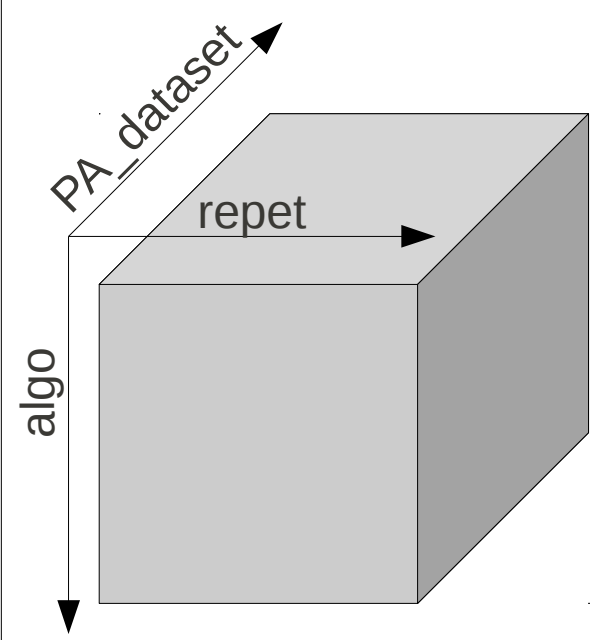
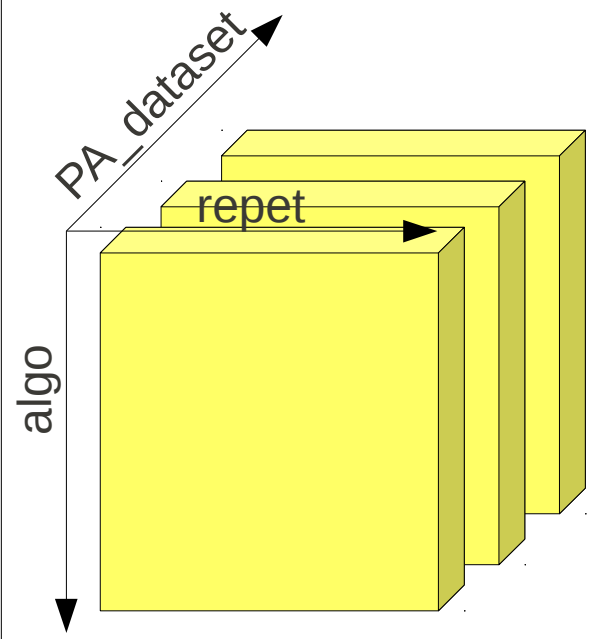
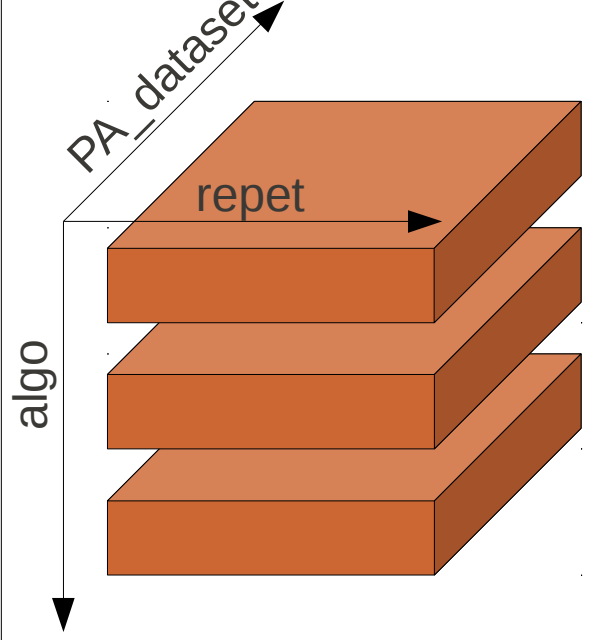
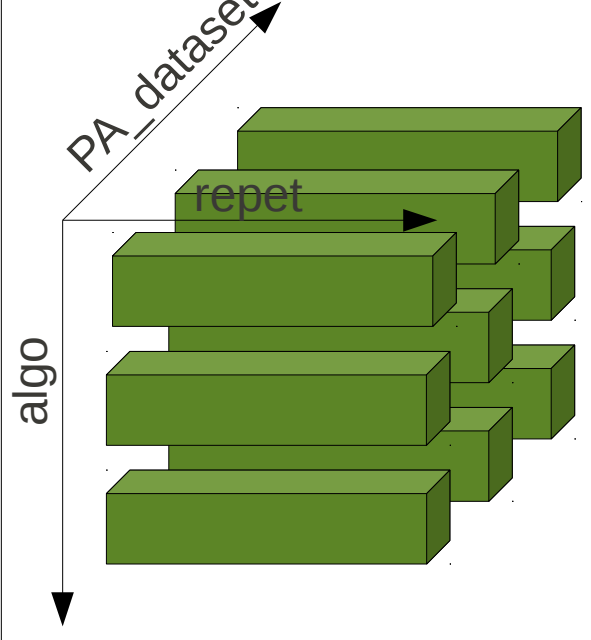
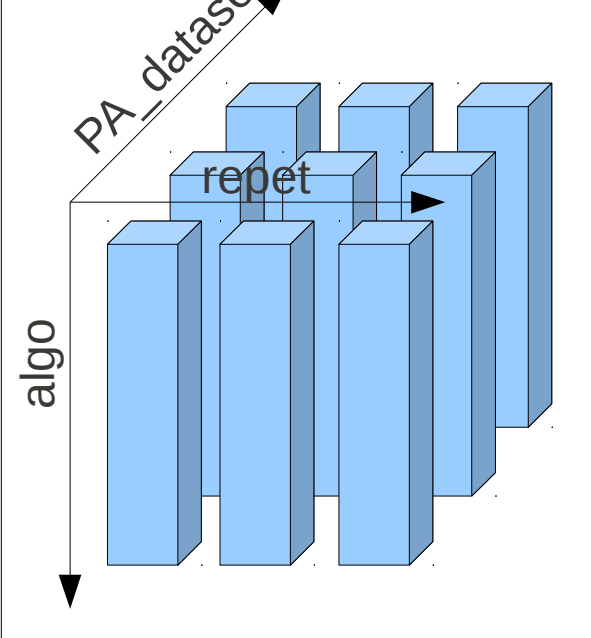


