

# Package ‘rds’

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**Type** Package

**Title** Root diversity score (RDS)

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**Description** R implementation of root diversity score (RDS) calculation (Reiter et al, Nature Genetics, 2020). Translated from the original python by Martin Blohmer. Packaged into an R library and maintained by Alexander Gorelick. Please cite: Reiter et al., Nature Genetics, 2020. <https://doi.org/10.1038/s41588-020-0633-2>

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**Imports** gmp

**RoxygenNote** 7.1.2

## R topics documented:

calculate_no_common_trees . . . . .	1
calculate_no_trees . . . . .	2
cluster_probability . . . . .	2
klm . . . . .	3
min_cluster_probability . . . . .	3
multinomial . . . . .	4
no_trees_min_cluster . . . . .	4
no_trees_with_clusters . . . . .	5
rds . . . . .	5
<b>Index</b>	<b>6</b>

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calculate_no_common_trees
<i>calculate_no_common_trees</i>

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## Description

Calculate the number of monophyletic trees given by Theorem 3 in the SI of Reiter et al. 2020 Nat Gen.

**Usage**

```
calculate_no_common_trees(k, m)
```

**Arguments**

k	number of remaining samples
m	number of metastases samples

**Value**

number of monophyletic trees

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calculate_no_trees	<i>calculate_no_trees</i>
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**Description**

Calculate the total number of distinct trees given by Edwards and Cavalli-Sforza, 1963

**Usage**

```
calculate_no_trees(n)
```

**Arguments**

n	number of samples
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**Value**

number of distinct trees

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cluster_probability	<i>cluster_probability</i>
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**Description**

Calculate the probability that a tree where all m metastases form a cluster (have one root) exists by chance

**Usage**

```
cluster_probability(k, m)
```

**Arguments**

k	number of remaining cancer samples of the same phylogeny
m	number of metastases samples

**Value**

probability of cluster by chance

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klm

*klm*


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**Description**

klm

**Usage**

```
klm(phy, drop_na = T, primary_as_PT = T)
```

**Arguments**

phy                      Either a phylo-object (as from `ape::nj()`) or a distance matrix (square matrix).

**Value**

data.frame where rows are metastasis sample-types and columns are k, l, m, and RDS values.

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min\_cluster\_probability

*min\_cluster\_probability*


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**Description**

Calculates the probability that a tree where all m metastases form a cluster (have one root) exists by chance

**Usage**

```
min_cluster_probability(k, m, l)
```

**Arguments**

k                      number of primary tumor region samples  
m                      total number of metastases samples  
l                      number of metastases that actually cluster together

**Value**

probability that a cluster of size l arises by chance

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multibinomial

*multibinomial*


---

### Description

Calculate the product of the binomials

### Usage

```
multibinomial(m, l, cluster_numbers)
```

### Arguments

m	number of remaining cancer samples
l	size of observed metastases cluster
cluster_numbers	vector of possible coexisting clusters of size l for a given phylogeny

### Value

product of binomials

---

no\_trees\_min\_cluster

*no\_trees\_min\_cluster*


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### Description

Calculates the number of trees where m metastases form a cluster of size at least l. Implements Formula (S1) from SI.

### Usage

```
no_trees_min_cluster(k, m, l)
```

### Arguments

k	number of primary tumor region samples
m	number of metastases samples
l	minimal cluster size

### Value

number of distinct tree topologies where l out of m metastases form a cluster

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no_trees_with_clusters	
	<i>no_trees_with_clusters</i>

---

**Description**

Calculates the number of trees where m1, m2, ..., mC, metastases form a cluster (have one root)

**Usage**

```
no_trees_with_clusters(k, clusters)
```

**Arguments**

k	number of remaining cancer samples of the same phylogeny
clusters	vector of number of metastases samples per C clusters

**Value**

number of trees where the given clusters have independent origin

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rds	<i>rds</i>
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**Description**

Calculates the root diversity scores as the probability that a tree where l metastases form a cluster (have one root) exists by chance as defined by Equation (2).

**Usage**

```
rds(k, m, l)
```

**Arguments**

k	number of primary tumor region samples
m	total number of metastases samples
l	number of metastases that actually cluster together

**Value**

probability that a cluster of size l arises by chance

# Index

calculate\_no\_common\_trees, [1](#)

calculate\_no\_trees, [2](#)

cluster\_probability, [2](#)

klm, [3](#)

min\_cluster\_probability, [3](#)

multibinomial, [4](#)

no\_trees\_min\_cluster, [4](#)

no\_trees\_with\_clusters, [5](#)

rds, [5](#)