

# Package: rseedcalc (via r-universe)

August 21, 2024

**Title** Estimating the Proportion of Genetically Modified Seeds in Seedlots via Multinomial Group Testing

**Version** 1.3

**Type** Package

**Date** 2013-10-10

**Description** Estimate the percentage of seeds in a seedlot that contain stacks of genetically modified traits. Estimates are calculated using a multinomial group testing model with maximum likelihood estimation of the parameters.

**License** GPL-2

**Imports** stats

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**NeedsCompilation** no

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

**RemoteUrl** <https://github.com/cran/rseedcalc>

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rseedcalc-package	<i>Estimation of the proportion of genetically modified stacked seeds in seedlots</i>
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### Description

Estimate the percentage of seeds in a seedlot that contain stacks of genetically modified traits.

### Details

The main functions for this package are [stack2](#) and [stack3](#).

For a complete list of functions, use `library(help="rseedcalc")`

### Author(s)

Kevin Wright, Jean-Louis Laffont

Maintainer: Kevin Wright <kw.stat@gmail.com>

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stack3	<i>Multinomial group testing estimation of stacked genes</i>
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### Description

Assuming qualitative tests are performed on  $n$  pools of  $m$  seeds, use multinomial group testing to estimate the percent of seeds with single genetic traits and the percentage of seeds with stacked genetic traits.

Print method for seedstack object.

### Usage

```
stack3(n, m, nA, nB, nC, nAB, nAC, nBC, nABC, existAB = "Yes",
      existAC = "Yes", existBC = "Yes", existABC = "Yes", fpr = 0,
      fnr = 0, check = TRUE)
```

```
stack2Excel(...)
```

```
stack3Excel(...)
```

```
stack2(n, m, nA, nB, nAB, existAB = "Yes", fpr = 0, fnr = 0,
      check = TRUE)
```

```
## S3 method for class 'seedstack'
print(x, ...)
```

**Arguments**

n	the number of pools
m	the number of seeds in each pool
nA	the number of positive pools for event A only
nB	the number of positive pools for event B only
nAB	the number of positive pools for both A and B
nC	the number of positive pools for event C only
nAC	the number of positive pools for both A and C
nBC	the number of positive pools for both B and C
nABC	the number of positive pools for both A and B and C
existAB	do seeds with a stacked event 'AB' exist?
existAC	do seeds with a stacked event 'AC' exist?
existBC	do seeds with a stacked event 'BC' exist?
existABC	do seeds with a stacked event 'ABC' exist?
fpr	false positive rate (proportion) for detecting GM events
fnr	false negative rate (proportion) for detecting GM events
check	Should simple checks be performed? Defaults to TRUE
...	Other arguments passed
x	A data frame to print pretty.

**Details**

The 'stack2Excel' and 'stack3Excel' functions are simple wrappers that are intended to be called from Excel and should not issue any warnings.

**Value**

A data frame with the estimated proportion of seeds for each event, the observed and expected number of positive pools, and whether or not each event can exist.

**Author(s)**

Kevin Wright, Jean-Louis Laffont

**Examples**

```
stack2(10, 300, 0, 1, 2)
stack3(20,150, 2,2,2,2,2,2,3, existAB="no", fnr=.02, fpr=.02)
```

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```
valid          #' Ensure probabilities are valid
```

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**Description**

Force calculated probabilities into the range [0,1].

**Usage**

```
valid(x)
```

**Arguments**

x            probability

**Details**

Due to floating-point arithmetic, a number that should represent a probability can be calculated as being less than zero or greater than one. This function returns a value that is a valid probability.

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