Package ‘branchingprocess’

April 25, 2025

Title Calculate Outbreak Probabilities for a Branching Process Model

Version 0.1.0

Description Quantify outbreak risk posed by individual importers of a transmissible pathogen. Input parameters of negative binomial offspring distributions for the number of transmissions from each infected individual and initial number of infected. Calculate probabilities of final outbreak size and generations of transmission, as described in Toth et al. (2015) <doi:10.3201/eid2108.150170> and Toth et al. (2016) <doi:10.1016/j.epidem.2016.04.002>.

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Encoding UTF-8

URL `https://github.com/EpiForeSITE/branchingprocess`, `https://epiforesite.github.io/branchingprocess/`

BugReports `https://github.com/EpiForeSITE/branchingprocess/issues`

RoxygenNote 7.3.2

Imports stats

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-04-25 12:50:05 UTC

Contents

`pExtinct` *Probability that one initial case leads to an outbreak that eventually dies out (stochastic extinction)*

Description

Probability that one initial case leads to an outbreak that eventually dies out (stochastic extinction)

Usage

```
pExtinct(R, k)
```

Arguments

`R`	Reproduction number: mean of negative binomial offspring distribution
`k`	Dispersion parameter of negative binomial offspring distribution

Value

The probability of outbreak extinction

Author(s)

Damon Toth

Examples

```
# Probability that a single case leads to an extinct outbreak when the offspring distribution
# is negative binomial with mean 2 and dispersion parameter 0.5:
pExtinct(R=2,k=0.5)
```

`pFinalSize` *Final outbreak size probability*

Description

Final outbreak size probability

Usage

```
pFinalSize(n, j, R, k)
```

Arguments

`n`	Number of initial cases in generation 0
`j`	Total outbreak size (>= n).
`R`	Mean of negative binomial offspring distribution
`k`	Dispersion of negative binomial offspring distribution

Value

The final size probability

Examples

```
# With 5 initial individuals and negative binomial offspring distribution with mean R=0.2
# and dispersion k=0.1, gives the probability of outbreak extinction with a total number
# final outbreak size of exactly 5 to 20 individuals (including the initial 5):
pFinalSize(5, 5:20, R=0.2, k=0.1)
```

`pFinalSizeAndGen` *Joint probability of outbreak final size and number of transmission generations*

Description

Joint probability of outbreak final size and number of transmission generations

Usage

```
pFinalSizeAndGen(g, n, j, R, k)
```

Arguments

`g`	Number of generations.
`n`	Number of initial cases
`j`	Final size
`R`	Reproduction number
`k`	Dispersion parameter

Value

The joint probability of the final outbreak size and number of transmission generations

Author(s)

Damon Toth

Examples

```
# Probability that 1 initial infection leads to an outbreak of final size 20 over exactly
# 3 generations of transmission:
pFinalSizeAndGen(g=3,n=1,j=20,R=0.8,k=0.1)
```

`pFinalSizeAndGenSwitch1` *Joint probability of outbreak final size and number of transmission generations with offspring distribution parameters switched after generation one*

Description

Joint probability of outbreak final size and number of transmission generations with offspring distribution parameters switched after generation one

Usage

```
pFinalSizeAndGenSwitch1(g, n, j, R0, k0, Rc, kc)
```

Arguments

`g`	Number of generations
`n`	Number of initial cases
`j`	Final size
`R0`	Mean of negative binomial offspring distribution from generation one
`k0`	Dispersion of negative binomial offspring distribution from generation one
`Rc`	Mean of negative binomial offspring distribution from generation two on
`kc`	Dispersion of negative binomial offspring distribution from generation two on

Value

The joint probability of outbreak final size and number of transmission generations

Author(s)

Damon Toth

Examples

```
# Probability that 1 initial infection leads to an outbreak of final size 20 over exactly
# 3 generations of transmission:
pFinalSizeAndGenSwitch1(g=3,n=1,j=20,R0=2,k0=0.1,Rc=0.5,kc=1)
```

`pFinalSizeSwitch1` *Probability of final outbreak size with offspring distribution parameters switched after generation one*

Description

pFinalSizeSwitch1 is the probability that n initial cases lead to an extinguished outbreak of total size j after any number of transmission generations (j includes the n initial cases)

Usage

```
pFinalSizeSwitch1(n, j, R0, k0, Rc, kc)
```

Arguments

`n`	Number of initial cases in generation 0
`j`	Total outbreak size (>= n).
`R0`	Mean of negative binomial offspring distribution from generation one
`k0`	Dispersion of negative binomial offspring distribution from generation one
`Rc`	Mean of negative binomial offspring distribution from generation two on
`kc`	Dispersion of negative binomial offspring distribution from generation two on

Value

The probability of the final outbreak size

Examples

```
#With 5 initial cases, the probability that the final outbreak size is 5 to 20
#(including the initial 5):
pFinalSizeSwitch1(n=5, j=5:20, R0=2, k0=0.1, Rc=0.2, kc=0.1)
```

---

pGen *Probability that one initial case leads to an outbreak lasting less than g generations of transmission.*

Description

Probability that one initial case leads to an outbreak lasting less than g generations of transmission.

