Package ‘dkDNA’

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Type Package

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**

**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>
References


Examples

# 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)

snpgrid

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

snpgrid(X, theta)

Arguments

X A genotype matrix of n individuals with p SNPs (n × p).
theta The rate of diffusion.

Value

Diffusion kernel matrix of size n × 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>
snphamming

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)

snphamming

Diffusion kernels on SNP genotypes

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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