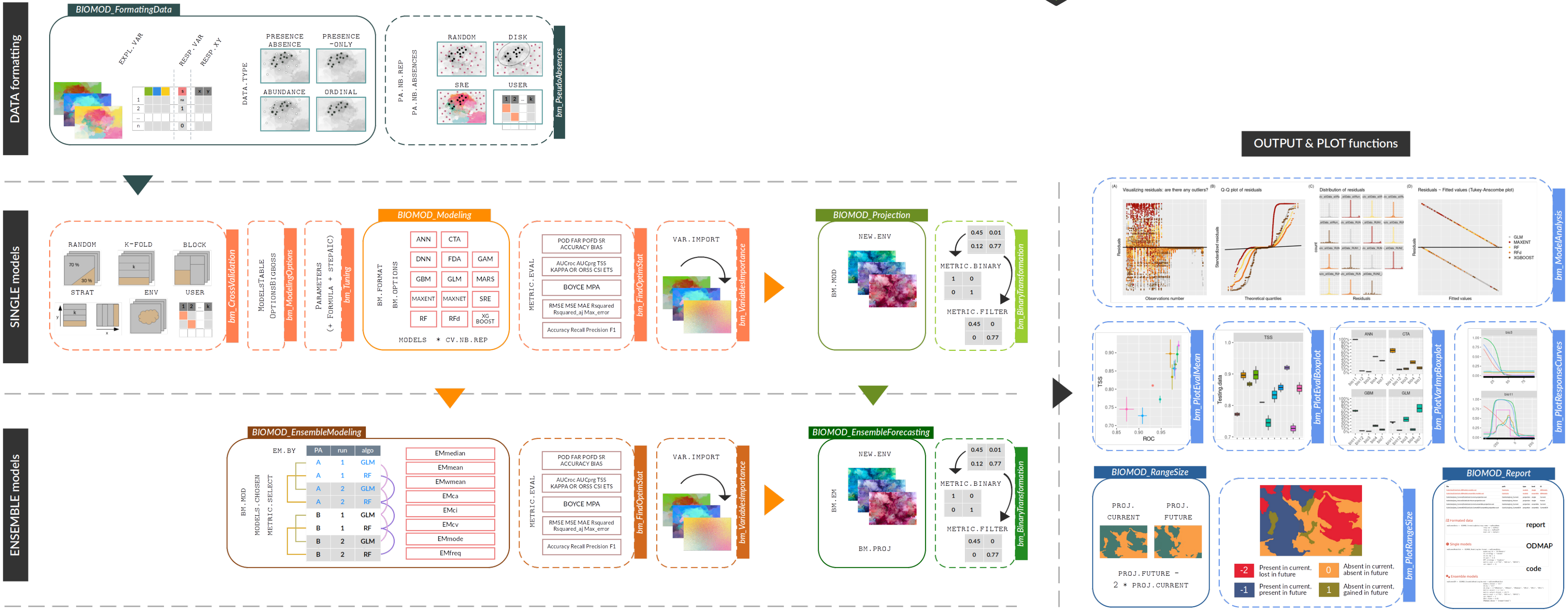
Species distribution modeling, calibration and evaluation, ensemble modeling

Laboratoire d'Ecologie Alpine



DATA formatting

BIOMOD_FormatingData

EXPL.VAR

RESP.VAR

RESP.XY

DATA.TYPE

PRESENCE ABSENCE

PRESENCE -ONLY

ABUNDANCE

ORDINAL

PA.NB.REP

PA.NB.ABSENCES

RANDOM

DISK

SRE

USER

bm_PseudoAbsences

SINGLE models

RANDOM

K-FOLD

BLOCK

STRAT

ENV

USER

bm_CrossValidation

MODELSTABLE

OPTIONSBIGBOSS

bm_ModelingOptions

PARAMETERS

(+ FORMULA + STEPAIC)

bm_Tuning

BIOMOD_Modeling

BM.FORMAT

BM.OPTIONS

ANN, CTA, DNN, FDA, GAM, GBM, GLM, MARS, MAXENT, MAXNET, SRE, RF, RFd, XG BOOST

MODELS * CV.NB.REP

METRIC.EVAL

POD FAR POFD SR ACCURACY BIAS

AUCroc AUCprg TSS KAPPA OR ORSS CSI ETS

BOYCE MPA

RMSE MSE MAE Rsquared Rsquared_aj Max_error

Accuracy Recall Precision F1

bm_FindOptimStat

VAR.IMPORT

bm_VariablesImportance

BIOMOD_Projection

NEW.ENV

BM.MOD

METRIC.BINARY

METRIC.FILTER

bm_BinaryTransformation

ENSEMBLE models

BIOMOD_EnsembleModeling

BM.MOD

MODELS.CHOSEN

METRIC.SELECT

EM.BY

PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

EMmedian, EMmean, EMwmean, EMca, EMci, EMcv, EMmode, EMfreq

METRIC.EVAL

POD FAR POFD SR ACCURACY BIAS

AUCroc AUCprg TSS KAPPA OR ORSS CSI ETS

BOYCE MPA

RMSE MSE MAE Rsquared Rsquared_aj Max_error

Accuracy Recall Precision F1

bm_FindOptimStat

VAR.IMPORT

bm_VariablesImportance

BIOMOD_EnsembleForecasting

NEW.ENV

BM.EM

BM.PROJ

METRIC.BINARY

METRIC.FILTER

bm_BinaryTransformation

OUTPUT & PLOT functions

bm_ModelAnalysis

bm_PlotEvalMean

bm_PlotEvalBoxplot

bm_PlotVarImpBoxplot

bm_PlotResponseCurves

BIOMOD_RangeSize

PROJ. CURRENT

PROJ. FUTURE

PROJ.FUTURE - 2 * PROJ.CURRENT

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

bm_PlotRangeSize

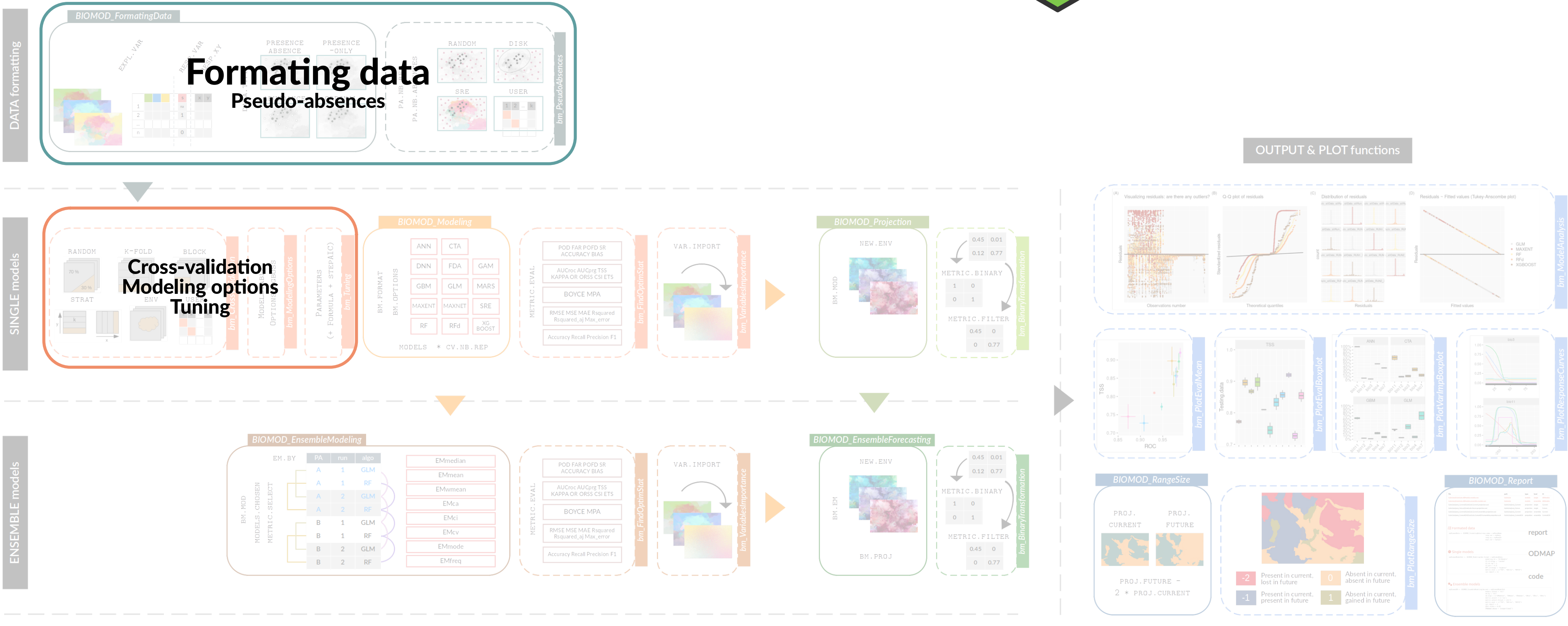
BIOMOD_Report

report

ODMAP

code

Species distribution modeling, calibration and evaluation, ensemble modeling



Formating data

Pseudo-absences

Cross-validation

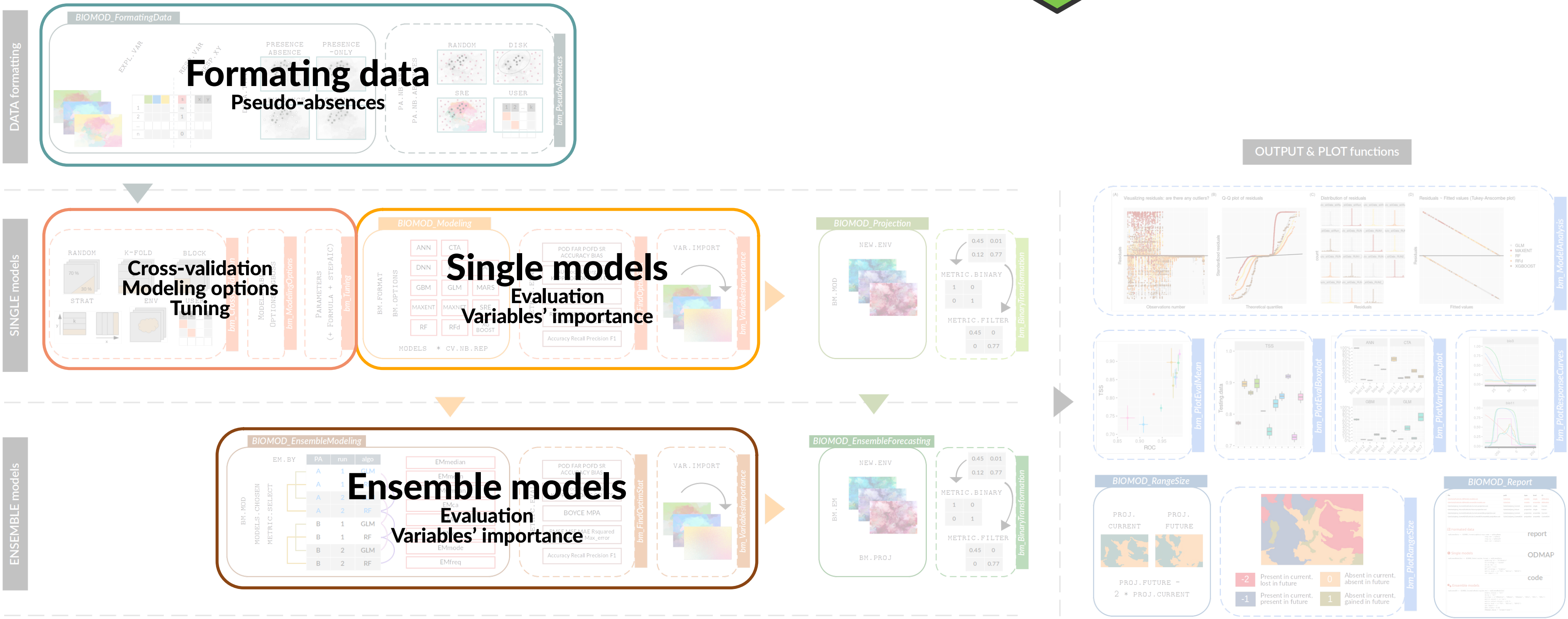
Modeling options

Tuning

Species distribution modeling, calibration and evaluation, ensemble modeling

biomod2

LECA
Laboratoire d'Ecologie Alpine



Formating data
Pseudo-absences

Cross-validation
Modeling options
Tuning

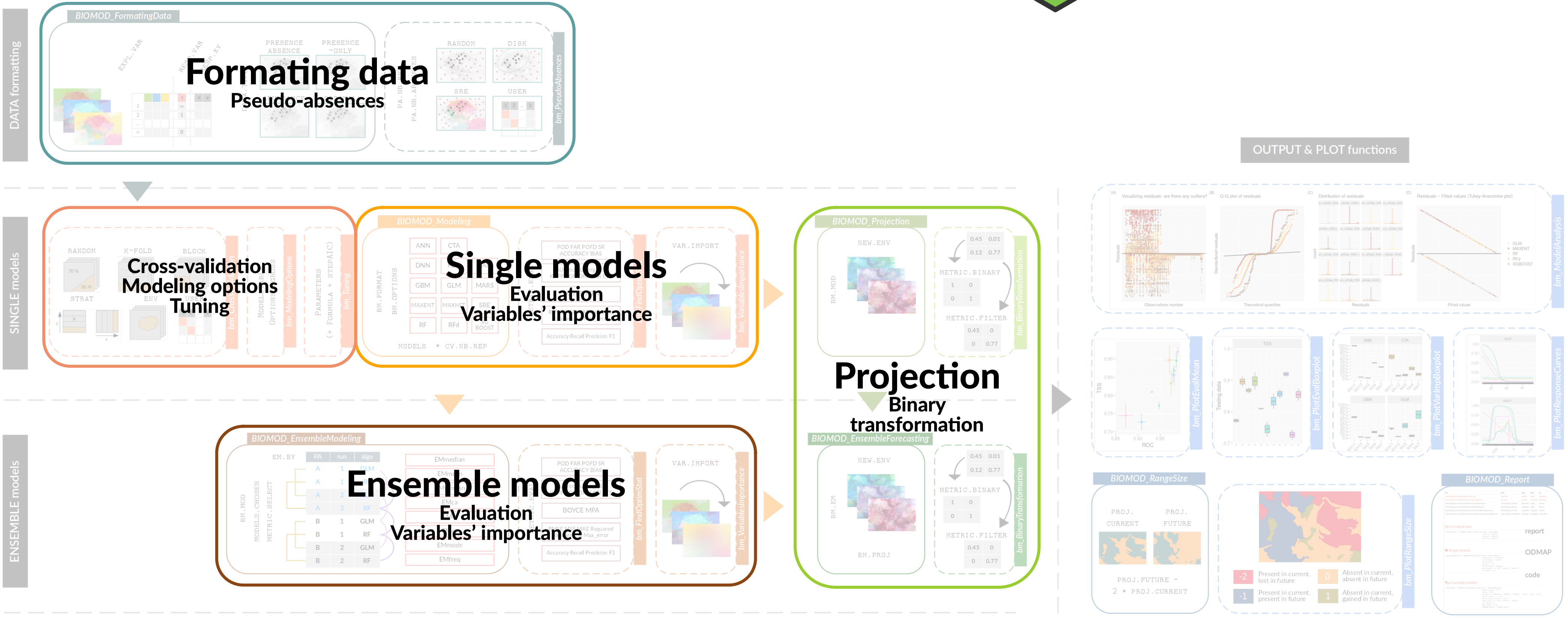
Single models
Evaluation
Variables' importance

