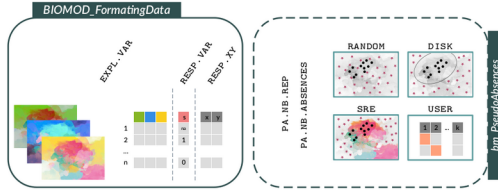


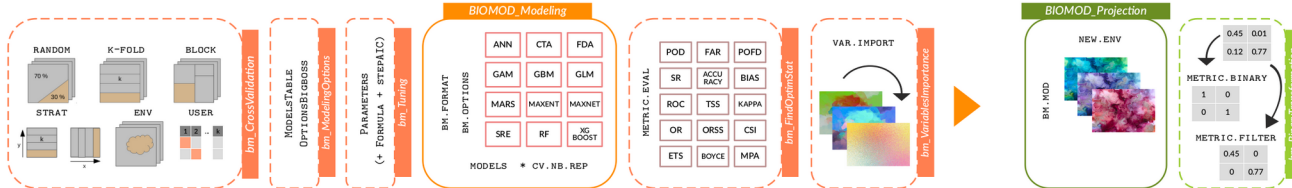


Species distribution modeling, calibration and evaluation, ensemble modeling

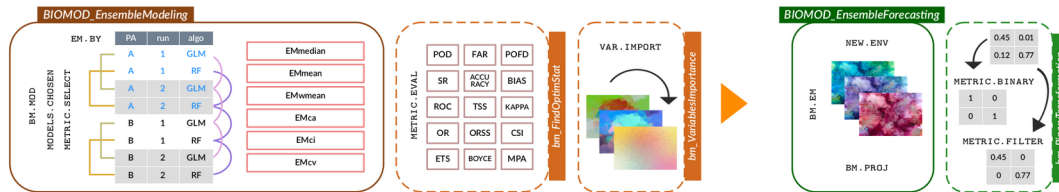
DATA formatting



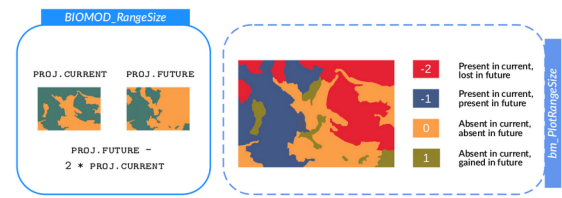
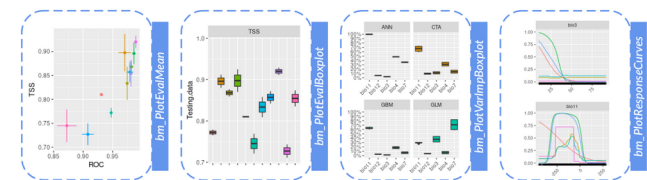
SINGLE models



ENSEMBLE models



OUTPUT & PLOT functions





Species distribution modeling, calibration and evaluation, ensemble modeling

DATA formatting

BIOMOD_FormatingData

Formating data Pseudo-absences

SINGLE models

Cross-validation Modeling options Tuning

BIOMOD_Modeling

ANN	CTA	FDA
GAM	GBM	GLM
MARS	MAXENT	MAXNET
SRE	RF	SISBOOST

MODELS * CV.NB.REP

METRIC_EVAL

POD	FAR	POFD
SR	ACCURACY	BIAS
ROC	TSS	KAPPA
OR	ORSS	CSI
ETS	BOYCE	MPA

VAR_IMPORT

bm_VariableImportance

BIOMOD_Projection

NEW_ENV

BM_MOD

METRIC_BINARY

0.45	0.01
0.12	0.77
1	0
0	1

METRIC_FILTER

0.45	0
0	0.77

bm_BinaryTransformation

OUTPUT & PLOT functions

bm_PlotEvalMean

bm_PlotEvalBoxplot

bm_PlotEvalBoxplot

bm_PlotResponseCurves

ENSEMBLE models

BIOMOD_EnsembleModeling

EH_BY	PA	run	algo	
A	1	1	GLM	EMmedian
		2	RF	EMmean
		2	GLM	EMvmean
B	1	1	RF	EMca
		2	GLM	EMcl
B	2	1	RF	EMcv
		2	RF	

METRIC_EVAL

POD	FAR	POFD
SR	ACCURACY	BIAS
ROC	TSS	KAPPA
OR	ORSS	CSI
ETS	BOYCE	MPA

VAR_IMPORT

bm_VariableImportance

BIOMOD_EnsembleForecasting

NEW_ENV

BM_EH

BM_PROJ

METRIC_BINARY

0.45	0.01
0.12	0.77
1	0
0	1

METRIC_FILTER

0.45	0
0	0.77

bm_BinaryTransformation

BIOMOD_RangeSize

PROJ_CURRENT

PROJ_FUTURE

2 * PROJ_CURRENT

bm_PlotRangeSize

- 2 Present in current, lost in future
- 1 Present in current, present in future
- 0 Absent in current, absent in future
- 1 Absent in current, gained in future



Species distribution modeling,
calibration and evaluation,
ensemble modeling

DATA formatting

BIOMOD_FormingData

Formating data
Pseudo-absences

SINGLE models

Cross-validation
Modeling options
Tuning

BIOMOD_Modeling

Single models
Evaluation
Variables' importance

BIOMOD_Projection

NEW_ENV

BM_H0D

METRIC_BINARY

0.45	0.01
0.12	0.77
1	0
0	1

METRIC_FILTER

0.45	0
0	0.77

bm_BinaryTransformation

OUTPUT & PLOT functions

bm_PlotEvalMean
bm_PlotEvalBoxplot
bm_PlotEvalBarplot
bm_PlotEvalResponseCurves

ENSEMBLE models

BIOMOD_EnsembleModeling

Ensemble models
Evaluation
Variables' importance

BIOMOD_EnsembleForecasting

NEW_ENV

BM_EN

BM_PROJ

METRIC_BINARY

0.45	0.01
0.12	0.77
1	0
0	1

METRIC_FILTER

0.45	0
0	0.77

bm_BinaryTransformation

BIOMOD_RangeSize

PROJ_CURRENT PROJ_FUTURE

2 * PROJ_CURRENT

bm_ProfRangeSize

- 2 Present in current, lost in future
- 1 Present in current, present in future
- 0 Absent in current, absent in future
- 1 Absent in current, gained in future

Species distribution modeling,
calibration and evaluation,
ensemble modeling



DATA formatting

BIOMOD_FormatingData

Formating data
Pseudo-absences

SINGLE models

BIOMOD_Modeling

Cross-validation
Modeling options
Tuning

Single models
Evaluation
Variables' importance

ENSEMBLE models

BIOMOD_EnsembleModeling

Ensemble models
Evaluation
Variables' importance

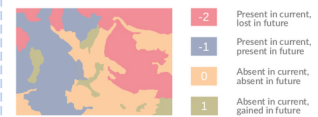
BIOMOD_Projection

Projection
Binary transformation

OUTPUT & PLOT functions

BIOMOD_RangeSize

OUTPUT & PLOT functions





Species distribution modeling,
calibration and evaluation,
ensemble modeling

DATA formatting

BIOMOD_FormatingData

Formating data
Pseudo-absences

SINGLE models

Cross-validation
Modeling options
Tuning

BIOMOD_Modeling

Single models
Evaluation
Variables' importance

BIOMOD_Projection

Projection
Binary transformation

OUTPUT & PLOT functions

Graphical representations

ENSEMBLE models

BIOMOD_EnsembleModeling

Ensemble models
Evaluation
Variables' importance

BIOMOD_EnsembleModeling

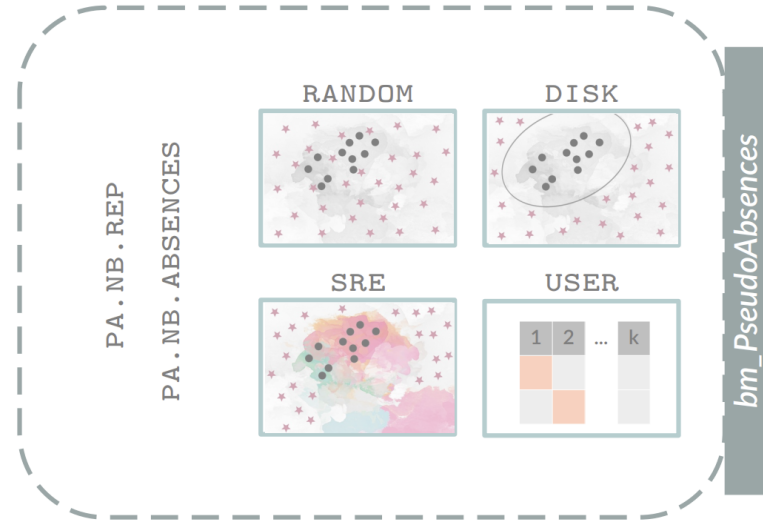
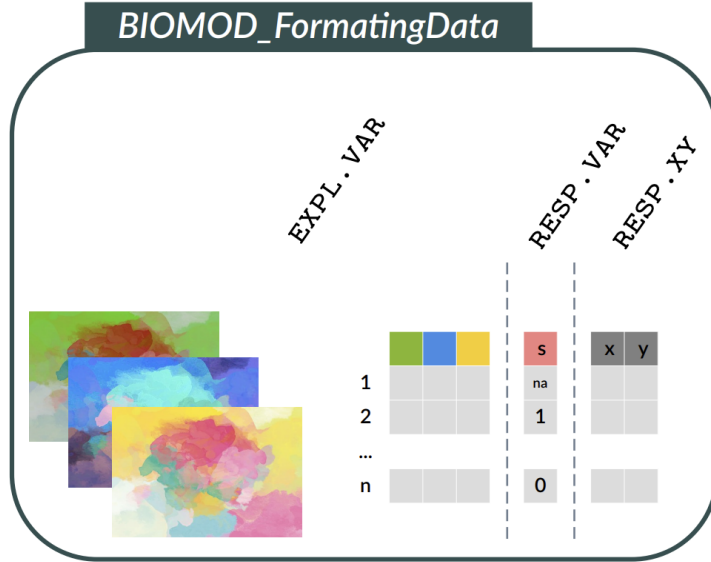
Projection
Binary transformation

BIOMOD_RangeSize

Range change

1. Formatting data

► presences-absences

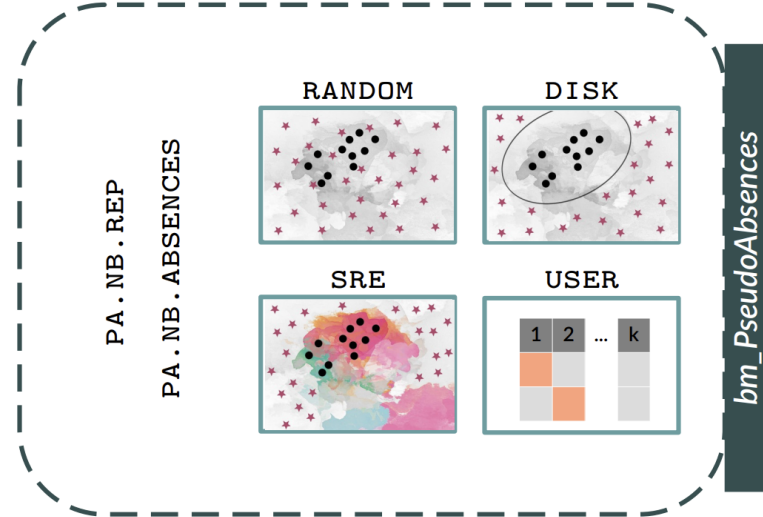
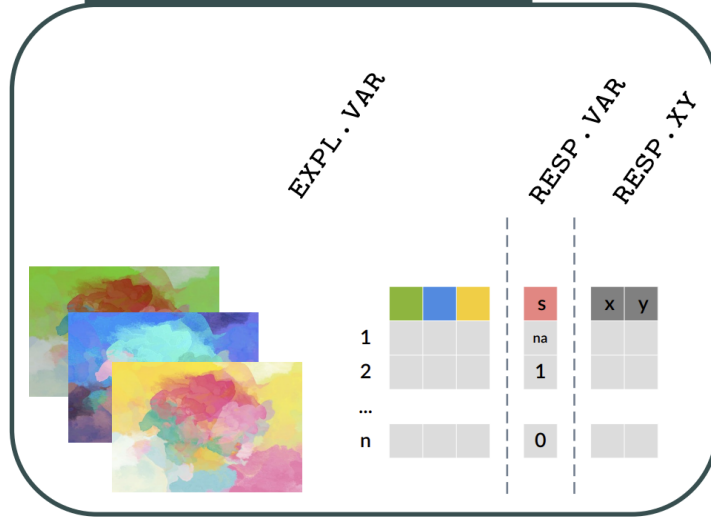


Species occ
Environment

1. Formating data

- › presence-only data
- › avoid to mix with real absences

BIOMOD_FormatingData



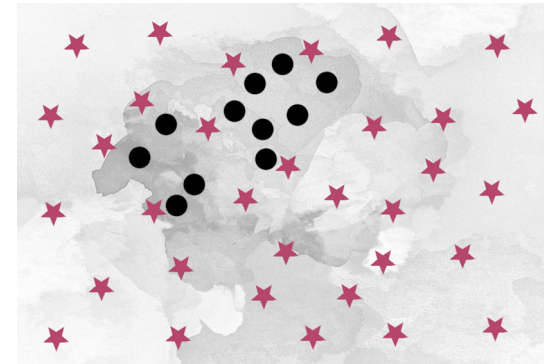
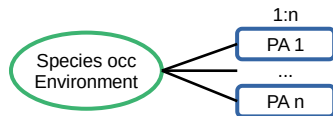
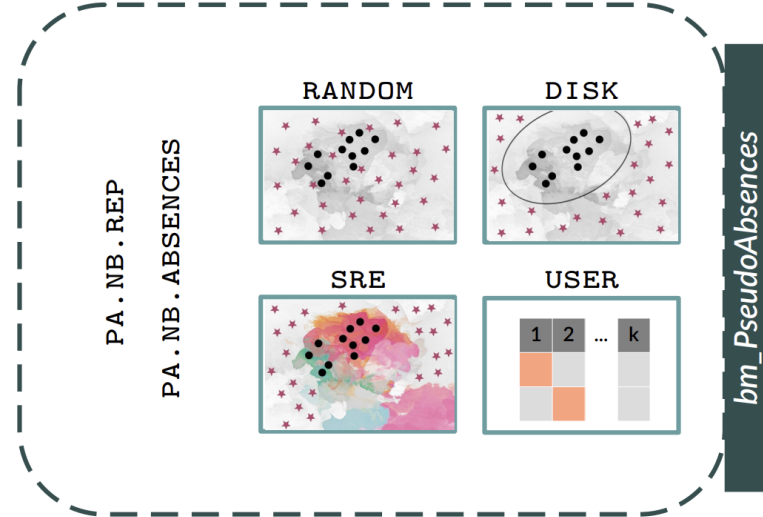
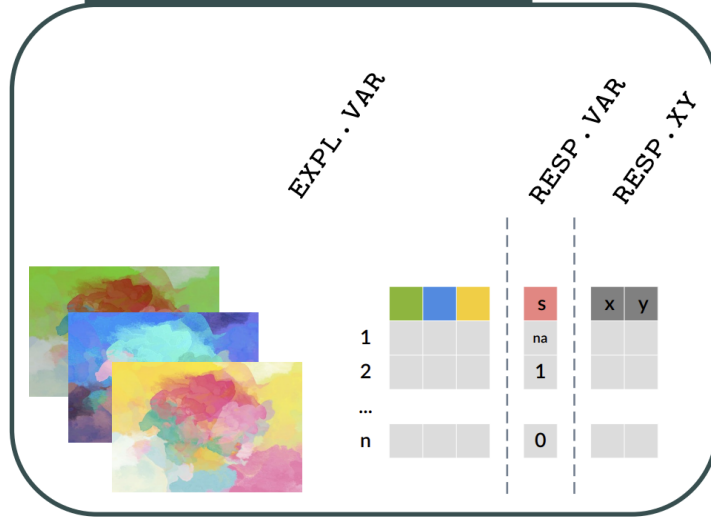
Species occ
Environment



1. Formating data

- **presence-only** data
- *avoid to mix with real absences*
- **random** : sampling potentially biased / non-exhaustive

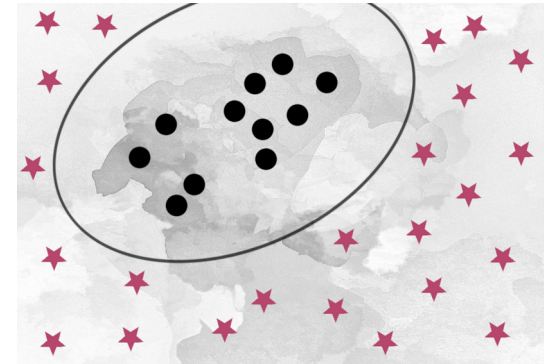
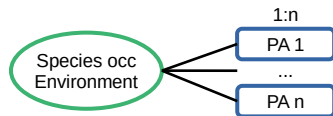
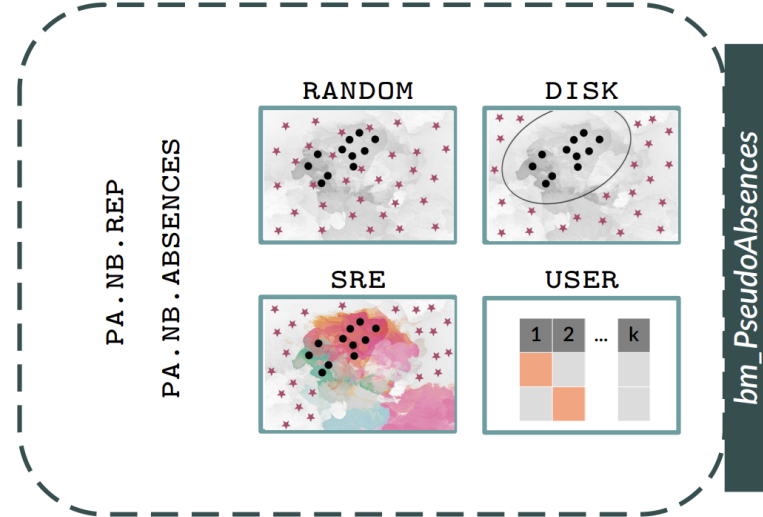
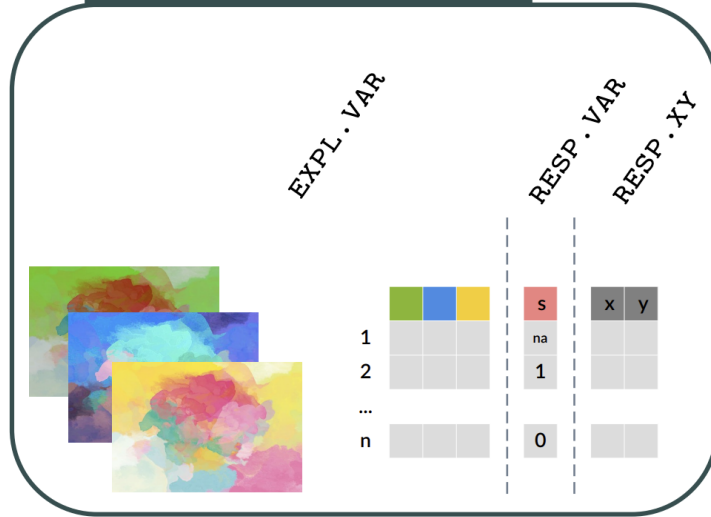
BIOMOD_FormatingData



1. Formating data

- **presence-only** data
- *avoid to mix with real absences*
- **random** : sampling potentially biased / non-exhaustive
- **disk** : geographic niche well sampled

