

# bcRep news

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## Contents

Changes in version 1.3.3 (2016-04-15) . . . . .	1
BUG FIXES . . . . .	1
NEW FEATURES AND FUNCTIONS . . . . .	1
Changes in version 1.3.2 (2016-03-17) . . . . .	1
BUG FIXES . . . . .	1
Changes in version 1.3 (2016-02-25) . . . . .	2
BUG FIXES . . . . .	2
NEW FEATURES AND FUNCTIONS . . . . .	2
Changes in version 1.3 (2016-02-15) . . . . .	2
BUG FIXES . . . . .	2
NEW FEATURES AND FUNCTIONS . . . . .	2
Changes in version 1.2.2 (2015-10-28) . . . . .	2
BUG FIXES . . . . .	2
NEW FEATURES AND FUNCTIONS . . . . .	2
Version 1.0 (2015-10-09) . . . . .	3

### Changes in version 1.3.3 (2016-04-15)

#### BUG FIXES

- \* `clones.filterSize()`: eliminated errors
- \* `clones.shared()`: eliminated errors
- \* `clones.compareGeneUsage()`: eliminated errors

#### NEW FEATURES AND FUNCTIONS

- \* `plotTrueDiversity()`: added option to plot mean diversities
- \* `plotCompareTrueDiversity()`: added option to plot mean diversities

### Changes in version 1.3.2 (2016-03-17)

#### BUG FIXES

- \* `sequences.geneComb()`: eliminated errors
- \* `compare.geneUsage()`: eliminated errors

## Changes in version 1.3 (2016-02-25)

### BUG FIXES

- \* readIMGT(): eliminated errors
- \* clones(): eliminated error message when no clone was found
- \* geneUsage(): eliminated error for JH subgroup usage

### NEW FEATURES AND FUNCTIONS

- \* sequences.mutation.AA() added (proportions of amino acid mutations)
- \* plotSequencesMutationAA() added
- \* sequences.mutation.base() added (proportions of bases around mutations)
- \* plotSequencesMutationBase() added

## Changes in version 1.3 (2016-02-15)

### BUG FIXES

- \* clones.shared(): reduced computation time and memory; copy number of CDR3 sequences changed
- \* sequences.mutation(): added sequence ID's

### NEW FEATURES AND FUNCTIONS

- \* added NEWS
- \* sequences.distance() added (distance/dissimilarity measurements on sequence data)
- \* geneUsage.distance() added (distance/dissimilarity measurements on gene usage data)
- \* dist.PCoA() and plotDistPCoA() added (Principal coordinate analysis on distance data and visualization)

## Changes in version 1.2.2 (2015-10-28)

### BUG FIXES

- \* plotClonesCopyNumber(): added parameter to plot with and without outliers (clone sizes > 75% quantile)
- \* geneUsage(): Combination of gene usage and functionality didn't work for alleles before
- \* sequences.geneComb(): added parallel processing option

### NEW FEATURES AND FUNCTIONS

- \* added Vignette
- \* combineIMGT(): combines IMGT output files from different folders
- \* clones.giniIndex(): calculates Gini Index of clones
- \* clones.filterSize(): filters clones for their size (number, percentage)
- \* clones.filterFunctionality(): filters clones for their functionality
- \* clones.filterJunctionFrame(): filters clones for their junction frame usage
- \* compare.aaDistribution(), plotCompareAADistribution(): compare amino acid distribution

- of different samples
- \* `compare.trueDiversity()`, `plotCompareTrueDiversity()`: compare richness and diversity of different samples
- \* `compare.geneUsage()`, `plotCompareGeneUsage()`: compare gene usage of different samples (subgroup, gene, allele)

**Version 1.0 (2015-10-09)**