Ensemble models
Evaluation
Variables' importance

OUTPUT & PLOT functions

Species distribution modeling, calibration and evaluation, ensemble modeling

Laboratoire d'Ecologie Alpine



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

BIOMOD_EnsembleForecasting

ENSEMBLE models

BIOMOD_EnsembleModeling

Ensemble models
Evaluation
Variables' importance

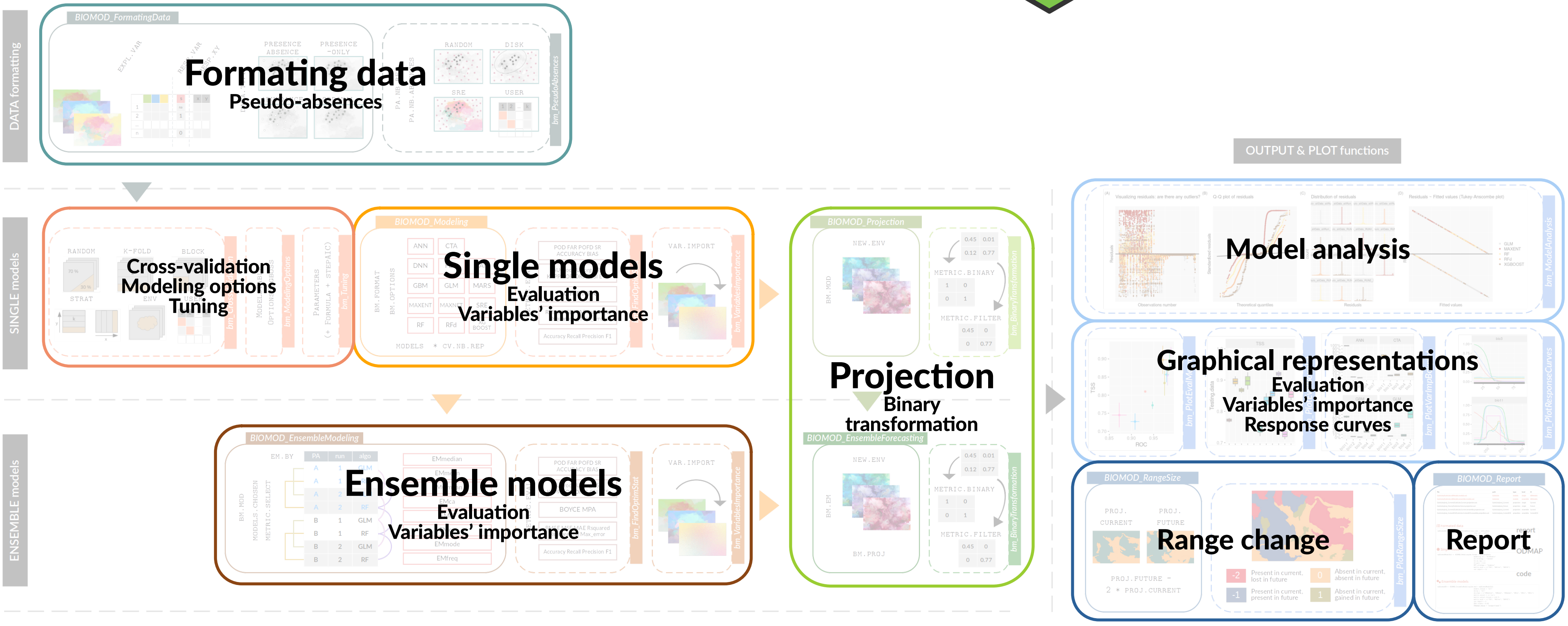
OUTPUT & PLOT functions

BIOMOD_RangeSize

BIOMOD_Report

Species distribution modeling, calibration and evaluation, ensemble modeling

Laboratoire d'Ecologie Alpine



Formating data
Pseudo-absences

Cross-validation
Modeling options
Tuning

Single models
Evaluation
Variables' importance

Ensemble models
Evaluation
Variables' importance

Projection
Binary transformation

Model analysis

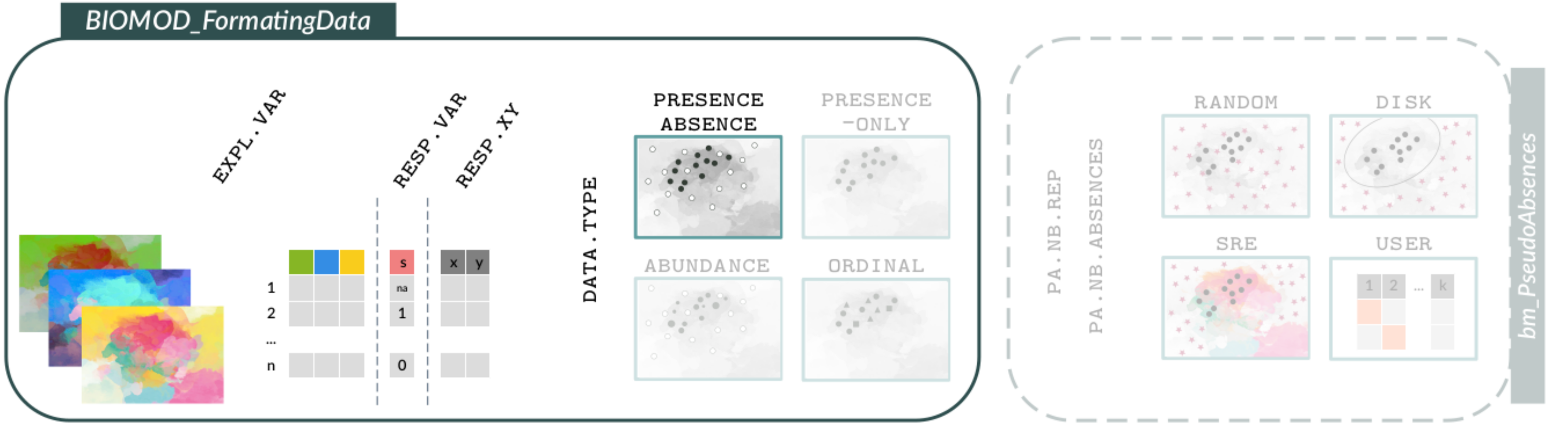
Graphical representations
Evaluation
Variables' importance
Response curves

Range change

Report

1. Formating data

- **presences-absences**



Species occ
Environment

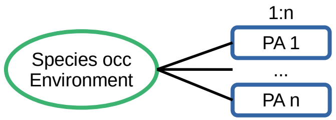
1. Formating data

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

Species occ
Environment

1. Formating data

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



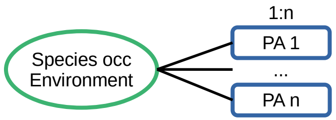
1:n

Species occ
Environment

PA 1
...
PA n

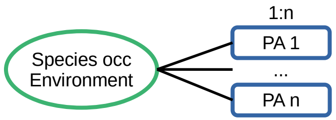
1. Formating data

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

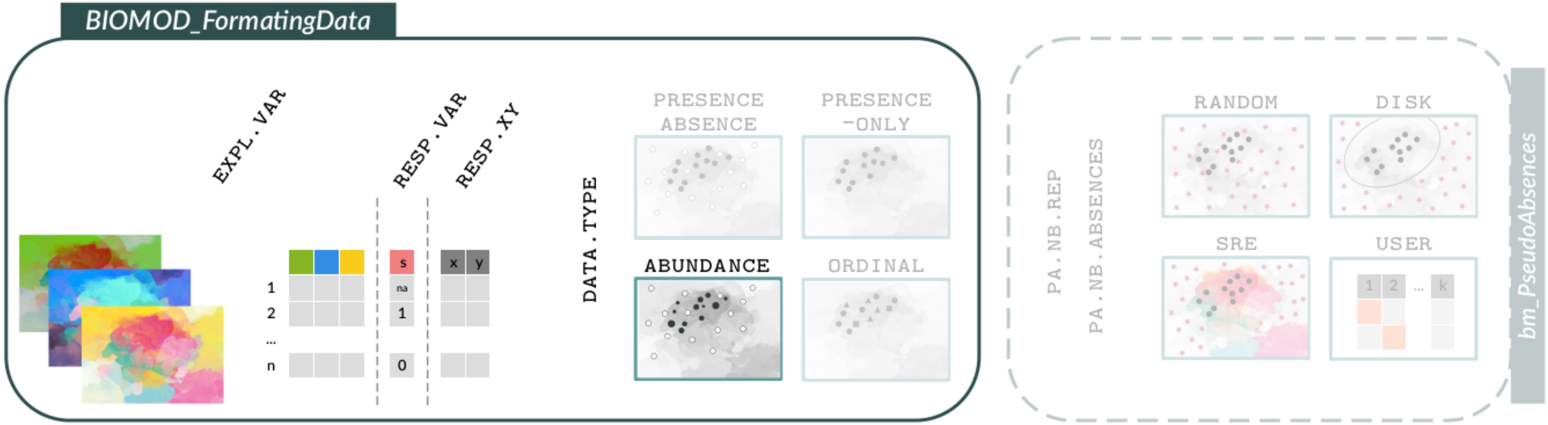


1. Formating data

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



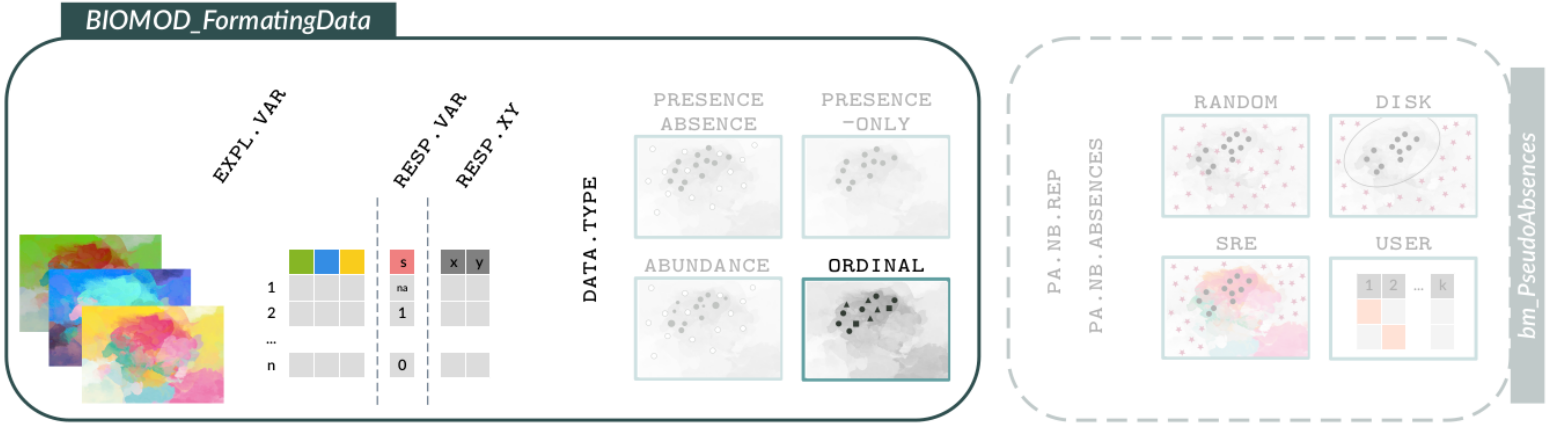
1. Formating data



- **abundance** data

Species occ
Environment

1. Formating data

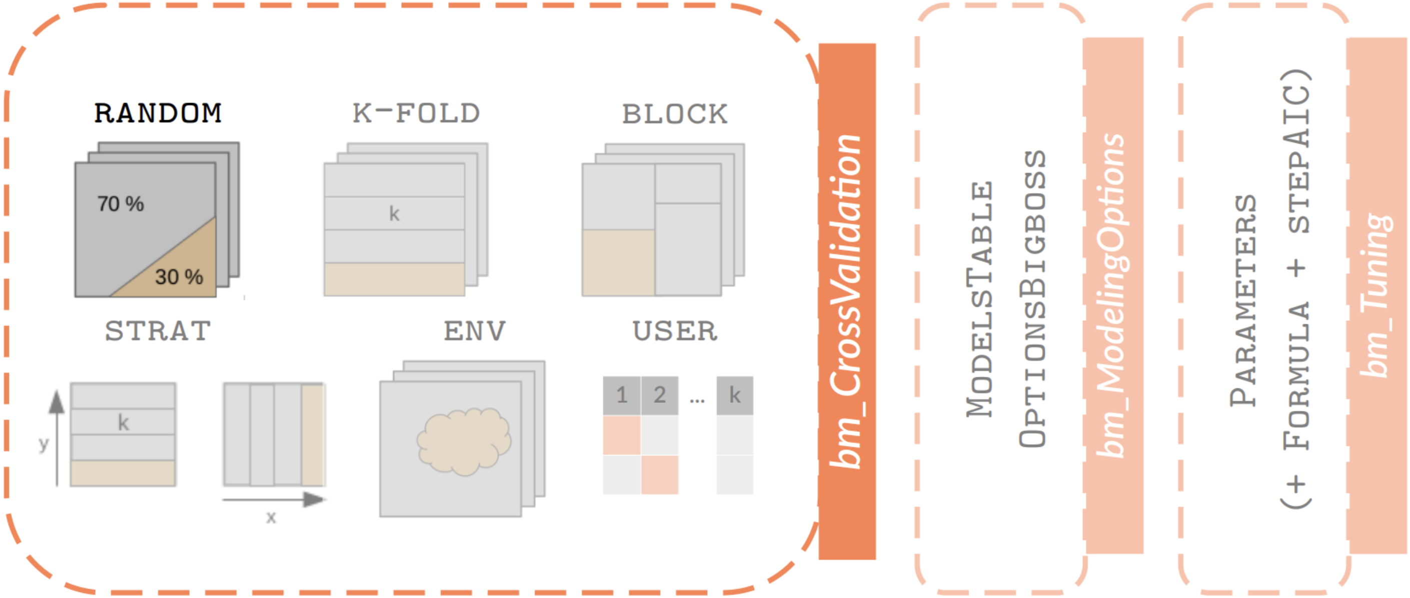


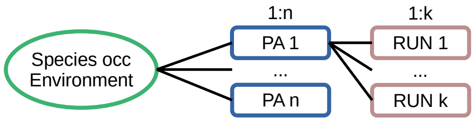
- **ordinal** data

Species occ
Environment

1. Formating data

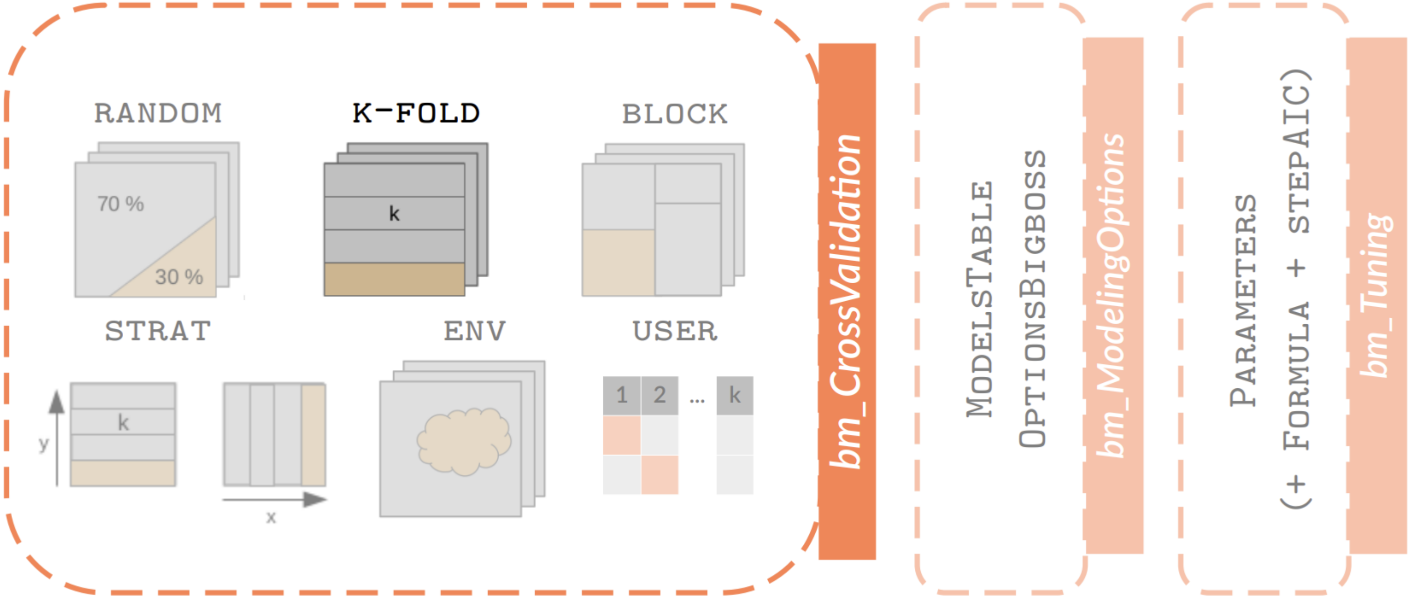
- simple calibration / validation split at the modeling step, and repeated nb.rep times