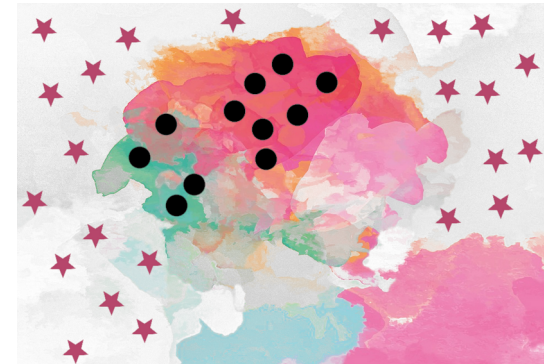
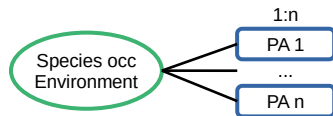
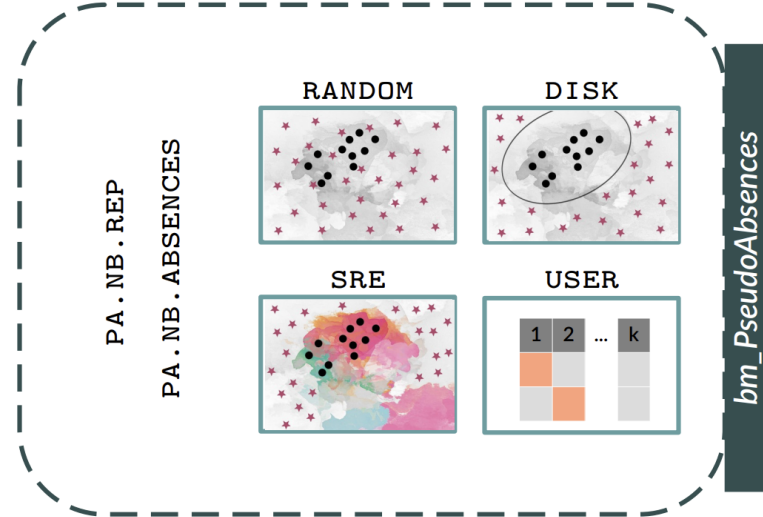
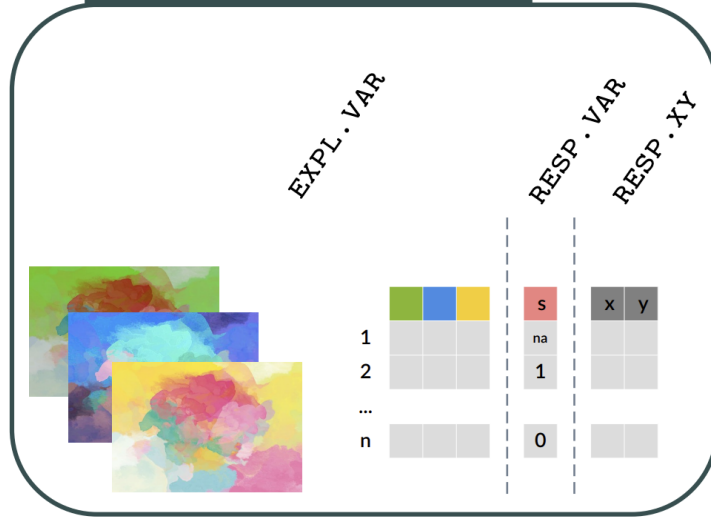
BIOMOD_FormatingData



1. Formating data

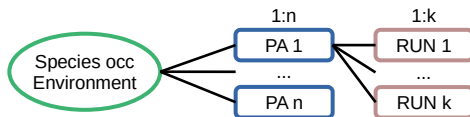
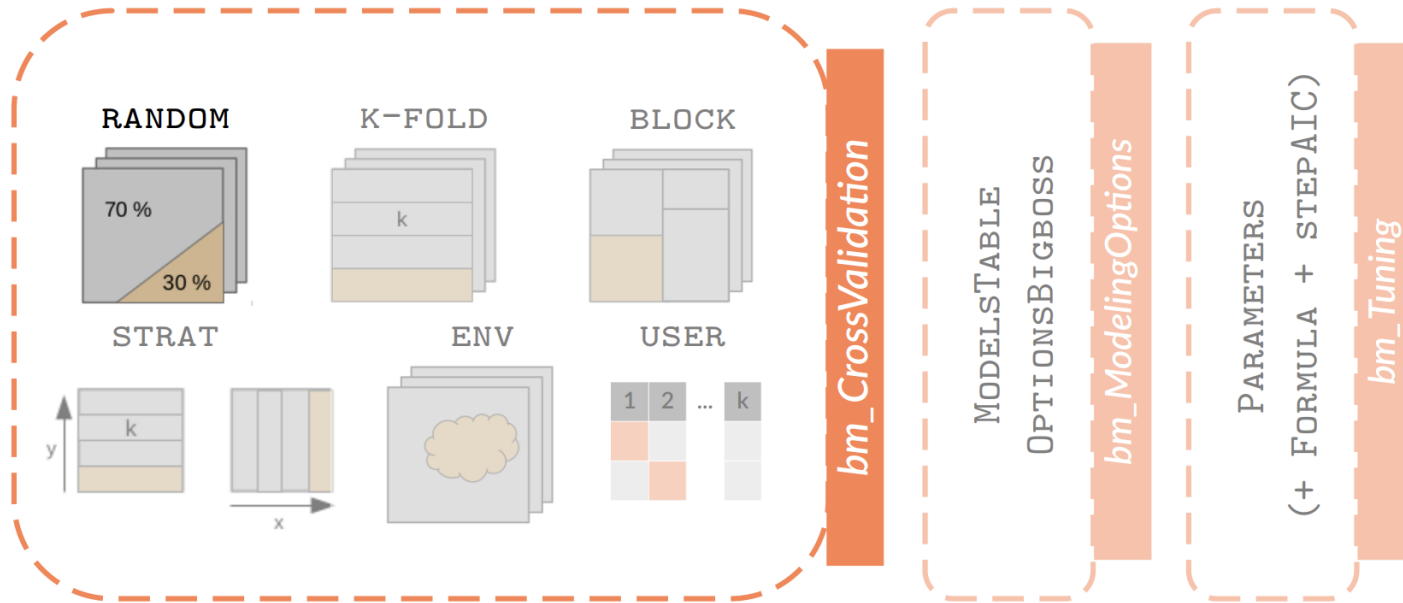
BIOMOD_FormatingData

- **presence-only** data
- *avoid to mix with real absences*
- **random** : sampling potentially biased / non-exhaustive
- **disk** : geographic niche well sampled
- **SRE** : environmental niche well sampled



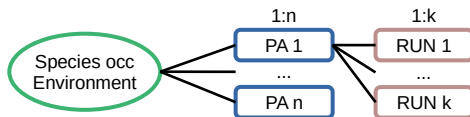
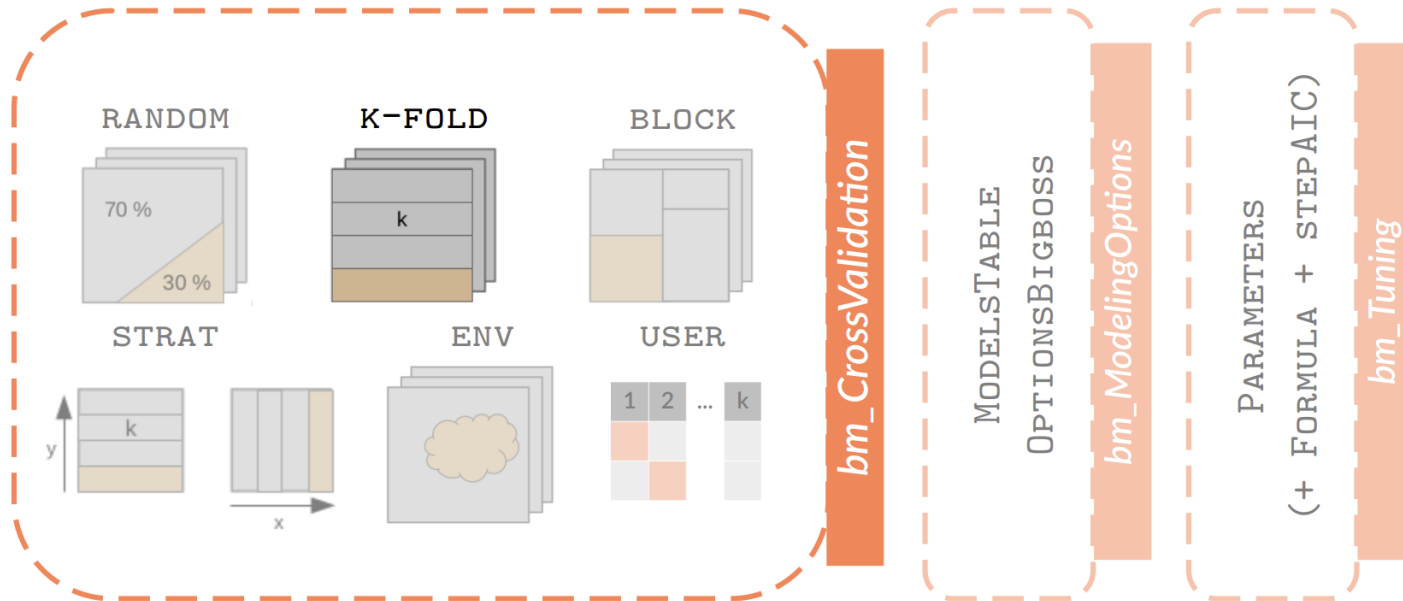
1. Formating data

- ▶ simple calibration / validation split at the modeling step, and repeated nb.rep times



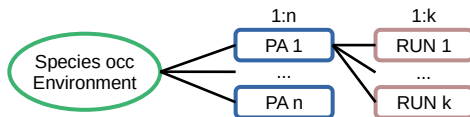
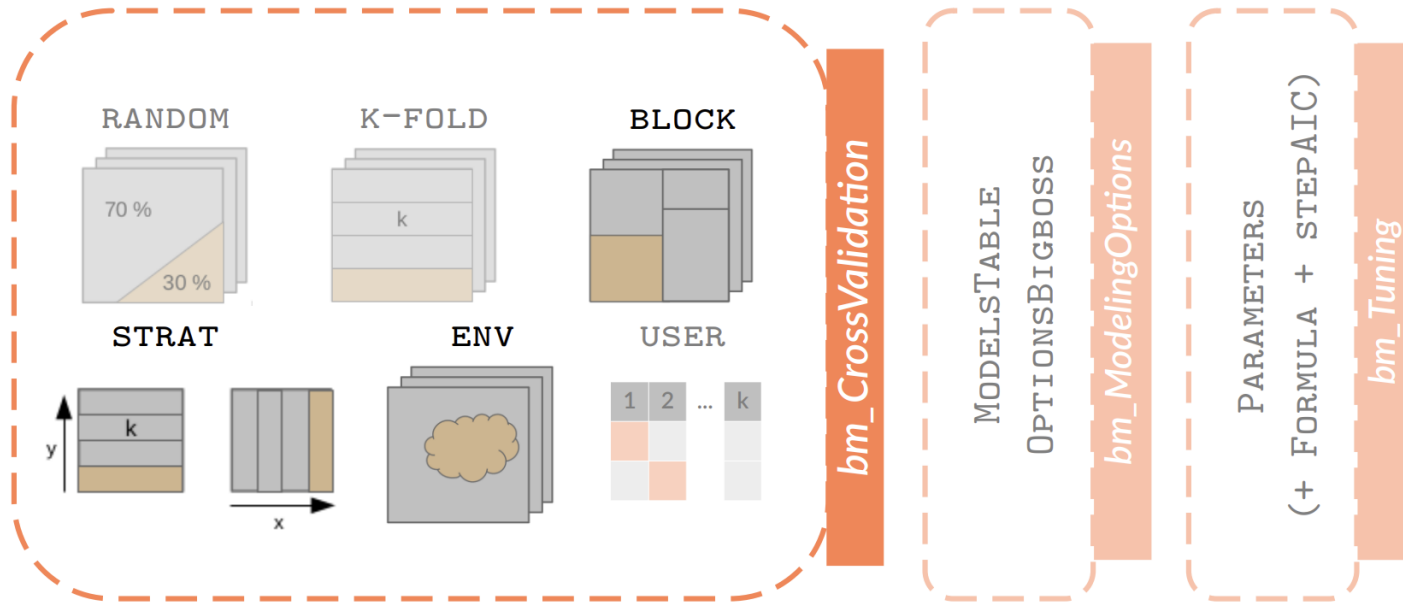
1. Formating data

- ▶ simple calibration / validation split at the modeling step, and repeated nb.rep times
- ▶ **k-fold** : partition data into k sub-dataset, and repeated nb.rep times



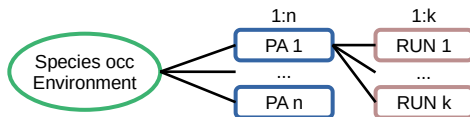
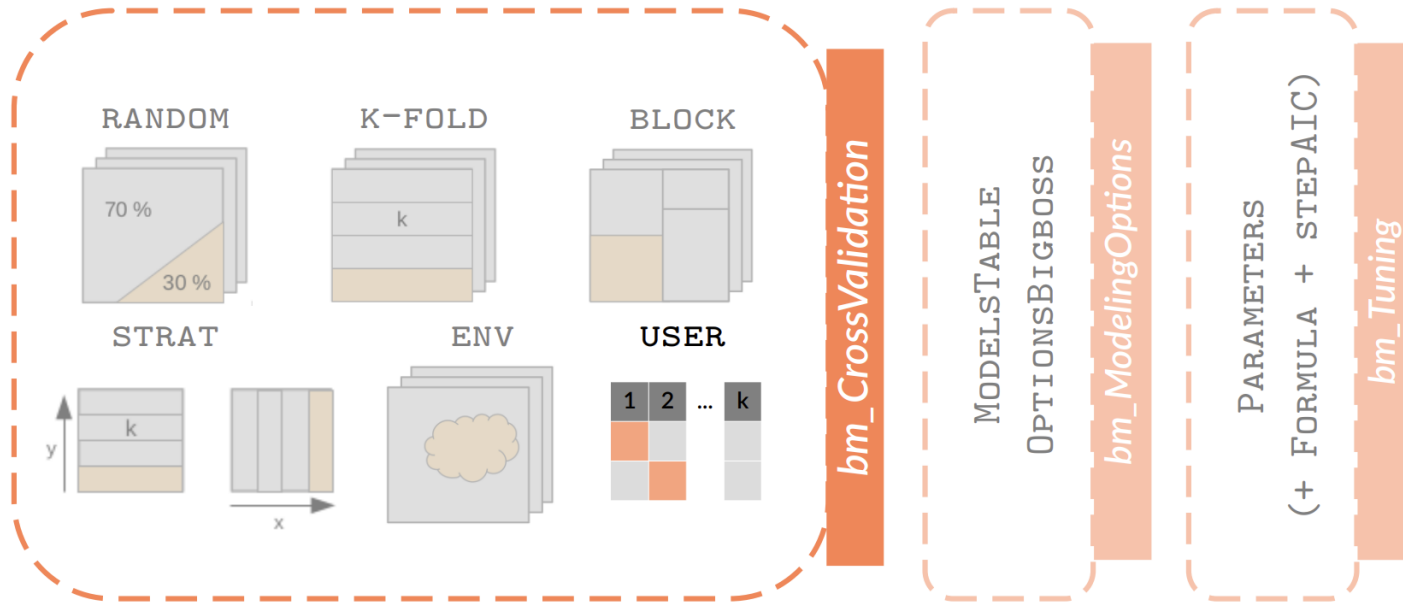
1. Formating data

- ▶ simple calibration / validation split at the modeling step, and repeated nb.rep times
- ▶ **k-fold** : partition data into k sub-dataset, and repeated nb.rep times
- ▶ **stratified** : partition data into k sub-dataset (x, y, both, block, env)



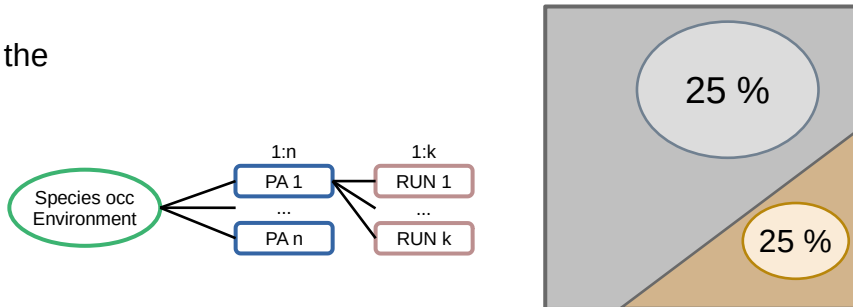
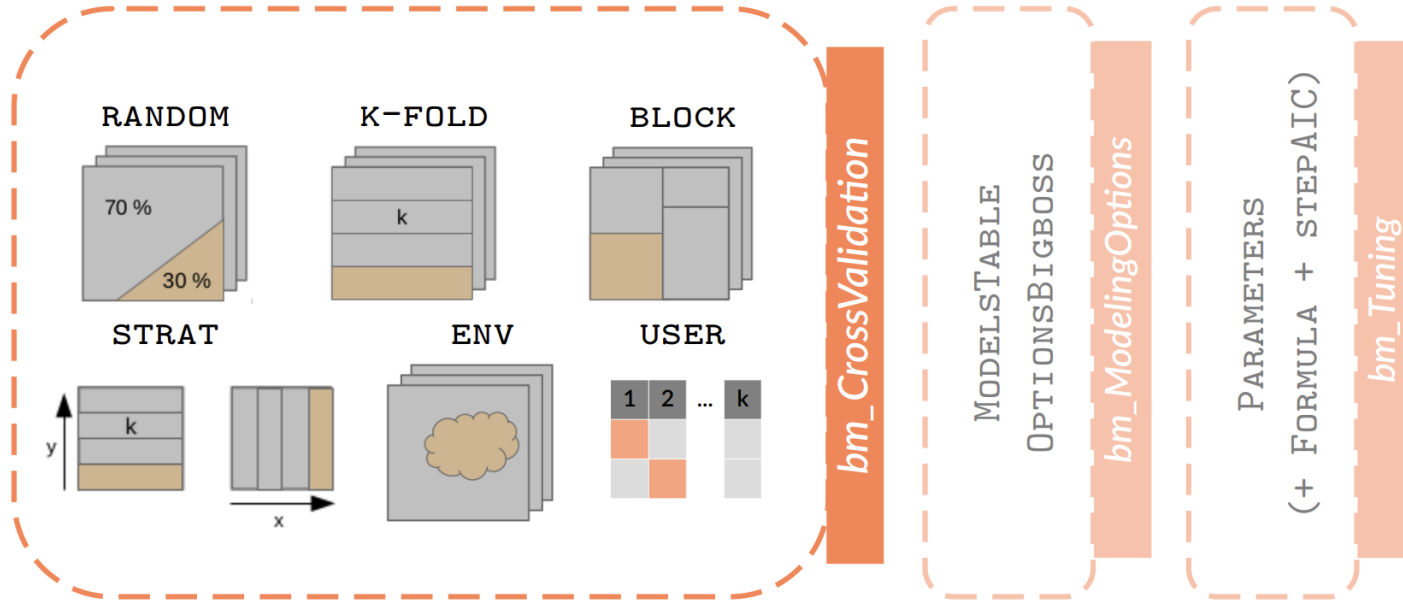
1. Formating data

- ▶ simple calibration / validation split at the modeling step, and repeated nb.rep times
- ▶ **k-fold** : partition data into k sub-dataset, and repeated nb.rep times
- ▶ **stratified** : partition data into k sub-dataset (x, y, both, block, env)
- ▶ **user defined**



