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:

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calculate_no_common_trees

calculate_no_common_trees

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

---

calculate_no_trees   *calculate_no_trees*

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

Value

number of distinct trees

---

cluster_probability   *cluster_probability*

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

probabilility of cluster by chance

---

min_cluster_probability

min_cluster_probability

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

probabilility that a cluster of size l arises by chance

---

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*

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

---

no_trees_with_clusters

no_trees_with_clusters

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

rds *rds*

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

probabilility that a cluster of size l arises by chance

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