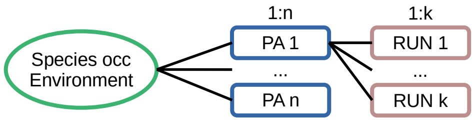




1. Formating data

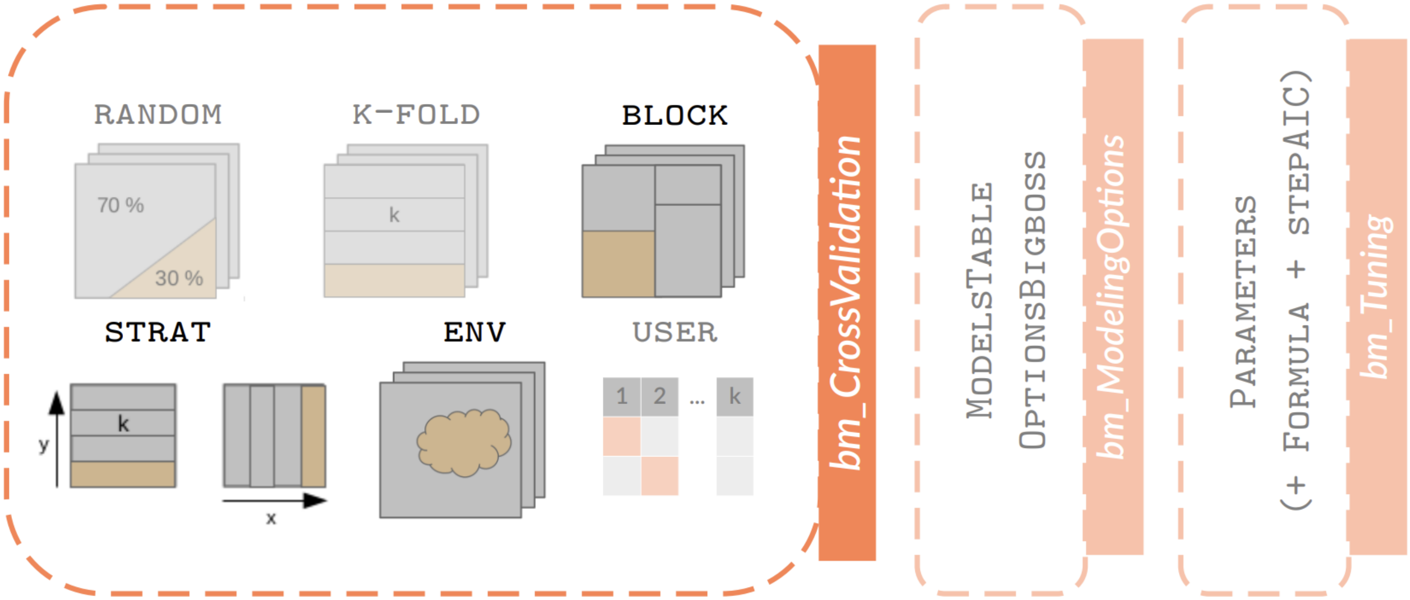
- simple calibration / validation split at the modeling step, and repeated nb.rep times
- **k-fold** : partition data into k sub-dataset, and repeated nb.rep times

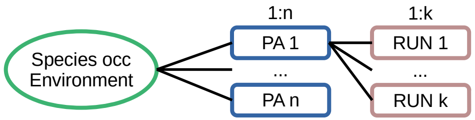




1. Formating data

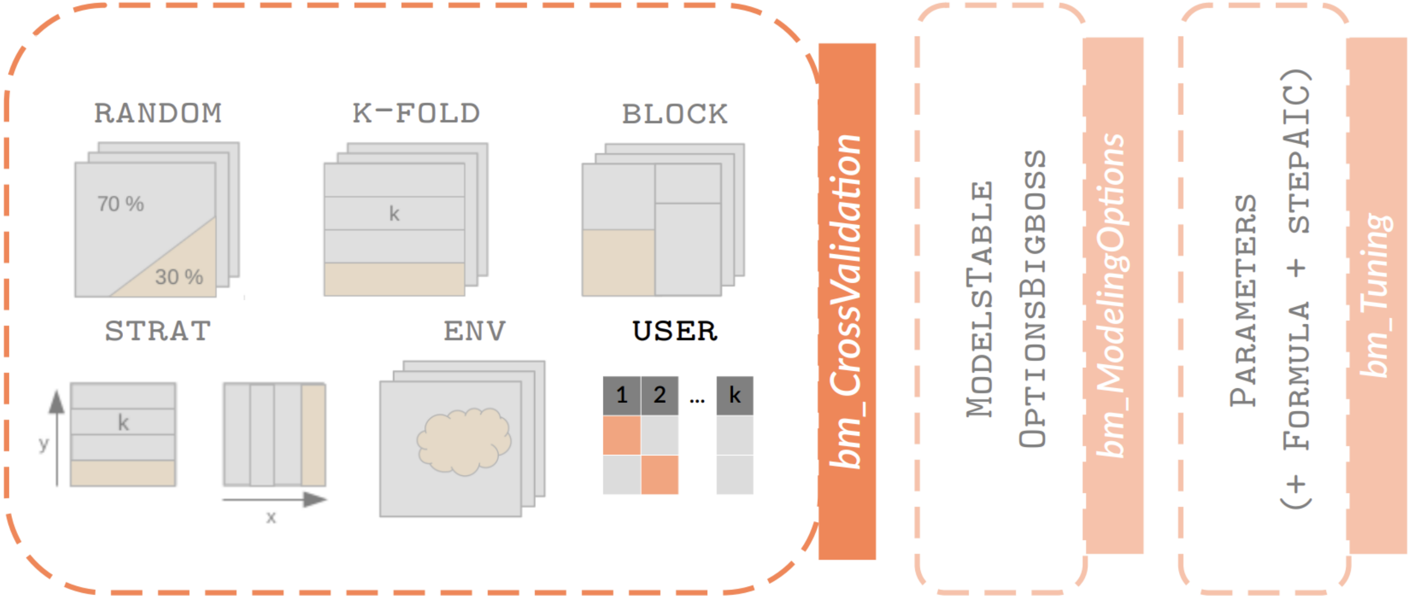
- simple calibration / validation split at the modeling step, and repeated nb.rep times
- **k-fold** : partition data into k sub-dataset, and repeated nb.rep times
- **stratified** : partition data into k sub-dataset (x, y, both, block, env)

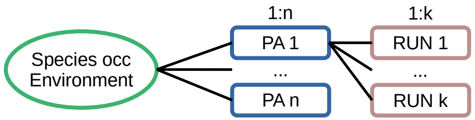




1. Formating data

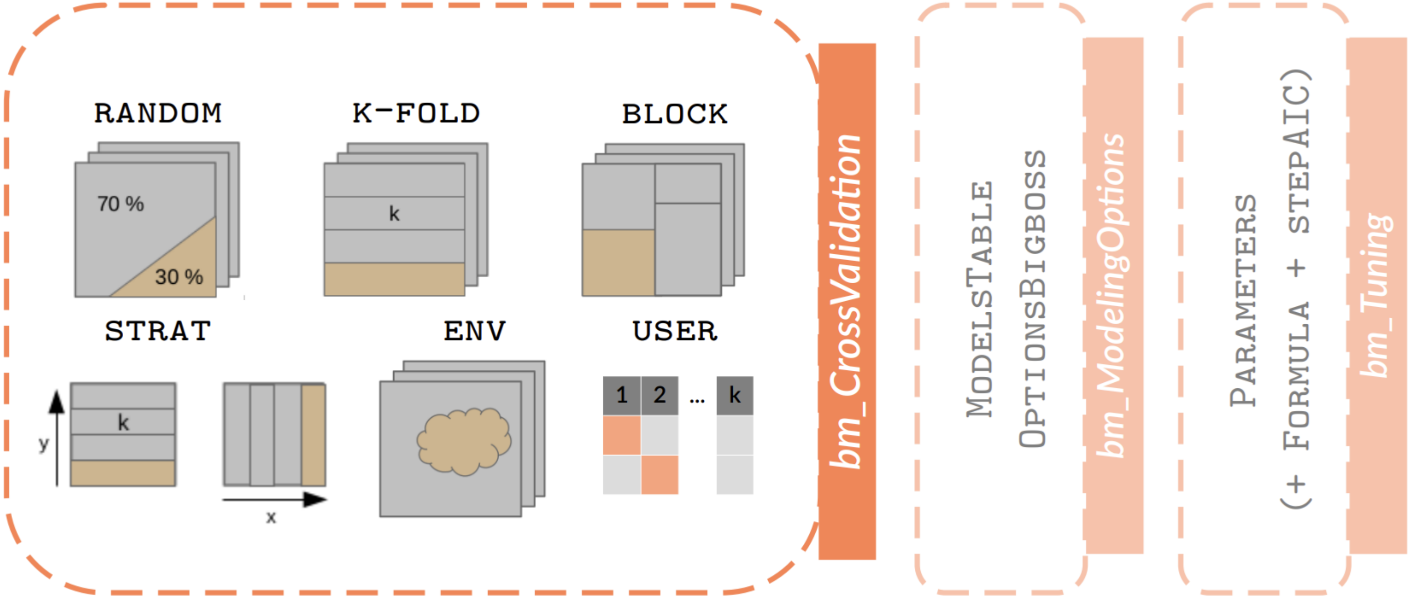
- simple calibration / validation split at the modeling step, and repeated nb.rep times
- **k-fold** : partition data into k sub-dataset, and repeated nb.rep times
- **stratified** : partition data into k sub-dataset (x, y, both, block, env)
- **user defined**

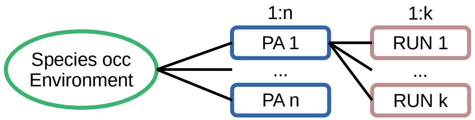


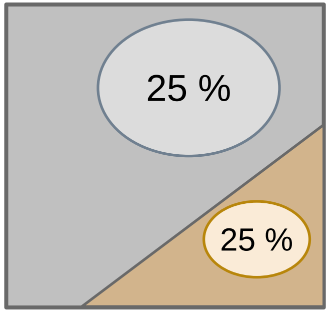


1. Formating data

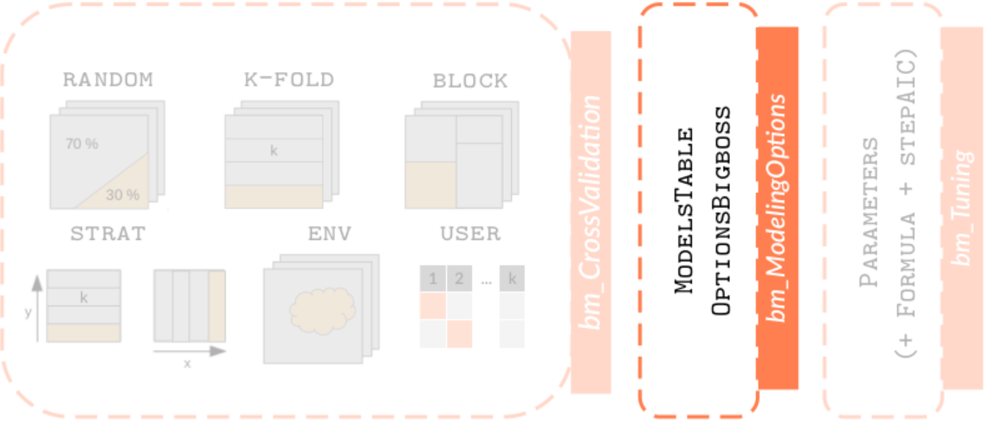
- simple calibration / validation split at the modeling step, and repeated nb.rep times
- **k-fold** : partition data into k sub-dataset, and repeated nb.rep times
- **stratified** : partition data into k sub-dataset (x, y, both, block, env)
- **user defined**
- **balance** : keep the prevalence of presences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





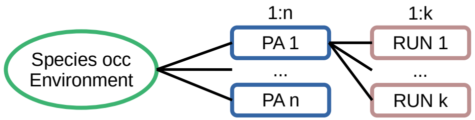


1. Formating data

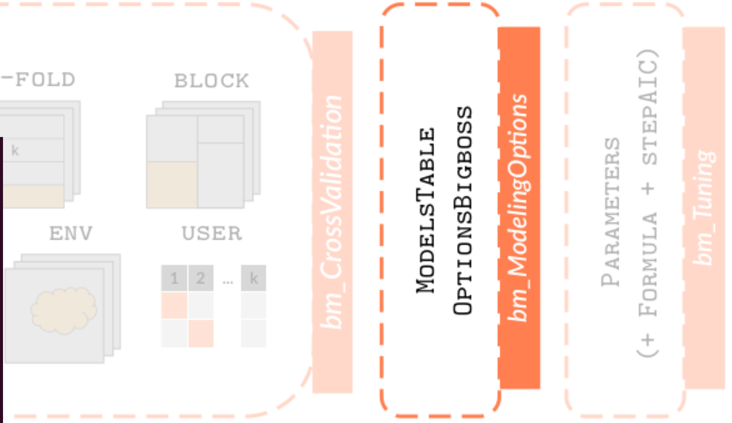


- 12 types of models,
  16 single models,
  11 that can use non-binary data
- 1 coded in biomod2,
  1 external software,
  13 other R packages

```
> ModelsTable
     model      type      package         func       train
1      ANN    binary         nnet         nnet      avNNet
2      CTA    binary        rpart        rpart       rpart
3      DNN    binary         cito          dnn        tune
4      FDA    binary          mda          fda         fda
5      GAM    binary          gam          gam    gamLoess
6      GAM    binary         mgcv          bam         bam
7      GAM    binary         mgcv          gam         gam
8      GBM    binary          gbm          gbm         gbm
9      GLM    binary        stats          glm         glm
10    MARS    binary        earth        earth       earth
11  MAXENT    binary       MAXENT       MAXENT ENMevaluate
12  MAXNET    binary       maxnet       maxnet      maxnet
13      RF    binary randomForest randomForest          rf
14     RFd    binary randomForest randomForest          rf
15     SRE    binary      biomod2       bm_SRE      bm_SRE
16 XGBOOST    binary      xgboost      xgboost     xgbTree
17     CTA nonbinary        rpart        rpart       rpart
18     DNN nonbinary         cito          dnn        tune
19     FDA nonbinary          mda          fda         fda
20     GAM nonbinary          gam          gam    gamLoess
21     GAM nonbinary         mgcv          bam         bam
22     GAM nonbinary         mgcv          gam         gam
23     GBM nonbinary          gbm          gbm         gbm
24     GLM nonbinary        stats          glm         glm
25    MARS nonbinary        earth        earth       earth
26      RF nonbinary randomForest randomForest          rf
27 XGBOOST nonbinary      xgboost      xgboost     xgbTree
```