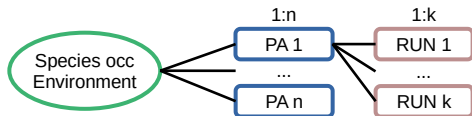
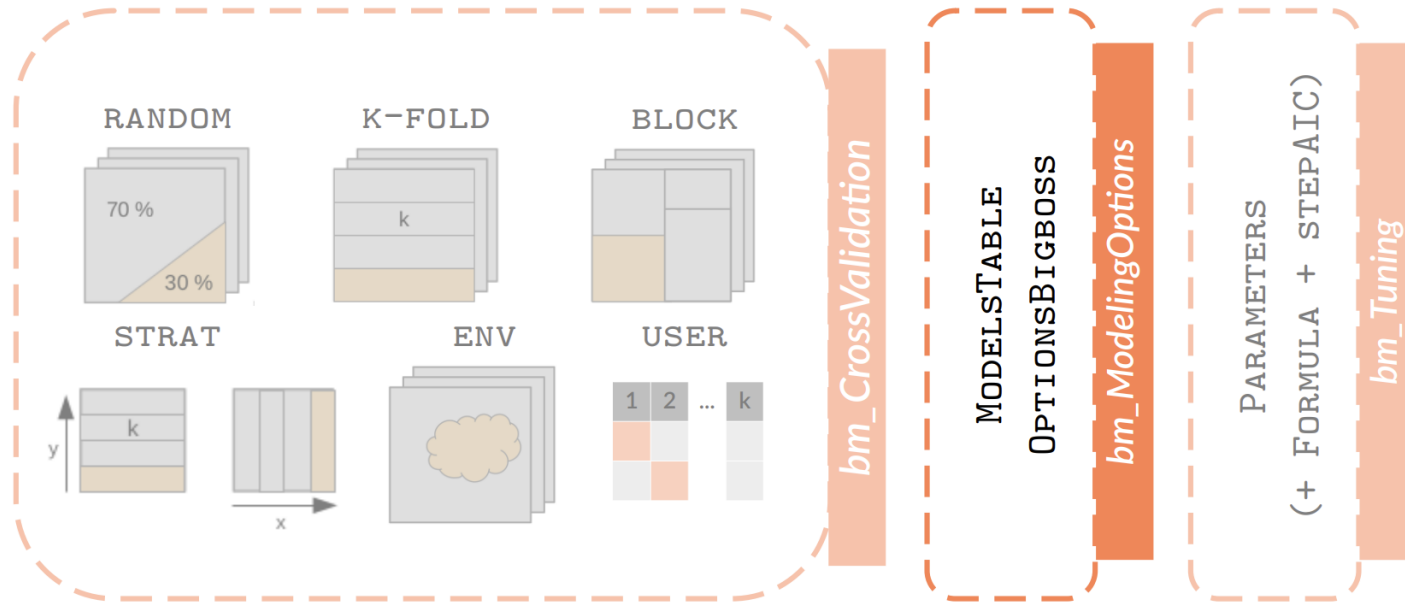
1. Formating data

- ▶ simple calibration / validation split at the modeling step, and repeated nb.rep times
- ▶ **k-fold** : partition data into k sub-dataset, and repeated nb.rep times
- ▶ **stratified** : partition data into k sub-dataset (x, y, both, block, env)
- ▶ **user defined**
- ▶ **balance** : keep the prevalence of presences (or absences) in sub-dataset



1. Formating data

- ▶ 11 types of models, 14 single models
- ▶ 1 coded in biomod2, 1 external software, 12 other R packages



```
> ModelsTable
  model type package func train
1 ANN binary nnet nnet avNNet
2 CTA binary rpart rpart rpart
3 FDA binary mda fda fda
4 GAM binary gam gam gamLoess
5 GAM binary mgcv bam bam
6 GAM binary mgcv gam gam
7 GBM binary gbm gbm gbm
8 GLM binary stats glm glm
9 MARS binary earth earth earth
10 MAXENT binary MAXENT MAXENT ENMevaluate
11 MAXNET binary maxnet maxnet maxnet
12 RF binary randomForest randomForest rf
13 SRE binary biomod2 bm_SRE bm_SRE
14 XGBOOST binary xgboost xgboost xgbTree
```


1. Formating data

- ▶ 11 types of models, 14 single models
- ▶ 1 coded in biomod2, 1 external software, 12 other R packages
- ▶ **default** : extracted from functions

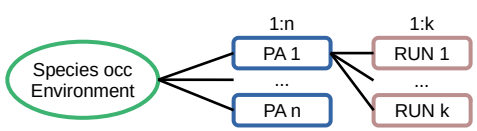
```
nnet package:nnet R Documentation
Fit Neural Networks
Description:
  Fit single-hidden-layer neural network, possibly with skip-layer
  connections.
Usage:
  nnet(x, ...)
## S3 method for class 'formula'
nnet(formula, data, weights, ...,
      subset, na.action, contrasts = NULL)
## Default S3 method:
nnet(x, y, weights, size, Wts, mask,
      linout = FALSE, entropy = FALSE, softmax = FALSE,
      censored = FALSE, skip = FALSE, rang = 0.7, decay = 0,
      maxit = 100, Hess = FALSE, trace = TRUE, MaxNWts = 1000,
      abstol = 1.0e-4, reltol = 1.0e-8, ...)
```

MODELSTABLE
OPTIONSBIGBOSS

bm_ModelingOptions

PARAMETERS
(+ FORMULA + STEPAIC)

bm_Tuning

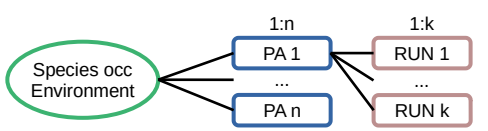


> ModelsTable					
	model	type	package	func	train
1	ANN	binary	nnet	nnet	avNNet
2	CTA	binary	rpart	rpart	rpart
3	FDA	binary	mda	fda	fda
4	GAM	binary	gam	gam	gamLoess
5	GAM	binary	mgcv	bam	bam
6	GAM	binary	mgcv	gam	gam
7	GBM	binary	gbm	gbm	gbm
8	GLM	binary	stats	glm	glm
9	MARS	binary	earth	earth	earth
10	MAXENT	binary	MAXENT	MAXENT	ENMevaluate
11	MAXNET	binary	maxnet	maxnet	maxnet
12	RF	binary	randomForest	randomForest	rf
13	SRE	binary	biomod2	bm_SRE	bm_SRE
14	XGBOOST	binary	xgboost	xgboost	xgbTree

1. Formating data

- ▶ 11 types of models, 14 single models
- ▶ 1 coded in biomod2, 1 external software, 12 other R packages
- ▶ **default** : extracted from functions
- ▶ **bigboss** : redefined by biomod2 team

```
nnet package:nnet R Documentation
Fit Neural Networks
Description:
Fit single-hidden-layer neural network, possibly with skip-layer
connections.
Usage:
nnet(x, ...)
## S3 method for class 'formula'
nnet(formula, data, weights, ...,
      subset, na.action, contrasts = NULL)
## Default S3 method:
nnet(x, y, weights, size, Wts, mask,
      linout = FALSE, entropy = FALSE, softmax = FALSE,
      censored = FALSE, skip = FALSE, rang = 0.7, decay = 0,
      maxit = 100, Hess = FALSE, trace = TRUE, MaxNWts = 1000,
      abstol = 1.0e-4, reltol = 1.0e-8, ...)
> ANN options (datatype: binary , package: nnet , function: nnet ) :
( dataset allData allRun )
- size = 5 (default: 2 )
- decay = 5 (default: NULL )
- trace = FALSE (default: NULL )
- rang = 0.1 (default: NULL )
- maxit = 200 (default: NULL )
```

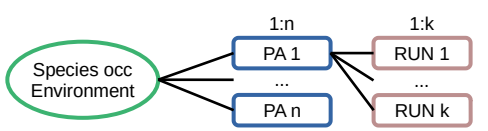


	model	type	package	func	train
1	ANN	binary	nnet	nnet	avNNet
2	CTA	binary	rpart	rpart	rpart
3	FDA	binary	mda	fda	fda
4	GAM	binary	gam	gam	gamLoess
5	GAM	binary	mgcv	bam	bam
6	GAM	binary	mgcv	gam	gam
7	GBM	binary	gbm	gbm	gbm
8	GLM	binary	stats	glm	glm
9	MARS	binary	earth	earth	earth
10	MAXENT	binary	MAXENT	MAXENT	ENMevaluate
11	MAXNET	binary	maxnet	maxnet	maxnet
12	RF	binary	randomForest	randomForest	rf
13	SRE	binary	biomod2	bm_SRE	bm_SRE
14	XGBOOST	binary	xgboost	xgboost	xgbTree

1. Formating data

- ▶ 11 types of models, 14 single models
- ▶ 1 coded in biomod2, 1 external software, 12 other R packages
- ▶ **default** : extracted from functions
- ▶ **bigboss** : redefined by biomod2 team
- ▶ **user-defined**

```
nnet package:nnet R Documentation
Fit Neural Networks
Description:
Fit single-hidden-layer neural network, possibly with skip-layer connections.
Usage:
nnet(x, ...)
## S3 method for class 'formula'
nnet(formula, data, weights, ...,
      subset, na.action, contrasts = NULL)
## Default S3 method:
nnet(x, y, weights, size, Wts, mask,
      linout = FALSE, entropy = FALSE, softmax = FALSE,
      censored = FALSE, skip = FALSE, rang = 0.7, decay = 0,
      maxit = 100, Hess = FALSE, trace = TRUE, MaxNwts = 1000,
      abstol = 1.0e-4, reltol = 1.0e-8, ...)
> ANN options (datatype: binary , package: nnet , function: nnet ) :
( dataset _allData_allRun )
- size = 5 (default: 2 )
- decay = 5 (default: NULL )
- trace = FALSE (default: NULL )
- rang = 0.1 (default: NULL )
- maxit = 200 (default: NULL )
```

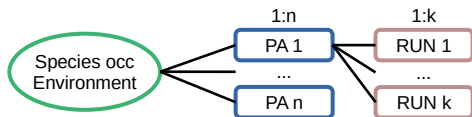
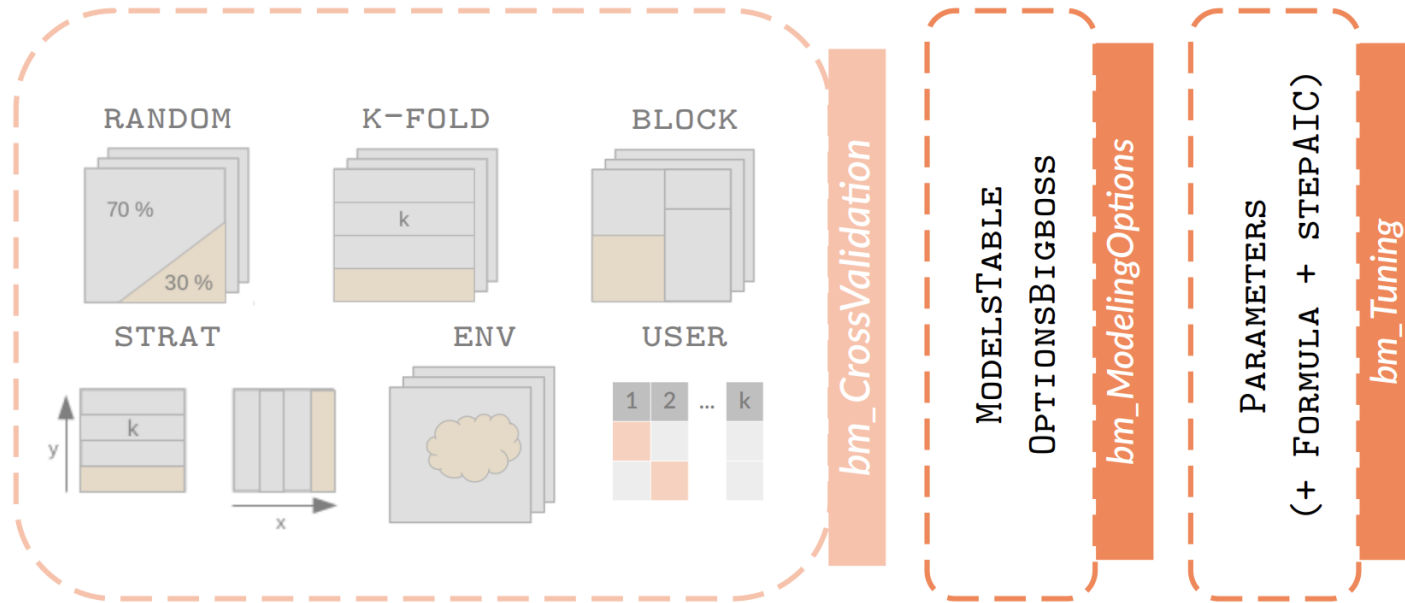


```
> ModelsTable
  model type package func train
1 ANN binary nnet nnet avNNet
2 CTA binary rpart rpart rpart
3 FDA binary mda fda fda
4 GAM binary gam gam gamLoess
5 GAM binary mgcv bam bam
6 GAM binary mgcv gam gam
7 GBM binary gbm gbm gbm
8 GLM binary stats glm glm
9 MARS binary earth earth earth
10 MAXENT binary MAXENT MAXENT ENMevaluate
11 MAXNET binary maxnet maxnet maxnet
12 RF binary randomForest randomForest rf
13 SRE binary biomod2 bm_SRE bm_SRE
14 XGBOOST binary xgboost xgboost xgbTree
```

```
user.ANN = list('_allData_allRun' =
list( size = 5,
      decay = 0.5,
      trace = FALSE,
      rang = 0.1,
      maxit = 500))
```

1. Formating data

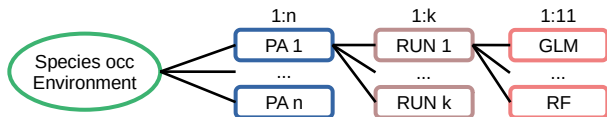
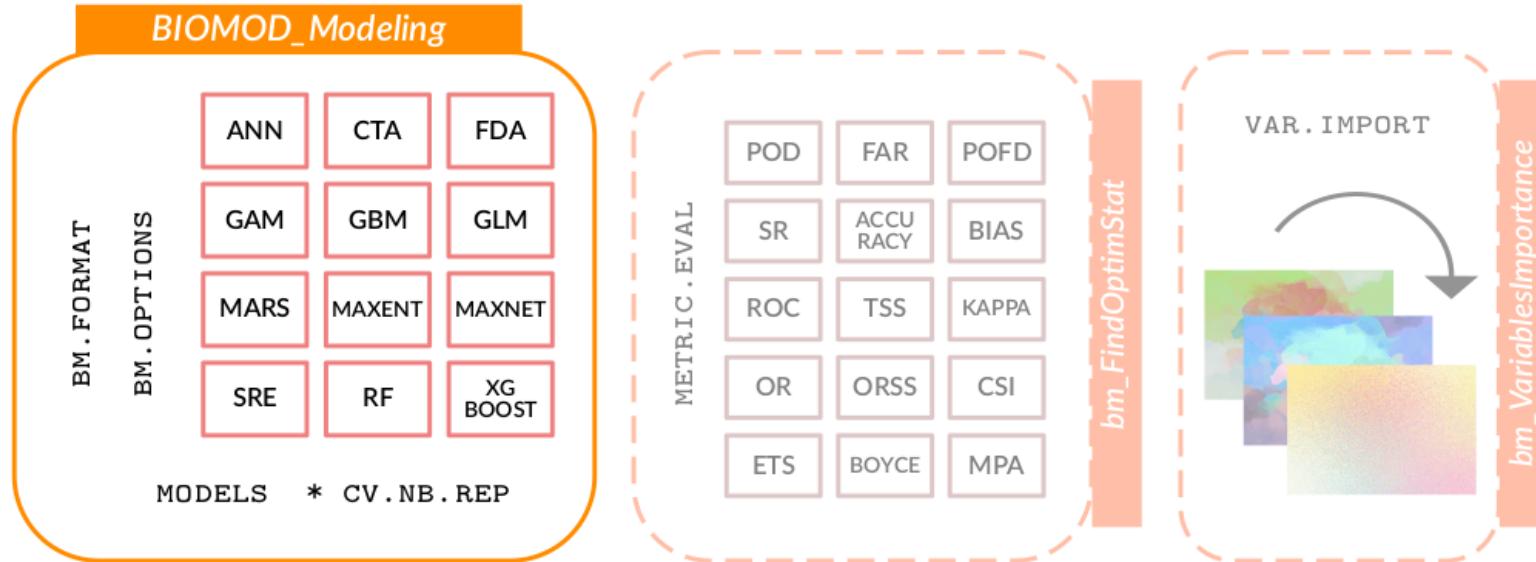
- ▶ 11 types of models, 14 single models
- ▶ 1 coded in biomod2, 1 external software, 12 other R packages
- ▶ **default** : extracted from functions
- ▶ **bigboss** : redefined by biomod2 team
- ▶ **user-defined**
- ▶ **tuned** : with *train* function from *caret* package



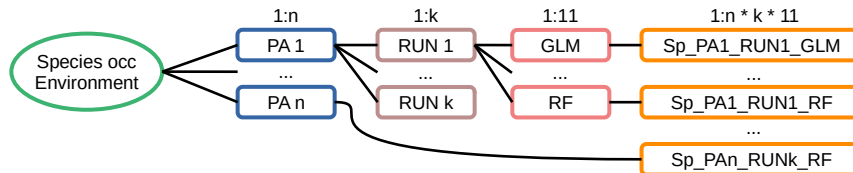
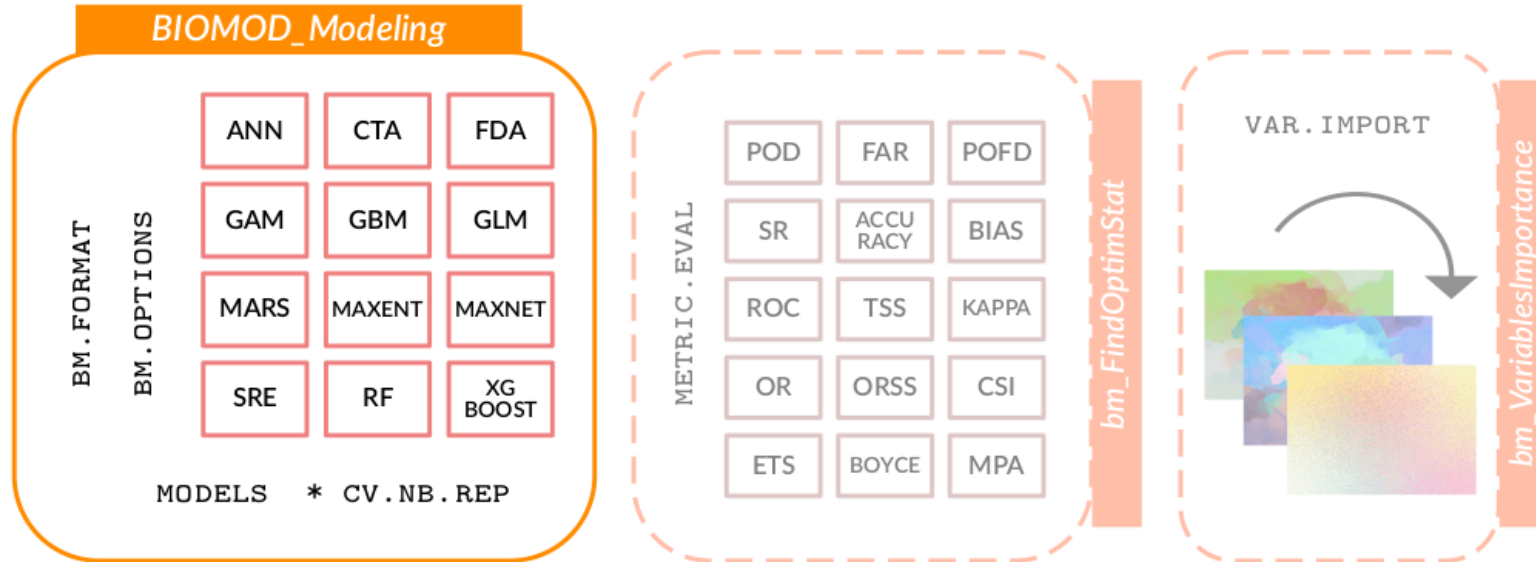
```
> ModelsTable
  model type package func train
1 ANN binary nnet nnet avNNet
2 CTA binary rpart rpart rpart
3 FDA binary mda fda fda
4 GAM binary gam gam gamLoess
5 GAM binary mgcv bam bam
6 GAM binary mgcv gam gam
7 GBM binary gbm gbm gbm
8 GLM binary stats glm glm
9 MARS binary earth earth earth
10 MAXENT binary MAXENT MAXENT ENMevaluate
11 MAXNET binary maxnet maxnet maxnet
12 RF binary randomForest randomForest rf
13 SRE binary biomod2 bm_SRE bm_SRE
14 XGBOOST binary xgboost xgboost xgbTree
```

- ▶ test a bunch of parameters, and try to keep the « best » according to some evaluation metrics (TSS or ROC)

