

# bcRep news

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## Contents

Changes in version 1.3 (2016-02-15) . . . . .	1
BUG FIXES . . . . .	1
NEW FEATURES AND FUNCTIONS . . . . .	1
Changes in version 1.2.2 (2015-10-28) . . . . .	1
BUG FIXES . . . . .	1
NEW FEATURES AND FUNCTIONS . . . . .	2
Version 1.0 (2015-10-09) . . . . .	2

## 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
- \* `combineIMG()`: combines IMG 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)