1. Formating data



- 12 types of models, 16 single models, 11 that can use non-binary data
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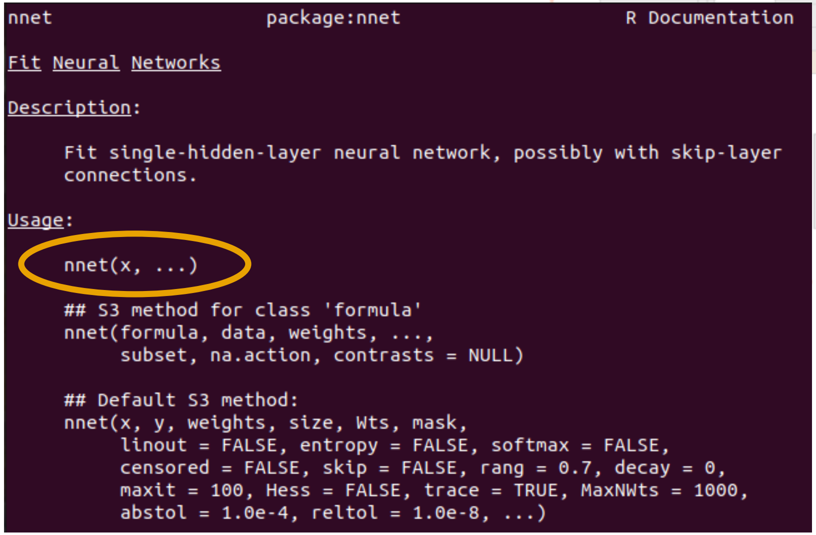

```
nnet                   package:nnet                    R Documentation

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
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1      ANN    binary         nnet         nnet      avNNet
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6      GAM    binary         mgcv          bam         bam
7      GAM    binary         mgcv          gam         gam
8      GBM    binary          gbm          gbm         gbm
9      GLM    binary        stats          glm         glm
10    MARS    binary        earth        earth       earth
11  MAXENT    binary       MAXENT       MAXENT ENMevaluate
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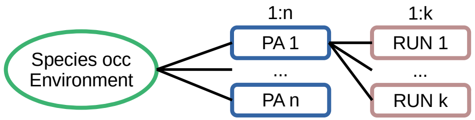

1. Formating data

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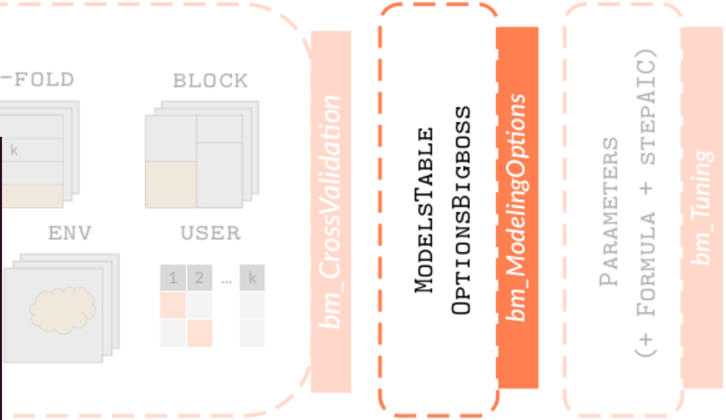

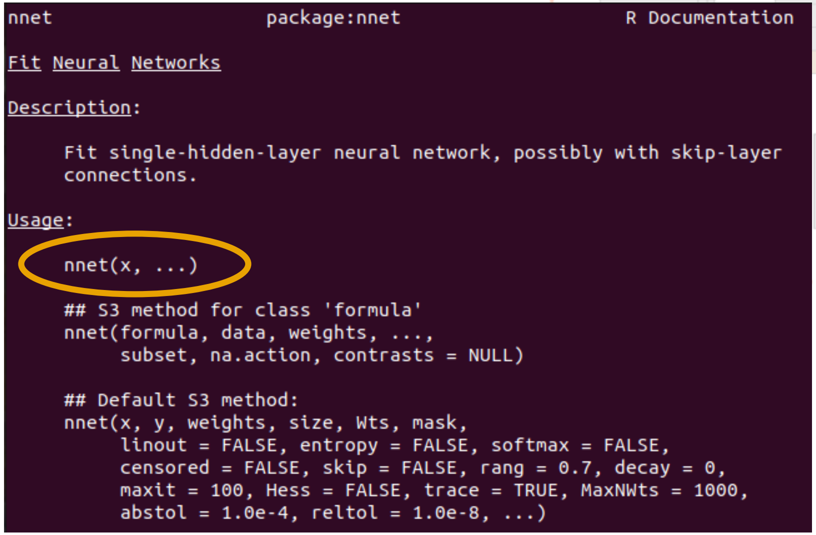

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nnet                      package:nnet                   R Documentation

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     ## S3 method for class 'formula'
     nnet(formula, data, weights, ...,
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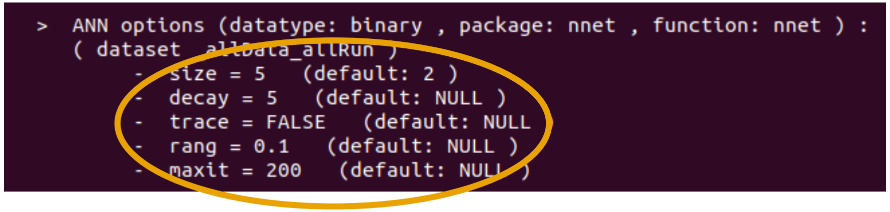
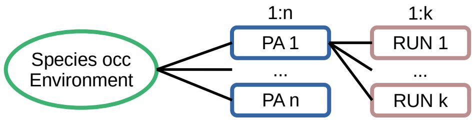
     ## Default S3 method:
     nnet(x, y, weights, size, Wts, mask,
          linout = FALSE, entropy = FALSE, softmax = FALSE,
          censored = FALSE, skip = FALSE, rang = 0.7, decay = 0,
          maxit = 100, Hess = FALSE, trace = TRUE, MaxNWts = 1000,
          abstol = 1.0e-4, reltol = 1.0e-8, ...)
```



```
 >  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 )
```



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5      GAM     binary           gam           gam   gamLoess
6      GAM     binary          mgcv           bam        bam
7      GAM     binary          mgcv           gam        gam
8      GBM     binary           gbm           gbm        gbm
9      GLM     binary         stats           glm        glm
10    MARS     binary         earth         earth      earth
11  MAXENT     binary        MAXENT        MAXENT ENMevaluate
12  MAXNET     binary        maxnet        maxnet     maxnet
13      RF     binary randomForest randomForest         rf
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15     SRE     binary       biomod2        bm_SRE     bm_SRE
16 XGBOOST     binary       xgboost       xgboost    xgbTree
17     CTA  nonbinary         rpart         rpart      rpart
18     DNN  nonbinary          cito           dnn       tune
19     FDA  nonbinary           mda           fda        fda
20     GAM  nonbinary           gam           gam   gamLoess
21     GAM  nonbinary          mgcv           bam        bam
22     GAM  nonbinary          mgcv           gam        gam
23     GBM  nonbinary           gbm           gbm        gbm
24     GLM  nonbinary         stats           glm        glm
25    MARS  nonbinary         earth         earth      earth
26      RF  nonbinary randomForest randomForest         rf
27 XGBOOST  nonbinary       xgboost       xgboost    xgbTree
```

1. Formating data

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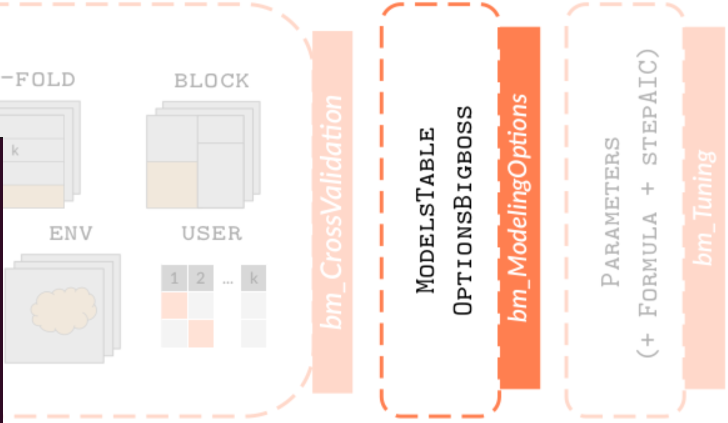
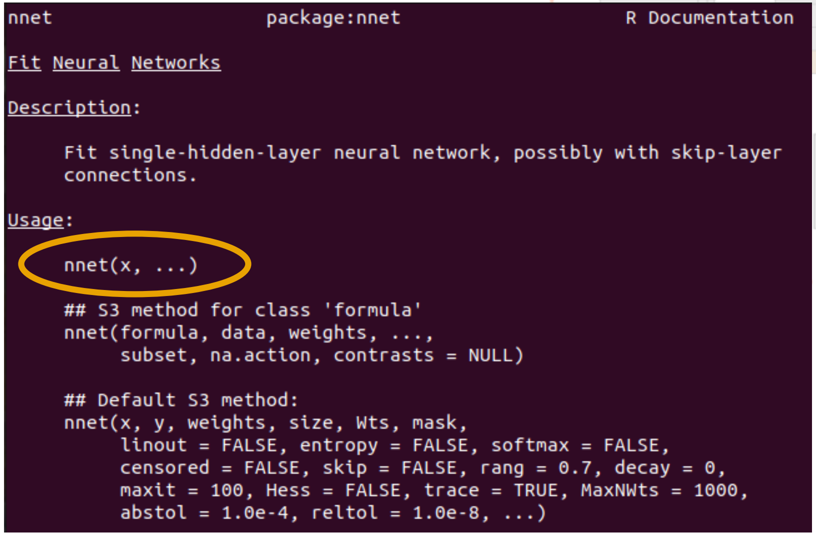
- **user-defined**





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nnet                    package:nnet                    R Documentation

Fit Neural Networks

Description:

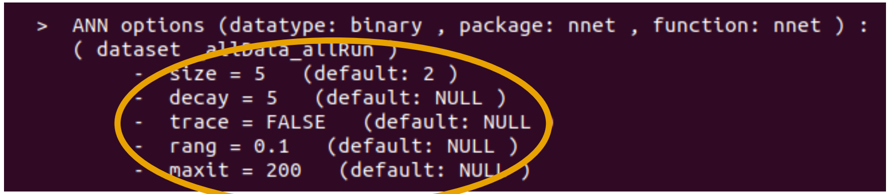
     Fit single-hidden-layer neural network, possibly with skip-layer
     connections.

Usage:

     nnet(x, ...)

     ## S3 method for class 'formula'
     nnet(formula, data, weights, ...,
          subset, na.action, contrasts = NULL)

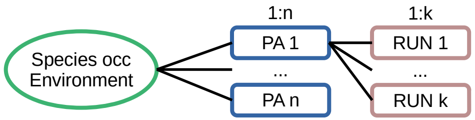
     ## Default S3 method:
     nnet(x, y, weights, size, Wts, mask,
          linout = FALSE, entropy = FALSE, softmax = FALSE,
          censored = FALSE, skip = FALSE, rang = 0.7, decay = 0,
          maxit = 100, Hess = FALSE, trace = TRUE, MaxNWts = 1000,
          abstol = 1.0e-4, reltol = 1.0e-8, ...)
```



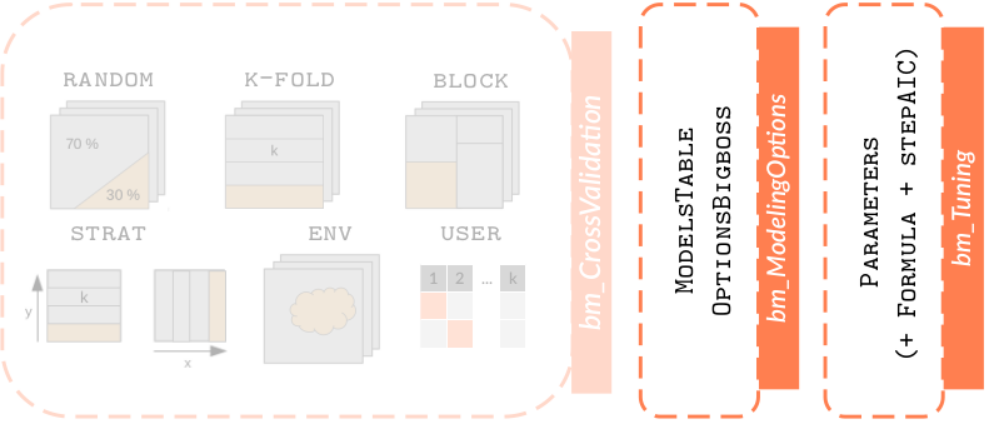
```
 >  ANN options (datatype: binary , package: nnet , function: nnet ) :
    ( dataset  allData_allRun )
         -  size = 5   (default: 2 )
         -  decay = 5   (default: NULL )
         -  trace = FALSE   (default: NULL )
         -  rang = 0.1   (default: NULL )
         -  maxit = 200   (default: NULL )
```

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

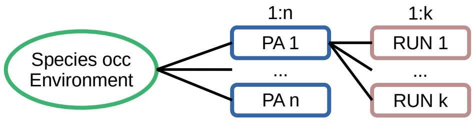
```
> ModelsTable
     model      type       package         func       train
1      ANN    binary          nnet         nnet     avNNet
2      CTA    binary         rpart        rpart      rpart
3      DNN    binary          cito          dnn       tune
4      FDA    binary           mda          fda        fda
5      GAM    binary           gam          gam   gamLoess
6      GAM    binary          mgcv          bam        bam
7      GAM    binary          mgcv          gam        gam
8      GBM    binary           gbm          gbm        gbm
9      GLM    binary         stats          glm        glm
10    MARS    binary         earth        earth      earth
11  MAXENT    binary        MAXENT       MAXENT ENMevaluate
12  MAXNET    binary        maxnet       maxnet     maxnet
13      RF    binary randomForest randomForest         rf
14     RFd    binary randomForest randomForest         rf
15     SRE    binary       biomod2       bm_SRE     bm_SRE
16 XGBOOST    binary       xgboost      xgboost    xgbTree
17     CTA nonbinary         rpart        rpart      rpart
18     DNN nonbinary          cito          dnn       tune
19     FDA nonbinary           mda          fda        fda
20     GAM nonbinary           gam          gam   gamLoess
21     GAM nonbinary          mgcv          bam        bam
22     GAM nonbinary          mgcv          gam        gam
23     GBM nonbinary           gbm          gbm        gbm
24     GLM nonbinary         stats          glm        glm
25    MARS nonbinary         earth        earth      earth
26      RF nonbinary randomForest randomForest         rf
27 XGBOOST nonbinary       xgboost      xgboost    xgbTree
```



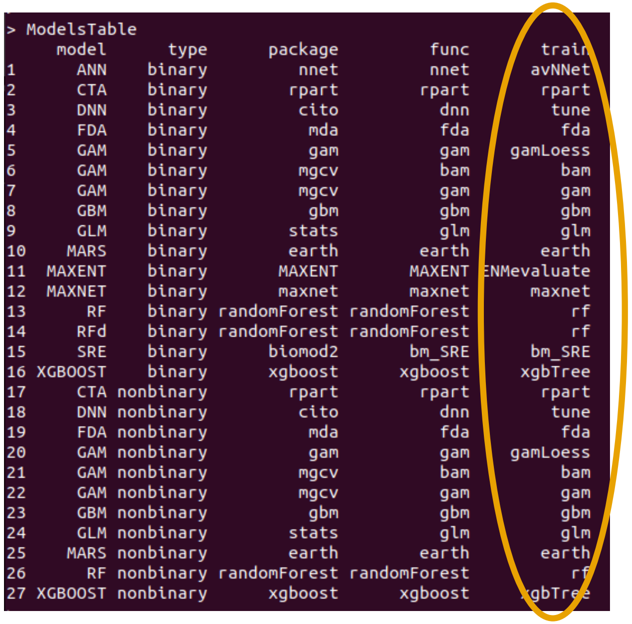
1. Formating data



- 12 types of models,
  16 single models,
  11 that can use non-binary data
- 1 coded in biomod2,
  1 external software,
  13 other R packages
- **default** : extracted from functions
- **bigboss** : redefined by biomod2 team
- **user-defined**
- **tuned** : with *train* function from *caret* package



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



```
> ModelsTable
     model      type      package         func       train
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2      CTA    binary        rpart        rpart       rpart
3      DNN    binary         cito          dnn        tune
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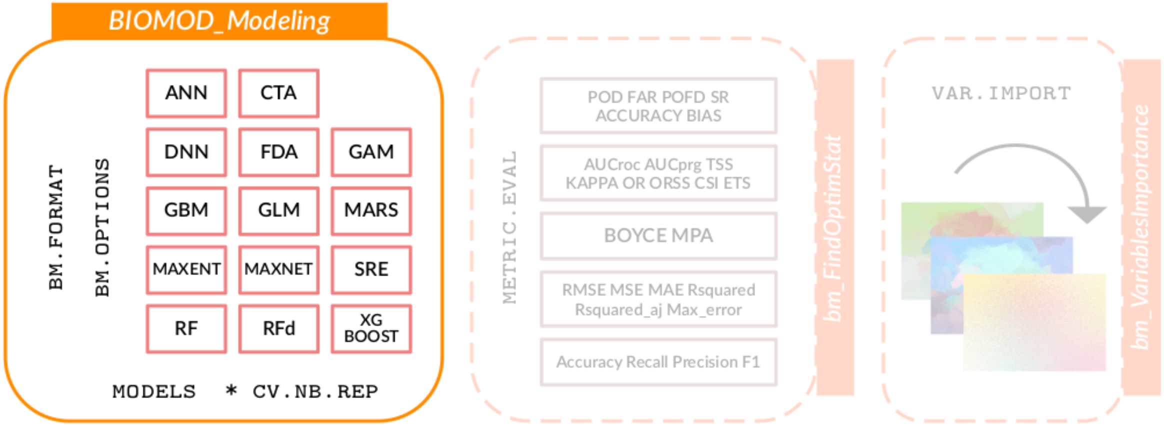
5      GAM    binary          gam          gam    gamLoess
6      GAM    binary         mgcv          bam         bam
7      GAM    binary         mgcv          gam         gam
8      GBM    binary          gbm          gbm         gbm
9      GLM    binary        stats          glm         glm
10    MARS    binary        earth        earth       earth
11  MAXENT    binary       MAXENT       MAXENT ENMevaluate
12  MAXNET    binary       maxnet       maxnet      maxnet
13      RF    binary randomForest randomForest          rf
14     RFd    binary randomForest randomForest          rf
15     SRE    binary      biomod2       bm_SRE      bm_SRE
16 XGBOOST    binary      xgboost      xgboost     xgbTree
17     CTA nonbinary        rpart        rpart       rpart
18     DNN nonbinary         cito          dnn        tune
19     FDA nonbinary          mda          fda         fda
20     GAM nonbinary          gam          gam    gamLoess
21     GAM nonbinary         mgcv          bam         bam
22     GAM nonbinary         mgcv          gam         gam
23     GBM nonbinary          gbm          gbm         gbm
24     GLM nonbinary        stats          glm         glm
25    MARS nonbinary        earth        earth       earth
26      RF nonbinary randomForest randomForest          rf
27 XGBOOST nonbinary      xgboost      xgboost     xgbTree
```

2.a Single models



BIOMOD_Modeling

BM.FORMAT

BM.OPTIONS

ANN CTA

DNN FDA GAM

GBM GLM MARS

MAXENT MAXNET SRE

RF RFd XG BOOST

MODELS * CV.NB.REP

METRIC.EVAL

POD FAR POFD SR ACCURACY BIAS

AUCroc AUCprg TSS KAPPA OR ORSS CSI ETS

BOYCE MPA

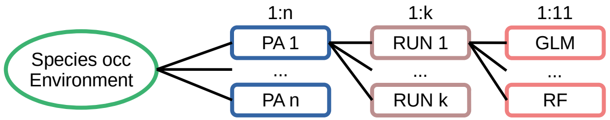
RMSE MSE MAE Rsquared Rsquared_aj Max_error

Accuracy Recall Precision F1

bm_FindOptimStat

VAR.IMPORT

bm_VariablesImportance



Species occ Environment

1:n

PA 1

...

