### Package ‘Kernelize’

#### July 27, 2014

**Type** Package

**Title** Computation of Useful Kernel Matrices

**Version** 1.85

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**Description** This is simply a useful package for computing a number of kernel matrices in R. The C back end speeds up computation of the n by n kernel matrices.

**License** GPL(>=2)

**LazyLoad** yes

**Archs** i386, x64

### R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Pages</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kernelize-package</td>
<td>2</td>
</tr>
<tr>
<td>getKernel.2wayIX</td>
<td>2</td>
</tr>
<tr>
<td>getKernel.dPoly</td>
<td>3</td>
</tr>
<tr>
<td>getKernel.gaussian</td>
<td>3</td>
</tr>
<tr>
<td>getKernel.IBS</td>
<td>4</td>
</tr>
<tr>
<td>getKernel.IBS.weighted</td>
<td>5</td>
</tr>
<tr>
<td>getKernel.linear</td>
<td>5</td>
</tr>
<tr>
<td>getKernel.quadratic</td>
<td>6</td>
</tr>
<tr>
<td>getKernel.squareDiff</td>
<td>6</td>
</tr>
<tr>
<td>getKernel.triangle</td>
<td>7</td>
</tr>
</tbody>
</table>

**Index** 8

1
Kernelize-package  Package for obtaining kernels. ~ package title ~

Description

This package contains functions for obtaining the kernel matrices for use in the kernel machine test. The back end for some kernels is in C.

Details

Package: Kernelize
Type: Package
Version: 1.7
Date: 2012-10-24
License: GNU General License

Author(s)

Michael C. Wu, Seunggeun Lee

References

None

See Also

None

getKernel.2wayIX  Function for estimating the two-way interaction kernel.

Description

This function estimates the linear kernel based on an arbitrary set of inputs. No missing data are allowed.

Usage

getKernel.2wayIX(Z, n, p)

Arguments

Z  n by p matrix of genetic features (e.g. SNP/SNV/CpG/genes etc)

n  Sample size: number of individuals on whom the features have been measured

p  The number of measured features.
getKernel.dPoly

Value
returns an n by n kernel matrix

Author(s)
Michael C. Wu, Seunggeun Lee

getKernel.dPoly Function for estimating the d-th order polynomial kernel.

Description
This function estimates the d-th order polynomial kernel based on an arbitrary set of inputs and fixed d. No missing data are allowed.

Usage
getKernel.dPoly(Z, n, p, d)

Arguments
Z n by p matrix of genetic features (e.g. SNP/SNV/CpG/genes etc)
n Sample size: number of individuals on whom the features have been measured
p The number of measured features.
d The order of the polynomial.

Value
returns an n by n kernel matrix

Author(s)
Michael C. Wu, Seunggeun Lee

getKernel.gaussian Function for estimating the gaussian kernel.

Description
This function estimates the gaussian kernel based on an arbitrary set of inputs. No missing data are allowed.

Usage
getKernel.gaussian(Z, n, p, rho = 1)
Arguments

- **Z**: n by p matrix of genetic features (e.g. SNP/SNV/CpG/genes etc)
- **n**: Sample size: number of individuals on whom the features have been measured
- **p**: The number of measured features.
- **rho**: The scale parameter for the gaussian kernel.

Value

returns an n by n kernel matrix

Author(s)

Michael C. Wu, Seunggeun Lee

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**getKernel.IBS**

*Function for estimating the IBS kernel.*

Description

This function estimates the IBS kernel based on an arbitrary set of inputs. No missing data are allowed.

Usage

getKernel.IBS(Z, n, p)

Arguments

- **Z**: n by p matrix of genetic features (e.g. SNP/SNV etc). This function only really works for genotype data.
- **n**: Sample size: number of individuals on whom the features have been measured
- **p**: The number of measured features.

Value

returns an n by n kernel matrix

Author(s)

Michael C. Wu, Seunggeun Lee
getKernel.IBS.weighted

Function for estimating the weighted IBS kernel.

Description
This function estimates the weighted IBS kernel based on an arbitrary set of inputs. No missing data are allowed. By default the weights are set to be 1/MAF.

Usage
getKernel.IBS.weighted(Z, n, p, weights)

Arguments
Z n by p matrix of genetic features (e.g. SNP/SNV/CpG/genes etc)
n Sample size: number of individuals on whom the features have been measured
p The number of measured features.
weights The weights for the individual variants in the study. They default to 1/MAF

Value
returns an n by n kernel matrix

Author(s)
Michael C. Wu, Seunggeun Lee

getKernel.linear

Function for estimating the linear kernel.

Description
This function estimates the linear kernel based on an arbitrary set of inputs. No missing data are allowed.

Usage
getKernel.linear(Z, n, p)

Arguments
Z n by p matrix of genetic features (e.g. SNP/SNV/CpG/genes etc)
n Sample size: number of individuals on whom the features have been measured
p The number of measured features.

Value
returns an n by n kernel matrix
getKernel.squareDiff

Function for estimating the Square Difference kernel.

Description
This function estimates the Square Difference kernel based on an arbitrary set of inputs. No missing data are allowed.

Usage
getKernel.squareDiff(Z, n, p)

Arguments
Z  n by p matrix of genetic features (e.g. SNP/SNV/CpG/genes etc)
n  Sample size: number of individuals on whom the features have been measured
p  The number of measured features.

Value
returns an n by n kernel matrix

Author(s)
Michael C. Wu, Seunggeun Lee
**getKernel.triangle**  

*Function for estimating the triangle kernel.*

**Description**  
This function estimates the triangle kernel based on an arbitrary set of inputs. No missing data are allowed.

**Usage**  
```
getKernel.triangle(Z, n, p)
```

**Arguments**  
- `Z`  
  n by p matrix of genetic features (e.g. SNP/SNV/CpG/genes etc)  
- `n`  
  Sample size: number of individuals on whom the features have been measured  
- `p`  
  The number of measured features.

**Value**  
returns an n by n kernel matrix

**Author(s)**  
Michael C. Wu, Seunggeun Lee
Index

«Topic package
   Kernelize-package, 2
getKernel.2wayIX, 2
getKernel.dPoly, 3
getKernel.gaussian, 3
getKernel.IBS, 4
getKernel.IBS.weighted, 5
getKernel.linear, 5
getKernel.quadratic, 6
getKernel.squareDiff, 6
getKernel.triangle, 7

Kernelize (Kernelize-package), 2
Kernelize-package, 2