Ensemble Modelling : available models combination
(em.by argument setting)

The following table shows how models built at **BIOMOD_Modelling(...)** step can be combined to construct some ensemble models. This models associations are controlled by the **em.by** parameter of **BIOMOD_EnsembleModeling(...)** function. Several ensemble modelling algorithms can be set up (e.g. Mean of probabilities, median of probabilities, confidence intervals, committee averaging... see **BIOMOD_EnsembleModeling(...)** help file for more details) All ensemble models are evaluated according to defined evaluation metrics (data used for models evaluation exposed in table) and could be projected later using **BIOMOD_EnsembleForecasting(...)** function.

Models can be assembled following 3 dimensions : algo (e.g. GLM, GAM...), PA_dataset (e.g. PA1, PA2... or AllData if no pseudo-absences selection done) and repetition (full, rep1, rep2...). If one of these dimension is 1 (e.g. If no pseudo absences selection done then PA_dataset will be only 'AllData', if no repetition done then repet will be only 'full'...), some ensemble models can be equivalent.

Graphical representation	'em.by' value	Remarks
	'all'	<ul style="list-style-type: none">• 1 ensemble model built.• Ensemble models evaluated over evaluation data if some have been entered at BIOMOD_FormatingData(...) step. If not, the union of all PA_dataset points is used as reference. In the latest case, all 'NA' points (pseudo-absences) are considered as absences. This approach is not perfectly fair because some points used for individual models calibration are reused for ensemble models evaluation.
	'PA_dataset'	<ul style="list-style-type: none">• Number of Pseudo absences selection computed ensemble model built.• Ensemble models evaluated over evaluation data if some have been entered at BIOMOD_FormatingData(...) step. If not the whole corresponding PA_dataset is taken as reference.
	'algo'	<ul style="list-style-type: none">• Number of model algorithms ensemble model built.• Ensemble models evaluated over evaluation data if some have been entered at BIOMOD_FormatingData(...) step. If not, the union of all PA_dataset points is used as reference. In the latest case, all 'NA' points (pseudo-absences) are considered as absences. This approach is not perfectly fair because some points used for individual models calibration are reused for ensemble models evaluation.
	'PA_dataset+algo'	<ul style="list-style-type: none">• Number of model algorithms x Number of Pseudo absences selection computed ensemble model built.• Ensemble models evaluated over evaluation data if some have been entered at BIOMOD_FormatingData(...) step. If not the whole corresponding PA_dataset is taken as reference.
	'PA_dataset+repet'	<ul style="list-style-type: none">• Number of Pseudo absences selection computed x Number of repetitions ensemble model built.• Ensemble models evaluated over evaluation data if some have been entered at BIOMOD_FormatingData(...) step. If not, the union of all PA_dataset points is used as reference. In the latest case, all 'NA' points (pseudo-absences) are considered as absences. This approach is not perfectly fair because some points used for individual models calibration are reused for ensemble models evaluation.