

# Package: nih.joinpoint (via r-universe)

September 9, 2024

**Version** 0.1.0.9004

**Title** R Interface for NIH's Joinpoint Regression Software

**Description** Functions to easily use National Institute of Health (NIH)'s 'Joinpoint Regression Software'. You **must** download and install the software beforehand at <https://surveillance.cancer.gov/joinpoint/callable/>. NIH's approval will be needed to download the executable.

**License** GPL-3

**URL** <https://github.com/DanChaltiel/nih.joinpoint/>

**BugReports** <https://github.com/DanChaltiel/nih.joinpoint/issues/>

**Depends** R (>= 3.1.0)

**Imports** dplyr (>= 1.0.0), forcats, glue, ggplot2, janitor, purrr, rlang (>= 0.4.7), readr, tibble, tidyselect, patchwork, zoo

**Suggests** covr, crayon, knitr, lifecycle, rmarkdown, systemfonts, testthat, tidyverse, withr, waldo

**VignetteBuilder** knitr

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Repository** <https://danchaltiel.r-universe.dev>

**RemoteUrl** <https://github.com/DanChaltiel/nih.joinpoint>

**RemoteRef** HEAD

**RemoteSha** f341f8f10ba0f0246bf6ded93e22e9b541b3767b

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browse	<i>Browse the joinpoint files</i>
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### Description

Open the directory in temporary files where joinpoint files are stored

### Usage

```
browse(jp)
```

### Arguments

jp                    the joinpoint analysis to browse

### Examples

```
jp = joinpoint_example()
print(dir)
#browseURL(dir)
```

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export_options	<i>Export options</i>
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### Description

Create a character representation of the .ini file needed for export options.

### Usage

```
export_options(
  models = c("best fit", "all"),
  remove_jp_flags = TRUE,
  remove_best_fit_flags = FALSE,
  output_bygroup_headers = FALSE,
  all_models_in_same_column = FALSE,
  include_jp_estimates = FALSE,
  include_apcs = TRUE,
  x_precision = 9,
```

```

y_precision = 9,
model_precision = 3,
estimated_joinpoint_precision = 3,
regression_coefficients_precision = 3,
covariance_matrix_precision = 3,
correlation_matrix_precision = 3,
apc_precision = 3,
aapc_precision = 3,
aapc_segment_ranges_precision = 3,
pvalue_precision = 3,
aapc_full_range = FALSE,
aapc_start_range1 = NULL,
aapc_end_range1 = NULL,
aapc_start_range2 = NULL,
aapc_end_range2 = NULL,
aapc_start_range3 = NULL,
aapc_end_range3 = NULL,
aapc_last_obs = FALSE,
export_bad_cohorts = TRUE,
export_report = TRUE,
export_data = TRUE,
export_apc = TRUE,
export_aapc = TRUE,
export_ftest = TRUE,
export_pairwise = TRUE,
export_jump_cr = TRUE
)

```

### Arguments

models	one of c("best fit", "all"). Using all might be insightful but rather messes with the output.
remove_jp_flags	remove_jp_flags
remove_best_fit_flags	removes the final_selected_model column
output_bygroup_headers	should only be used if models==best. If FALSE, result table has model, apc, joinpoints. If TRUE, result table has jp2, apc2 (if selected model is with 2 joinpoints) but rather messes with the output.
all_models_in_same_column	all_models_in_same_column
include_jp_estimates	include_jp_estimates
include_apcs	include_apcs
x_precision	x_precision
y_precision	y_precision

```
model_precision
    model_precision
estimated_joinpoint_precision
    estimated_joinpoint_precision
regression_coefficients_precision
    regression_coefficients_precision
covariance_matrix_precision
    covariance_matrix_precision
correlation_matrix_precision
    correlation_matrix_precision
apc_precision  apc_precision
aapc_precision aapc_precision
aapc_segment_ranges_precision
    aapc_segment_ranges_precision
pvalue_precision
    pvalue_precision
aapc_full_range
    aapc_full_range
aapc_start_range1
    aapc_start_range1
aapc_end_range1
    aapc_end_range1
aapc_start_range2
    aapc_start_range2
aapc_end_range2
    aapc_end_range2
aapc_start_range3
    aapc_start_range3
aapc_end_range3
    aapc_end_range3
aapc_last_obs  aapc_last_obs
export_bad_cohorts
    export_bad_cohorts
export_report  export_report
export_data    export_data
export_apc     export_apc
export_aapc    export_aapc
export_ftest   export_ftest
export_pairwise
    export_pairwise
export_jump_cr export_jump_cr
```