2.a Single models



2.a Single models

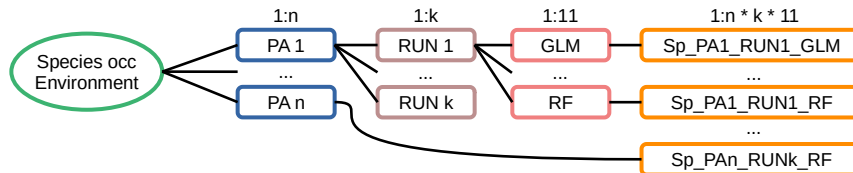
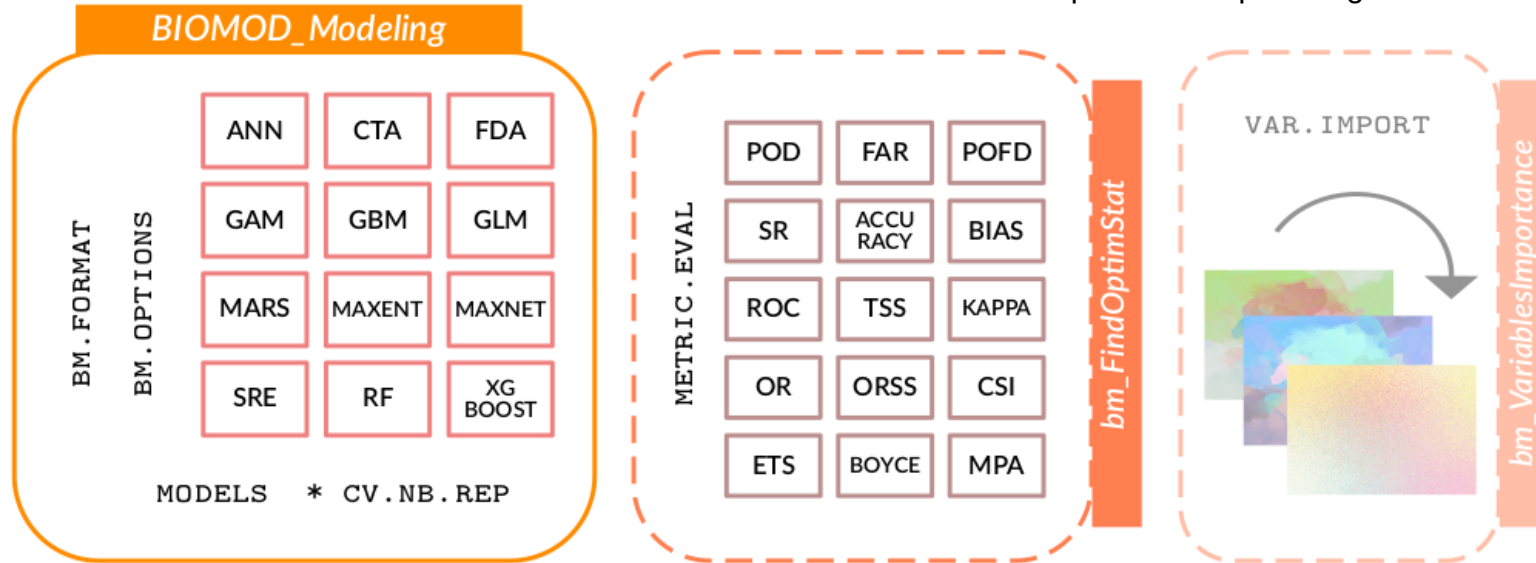


2.a Single models

» except ROC, all evaluation metrics obtained from contingency table (*containing TP, FP, TN, FN*)

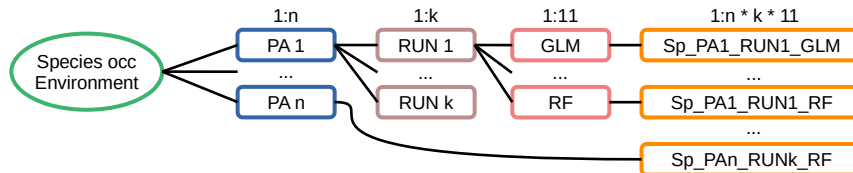
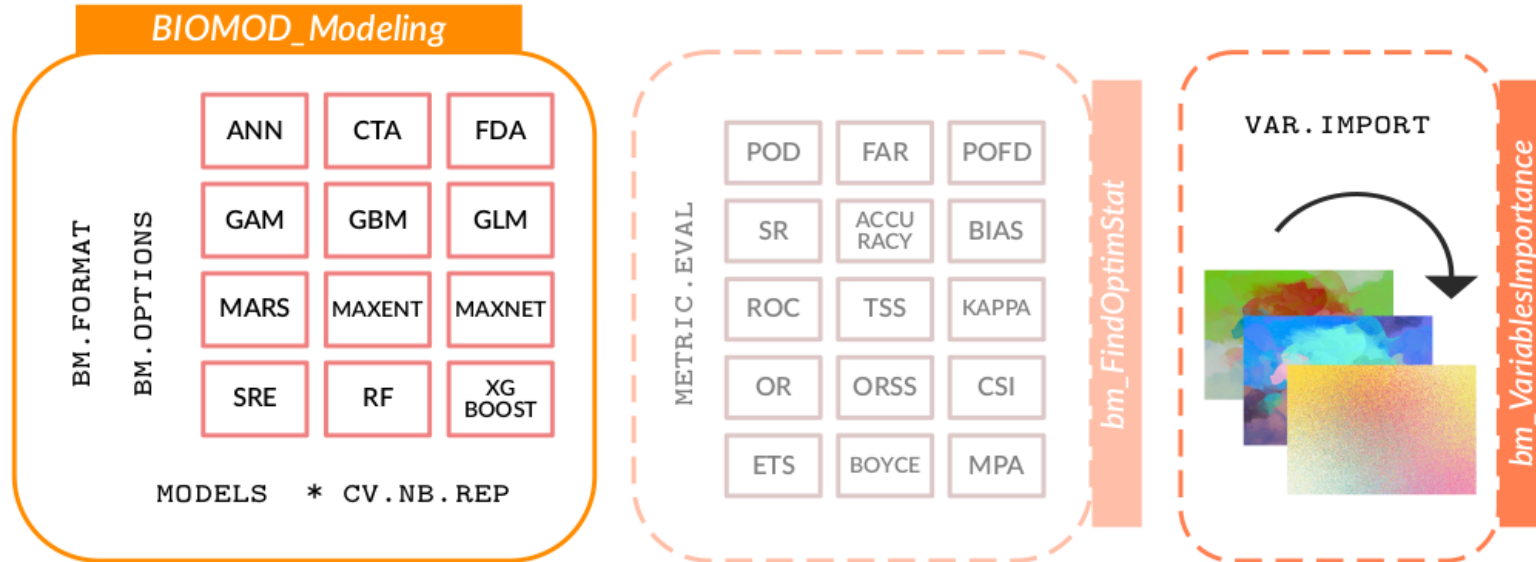
» require a **binary transformation** :

- range of thresholds tested
- keep threshold optimising the evaluation metric

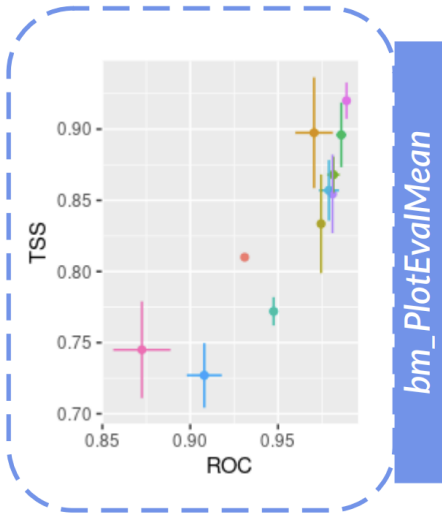


2.a Single models

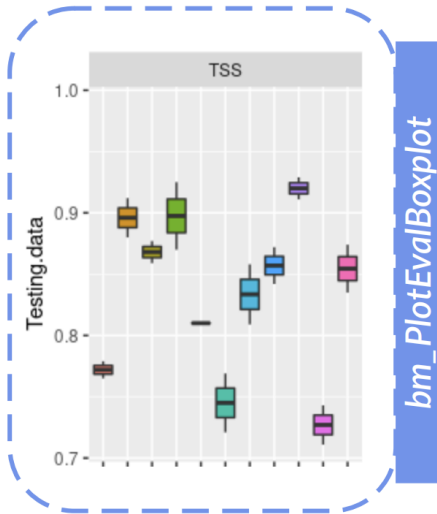
- » comparison of importance of variables between models
- » **Pearson correlation** between :
 - normal prediction
 - prediction with 1 variable randomised



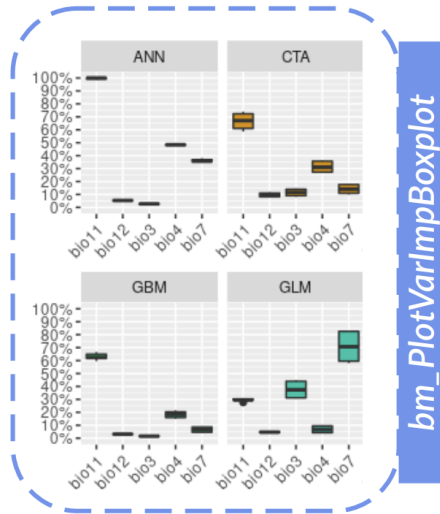
3.a Exploring single models



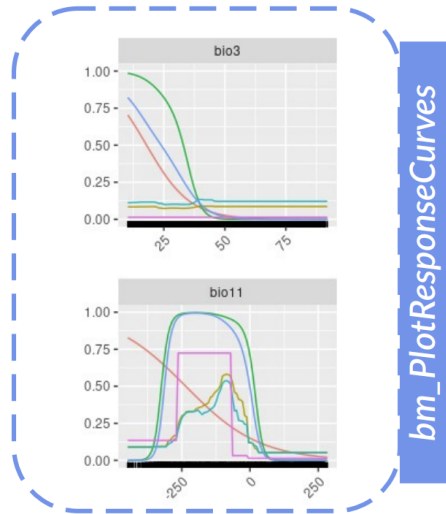
bm_PlotEvalMean



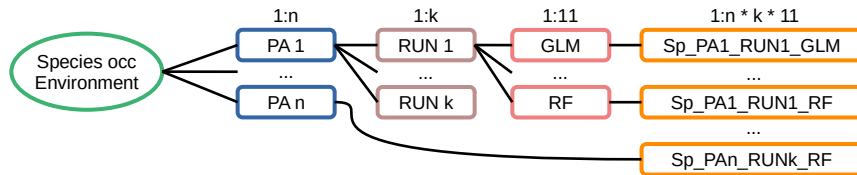
bm_PlotEvalBoxplot



bm_PlotVarImpBoxplot

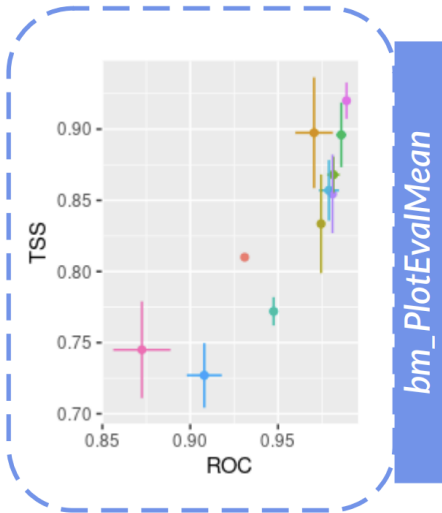


bm_PlotResponseCurves

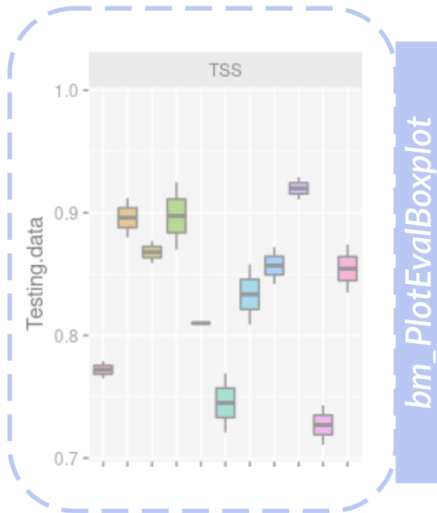


3.a Exploring single models

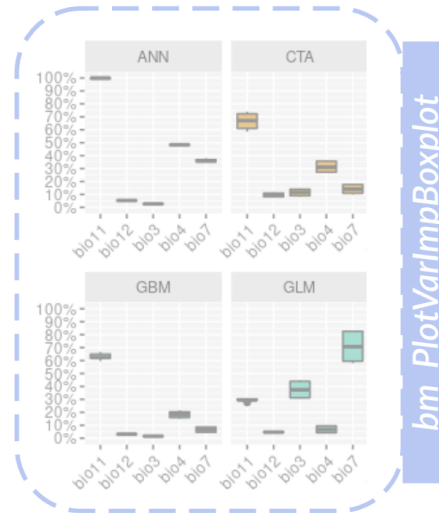
- » « evaluation space »
- » visualize the metrics consistency between models



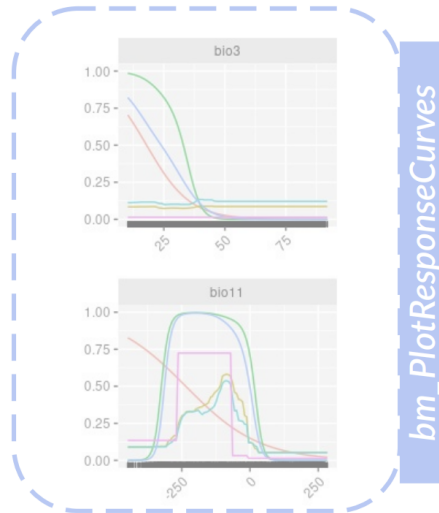
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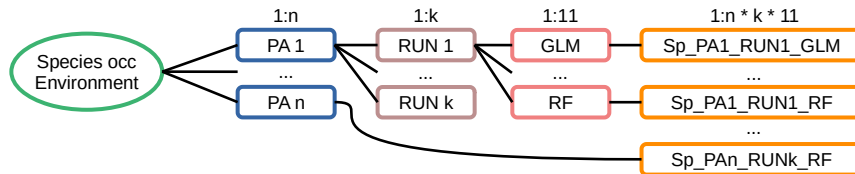
bm_PlotEvalBoxplot



bm_PlotVarImpBoxplot

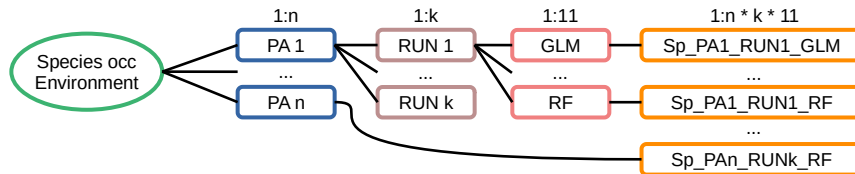
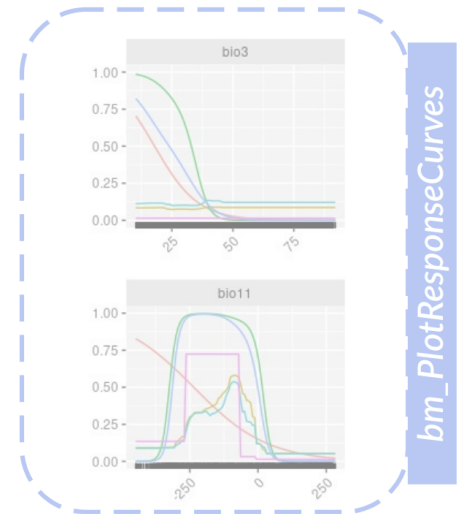
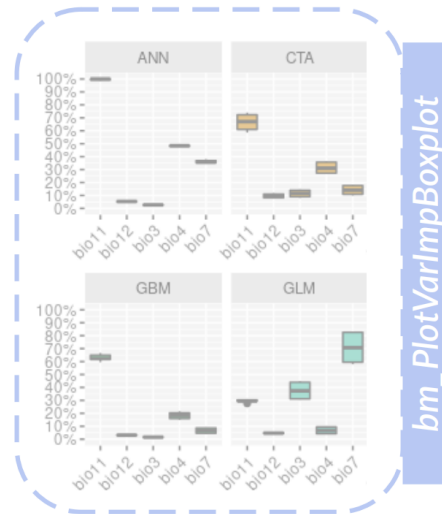
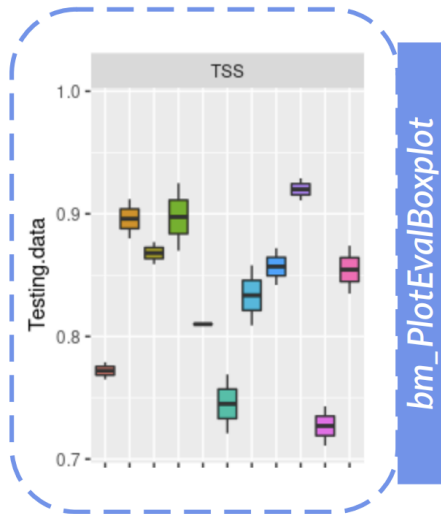
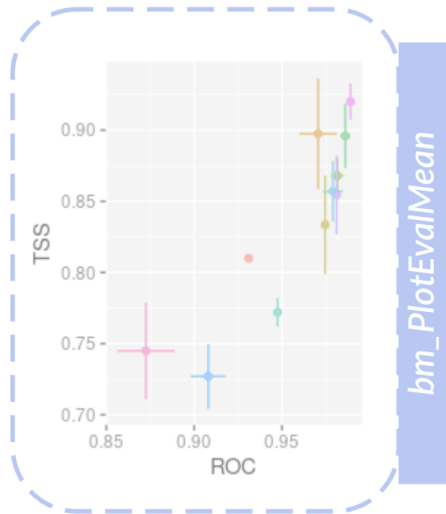


bm_PlotResponseCurves



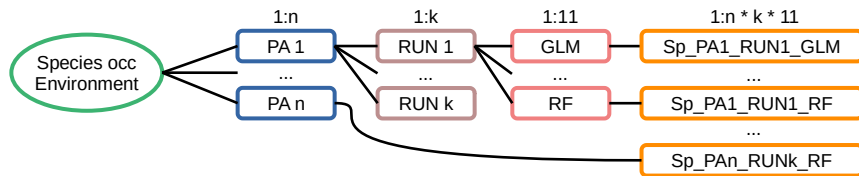
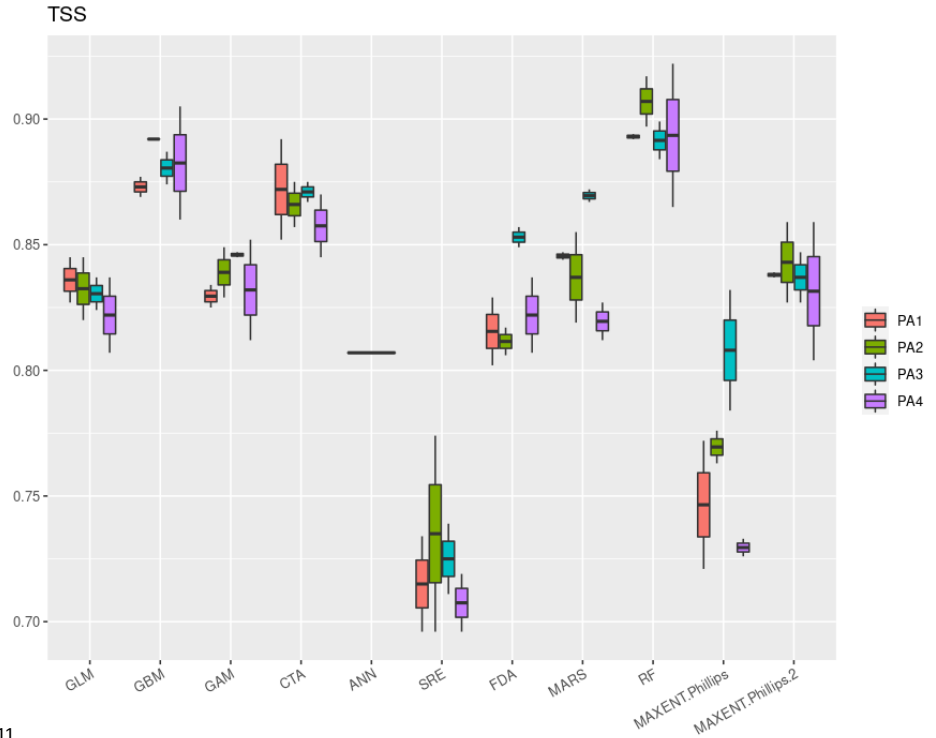
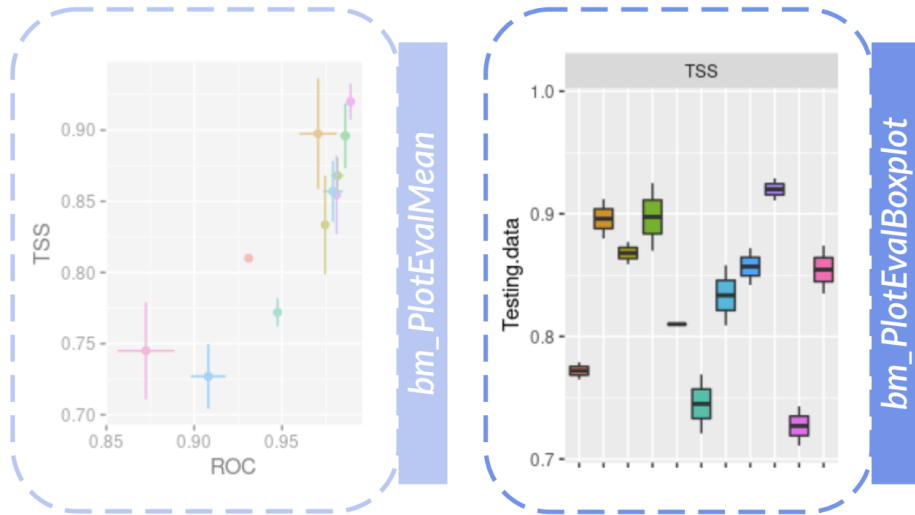
3.a Exploring single models

