

bcRep news

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Changes in version 1.3.5 (2016-06-03)

BUG FIXES

- * `geneUsage.distance()`: eliminated errors
- * `geneUsage()` & `compare.geneUsage()`: eliminated errors

NEW FEATURES AND FUNCTIONS

- * `sequences.mutation.base()`: Added function to calculate proportions of silent mutations from nucleotides
- * `plotSequencesMutationBase()`: added function to plot results of `sequences.mutation.base()`

Changes in version 1.3.4 (2016-04-21)

BUG FIXES

- * clones(): eliminated errors

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
- * `combineIMGOT()`: combines IMGOT 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)