**Value**

a string (character of length 1) representing the .ini file

**Source**

[https://surveillance.cancer.gov/joinpoint/Joinpoint\\_Help\\_4.8.0.1.pdf](https://surveillance.cancer.gov/joinpoint/Joinpoint_Help_4.8.0.1.pdf)

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get_tempdir	<i>Temporary directory for joinpoint files</i>
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**Description**

Creates a timestamped directory in Local/Temp

**Usage**

```
get_tempdir()
```

**Examples**

```
dir = get_tempdir()
print(dir)
#browseURL(dir)
```

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joinpoint	<i>API to run a joinpoint model</i>
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**Description**

Use the Command-Line version of "Joinpoint Regression Software" provided by the NIH to run a regression. The software must be downloaded at <https://surveillance.cancer.gov/joinpoint/callable/> and installed on a **Windows** computer. I am not aware of a version of this software for Linux or MacOS.

**Usage**

```
joinpoint(
  data,
  x,
  y,
  by = NULL,
  se = NULL,
  export_opts = export_options(),
  run_opts = run_options(),
  cmd_path = getOption("joinpoint_path",
    "C:/Program Files (x86)/Joinpoint Command/jpCommand.exe"),
```

```

    dir = get_tempdir(),
    verbose = FALSE
  )

```

### Arguments

data	A data frame
x	<tidy-select> the independent variable (for instance the year)
y	<tidy-select> the dependent variable
by	<tidy-select> one or several stratification variable (for instance sex)
se	<tidy-select> the standard error of the dependent variable. Can be left as NULL at the cost of a longer computation. See <a href="https://seer.cancer.gov/seerstat/WebHelp/Rate_Algorithms.htm">https://seer.cancer.gov/seerstat/WebHelp/Rate_Algorithms.htm</a> for calculation formulas.
export_opts	the result of <code>export_options()</code>
run_opts	the result of <code>run_options()</code>
cmd_path	the path to the executable. Can usually be left default to "C:/Program Files (x86)/Joinpoint Command/jpCommand.exe". Can also be set through <code>options(joinpoint_path="my...")</code>
dir	The temporary directory where all the temporary files will be written
verbose	Logical indicating whether or not to print out progress

### Details

This function will generate the .ini files, run the software, and then parse the result files as an plain old R list.

### Value

the list of the output tables

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jp_plot	<i>Plot the output of a joinpoint analysis.</i>
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---

### Description

Plot the output of a joinpoint analysis.

### Usage

```

jp_plot(
  jp,
  by_level = NULL,
  legend_pattern = getOption("jp_plot_legend_pattern", "{xmin}-{xmax}: {slope}"),
  title_pattern = getOption("jp_plot_title_pattern", "{key}={val}"),
  ncol = 1,
  return_patchwork = TRUE,
  ...
)

```

**Arguments**

jp	A list generated using <code>joinpoint()</code> .
by_level	One or several stratification levels. Works only if jp was made using one single stratification variable.
legend_pattern	<code>glue::glue()</code> pattern for the legend. Can use variables <code>slope</code> , <code>xmin</code> , and <code>xmax</code> . Can be set through options, e.g. <code>options(jplot_legend_pattern="{slope}-")</code> .
title_pattern	<code>glue::glue()</code> pattern for the title. Can use variables <code>key</code> (grouping variable) and <code>val</code> (current group). Can be set through options, e.g. <code>options(jplot_title_pattern="{val}-")</code> .
...	passed on to <code>patchwork::wrap_plots()</code>

**Value**

a patchwork if `return_patchwork==TRUE`, a list of ggplots otherwise

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nih_sample_data	<i>Sample dataset</i>
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**Description**

Sample dataset

**Usage**

```
nih_sample_data
```

**Format**

A dataframe with 105 observations on 4 variables

**Source**

Dataset that comes with NIH's Joinpoint software

run\_options

*Design options***Description**

Create a character representation of the .ini file needed for run options.

