle tables from old-style results to match format of new-style results*

Description

Wrangle tables from old-style results to match format of new-style results

Usage

```
shim_results(results)
```

Arguments

`results`	List of old style NHP results tables

Value

List of NHP results tables in the "new" format

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