Usage

```
pGen(gMax, R, k)
```

Arguments

`gMax`	Maximum number of generations.
`R`	Reproduction number.
`k`	Dispersion parameter.

Value

A vector of probabilities for each number of generations from 1 to gmax

Author(s)

Damon Toth

Examples

```
# Probability of outbreak lasting less than 1,2,3,...,10 generations:
pGen(gMax=10, R=0.9, k=0.1)
```

---

pGenSwitch1 *Probability that one initial case leads to an outbreak lasting less than g generations of transmission, with offspring distribution parameters switched after generation one.*

Description

Probability that one initial case leads to an outbreak lasting less than g generations of transmission, with offspring distribution parameters switched after generation one.

Usage

```
pGenSwitch1(gMax, R0, k0, Rc, kc)
```

Arguments

`gMax`	Maximum number of generations
`R0`	Basic reproduction number: mean of negative binomial offspring distribution from generation one
`k0`	Dispersion of negative binomial offspring distribution from generation one
`Rc`	Control reproduction number: mean of negative binomial offspring distribution from generation two plus
`kc`	Dispersion of negative binomial offspring distribution from generation two plus

Value

A vector of probabilities for each number of generations from 1 to gmax

Author(s)

Damon Toth

Examples

```
# Probability of outbreak lasting less than 1,2,3,...,10 generations:
pGenSwitch1(gMax=10, R0=3, k0=0.1, Rc=0.5, kc=1)
```

`pNextGenSize` *Probability of y total transmission directly from x independent infected individuals*

Description

Probability of y total transmission directly from x independent infected individuals

Usage

```
pNextGenSize(x, y, R, k)
```

Arguments

`x`	Number of infected individuals in generation n
`y`	Number of total transmissions in generation n+1
`R`	Mean of negative binomial offspring distribution
`k`	Dispersion of negative binomial offspring distribution

Value

The probability of the given number of transmissions

Examples

```
# With 5 individuals in this generation, what is the probability of
# 0 to 15 transmissions in the next generation?
pNextGenSize(x=5, y=0:15, R=0.2, k=0.1)
```

`pSizeAtGen` *Probability that n initial cases lead to an outbreak that lasts at least g generations of transmission AND has exactly j total cases after generation g*

Description

Probability that n initial cases lead to an outbreak that lasts at least g generations of transmission AND has exactly j total cases after generation g

Usage

```
pSizeAtGen(g, n, j, R, k)
```

Arguments

`g`	Number of generations of transmission
`n`	Number of initial cases
`j`	Total size of outbreak after generation g
`R`	Reproduction number: mean of negative binomial offspring distribution
`k`	Dispersion parameter of negative binomial offspring distribution

Value

The probability of the given outbreak size at the given generation

Author(s)

Damon Toth

Examples

```
#Probability that 10 initial cases leads to an outbreak lasting at least
# 3 transmission generations and is of exact size 30 after 3 generations
pSizeAtGen(g=3,n=10,j=30,R=2,k=0.5)
```

`pSizeAtGenSwitch1` *Probability that n initial cases lead to an outbreak that lasts at least g generations of transmission AND has exactly j total cases after generation g, with offspring distribution parameters switched after generation one*

Description

Probability that n initial cases lead to an outbreak that lasts at least g generations of transmission AND has exactly j total cases after generation g, with offspring distribution parameters switched after generation one

Usage

```
pSizeAtGenSwitch1(g, n, j, R0, k0, Rc, kc)
```

Arguments

`g`	Number of generations of transmission
`n`	Number of initial cases
`j`	Total size of outbreak after generation g
`R0`	Basic reproduction number: mean of negative binomial offspring distribution from generation one
`k0`	Dispersion parameter of negative binomial offspring distribution from generation one
`Rc`	Control reproduction number: mean of negative binomial offspring distribution from generation two plus
`kc`	Dispersion parameter of negative binomial offspring distribution from generation two plus

Value

The probability of the given outbreak size at the given transmission generation

Author(s)

Damon Toth

Examples

```
#Probability that 10 initial cases leads to an outbreak lasting at least
# 3 transmission generations and is of exact size 30 after 3 generations
pSizeAtGenSwitch1(g=3,n=10,j=30,R0=2,k0=0.5,Rc=0.5,kc=1)
```

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