- ▶ more classical view
- ▶ visualize the metrics consistency between models



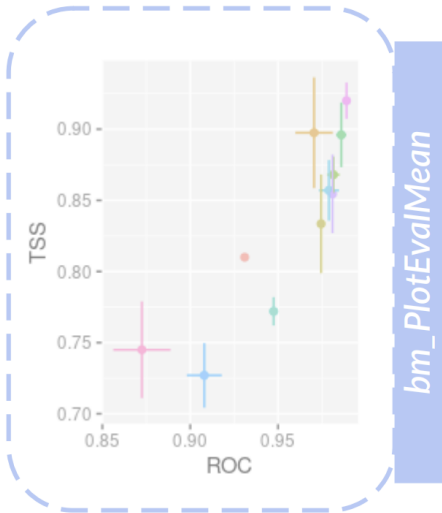
3.a Exploring single models

- ▶ more classical view
- ▶ visualize the metrics consistency between models
 - explore the different levels of subsets

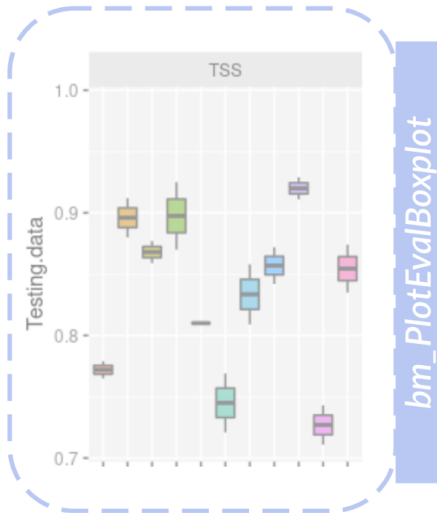


3.a Exploring single models

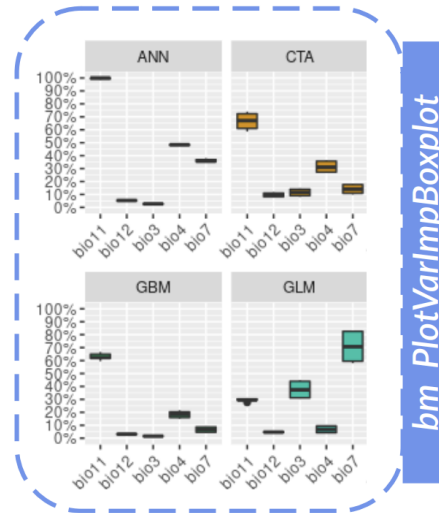
- ▶ compare importance of variables between models
- ▶ visualize the consistency between models (and different types of models)



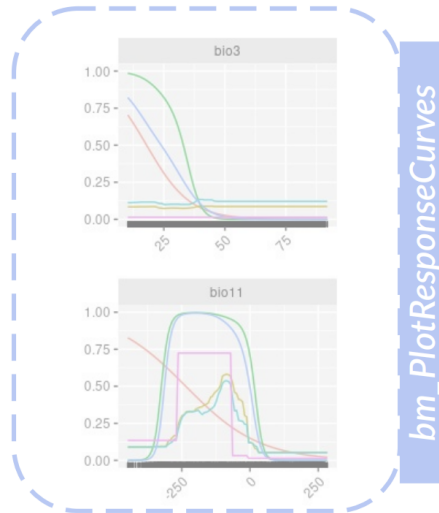
bm_PlotEvalMean



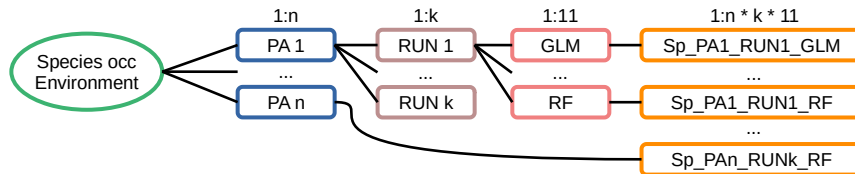
bm_PlotEvalBoxplot



bm_PlotVarImpBoxplot

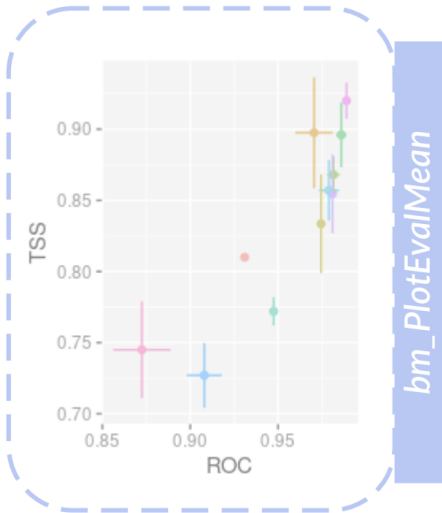


bm_PlotResponseCurves

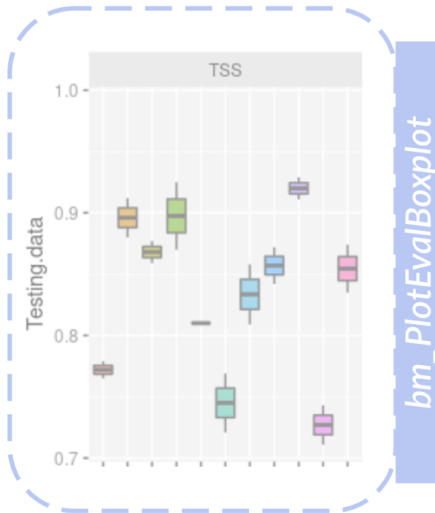


3.a Exploring single models

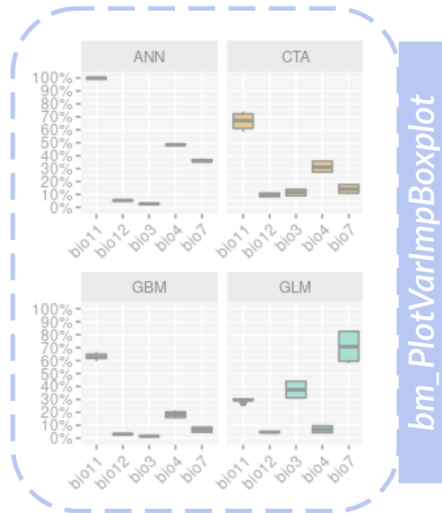
- ▶ better understand the effect of each variable along its gradient onto the probability of presence
- ▶ visualize the consistency between models (and different types of models)



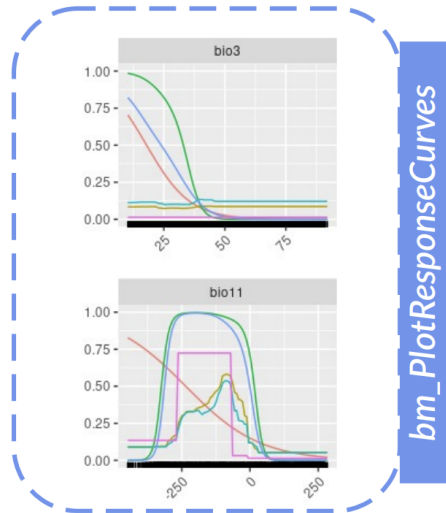
bm_PlotEvalMean



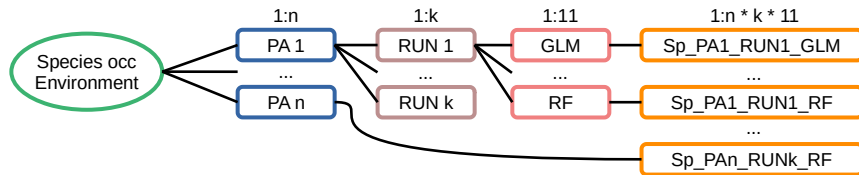
bm_PlotEvalBoxplot



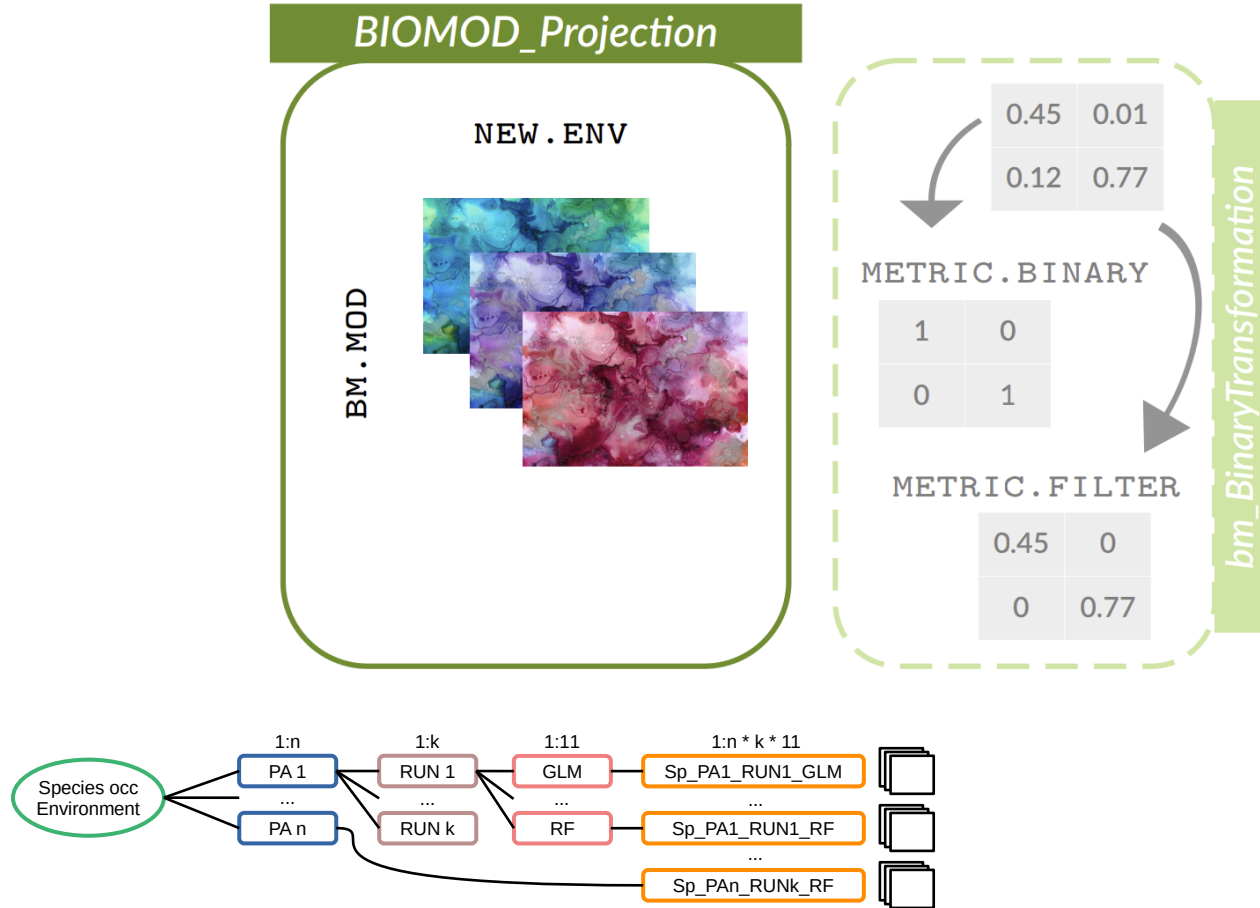
bm_PlotVarImpBoxplot



bm_PlotResponseCurves

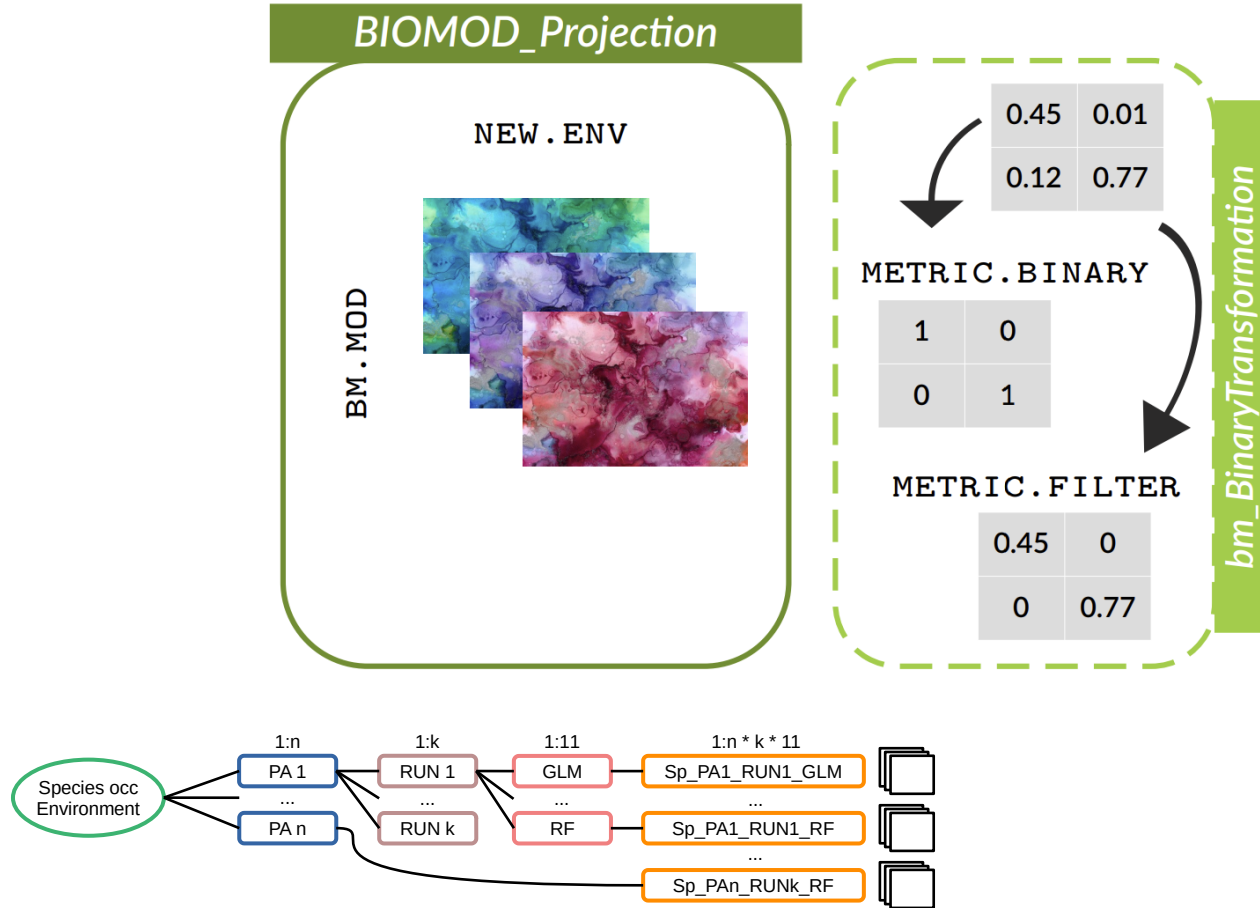


4.a Projecting single models



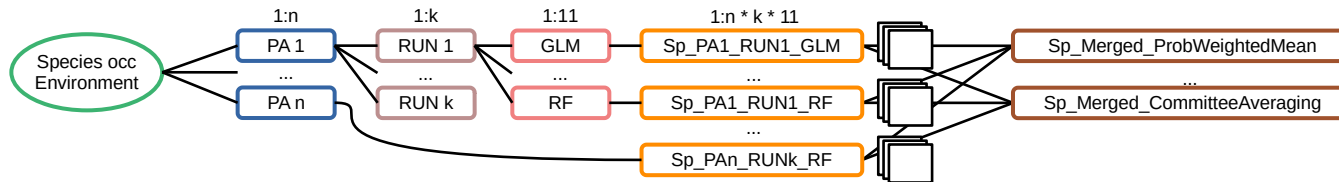
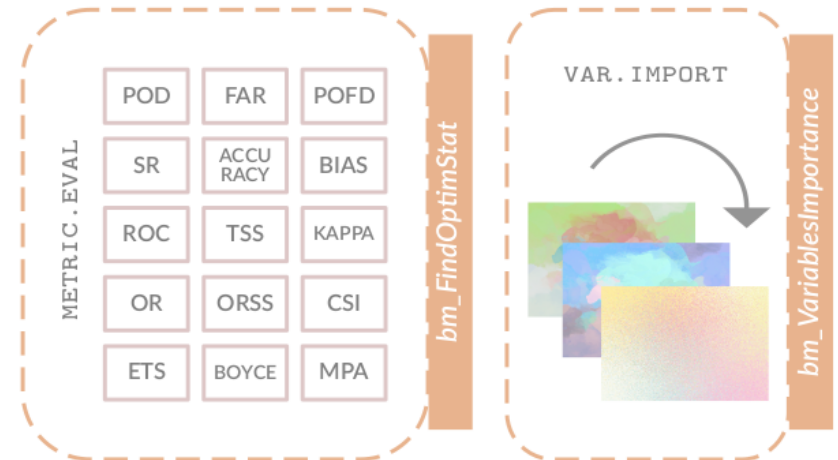
4.a Projecting single models

- › transformation associated to one evaluation metric (*one map created for each metric selected*)
- › use the threshold maximising the chosen metric



2.b Ensemble models

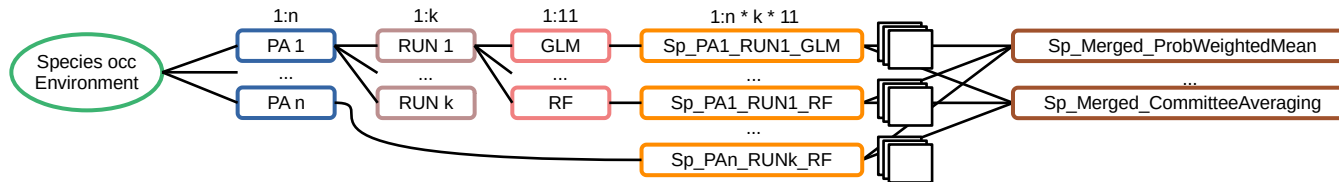
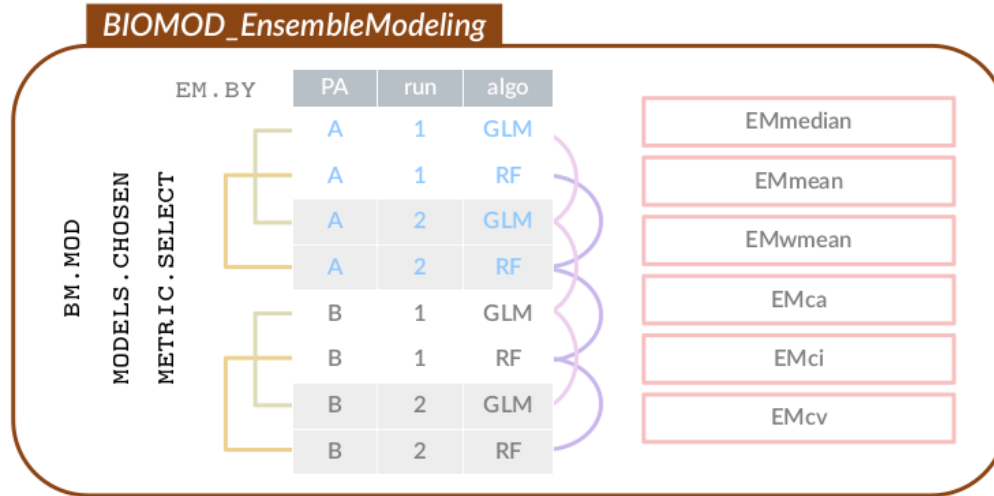
BIOMOD_EnsembleModeling



