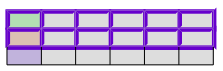
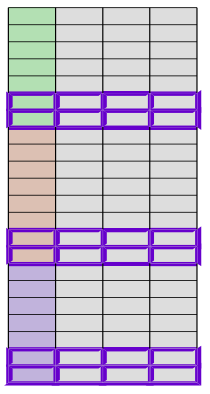
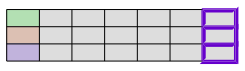
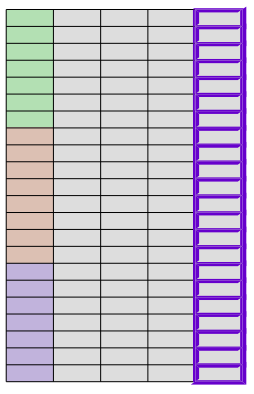
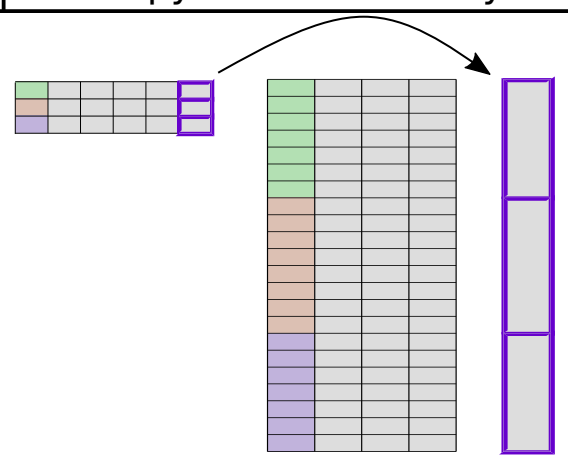
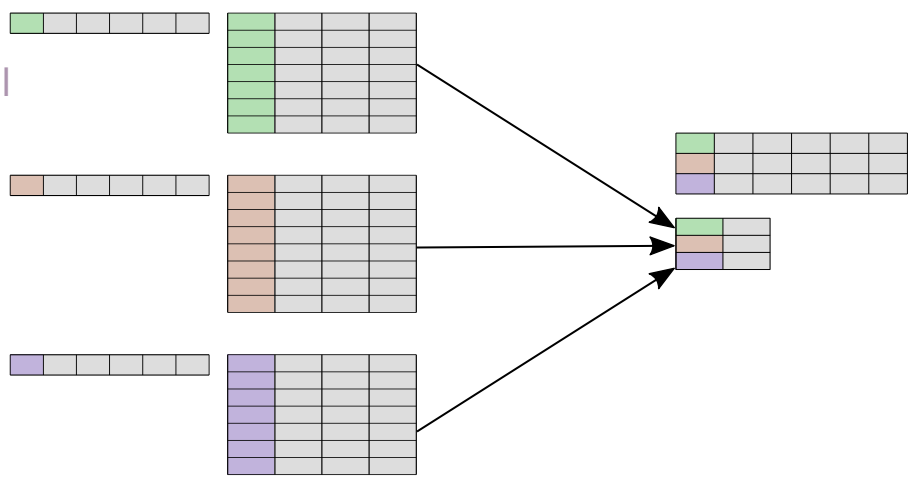
	Metadata	Data
Select	**dt[CRITERIA, meta = TRUE]**  *# to subet the metadata only for males* *> male_meta <- dt[sex == "M",* *meta = TRUE]*	**dt[CRITERIA]** *# to keep only data > 5s* *> late_dt <- dt[t > 5]* Note: metadata is updated when selection removes all data from one id. 
Alter, create & delete (meta)variables	**dt[, X := value, meta = TRUE]**  *# to create a metavariable set to "wt"* *> dt[, genotype := "wt", meta = TRUE]* *# delete* *> dt[, sex := NULL, meta = TRUE]*	**dt[, Y := value]** *# to create t_2 (t - 1)* *> dt[, t_2 := t - 1]* *# to delete t* *> dt[, t := NULL]* Note: update data in place. No copy of dt in memory. 
Expand metavariables as variables	**dt[xmv(X)]** *# to select data with sex* *> dt <- dt[xmv(sex) == "M"]* *# to copy a metavariable as a variable* *> dt[, s := xmv(sex)]*	
Aggregate & summary	**dt[, OPERATION, by = id]** *# to compute mean activity, per individual* *> dt <- dt[,.(* *mean_act = mean(activity)* *), by = id]* *# to count reads per id* *> dt[, .N, by = id]*	**OPERATION** 
Join data & metadata	**rejoin(dt)** *# to reunite data and metadata* *> full_table <- rejoin(dt)* Note: used mostly after aggregation or preprocessing	**REJOIN**