Package ‘dkDNA’

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Title Diffusion Kernels on a Set of Genotypes
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Description
Compute diffusion kernels on DNA polymorphisms, including SNP and bi-allelic genotypes.
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**Description**

Compute diffusion kernels on DNA polymorphisms, including SNP and binary genotypes.

**Author(s)**

Gota Morota <morota@unl.edu> and Masanori Koyama <koyama.masanori@gmail.com>

**References**


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**hypercube**

**Diffusion kernels on bi-allelic genotypes**

**Description**

This function constructs a diffusion kernel on a $p$-dimensional hypercube, where each genotype takes on two possible configurations. This graph is obtained by the $p$-Cartesian graph product of a complete graph $K_2$. It contains $2^p$ vertices corresponding to sequences of genotypes, and two vertices are adjacent if and only if just one SNP locus differs.

**Usage**

`hypercube(X, theta)`

**Arguments**

- `X`: A genotype matrix of $n$ individuals with $p$ bi-allelic genotypes ($n \times p$).
- `theta`: The rate of diffusion.

**Value**

Diffusion kernel matrix of size $n \times n$. This can be viewed as a covariance among individuals given the diffusion rate.

**Author(s)**

Gota Morota <morota@unl.edu> and Masanori Koyama <koyama.masanori@gmail.com>
**snpgird**

**References**


**Examples**

```r
# set a seed
set.seed(4321)

# create a genotype matrix of 5 individuals with 10 bi-allelic genotypes
X <- matrix(sample(c(0,1), 50, prob=c(0.6,0.4), replace=TRUE), ncol=10)

# set the rate of diffusion equal to 1
theta <- 1

# compute a hypercube kernel
hypercube(X, theta)
```

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**snpgird**

**Diffusion kernels on SNP genotypes**

**Description**

This function construct a diffusion kernel on a \( p \)-dimensional SNP grid graph, where each genotype takes on three possible configurations, namely 0 ('aa'), 1 ('Aa'), and 2 ('AA'). This graph is obtained by the \( p \)-Cartesian graph product of a path graph 0-1-2. It contains \( 3^p \) vertices corresponding to sequences of genotypes, and two vertices are adjacent if and only if just one SNP locus differs by 1.

**Usage**

```r
snpgird(X, theta)
```

**Arguments**

- **X**: A genotype matrix of \( n \) individuals with \( p \) SNPs \((n \times p)\).
- **theta**: The rate of diffusion.

**Value**

Diffusion kernel matrix of size \( n \times n \). This can be viewed as a covariance among individuals given the diffusion rate.

**Author(s)**

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References


See Also

snphamming

Examples

# set a seed
set.seed(4321)

# create a genotype matrix of 5 individuals with 10 SNPs
X <- matrix(sample(c(0,1,2), 50, prob=c(0.35, 0.3, 0.35), replace=TRUE), ncol=10)

# set the rate of diffusion equal to 1
theta <- 1

# compute a SNP grid kernel
snpgrid(X, theta)

Description

This function construct a diffusion kernel on a $p$-dimensional SNP hamming graph, where each genotype takes on three possible configurations, namely 0 (`aa`), 1 (`Aa`), and 2 (`AA`). This graph is obtained by the $p$-Cartesian graph product of a complete graph $K_3$. It contains $3^p$ vertices corresponding to sequences of genotypes, and two vertices are adjacent if and only if just one SNP locus differs.

Usage

snphamming(X, theta)

Arguments

X A genotype matrix of $n$ individuals with $p$ SNPs ($n \times p$).
theta The rate of diffusion.
Value

Diffusion kernel matrix of size $n \times n$. This can be viewed as a covariance among individuals given the diffusion rate.

Author(s)

Gota Morota <morota@unl.edu> and Masanori Koyama <koyama.masanori@gmail.com>

References


See Also

snpgrid

Examples

```r
# set a seed
set.seed(4321)

# create a genotype matrix of 5 individuals with 10 SNPs
X <- matrix(sample(c(0,1,2), 50, prob=c(0.35, 0.3, 0.35), replace=TRUE),
ncol=10)

# set the rate of diffusion equal to 1
theta <- 1

# compute a SNP hamming kernel
snphamming(X, theta)
```
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