A

Metadata

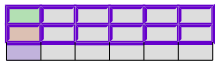| id	machine_name	date	...	condition	sex	...	p
xxx...xx|x	machine_001	2016-09-01	...	A	M	...	p_1
xxx...xx|y	machine_001	2016-09-01	...	B	M	...	p_2
xxx...xx|z	machine_002	2016-09-03	...	A	F	...	p_3
⋮	⋮	⋮	⋱	⋮	⋮	⋱	⋮
n	$machine_n$	$date_n$	...	$condition_n$	sex_n	...	p_n

Platform fields   Experiment fields

+

Data

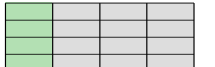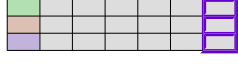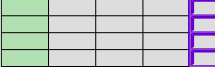| id	t	activity	...	q
xxx...xx|x	1	1	⋱	$q_{1,1}$
xxx...xx|x	2	0	⋱	$q_{1,2}$
xxx...xx|x	3	0	⋱	$q_{1,3}$
xxx...xx|x	⋮	⋮	⋱	⋮
xxx...xx|y	⋮	⋮	⋱	⋮
xxx...xx|z	1	0	⋱	$q_{3,1}$
xxx...xx|z	2	2	⋱	$q_{3,2}$
xxx...xx|z	3	0	⋱	$q_{3,3}$
xxx...xx|z	⋮	⋮	⋱	⋮
⋮	⋮	⋮	⋱	⋮
n	⋮	⋮	⋱	q_{n,k_n}

B

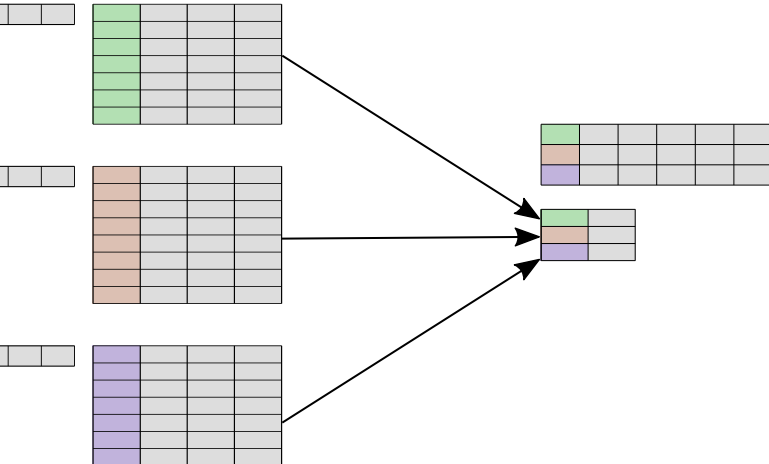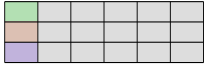|	Metadata	Data

Select	`dt[CRITERIA, meta = TRUE]`
	
	`> male_meta <- dt[sex == "M",`
	`                  meta = TRUE]`
		`dt[CRITERIA]`
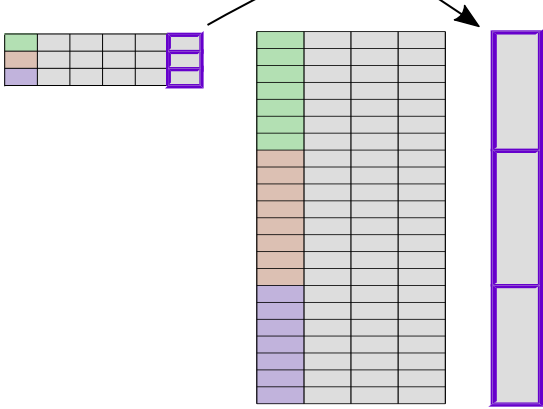		
		`> late_dt <- dt[t > 5]`
		
		Note: metadata is updated when selection removes all data from one id.

Alter, create & delete (meta)variables	`dt[, X := value, meta = TRUE]`
	
	`> dt[, genotype := "wt", meta = TRUE]`
	`> dt[, sex := NULL] #delete sex`
		`dt[, Y := value]`
		
		`> dt[, t_2 := t-1]`
		`> dt[, t := NULL] #delete t`
		
		Note: update data in place.
		No copy of dt in memory.

Expand metavariables as variables	`dt[xmv(X)]`
	
	`> dt <- dt[xmv(sex) == "M"]`
	`> dt[, s := xmv(sex)]`	

Aggregate & summary	`dt[, OPERATION, by = id]`
	
	`> dt <- dt[,.(`
	`         mean_act = mean(activity)`
	`         ), by = id]`
	
	`> dt[, .N, by = id] # count reads per id`
		OPERATION

Join data & metadata	`rejoin(dt)`
	
	`> full_table <- rejoin(dt)`
	
	Note: used mostly after aggregation or preprocessing
		REJOIN