PA n

1:k

RUN 1

...

RUN k

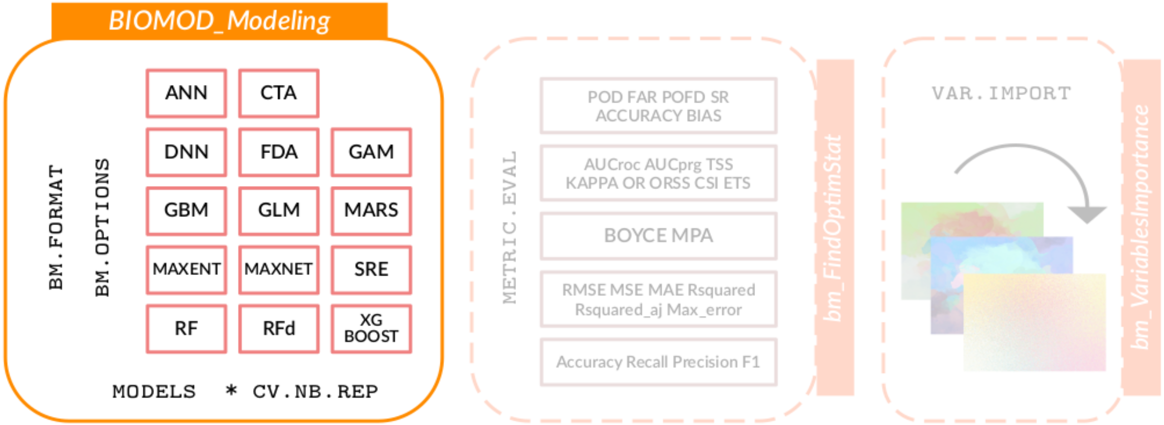
1:11

GLM

...

RF

2.a Single models



BIOMOD_Modeling

BM.FORMAT

BM.OPTIONS

ANN	CTA	
DNN	FDA	GAM
GBM	GLM	MARS
MAXENT	MAXNET	SRE
RF	RFd	XG BOOST

MODELS * CV.NB.REP

METRIC.EVAL

POD FAR POFD SR ACCURACY BIAS

AUCroc AUCprg TSS KAPPA OR ORSS CSI ETS

BOYCE MPA

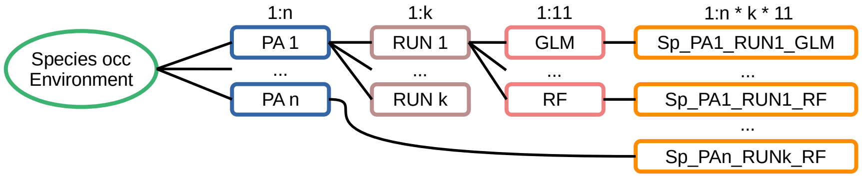
RMSE MSE MAE Rsquared Rsquared_aj Max_error

Accuracy Recall Precision F1

bm_FindOptimStat

VAR.IMPORT

bm_VariablesImportance



Species occ Environment

1:n

PA 1

...

PA n

1:k

RUN 1

...

RUN k

1:11

GLM

...

RF

1:n * k * 11

Sp_PA1_RUN1_GLM

...

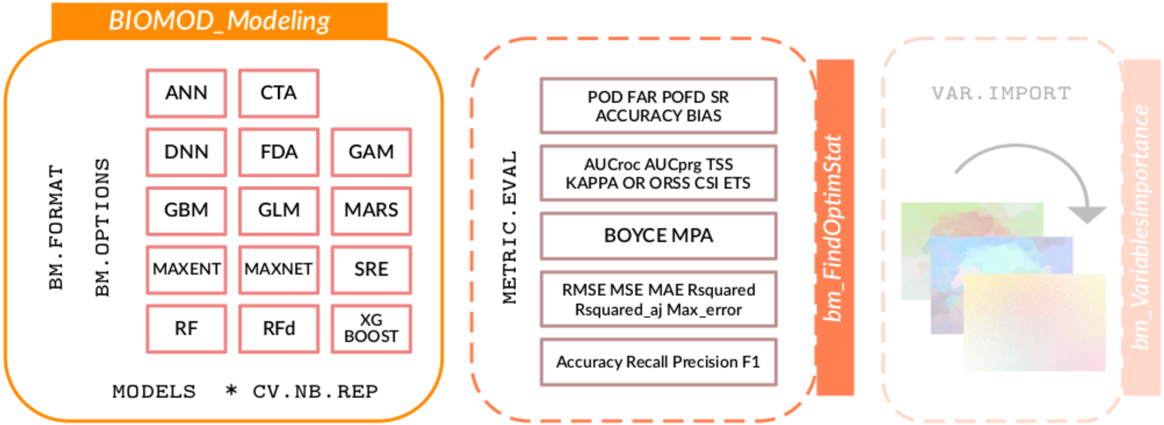
Sp_PA1_RUN1_RF

...

Sp_PAn_RUNk_RF

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 thresold optimising the evaluation metric



BIOMOD_Modeling

BM.FORMAT

BM.OPTIONS

ANN CTA
DNN FDA GAM
GBM GLM MARS
MAXENT MAXNET SRE
RF RFd XG BOOST

MODELS * CV.NB.REP

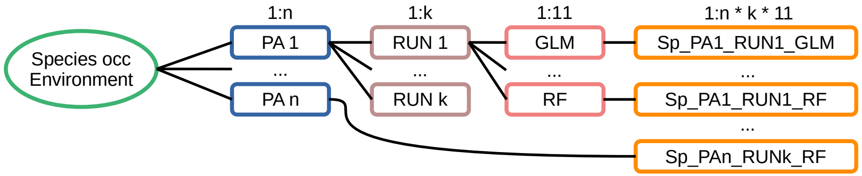
METRIC.EVAL

POD FAR POFD SR ACCURACY BIAS
AUCroc AUCprg TSS KAPPA OR ORSS CSI ETS
BOYCE MPA
RMSE MSE MAE Rsquared Rsquared_aj Max_error
Accuracy Recall Precision F1

bm_FindOptimStat

VAR.IMPORT

bm_VariablesImportance



Species occ Environment

1:n
PA 1
...
PA n

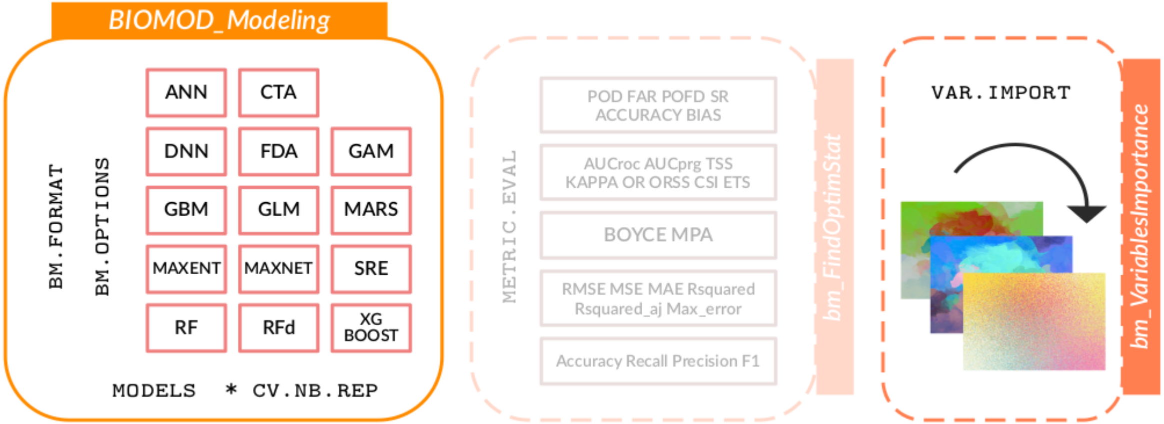
1:k
RUN 1
...
RUN k

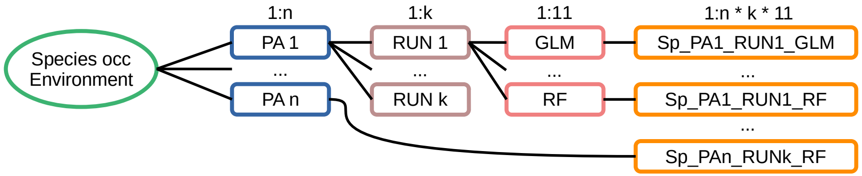
1:11
GLM
...
RF

1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

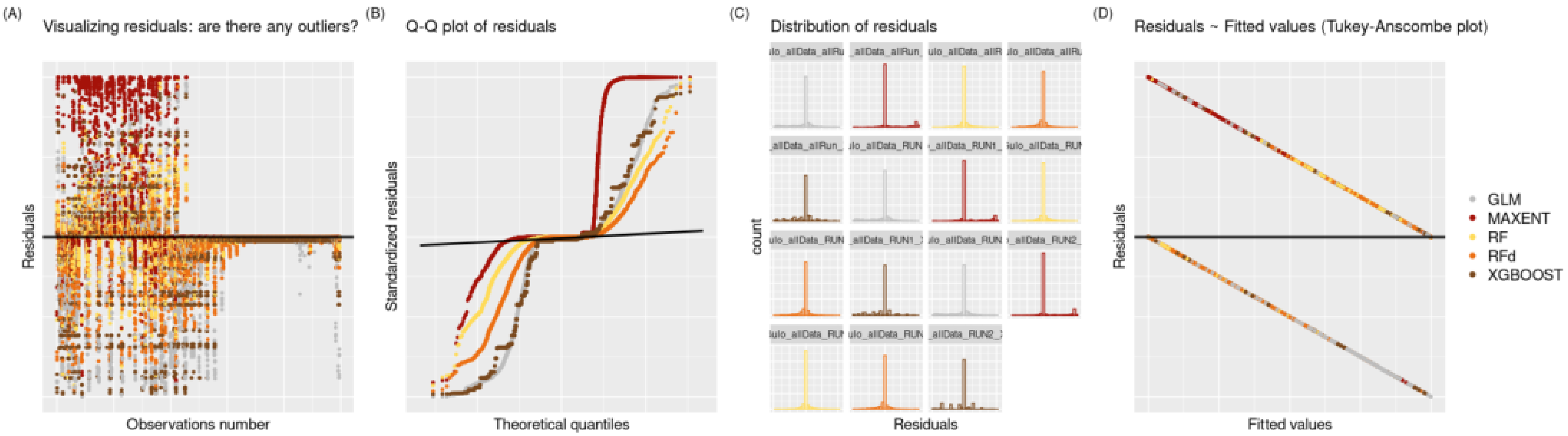
2.a Single models

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

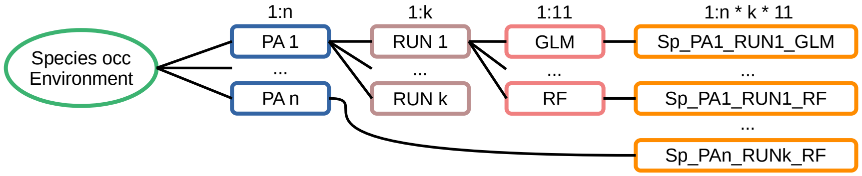




3.a Exploring single models



bm_ModelAnalysis


1:n
1:k
1:11
1:n * k * 11

Species occ
Environment

PA 1
...
PA n

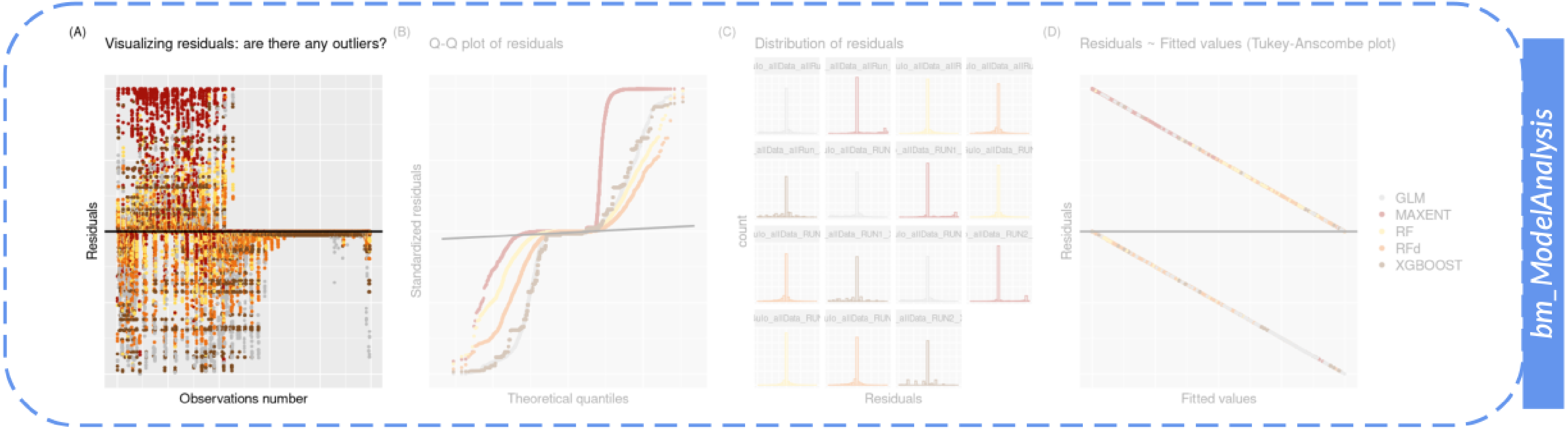
RUN 1
...
RUN k

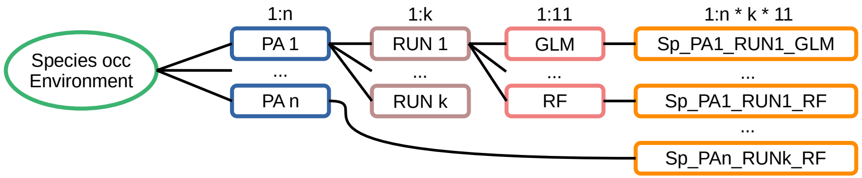
GLM
...
RF

Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

3.a Exploring single models

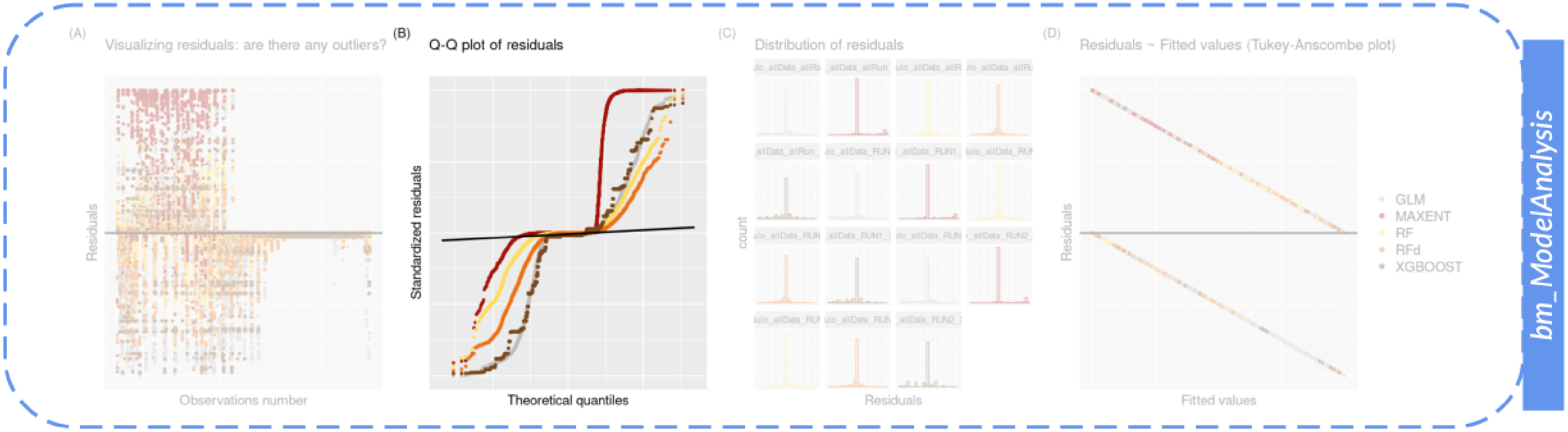
- *residuals ~ f(observations number)*
- visualize the potential outliers
  - x-axis only helps to find the outlier number

