Table 1. Summary of the MultiAssayExperiment API (Ramos et al. Can. Res. 2017; DOI: 10.1158/0008-5472.CAN-17-0344)

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
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)
Management		
complete.cases	Identify subjects with complete data in all experiments	vector (logical)
duplicated replicated*	Identify subjects with replicate observations per experiment	list of LogicalLists
anyReplicated	Displays whether there are any replicate observations in each assay	vector (logical)
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
prepMultiAssay	Troubleshoot common problems when constructing main class	list
Reshaping		
longFormat	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

Note. *assay* refers to a procedure for measuring the biochemical or immunological activity of a sample, e.g. RNA-seq, segmented copy number, and somatic mutation calls would be considered three different assays. *experiment* refers to the application of an assay to a set of samples. In general it is assumed that each experiment uses a different assay type, although an assay type may of course be repeated in different experiments. *mae* refers to a MultiAssayExperiment object. *subject* refers to patient, cell line, or other biological unit. *observation* refers to results of an assay, e.g. gene expression, somatic mutations, etc. *features* refer to measurements returned by the assays, labeled by row names or genomic ranges.

* "duplicated" was deprecated in Bioconductor 3.7 and replaced by "replicated"