2.b Ensemble models

Step 1 : filter single models

- » **filtering** associated to one evaluation metric
(one set of ensemble models created for each metric selected)
- » use a threshold to keep single models



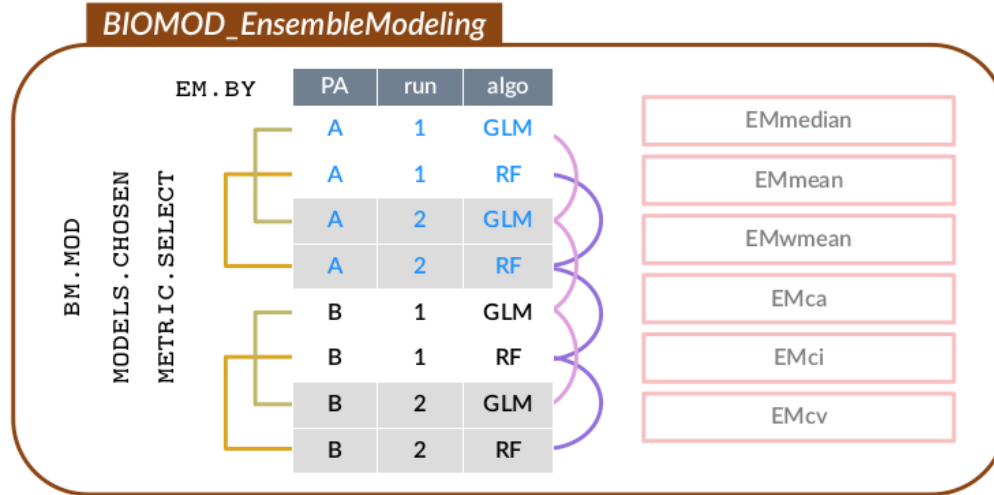
2.b Ensemble models

Step 1 : filter single models

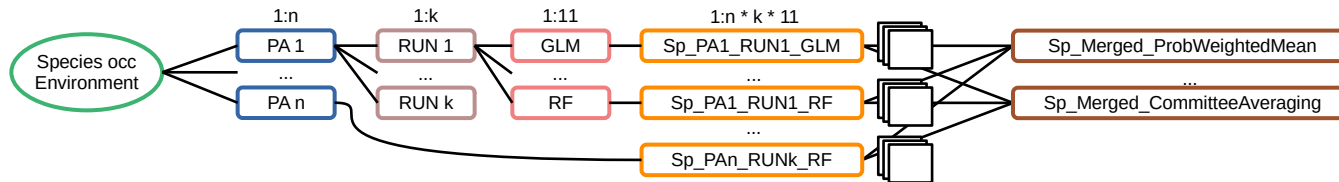
Step 2 : gather single models

» different ways of **combining** single models together :

- *all*
- *algo*
- *PA*
- *PA+algo*
- *PA+run*



PA1_RUN1_GLM	PA1_RUN1_RF
PA1_RUN2_GLM	PA1_RUN2_RF
PA1_RUN3_GLM	PA1_RUN3_RF
PA2_RUN1_GLM	PA2_RUN1_RF
PA2_RUN2_GLM	PA2_RUN2_RF
PA2_RUN3_GLM	PA2_RUN3_RF



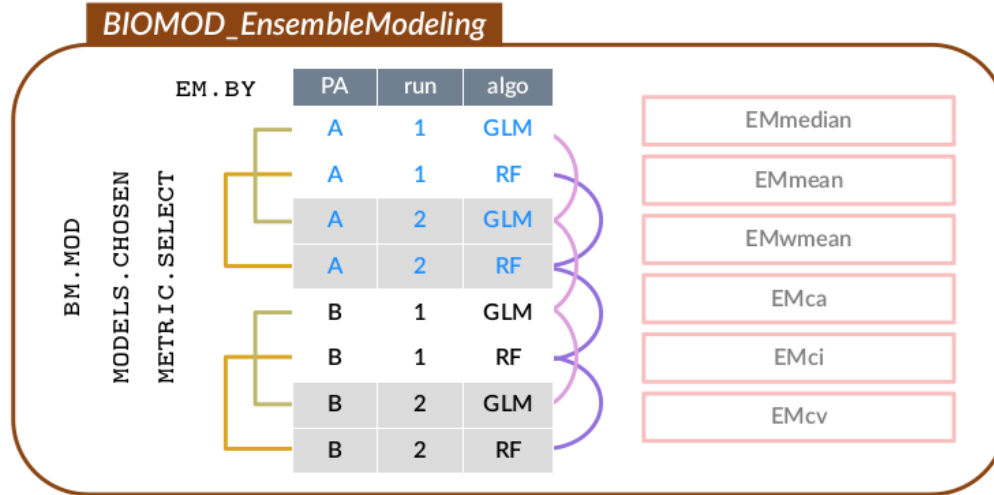
2.b Ensemble models

Step 1 : filter single models

Step 2 : gather single models

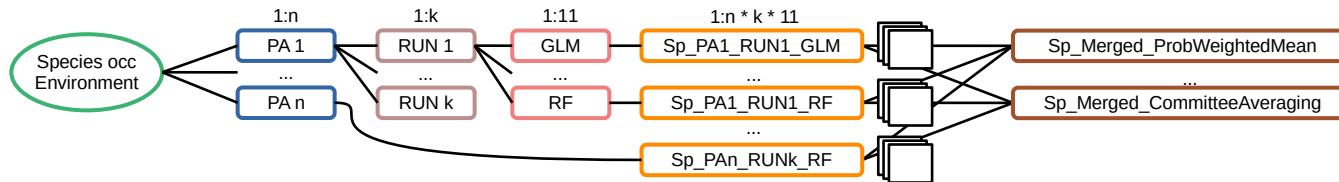
» different ways of **combining** single models together :

- *all*
- *algo*
- *PA*
- *PA+algo*
- *PA+run*



PA1_RUN1_GLM	PA1_RUN1_RF
PA1_RUN2_GLM	PA1_RUN2_RF
PA1_RUN3_GLM	PA1_RUN3_RF
PA2_RUN1_GLM	PA2_RUN1_RF
PA2_RUN2_GLM	PA2_RUN2_RF
PA2_RUN3_GLM	PA2_RUN3_RF

All models

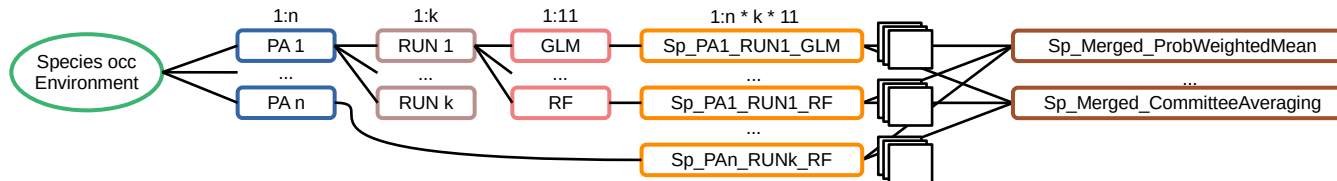
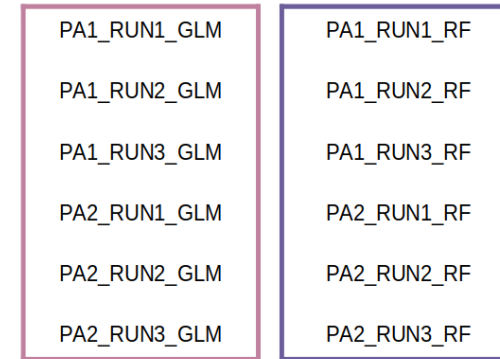
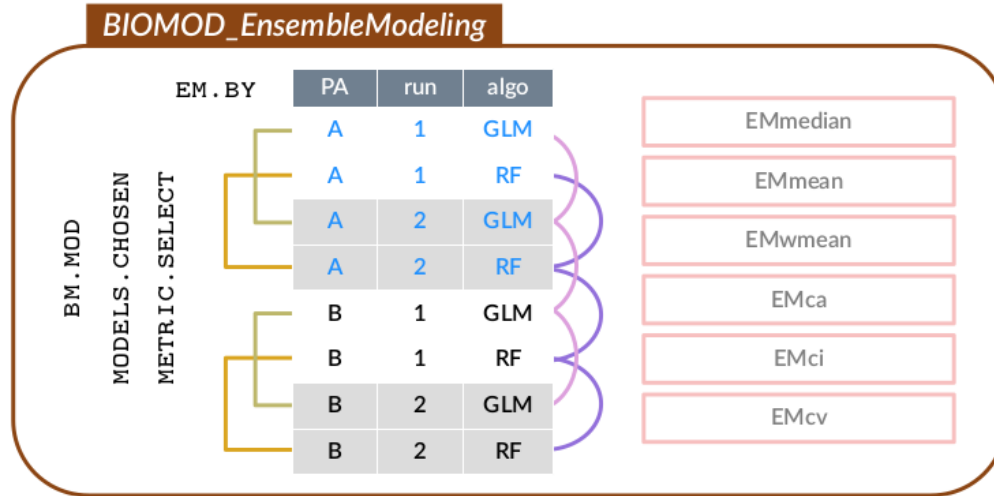


2.b Ensemble models

- Step 1 : filter single models
 Step 2 : gather single models

» different ways of **combining** single models together :

- *all*
- *algo*
- *PA*
- *PA+algo*
- *PA+run*



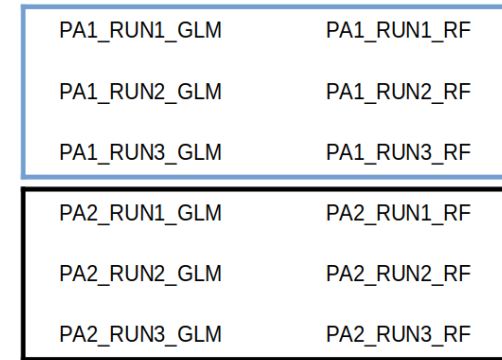
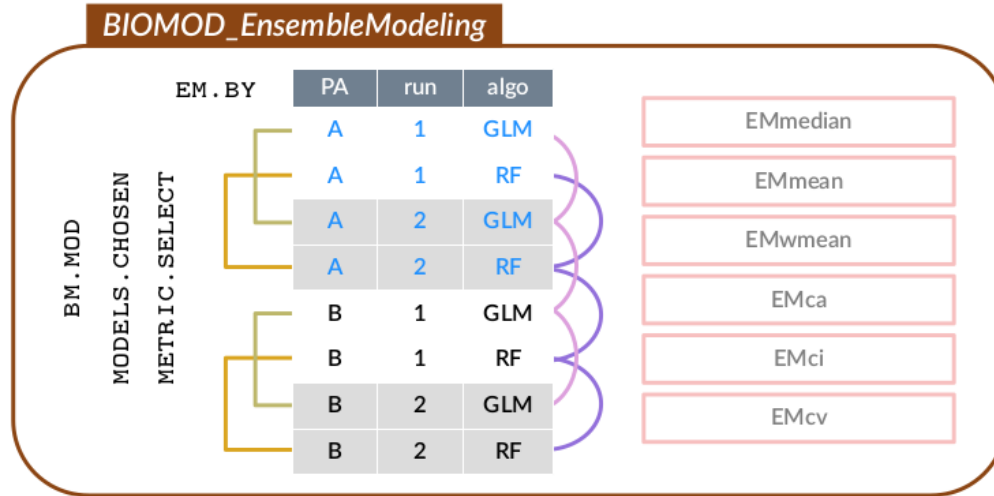
2.b Ensemble models

Step 1 : filter single models

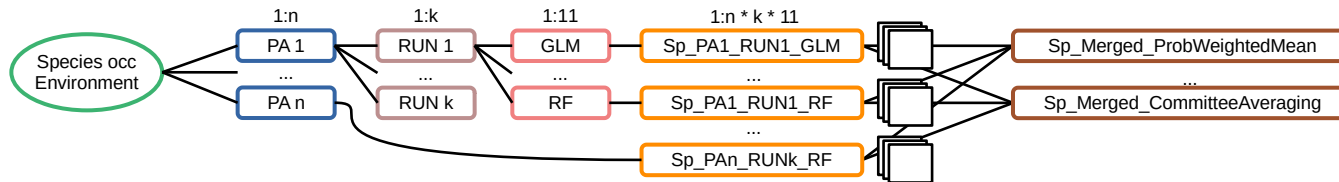
Step 2 : gather single models

» different ways of **combining** single models together :

- *all*
- *algo*
- *PA*
- *PA+algo*
- *PA+run*



Different PA



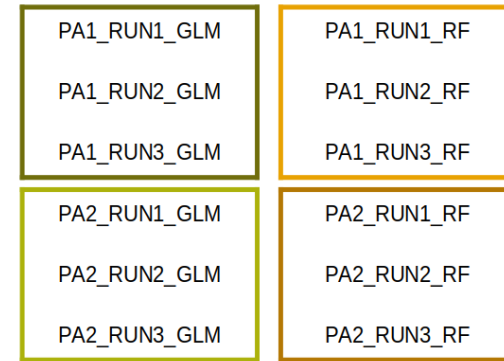
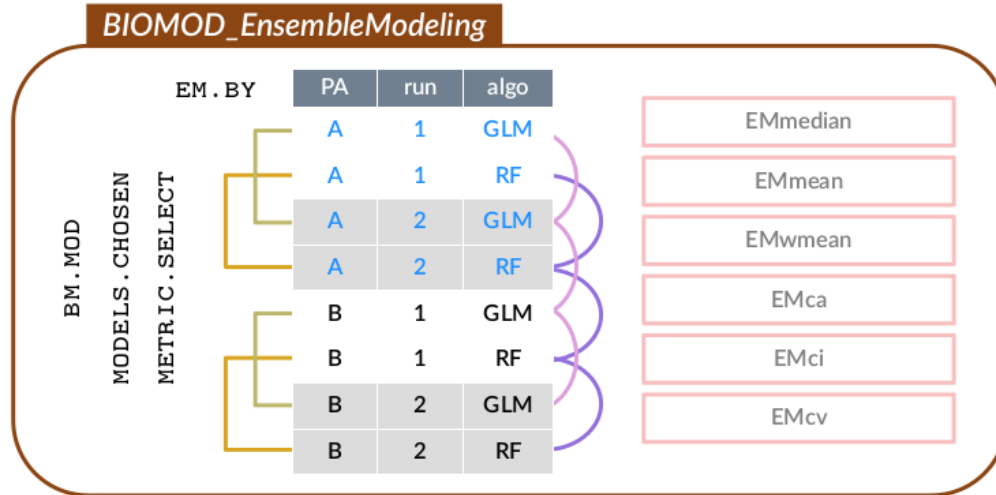
2.b Ensemble models

Step 1 : filter single models

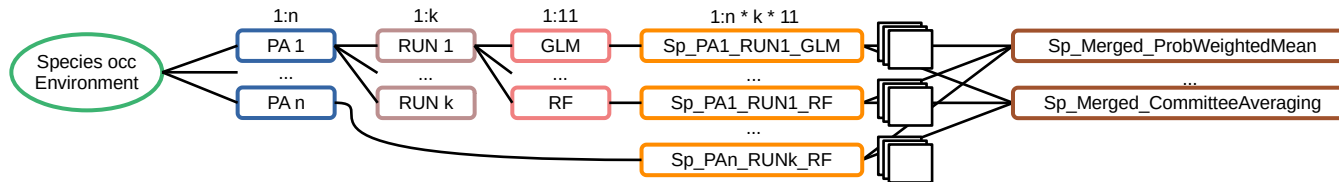
Step 2 : gather single models

» different ways of **combining** single models together :

- *all*
- *algo*
- *PA*
- *PA+algo*
- *PA+run*



Different PA and algo



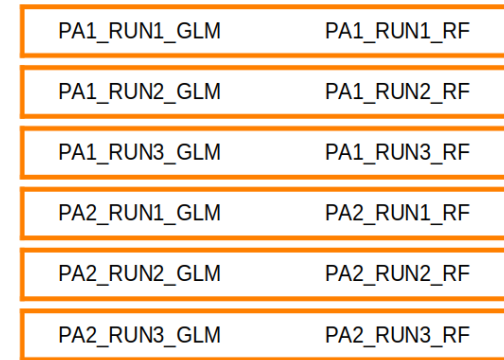
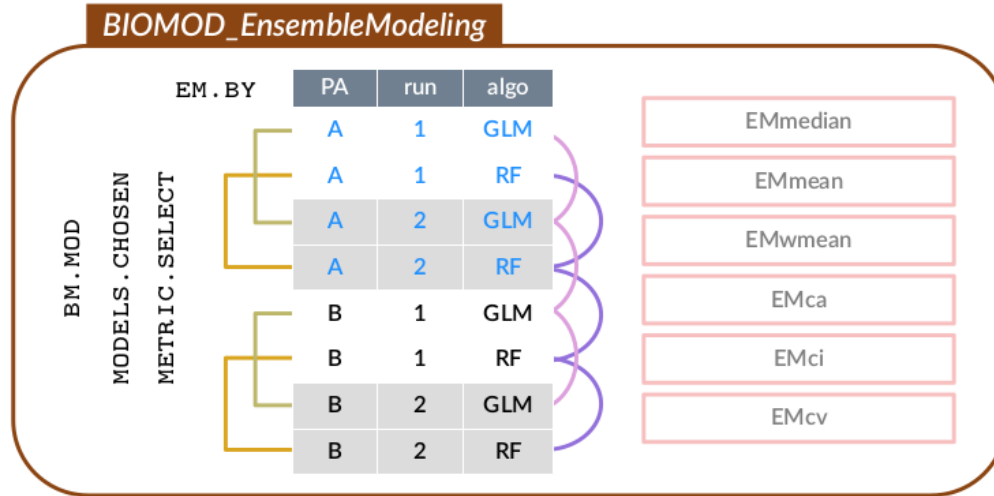
2.b Ensemble models

Step 1 : filter single models

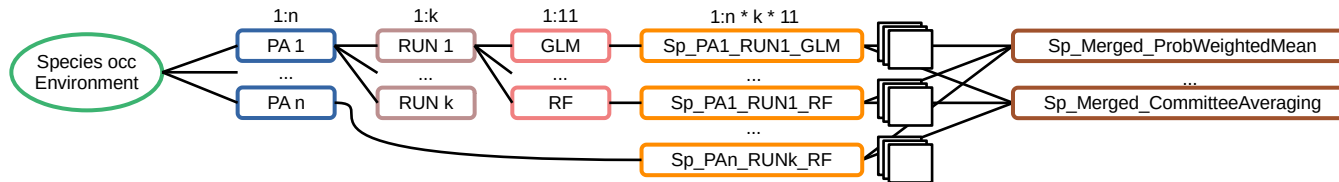
Step 2 : gather single models

» different ways of **combining** single models together :

