

# Package ‘Kernelize’

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**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

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

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### 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

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

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### 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.

**Value**

returns an n by n kernel matrix

**Author(s)**

Michael C. Wu, Seunggeun Lee

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

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**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

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getKernel.gaussian      *Function for estimating the gaussian kernel.*

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**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.*

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**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

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`getKernel.IBS.weighted`*Function for estimating the weighted IBS kernel.*

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**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

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`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

**Author(s)**

Michael C. Wu, Seunggeun Lee

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getKernel.quadratic    *Function for estimating the quadratic kernel.*

---

**Description**

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

**Usage**

```
getKernel.quadratic(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

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getKernel.squareDiff    *Function for estimating the Square Difference kernel.*

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**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

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`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

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