

# Package ‘collUtils’

October 12, 2022

**Type** Package

**Title** Auxiliary Package for Package ‘CollapsABEL’

**Version** 1.0.5

**Date** 2016-03-26

**Author** Kaiyin Zhong, Fan Liu

**Maintainer** Kaiyin Zhong <kindlychung@gmail.com>

**Depends** R (>= 3.1.3), rJava (>= 0.9-6), Rcpp (>= 0.11.2)

**LinkingTo** Rcpp

**Description** Provides some low level functions for processing PLINK input and output files.

**URL** <https://bitbucket.org/kindlychung/collutils>

**BugReports** <https://bitbucket.org/kindlychung/collutils/issues>

**Suggests** testthat

**SystemRequirements** Java (>= 1.6)

**License** GPL-3

**NeedsCompilation** yes

**Repository** CRAN

**Date/Publication** 2016-03-31 19:15:26

## R topics documented:

|                             |   |
|-----------------------------|---|
| collUtils-package . . . . . | 2 |
| countlines . . . . .        | 3 |
| getJArray . . . . .         | 3 |
| ncols . . . . .             | 4 |
| rBed . . . . .              | 4 |
| readcol . . . . .           | 5 |
| readcols . . . . .          | 5 |
| truncateEndOfFile . . . . . | 6 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>7</b> |
|--------------|----------|

---

collUtils-package      *A auxiliary package for CollapsABEL.*

---

## Description

This package includes some low level functions for processing PLINK input and output files written in Java or C++. Normally you shouldn't need to directly use functions from this package.

## Details

Package: collUtils  
Type: Package  
Version: 1.0  
Date: 2015-06-12  
License: GPL-3

## Author(s)

Kaiyin Zhong Maintainer: Kaiyin Zhong <kindlychung@gmail.com>

## References

To be updated.

## Examples

```
## Not run:  
require(collUtils)  
rbed_obj = rBed("test.bed")  
geno = rbed_obj$readBed()  
geno = getJArray(geno)  
print(geno)  
fn = tempfile()  
f = file(fn, "wb")  
writeBin("a", f)  
writeBin("b", f)  
writeBin("c", f)  
close(f)  
file.info(fn)$size == 6  
truncateEndOfFile(fn, 1)  
  
## End(Not run)
```

---

|            |  |
|------------|--|
| countlines | <i>Count the number of lines in a file</i> |
|------------|--|

---

**Description**

Count the number of lines in a file

**Usage**

```
countlines(fn)
```

**Arguments**

|    |                |
|----|----------------|
| fn | Input filepath |
|----|----------------|

**Value**

A integer for the number of lines

---

|           |                                 |
|-----------|---------------------------------|
| getJArray | <i>Import Java array into R</i> |
|-----------|---------------------------------|

---

**Description**

A thin wrapper around `rJava::.jevalArray`

**Usage**

```
getJArray(mat_ref, na_vals = -9)
```

**Arguments**

|         |                                    |
|---------|------------------------------------|
| mat_ref | Reference object of the Java array |
| na_vals | NA code. Default to -9.            |

**Author(s)**

Kaiyin Zhong

---

|       |   |
|-------|---|
| ncols | <i>Counts the number of columns of whitespace delimited file.</i> |
|-------|---|

---

**Description**

Counts the number of columns of whitespace delimited file.

**Usage**

```
ncols(fn)
```

**Arguments**

|    |                |
|----|----------------|
| fn | Input filepath |
|----|----------------|

**Value**

A integer for the number of columns

---

|      |   |
|------|---|
| rBed | <i>Wrapper for constructor of Bed class</i> |
|------|---|

---

**Description**

Wrapper for constructor of Bed class

**Usage**

```
rBed.bed_path, bytes_snp = NULL, nindiv = NULL)
```

**Arguments**

|           |                                 |
|-----------|---------------------------------|
| bed_path  | character. Path to bed file.    |
| bytes_snp | integer. Bytes per SNP.         |
| nindiv    | integer. Number of individuals. |

**Value**

jobRef object.

**Author(s)**

Kaiyin Zhong

**Examples**

```
## do not run
# rbed_obj = rBed("test.bed")
# geno = rbed_obj$readBed()
# geno = getJArray(geno)
# print(geno)
```

---

|         |  |
|---------|--|
| readcol | <i>Read one column of a whitespace delimited text file</i> |
|---------|--|

---

**Description**

Read one column of a whitespace delimited text file

**Usage**

```
readcol(fileName, colNum, nSkip, maxRowNum)
```

**Arguments**

|           |   |
|-----------|---|
| fileName  | Input filepath  |
| colNum    | An integer. The target column number                  |
| nSkip     | An integer. Number of lines to skip in the beginning. |
| maxRowNum | An Integer. Maximum number of lines to read           |

**Value**

A vector of strings containing the target column

---

|          |   |
|----------|---|
| readcols | <i>Read columns of a whitespace delimited text file</i> |
|----------|---|

---

**Description**

Read columns of a whitespace delimited text file

**Usage**

```
readcols(fn, colsel, nFirstSkipLines, nSkipUnit)
```

**Arguments**

|                 |  |
|-----------------|--|
| fn              | input filepath   |
| colsel          | a vector of target column numbers                        |
| nFirstSkipLines | Integer. Number of lines to skip in the beginning        |
| nSkipUnit       | Integer M. Let the function read one line out of every M |

**Value**

A matrix of strings from selected columns

---

|                   |  |
|-------------------|--|
| truncateEndOfFile | <i>Truncate n bytes from end of file</i> |
|-------------------|--|

---

**Description**

Truncate n bytes from end of file

**Usage**

```
truncateEndOfFile(filename, len)
```

**Arguments**

|          |                                      |
|----------|--------------------------------------|
| filename | character. Filename.                 |
| len      | numeric. Number of bytes to truncate |

**Author(s)**

Kaiyin Zhong

**Examples**

```
## Not run:  
fn = tempfile()  
f = file(fn, "wb")  
writeBin("a", f)  
writeBin("b", f)  
writeBin("c", f)  
close(f)  
file.info(fn)$size == 6  
truncateEndOfFile(fn, 1)  
file.info(fn)$size == 5  
  
## End(Not run)
```

# Index

\* **Compound heterozygosity**

collUtils-package, 2

\* **GWAS**

collUtils-package, 2

\* **Genomics**

collUtils-package, 2

\*

collUtils-package, 2

collUtils (collUtils-package), 2

collUtils-package, 2

countlines, 3

getJArray, 3

ncols, 4

rBed, 4

readcol, 5

readcols, 5

truncateEndOfFile, 6