- *all*
- *algo*
- *PA*
- *PA+algo*
- *PA+run*



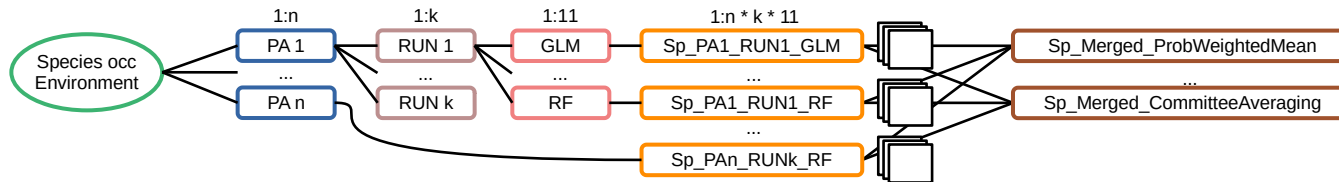
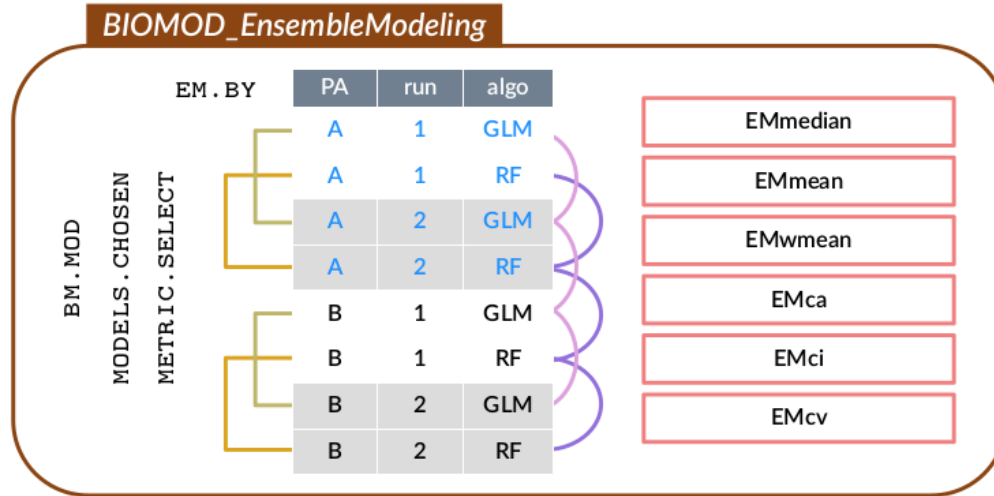
Different PA
and run



2.b Ensemble models

» « simple » ensemble models : **mean** or **median**

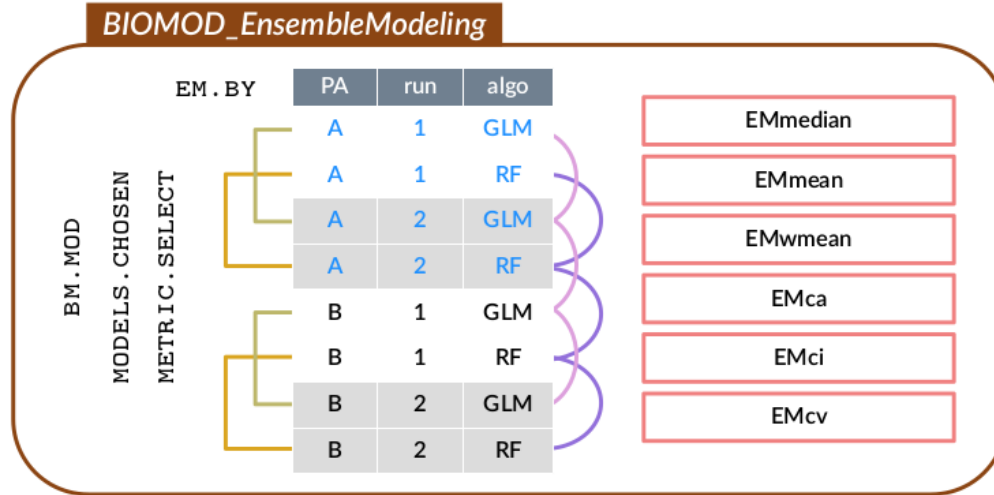
- Step 1** : filter single models
- Step 2** : gather single models
- Step 3** : build ensemble models



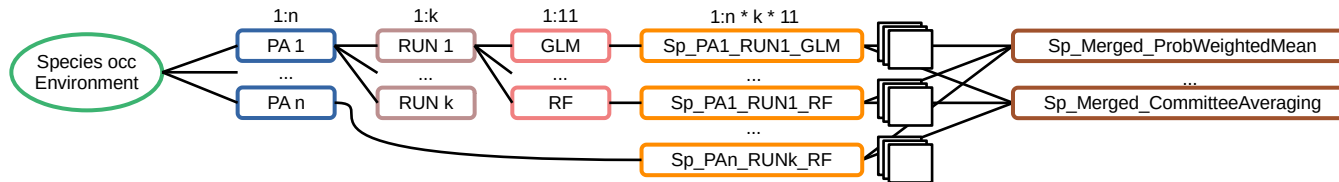
2.b Ensemble models

- Step 1 : filter single models
- Step 2 : gather single models
- Step 3 : build ensemble models

- » « simple » ensemble models : mean or median
- » « complex » ensemble models :
 - **probability weighted mean**



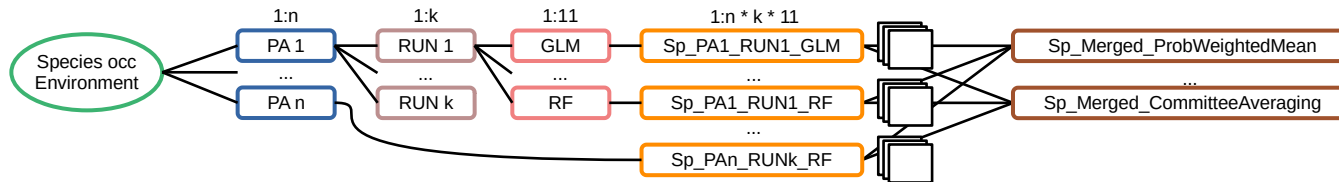
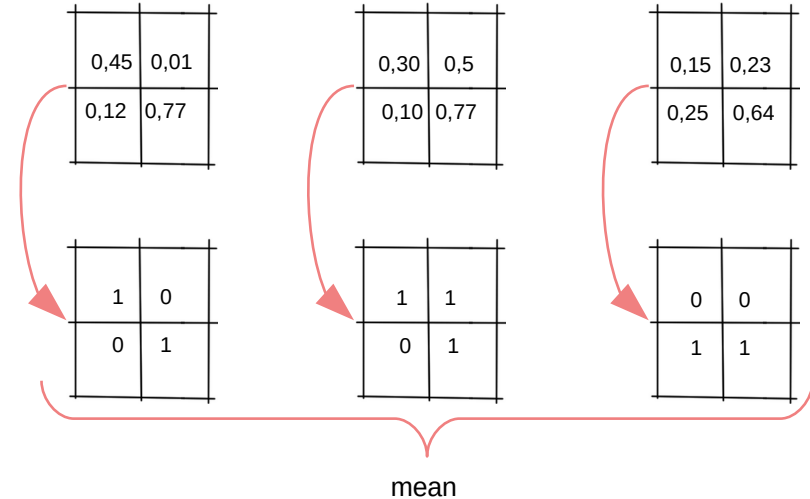
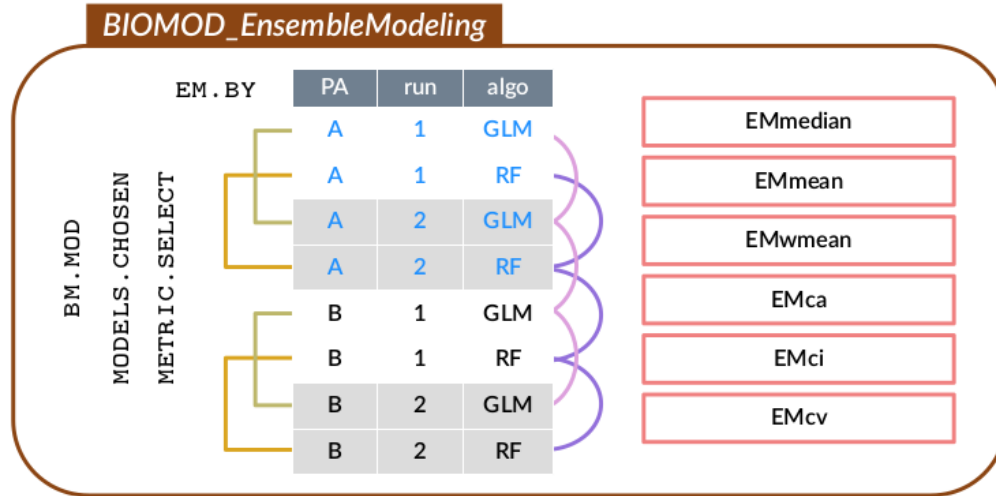
$$W1 * \begin{bmatrix} 0,45 & 0,01 \\ 0,12 & 0,77 \end{bmatrix} + W2 * \begin{bmatrix} 0,30 & 0,5 \\ 0,10 & 0,77 \end{bmatrix} + W3 * \begin{bmatrix} 0,15 & 0,23 \\ 0,25 & 0,64 \end{bmatrix}$$



2.b Ensemble models

- Step 1 : filter single models
- Step 2 : gather single models
- Step 3 : build ensemble models

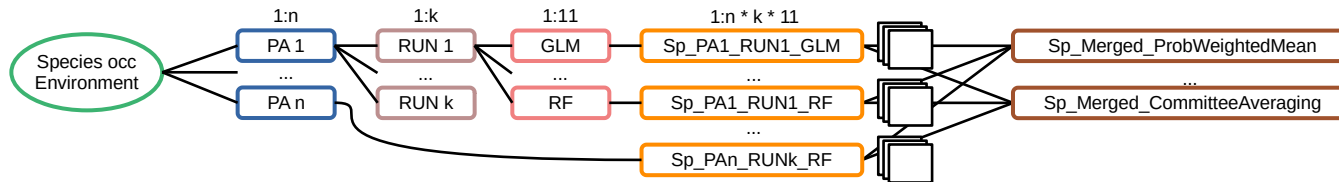
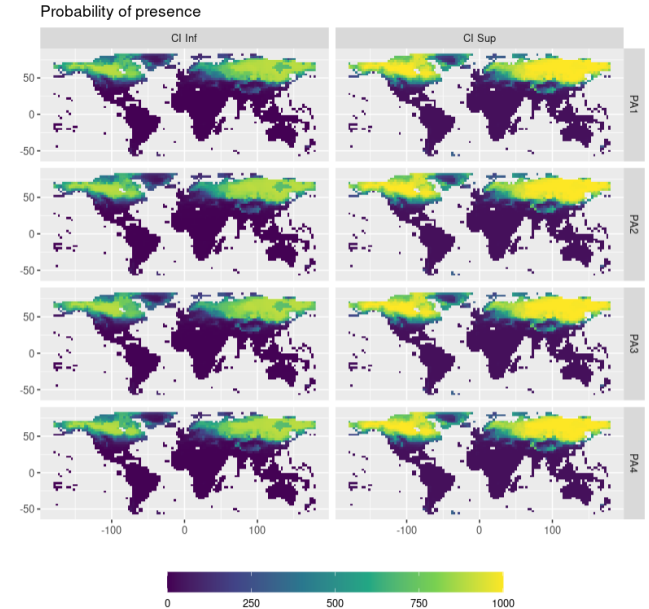
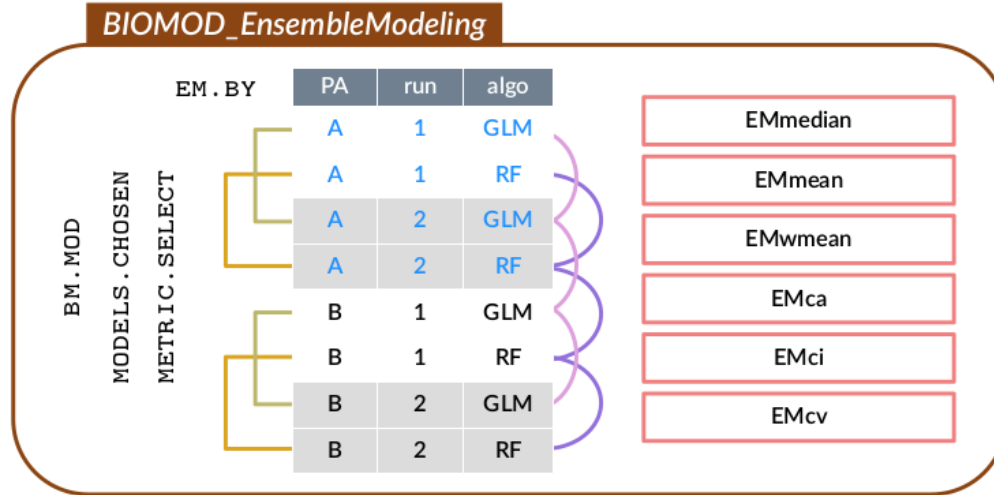
- » « simple » ensemble models : mean or median
- » « complex » ensemble models :
 - probability weighted mean
 - **committe averaging**



2.b Ensemble models

- Step 1 : filter single models
- Step 2 : gather single models
- Step 3 : build ensemble models

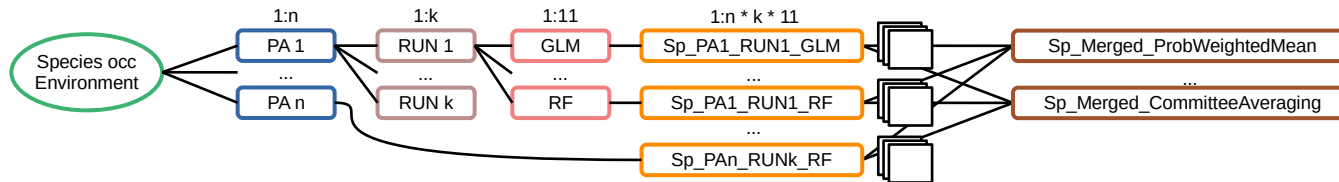
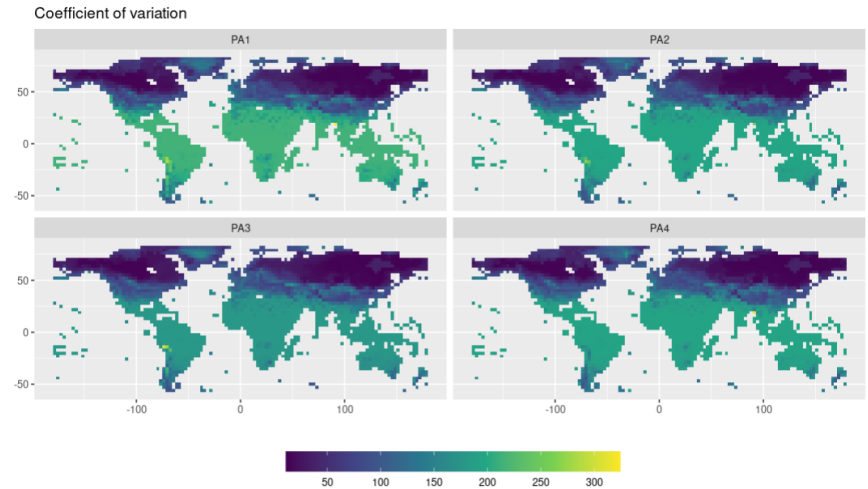
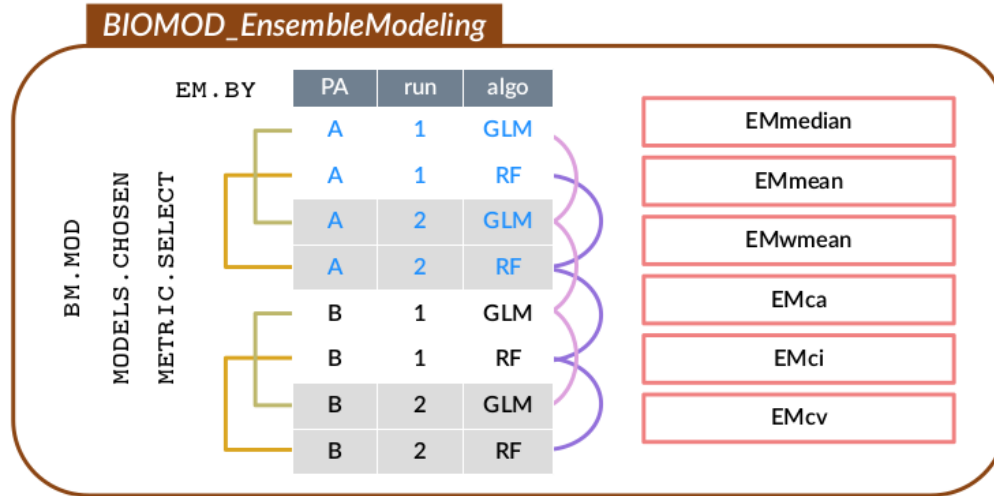
- » « simple » ensemble models : mean or median
- » « complex » ensemble models :
 - probability weighted mean
 - committee averaging
- » « exploratory » ensemble models :
 - **confidence intervals** or **coefficient of variation**



2.b Ensemble models

- Step 1** : filter single models
- Step 2** : gather single models
- Step 3** : build ensemble models

- » « simple » ensemble models : mean or median
- » « complex » ensemble models :
 - probability weighted mean
 - committee averaging
- » « exploratory » ensemble models :
 - **confidence intervals** or **coefficient of variation**

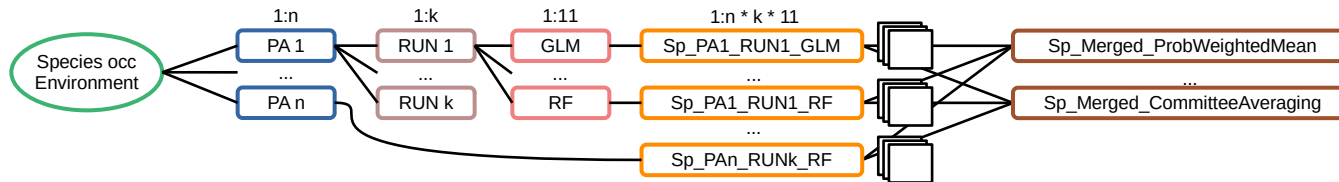
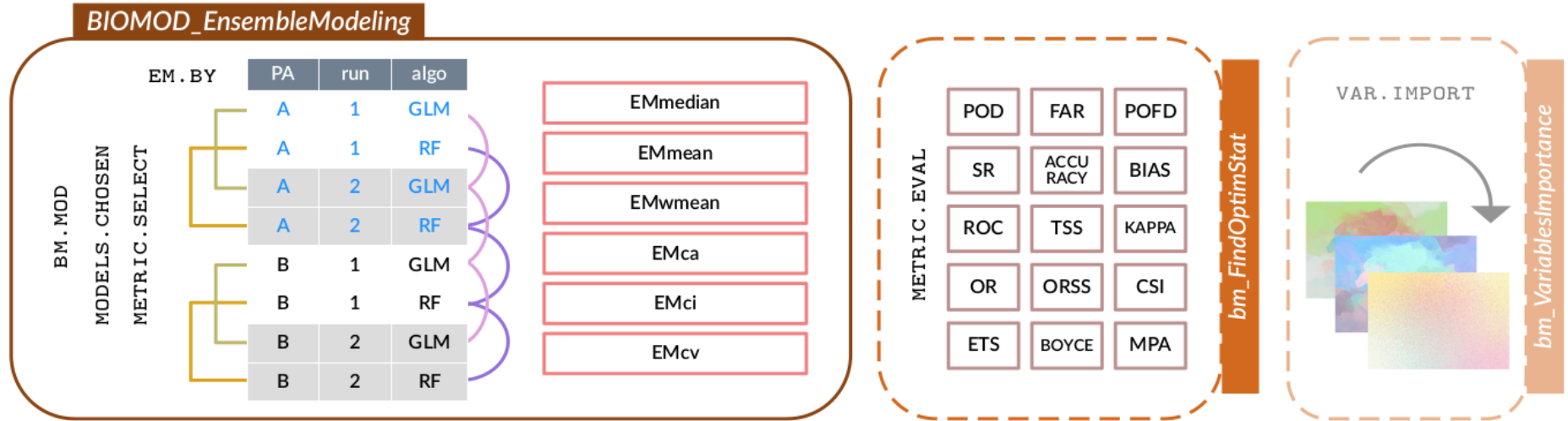


2.b Ensemble models

» except ROC, all evaluation metrics obtained from contingency table (*containing TP, FP, TN, FN*)

