MultiAssayExperiment API Summary (Bioconductor >= 3.21)

Category and Function	Description	Returned class
Constructors		
MultiAssayExperiment	Create a MultiAssayExperiment object	MultiAssayExperiment
ExperimentList	Create an ExperimentList from a List or list	ExperimentList
Accessors		
colData	Get or set data that describe patients / biological units	DataFrame
experiments	Get or set the list of experimental data objects as original classes	ExperimentList
assays	Get the list of experimental data numeric matrices	SimpleList
assay	Get the first experimental data numeric matrix	matrix, matrix-like
sampleMap	Get or set the map relating observations to subjects	DataFrame
metadata	Get or set additional data descriptions	list
rownames	Get row names for all experiments	CharacterList
colnames	Get column names for all experiments	CharacterList
getWithColData	Extract a single assay with whole or assay colData	(varies)
Subsetting		
mae[i, j, k]	Get rows, columns, and/or experiments	MultiAssayExperiment
mae[i, ,]	i: GRanges, character, integer, logical, List, list	MultiAssayExperiment
mae[, j,]	j: character, integer, logical, List, list	MultiAssayExperiment
mae[, , k]	k: character, integer, logical	MultiAssayExperiment
mae[[n]]	Get or set object of arbitrary class from experiments	(varies)
mae[[n]]	n: character, integer, logical	
mae$column	Get or set colData column	vector (varies)
getWithColData(mae, k)	Extract a single assay with associated colData; k: character, integer	(varies)
subsetByColData(mae, ...)	Select rows from the colData and re-harmonize remaining data	MultiAssayExperiment
Management		
prepMultiAssay	Troubleshoot common problems when constructing main class	list
complete.cases	Identify subjects with complete data in all experiments	vector (logical)
replicated	Identify subjects with replicate observations per experiment	list of LogicalLists
anyReplicated	Displays whether there are any replicate observations in each assay	vector (logical)
showReplicated	Show actual technical replicate columns in each assay	list of CharacterLists
mergeReplicates	Merge replicate observations within each experiment, using function	MultiAssayExperiment
intersectRows	Return features that are present for all experiments	MultiAssayExperiment
intersectColumns	Return subjects with data available for all experiments	MultiAssayExperiment
renameColname	Rename the assay column names for a single assay	MultiAssayExperiment
renamePrimary	Rename the colData rownames	MultiAssayExperiment
splitAssay	Separate columns from assays using a 'hitList' of logical vectors	MultiAssayExperiment
makeHitList	Create a 'hitList' list based on patterns for matching assay colnames	list
Reshaping		
longForm	Return a long and tidy DataFrame with optional colData columns	DataFrame
wideFormat	Create a wide DataFrame, 1 row per subject	DataFrame
Combining		
c	Concatenate an experiment to an existing MultiAssayExperiment	MultiAssayExperiment
Coercion		
MultiAssayExperimentToMAF	Convert a MultiAssayExperiment with 'non_syn' and 'syn' assays	maftools::MAF
Export		
exportClass	Save all data from a MultiAssayExperiment to a series of text files ('.csv')	(files)
saveHDF5MultiAssayExperiment	Save a MultiAssayExperient in '.h5' and '.rds' formats similar to HDF5Array::saveHDF5SummarizedExperiment	(files)