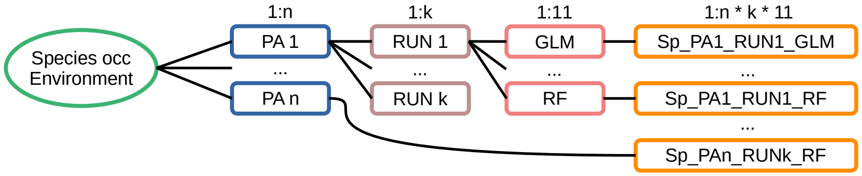




3.a Exploring single models

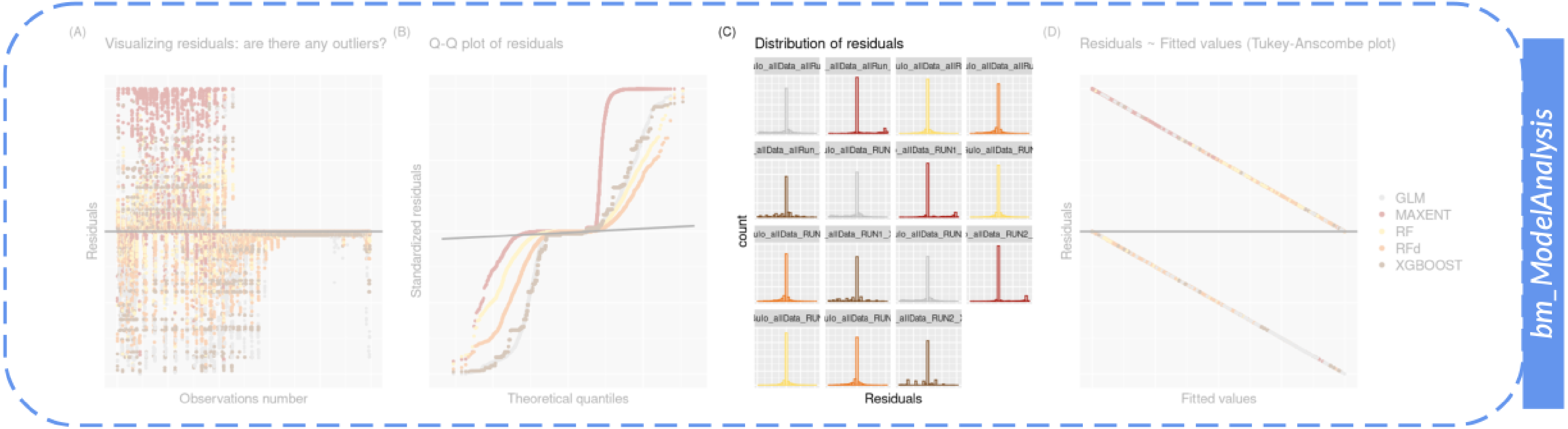
- *standardized residuals ~ f(theoretical quantiles)*
- Q-Q plot to assess if residuals follow a normal distribution

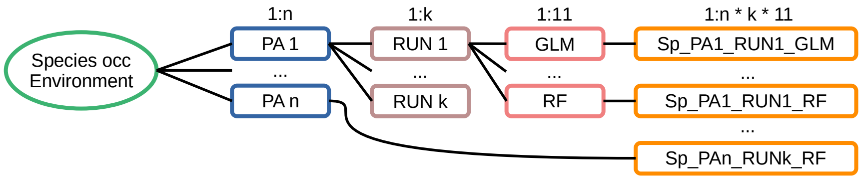



1:n
1:k
1:11
1:n * k * 11
Species occ
Environment
PA 1
...
PA n
RUN 1
...
RUN k
GLM
...
RF
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

3.a Exploring single models

- *residuals distribution*
- histogram to assess if residuals follow a normal distribution





Species occ
Environment

1:n
PA 1
...
PA n

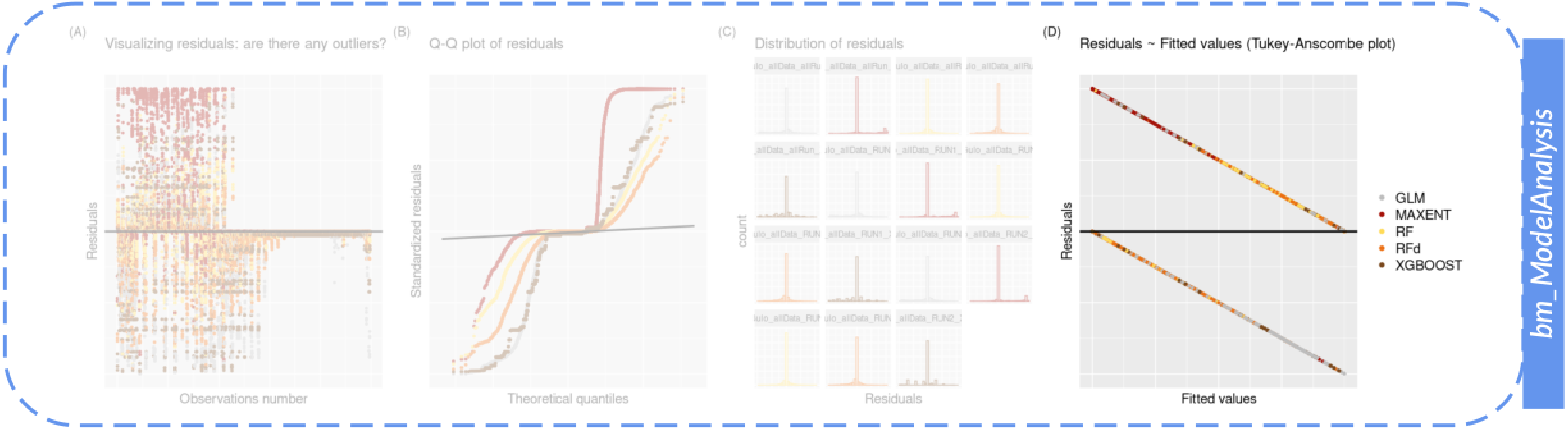
1:k
RUN 1
...
RUN k

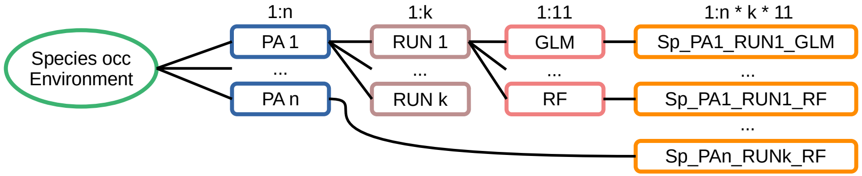
1:11
GLM
...
RF

1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

3.a Exploring single models

- *residuals ~ f(fitted values)*
- Tukey-Anscombe plot to detect heteroscedasticity
  - meaning residuals do not have a constant variance




1:n
1:k
1:11
1:n * k * 11

Species occ
Environment

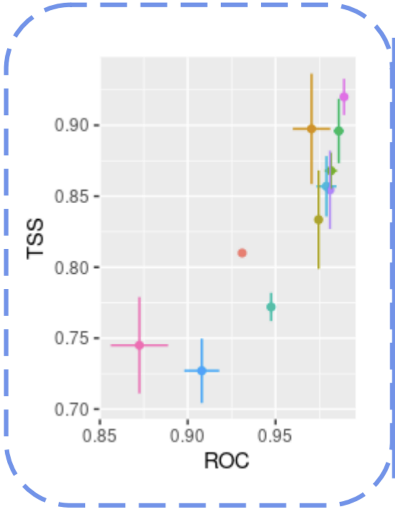
PA 1
...
PA n

RUN 1
...
RUN k

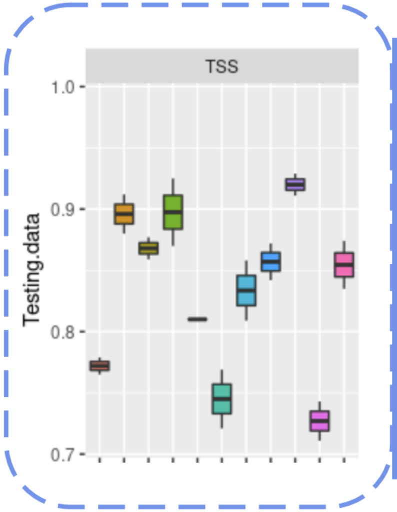
GLM
...
RF

Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

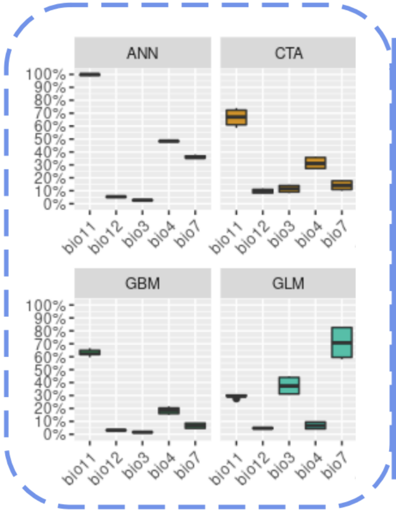
3.a Exploring single models



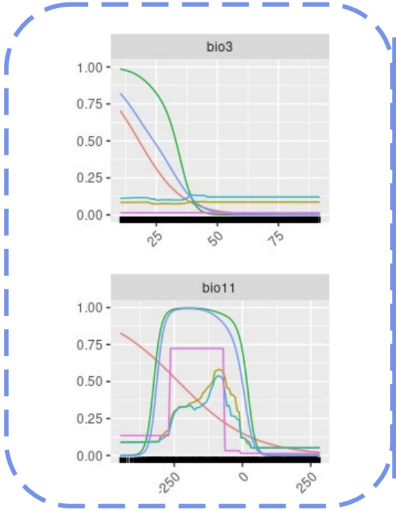
bm_PlotEvalMean



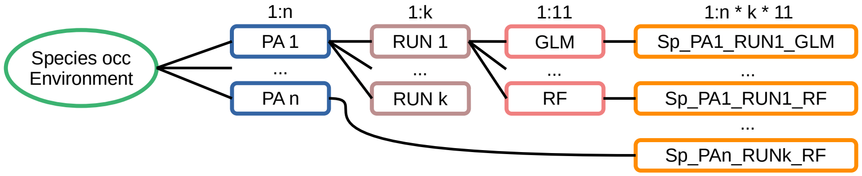
bm_PlotEvalBoxplot



bm_PlotVarImpBoxplot



bm_PlotResponseCurves



1:n
1:k
1:11
1:n * k * 11

Species occ
Environment

PA 1
...
PA n

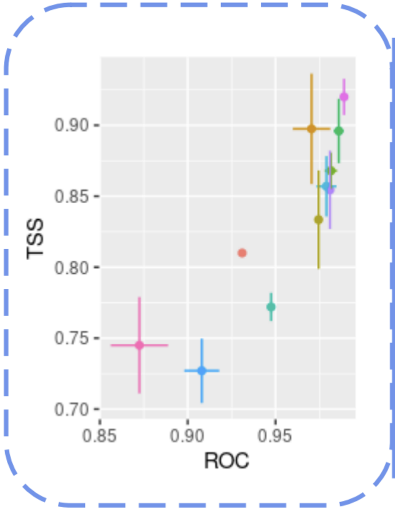
RUN 1
...
RUN k

GLM
...
RF

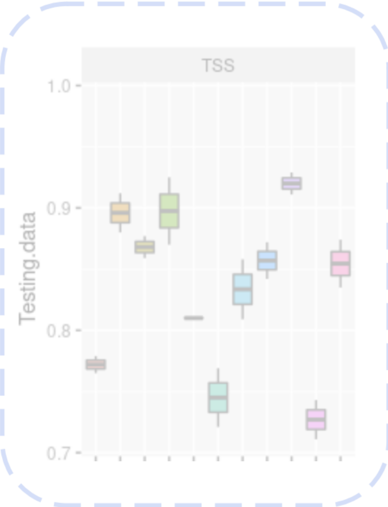
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

3.a Exploring single models

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

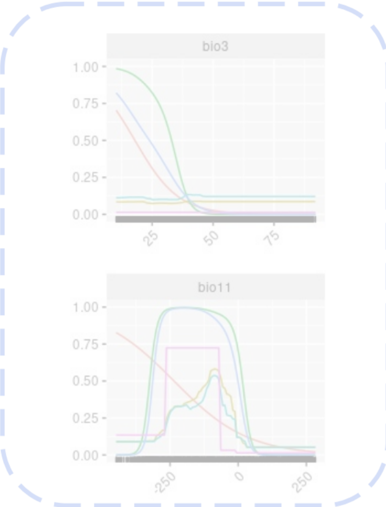


bm_PlotEvalMean

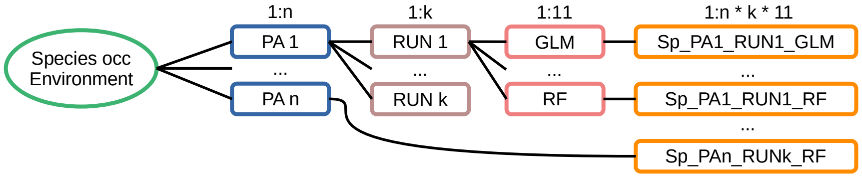


bm_PlotEvalBoxplot

bm_PlotVarImpBoxplot



bm_PlotResponseCurves



Species occ Environment

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PA 1
...
PA n

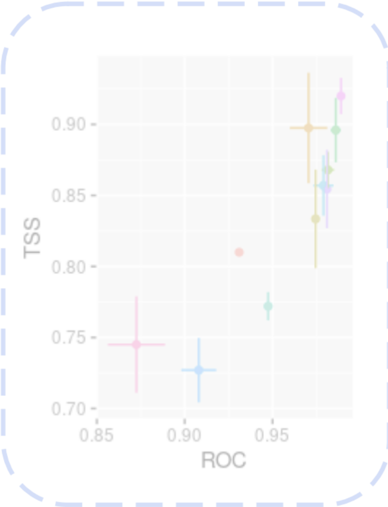
1:k
RUN 1
...
RUN k

1:11
GLM
...
RF

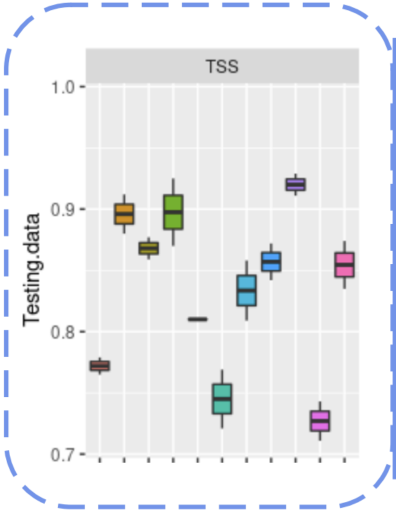
1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