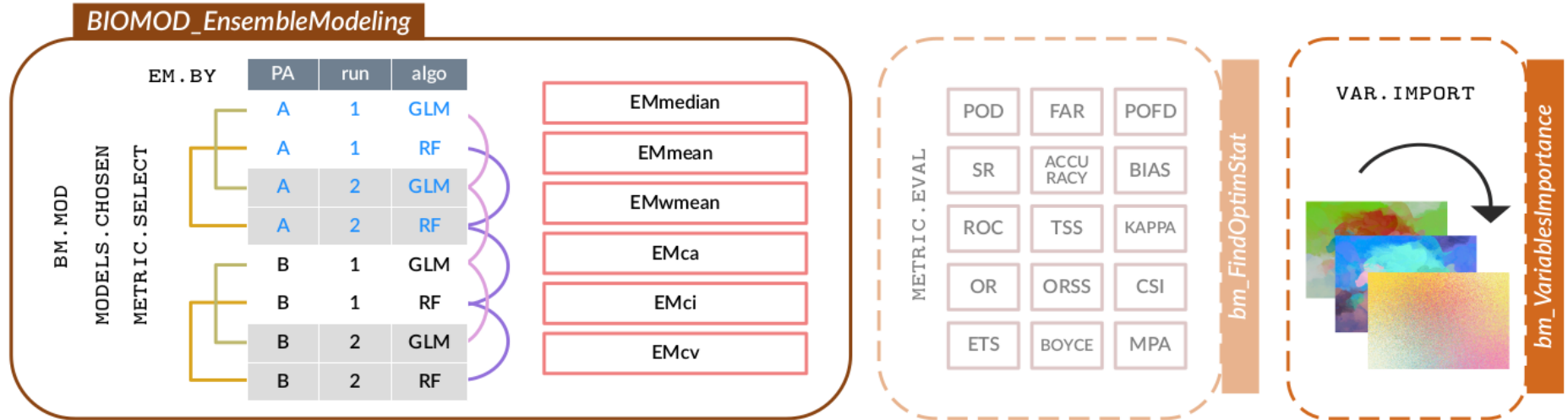
» require a **binary transformation** :

- range of thresholds tested
- keep threshold optimising the evaluation metric



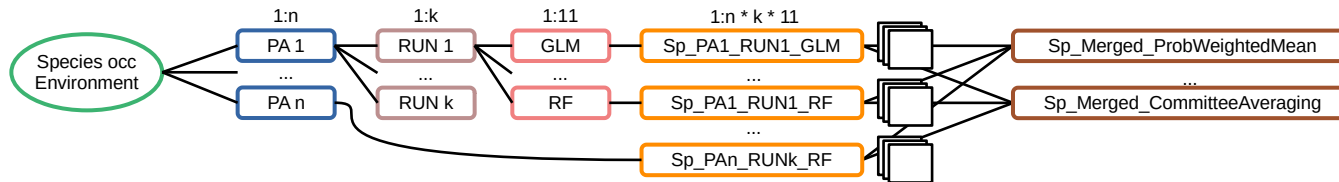
2.b Ensemble models

- » comparison of importance of variables between models
- » **Pearson correlation** between :
 - normal prediction
 - prediction with 1 variable randomised

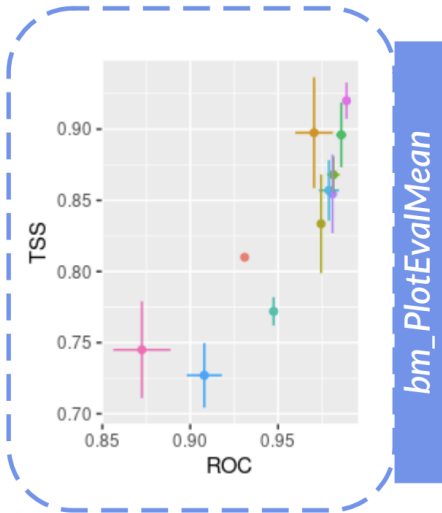


! IMPORTANT

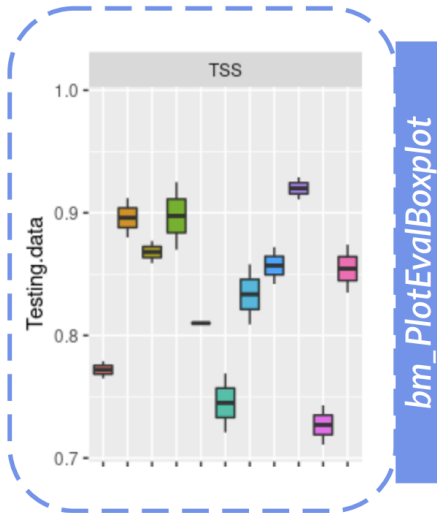
← Takes time ! Has to go through the whole workflow →



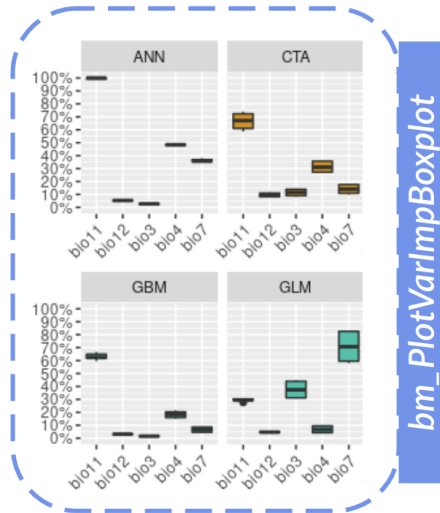
3.b Exploring ensemble models



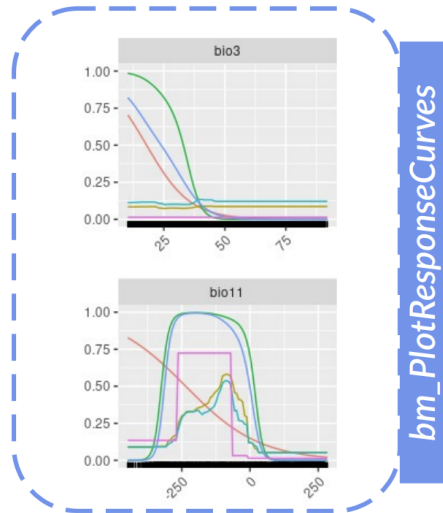
bm_PlotEvalMean



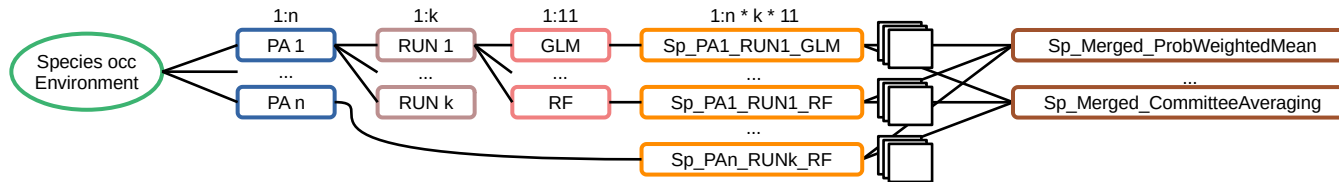
bm_PlotEvalBoxplot



bm_PlotVarImpBoxplot

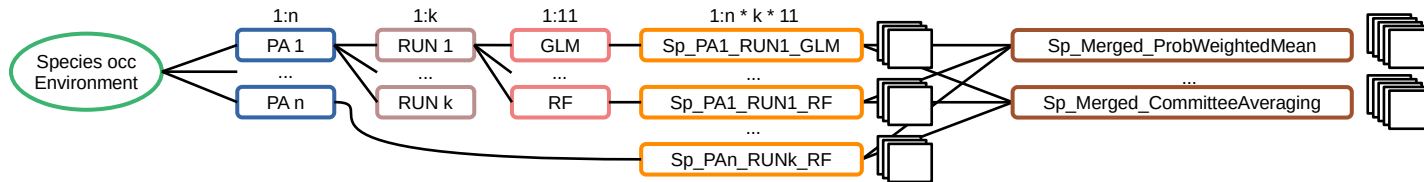
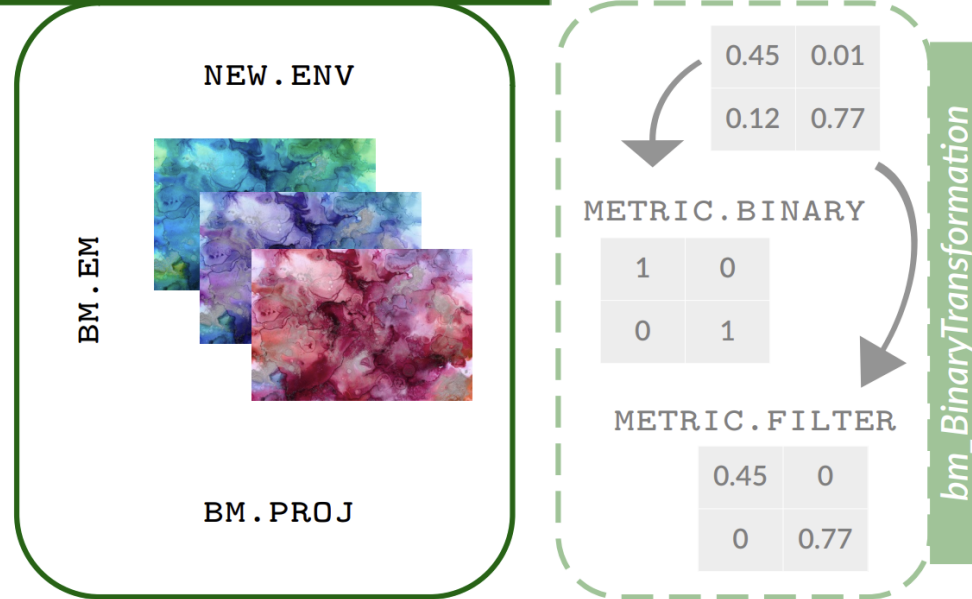


bm_PlotResponseCurves



4.b Projecting ensemble models

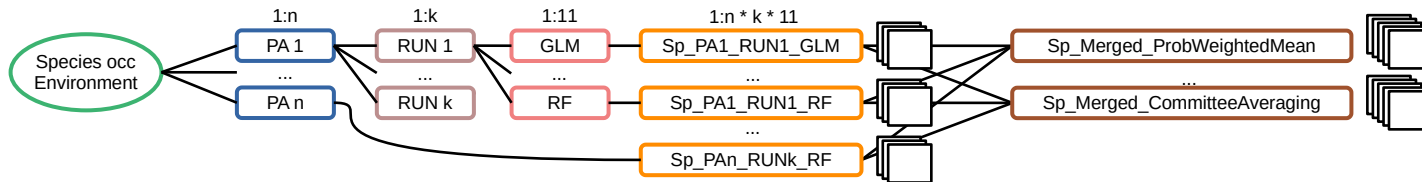
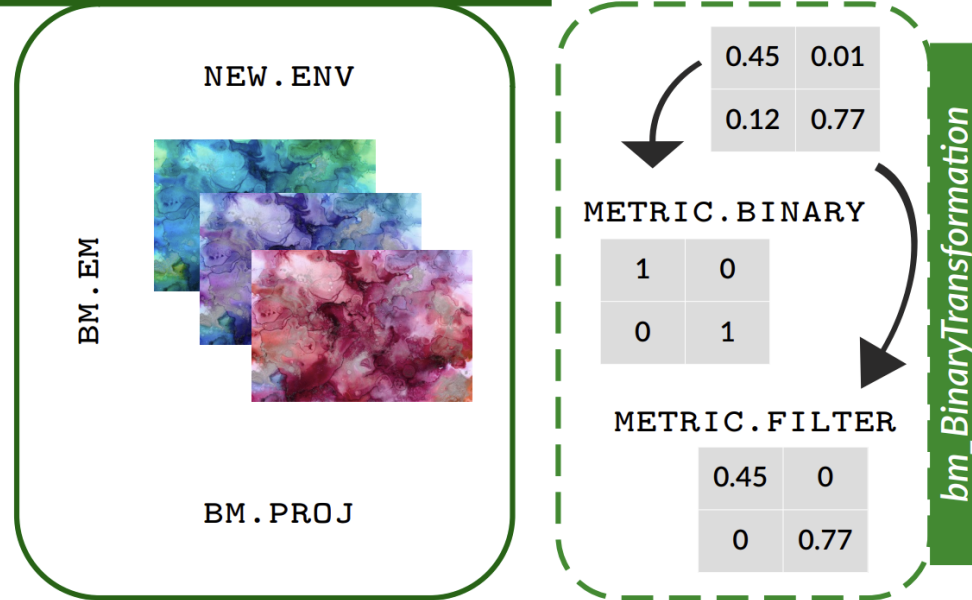
BIOMOD_EnsembleForecasting



4.b Projecting ensemble models

- › transformation associated to one evaluation metric (*one map created for each metric selected*)
- › use the threshold maximising the chosen metric

BIOMOD_EnsembleForecasting



5. Species range change

BIOMOD_RangeSize

PROJ . CURRENT



PROJ . FUTURE

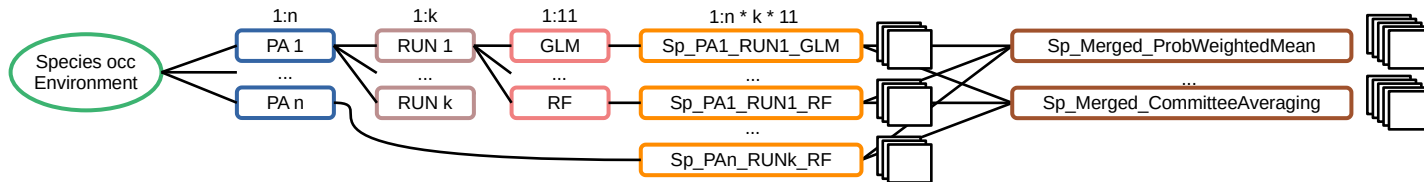


$$\text{PROJ . FUTURE} - 2 * \text{PROJ . CURRENT}$$



- 2 Present in current, lost in future
- 1 Present in current, present in future
- 0 Absent in current, absent in future
- 1 Absent in current, gained in future

bm_PlotRangeSize



5. Species range change

- » explore **spatially** the difference in predictions
- » provide **summary values** :
 - percentage of loss / gain
 - species range change

BIOMOD_RangeSize

PROJ . CURRENT



PROJ . FUTURE

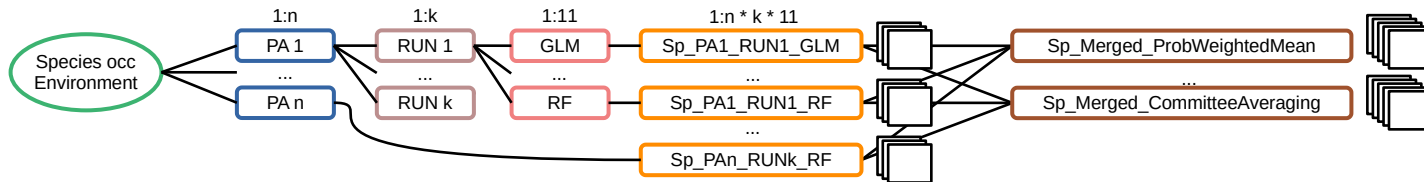


$$\text{PROJ . FUTURE} - 2 * \text{PROJ . CURRENT}$$



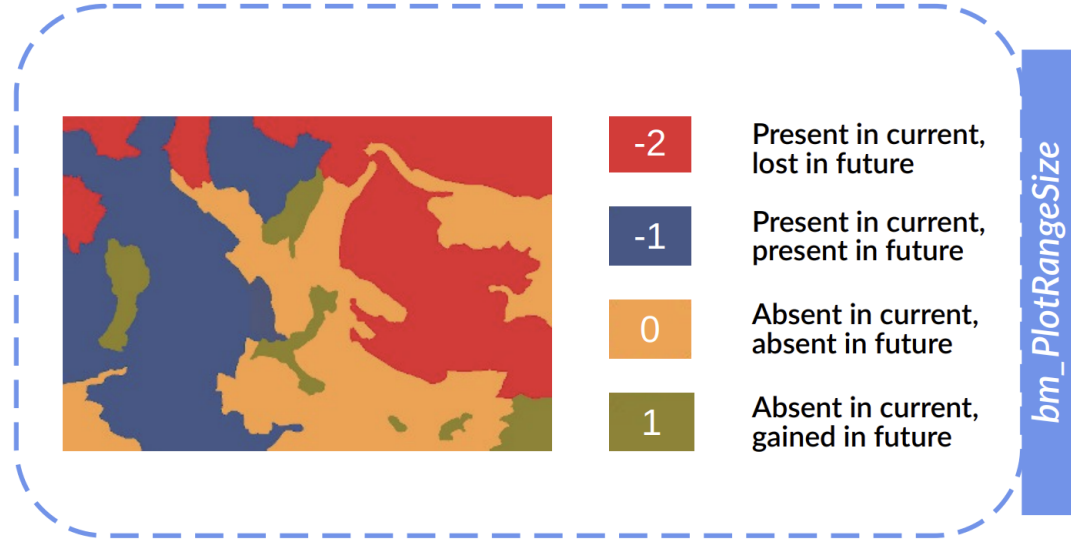
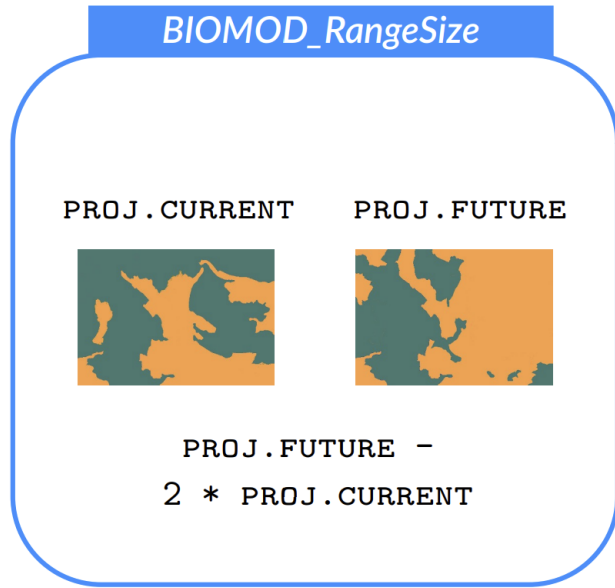
- 2 Present in current, lost in future
- 1 Present in current, present in future
- 0 Absent in current, absent in future
- 1 Absent in current, gained in future

bm_PlotRangeSize



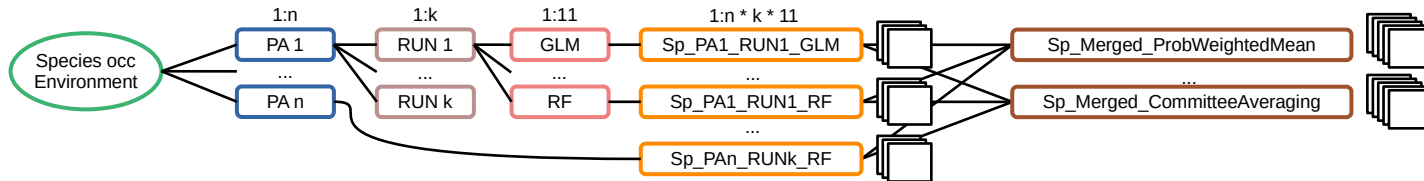
5. Species range change

- » explore **spatially** the difference in predictions
- » provide **summary values** :
 - percentage of loss / gain
 - species range change



! IMPORTANT

Work with binary maps (and not predictions between 0 and 1)



Species distribution modeling,
calibration and evaluation,
ensemble modeling



Thuiller, W. (2003), *BIOMOD – optimizing predictions of species distributions and projecting potential future shifts under global change*. **Global Change Biology**, 9: 1353-1362. <https://doi.org/10.1046/j.1365-2486.2003.00666.x>

Thuiller, W., Lafourcade, B., Engler, R. and Araújo, M.B. (2009), *BIOMOD – a platform for ensemble forecasting of species distributions*. **Ecography**, 32: 369-373. <https://doi.org/10.1111/j.1600-0587.2008.05742.x>

<https://github.com/biomodhub/biomod2/>

<https://biomodhub.github.io/biomod2/>