

# Package ‘npst’

July 2, 2014

**Type** Package

**Title** Generalization of Hewitt's Seasonality Test

**Version** 2.0

**Date** 2014-02-09

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**Maintainer** Roland Rau <roland.rau@gmail.com>

**Suggests** parallel

**Description** Package 'npst' generalizes Hewitt's (1971) test for seasonality and Rogerson's (1996) extension based on Monte-Carlo simulation.

**License** GPL-2

**LazyLoad** yes

**NeedsCompilation** yes

**Repository** CRAN

**Date/Publication** 2014-02-10 16:40:52

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npst-package

*npst*

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## Description

Package 'npst' generalizes Hewitt's (1971) test for seasonality and Rogerson's (1996) extension based on Monte-Carlo simulation.

## Details

Package: npst  
Type: Package  
Version: 1.6  
Date: 2011-08-26  
License: GPL-2  
LazyLoad: yes

## Author(s)

Roland Rau

Maintainer: Roland Rau <roland.rau@gmail.com>

## References

EDWARDS, J.H. (1961): The recognition and estimation of cyclic trends. *Annals of Human Genetics* 25:83-86

HEWITT, David and MILNER, Jean and CSIMA, Adele and PAKULA (1971): On Edwards' Criterion of Seasonality and a Non-Parametric Alternative. *British Journal of Preventive Social Medicine* 25:174-176

ROGERSON, Peter A. (1996): A Generalization of Hewitt's Test for Seasonality. *International Journal of Epidemiology* 25:644-648

WALTER, S.D. (1980): Exact significance levels for Hewitt's test for seasonality *Journal of Epidemiology and Community Health* 34:147-149

## Examples

```
npst(indata=c(1:6, 12:7), peak=6, repts=100000,  
     whole.distribution=FALSE, siglevels=c(0.01, 0.05, 0.1),  
     PARALLEL=FALSE)
```

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### Description

Package 'npst' generalizes Hewitt's (1971) test for seasonality and Rogerson's (1996) extension based on Monte-Carlo simulation.

### Usage

```
npst(indata=NULL, long=12, peak=6, repts=100000,
     whole.distribution=FALSE, siglevels=c(0.001,0.01,0.05,0.1),
     PARALLEL=FALSE, nodes=1)
```

### Arguments

|                    |   |
|--------------------|---|
| indata             | A numeric vector whose elements are the empirical number of events (e.g. deaths). The length of the data is typically 12 (=months), 52 or 53 (weeks), or 365 or 366 (days). Not providing 'indata' is also okay (slightly different output then). |
| long               | The basic length of the data analyzed, i.e. if we have monthly data, it would be 12 (hence it is an integer scalar). If 'indata' are provided, argument 'long' is calculated based on argument 'indata'.  |
| peak               | Length of peak period (integer scalar). For instance, if we assume that the 'peak season' lasts six months for monthly data, 'peak' would be six (=default value).  |
| repts              | How many Monte Carlo simulation runs should be conducted (integer scalar)?  |
| whole.distribution | Argument 'whole.distribution' indicates whether the whole distribution should be returned (=TRUE) or only the critical values (=FALSE) (Boolean Scalar).  |
| siglevels          | For which significance levels should the corresponding required rank sums be returned. Default settings are the 'typical' significance levels of 0.001,0.01, 0.05, and 0.1 (numeric vector).  |
| PARALLEL           | If TRUE, multi-core Monte Carlo Simulation; otherwise single-core Simulation (Boolean Scalar).  |
| nodes              | Specify on how many nodes the estimation should run (default=1). Only active if argument PARALLEL=TRUE.   |

### Value

|                  |   |
|------------------|---|
| maximum.rank.sum | The maximum rank sum theoretically possible with the given data (integer scalar)    |
| observed         | The observed maximum rank sum (with the given data) (integer scalar)                |
| observed.p.value | What is the p-value corresponding to the observed maximum rank sum (numeric scalar) |

critical values

What are the required rank sums for the entered significance levels (numeric data.frame)?

distribution

ONLY IF whole.distribution=TRUE: A numeric data.frame specifying all possible rank-sums and their associated p-values.

### Author(s)

Roland Rau

### References

EDWARDS, J.H. (1961): The recognition and estimation of cyclic trends. *Annals of Human Genetics* 25:83-86

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### Examples

```
npst(indata=c(1:6, 12:7), peak=6, repts=100000,
     whole.distribution=FALSE, siglevels=c(0.01, 0.05, 0.1),
     PARALLEL=FALSE)
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