3.a Exploring single models

- more classical view
- visualize the metrics consistency between models

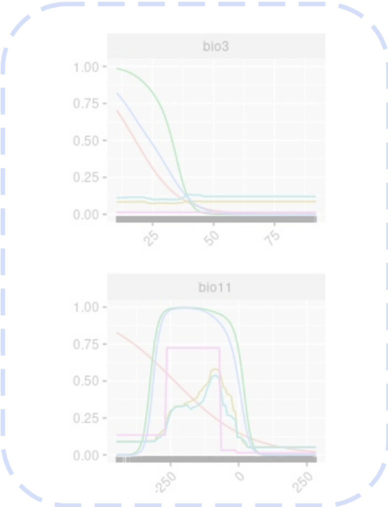


bm_PlotEvalMean

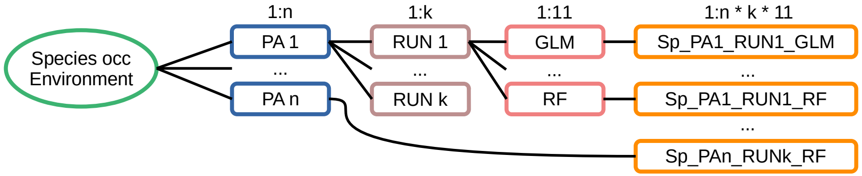


bm_PlotEvalBoxplot

bm_PlotVarImpBoxplot

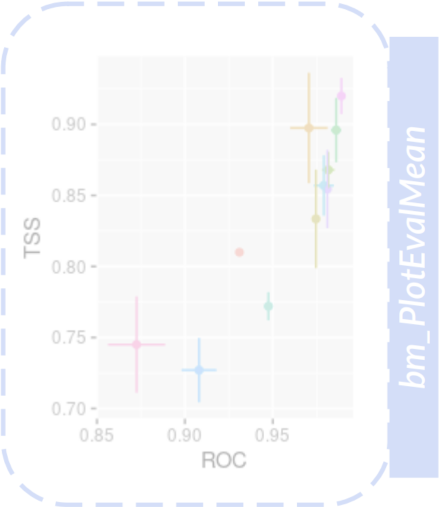


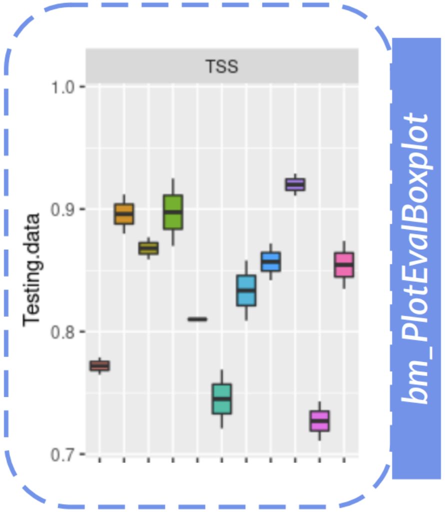
bm_PlotResponseCurves

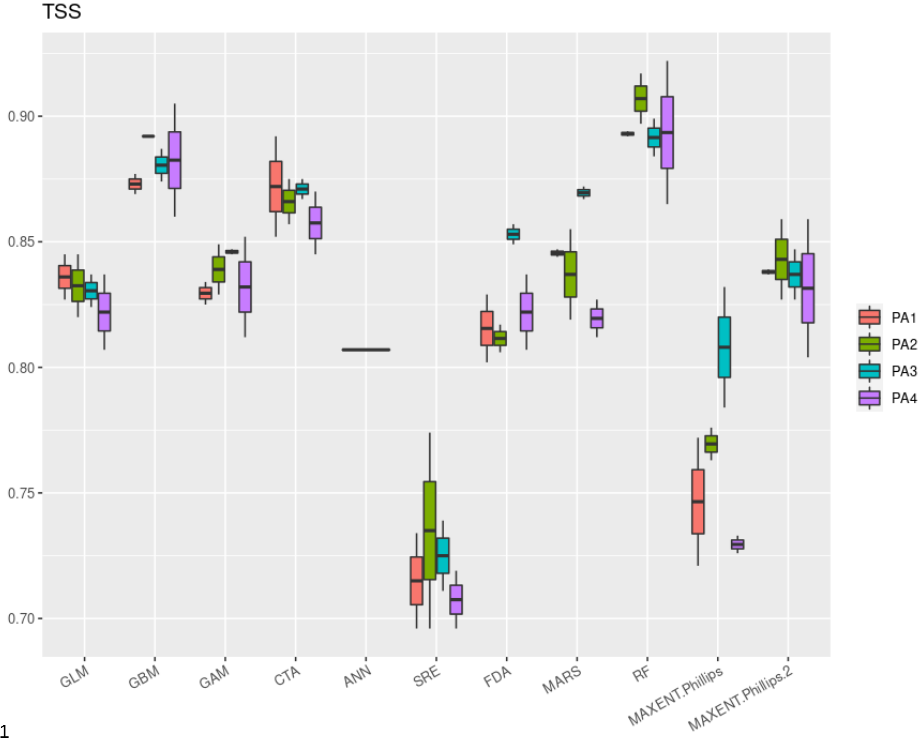


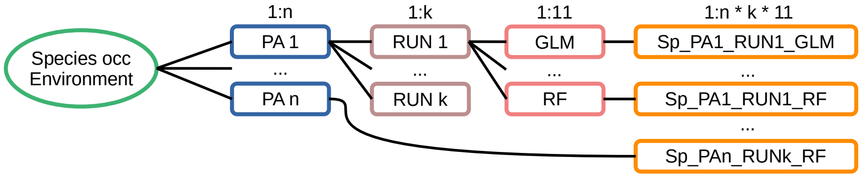
3.a Exploring single models

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









1:n
1:k
1:11
1:n * k * 11

Species occ
Environment

PA 1
...
PA n

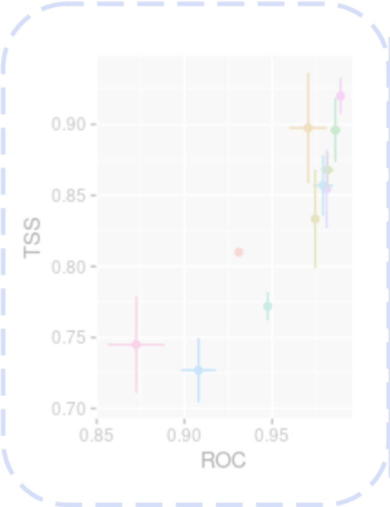
RUN 1
...
RUN k

GLM
...
RF

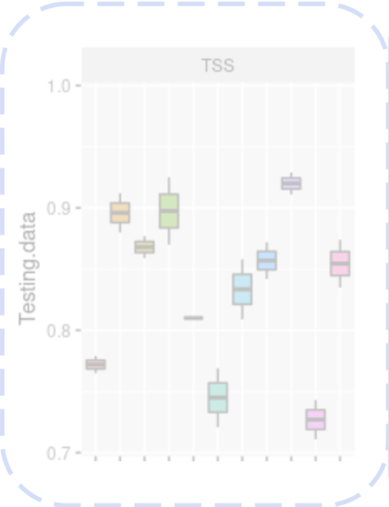
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

3.a Exploring single models

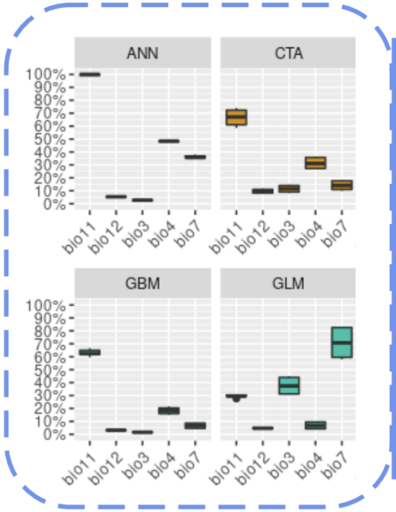
- compare importance of variables between models
- visualize the consistency between models
  (*and different types of models*)



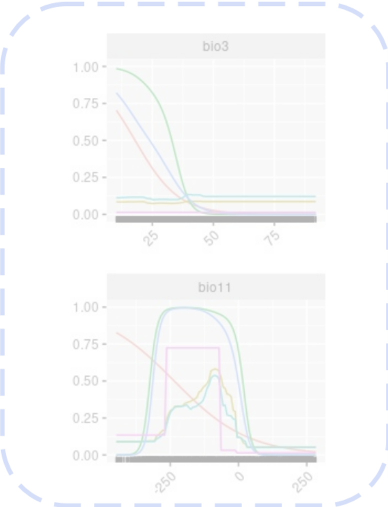
bm_PlotEvalMean



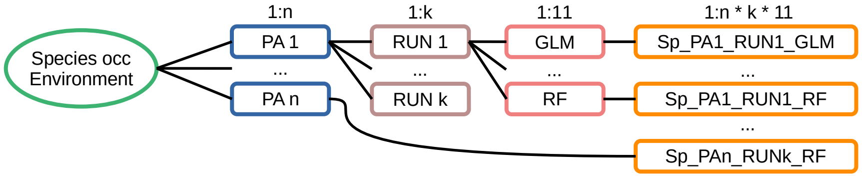
bm_PlotEvalBoxplot



bm_PlotVarImpBoxplot



bm_PlotResponseCurves



Species occ
Environment

1:n
PA 1
...
PA n

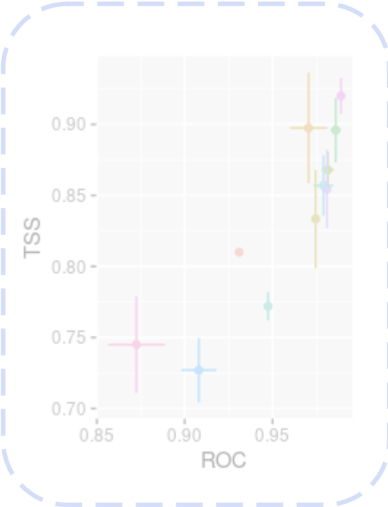
1:k
RUN 1
...
RUN k

1:11
GLM
...
RF

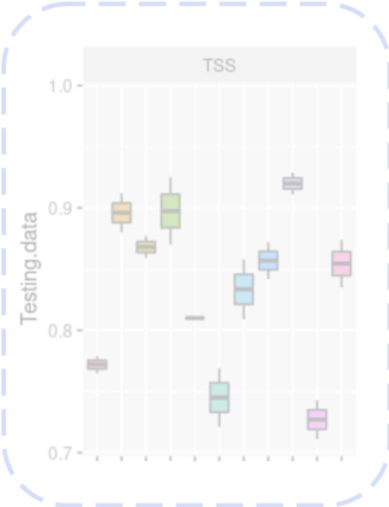
1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

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*)