**Usage**

```
run_options(
  model = c("linear", "ln"),
  data_shift = 0,
  min_joinpoints = 0,
  max_joinpoints = 4,
  pairwise = NULL,
  pairwise_signif_lvl = 0.05,
  pairwise_n_permut = 4499,
  method = c("grid", "hudsons"),
  min_obs_end = 2,
  min_obs_between = 2,
  n_obs_between = 0,
  model_selection_method = c("permutation test", "bic", "mbic",
    "data dependent selection", "wbic", "wbic-alt"),
  permutation_signif_lvl = 0.05,
  n_permutations = 4499,
  early_stopping = c("b-value", "curtailed", "fixed"),
  run_type = c("calculated", "provided"),
  rates_per_n = 1e+05,
  dependent_variable_type = c("count", "crude rate", "age-adjusted rate", "proportion",
    "percent"),
  het_error = c("constant variance", "standard error", "poisson rate", "poisson count"),
  het_error_var_location = NULL,
  ci_method = c("parametric", "empirical quantile method 1",
    "empirical quantile method 2"),
  n_cores = 1,
  delay_type = c("delay", "non-delay", "both"),
  autocorr_errors = c("number", "estimated"),
  jump_model = FALSE,
  comparability_ratio = FALSE,
  include_std_analysis = FALSE,
  jump_location = 9999,
  comparability_ratio_value = 0,
  cr_variance = 0,
  joinpoint_alpha_lvl = 0.05,
  apc_alpha_lvl = 0.05,
  aapc_alpha_lvl = 0.05,
  jump_cr_alpha_lvl = 0.05,
```



```

    random_seed = 7160,
    empirical_quantile_seed = 10000,
    empirical_quantile_seed_type = c("constant", "varying"),
    n_resample = 1000,
    madwd = FALSE,
    madwd_psi = 0
)

```

### Arguments

model	one of c("linear", "ln")
data_shift	data_shift
min_joinpoints	min_joinpoints
max_joinpoints	max_joinpoints
pairwise	pairwise
pairwise_signif_lvl	pairwise_signif_lvl
pairwise_n_permut	pairwise_n_permut
method	method
min_obs_end	min_obs_end
min_obs_between	min_obs_between
n_obs_between	n_obs_between
model_selection_method	model_selection_method
permutation_signif_lvl	permutation_signif_lvl
n_permutations	n_permutations
early_stopping	early_stopping
run_type	run_type
rates_per_n	rates_per_n
dependent_variable_type	dependent_variable_type
het_error	het_error
het_error_var_location	het_error_var_location
ci_method	ci_method
n_cores	n_cores
delay_type	delay_type
autocorr_errors	autocorr_errors

```
jump_model      jump_model
comparability_ratio
                comparability_ratio
include_std_analysis
                include_std_analysis
jump_location   jump_location
comparability_ratio_value
                comparability_ratio_value

cr_variance     cr_variance
joinpoint_alpha_lvl
                joinpoint_alpha_lvl

apc_alpha_lvl   apc_alpha_lvl
aapc_alpha_lvl  aapc_alpha_lvl
jump_cr_alpha_lvl
                jump_cr_alpha_lvl

random_seed     random_seed
empirical_quantile_seed
                empirical_quantile_seed
empirical_quantile_seed_type
                empirical_quantile_seed_type

n_resample      n_resample
madwd           madwd
madwd_psi       madwd_psi
```

**Value**

a string (character of length 1) representing the .ini file

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