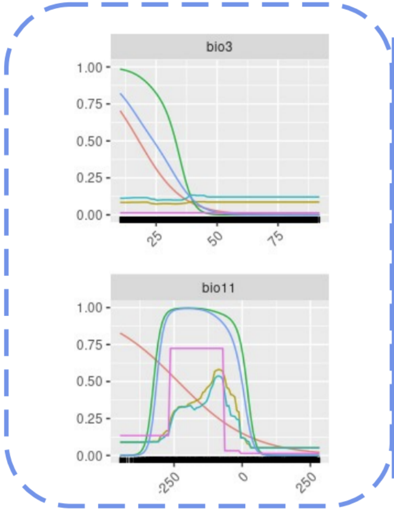


bm_PlotEvalMean

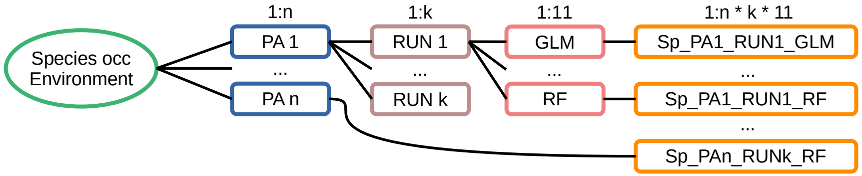


bm_PlotEvalBoxplot

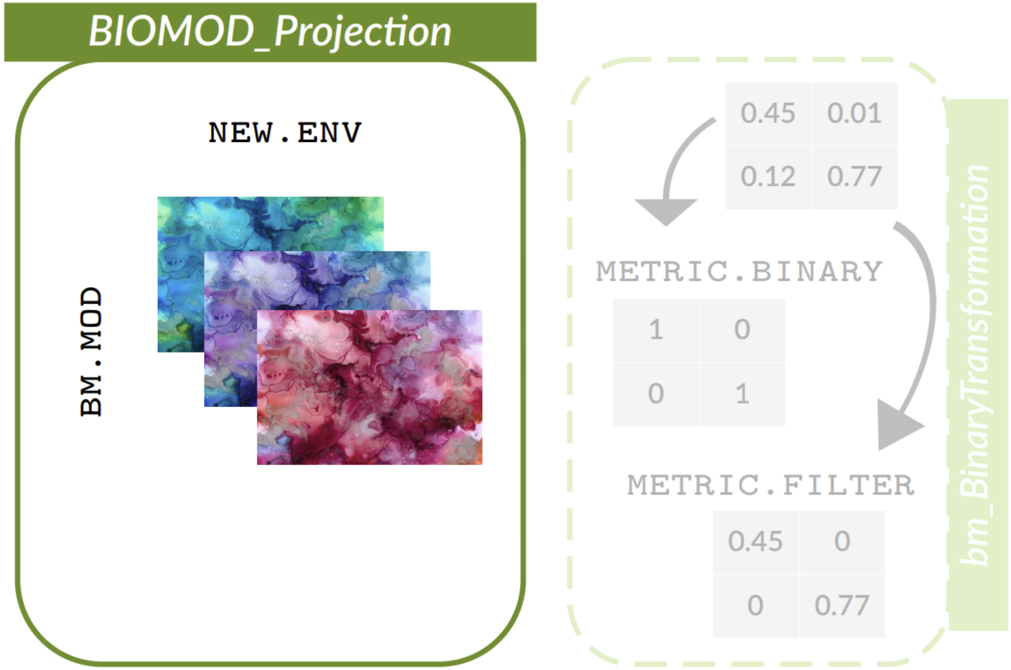
bm_PlotVarImpBoxplot



bm_PlotResponseCurves



4.a Projecting single models



BIOMOD_Projection

NEW.ENV

BM.MOD

bm_BinaryTransformation

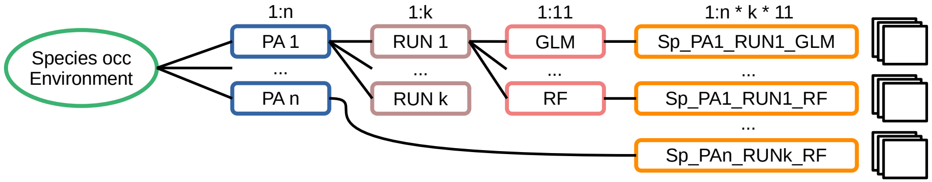
0.45	0.01
0.12	0.77

METRIC.BINARY

1	0
0	1

METRIC.FILTER

0.45	0
0	0.77



Species occ
Environment

1:n
PA 1
...
PA n

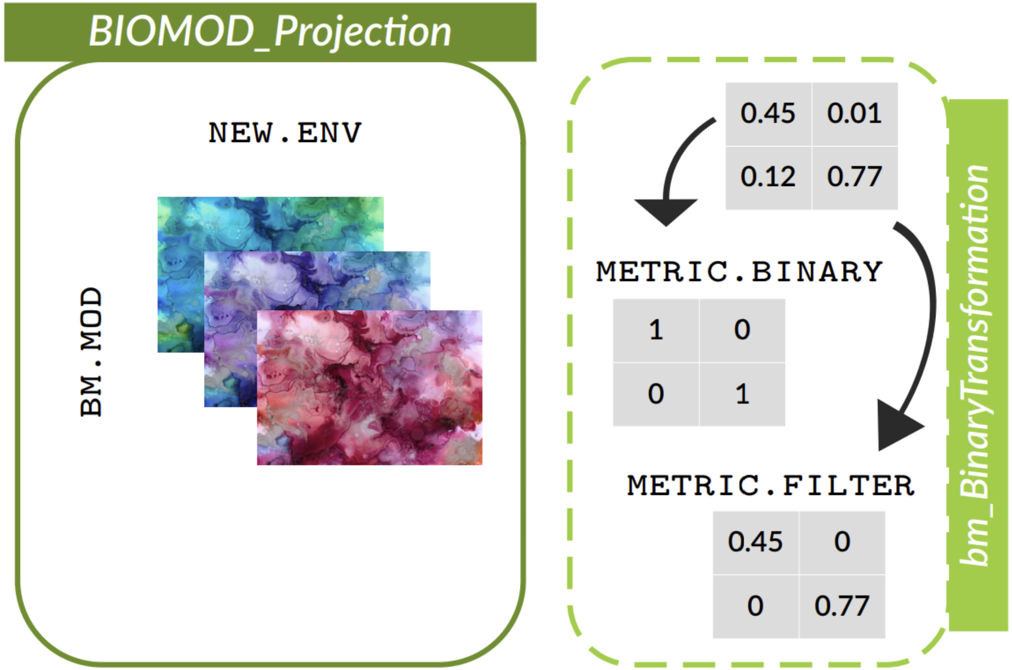
1:k
RUN 1
...
RUN k

1:11
GLM
...
RF

1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

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



BIOMOD_Projection

NEW.ENV

BM.MOD

0.45	0.01
0.12	0.77

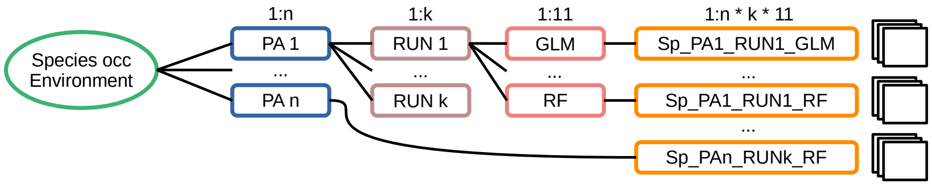
METRIC.BINARY

1	0
0	1

METRIC.FILTER

0.45	0
0	0.77

bm_BinaryTransformation



Species occ Environment

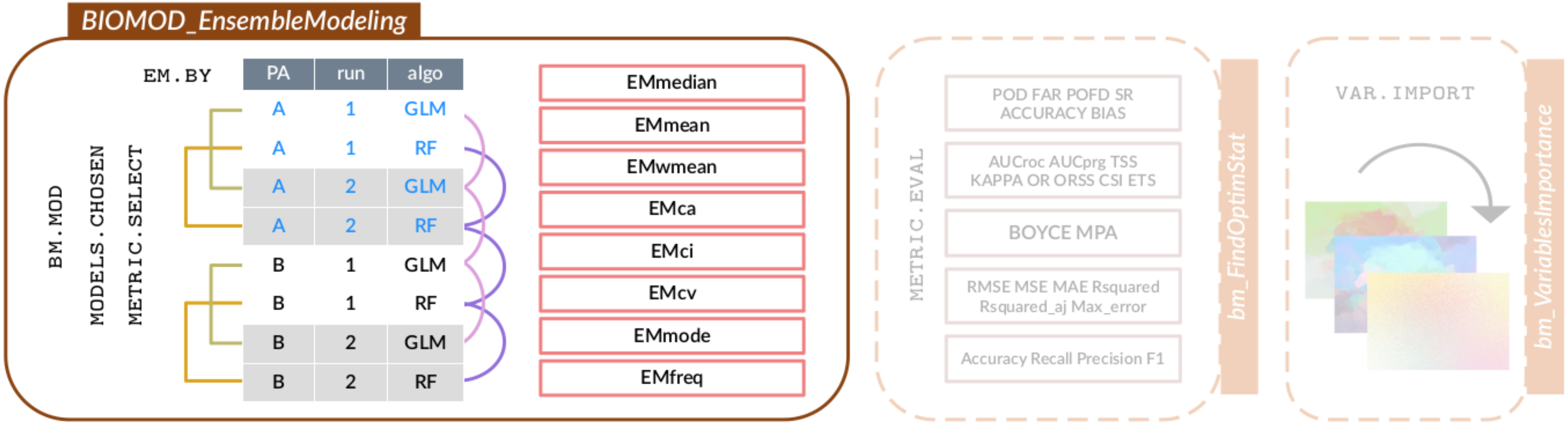
1:n
PA 1
...
PA n

1:k
RUN 1
...
RUN k

1:11
GLM
...
RF

1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

2.b Ensemble models



BIOMOD_EnsembleModeling

BM.MOD

MODELS.CHOSEN

METRIC.SELECT

EM.BY

PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

EMmedian

EMmean

EMwmean

EMca

EMci

EMcv

EMmode

EMfreq

METRIC.EVAL

POD FAR POFD SR ACCURACY BIAS

AUCroc AUCprg TSS KAPPA OR ORSS CSI ETS

BOYCE MPA

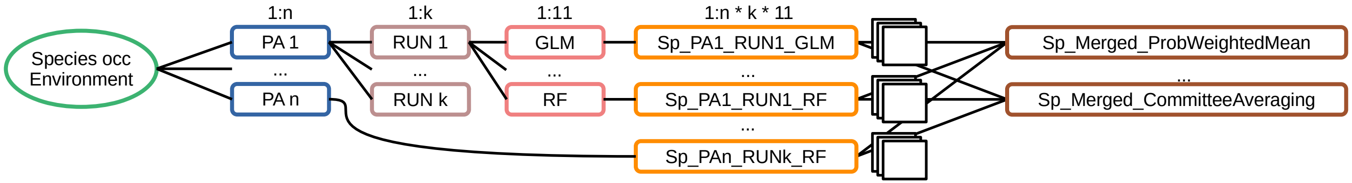
RMSE MSE MAE Rsquared Rsquared_aj Max_error

Accuracy Recall Precision F1

bm_FindOptimStat

VAR.IMPORT

bm_VariablesImportance



Species occ Environment

1:n

PA 1

...

PA n

1:k

RUN 1

...

RUN k

1:11

GLM

...

RF

1:n * k * 11

Sp_PA1_RUN1_GLM

...

Sp_PA1_RUN1_RF

...

Sp_PAn_RUNk_RF

Sp_Merged_ProbWeightedMean

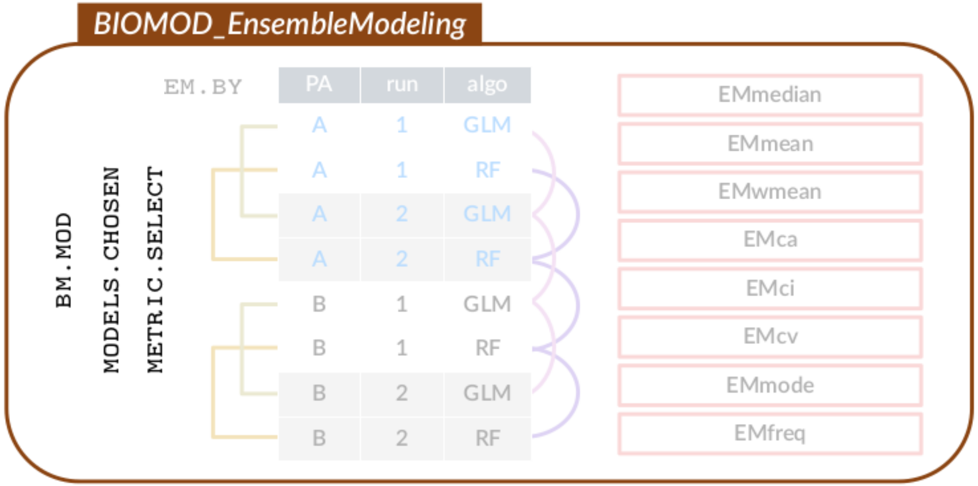
...

Sp_Merged_CommitteeAveraging

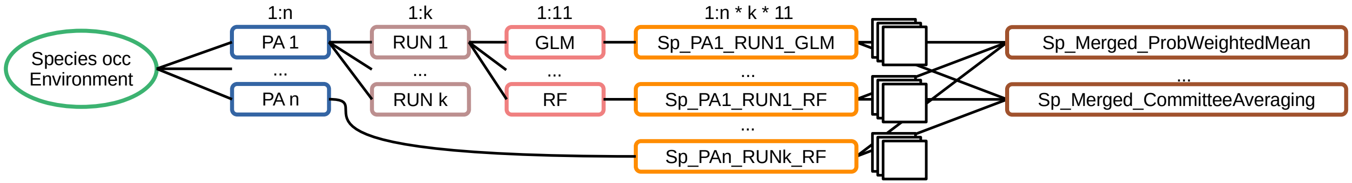
2.b Ensemble models

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



PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

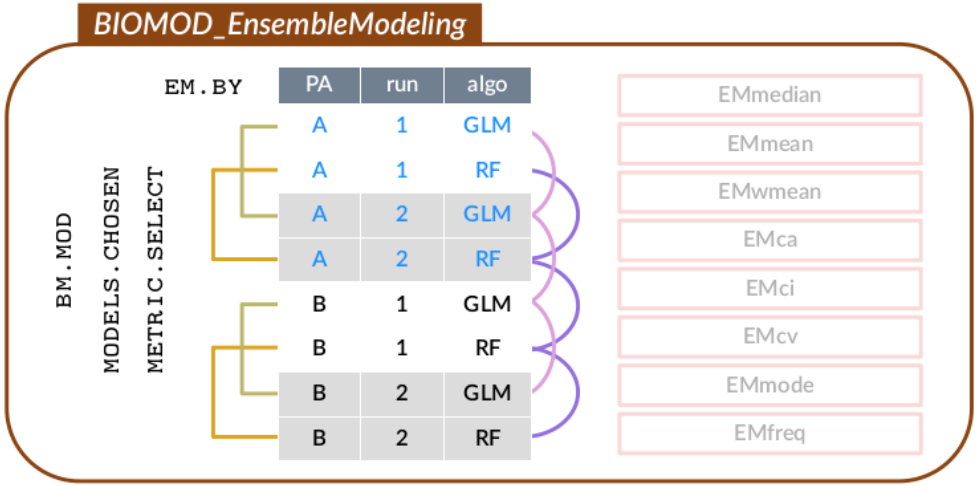


2.b Ensemble models

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

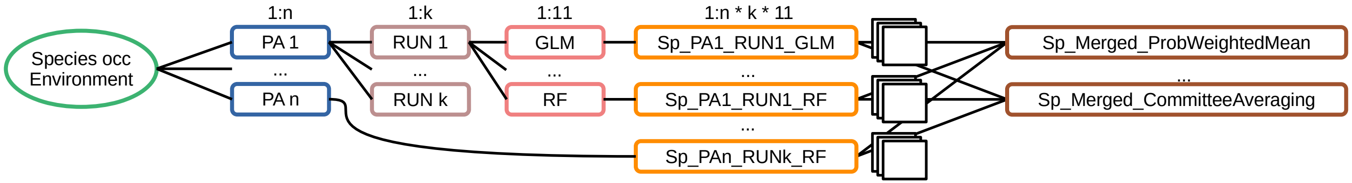
different ways of **combining** single models together :

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



PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

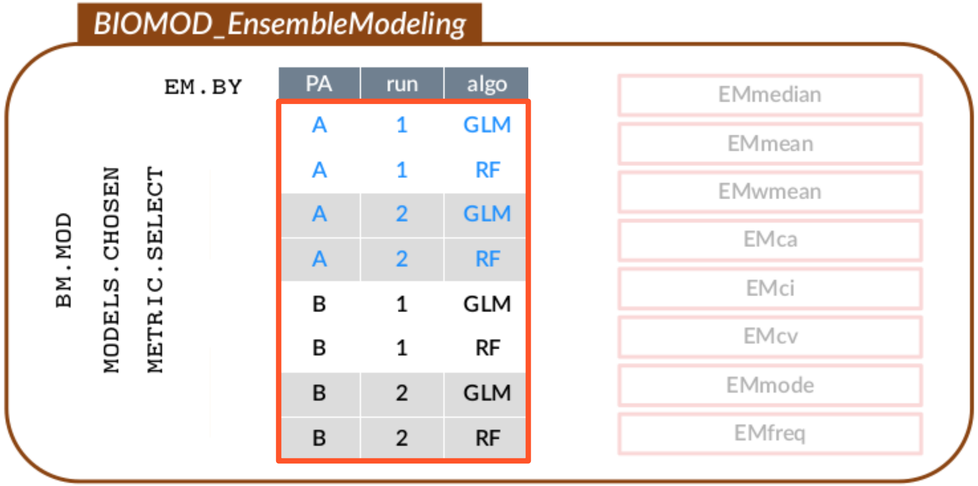
PA1_RUN1_GLM	PA1_RUN1_RF
PA1_RUN2_GLM	PA1_RUN2_RF
PA1_RUN3_GLM	PA1_RUN3_RF
PA2_RUN1_GLM	PA2_RUN1_RF
PA2_RUN2_GLM	PA2_RUN2_RF
PA2_RUN3_GLM	PA2_RUN3_RF



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*

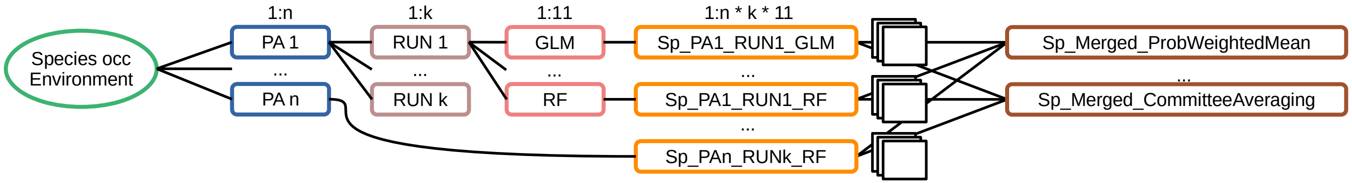


PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

- EMmedian
- EMmean
- EMwmean
- EMca
- EMci
- EMcv
- EMmode
- EMfreq

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

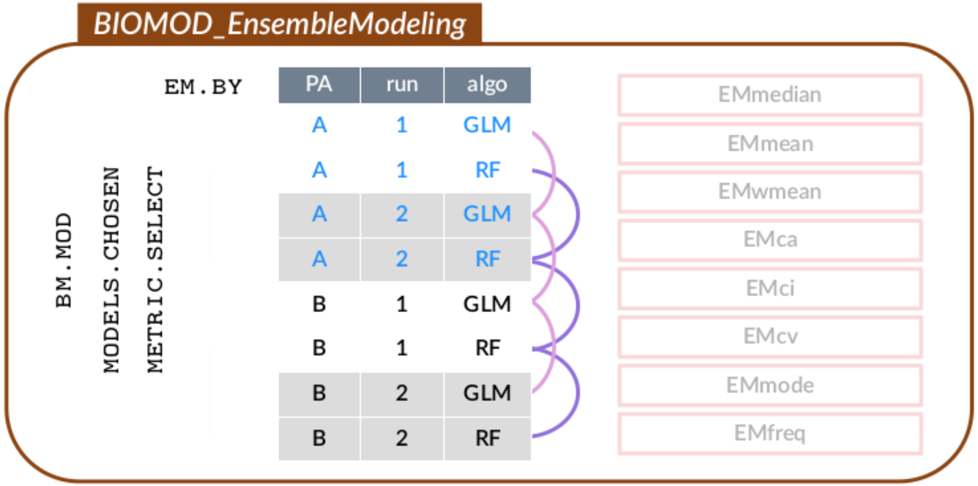
All models



2.b Ensemble models

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

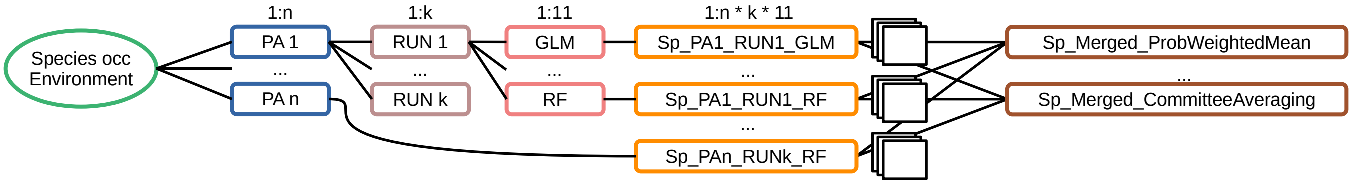
- different ways of **combining** single models together :
  - *all*
  - *algo*
  - *PA*
  - *PA+algo*
  - *PA+run*



PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

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

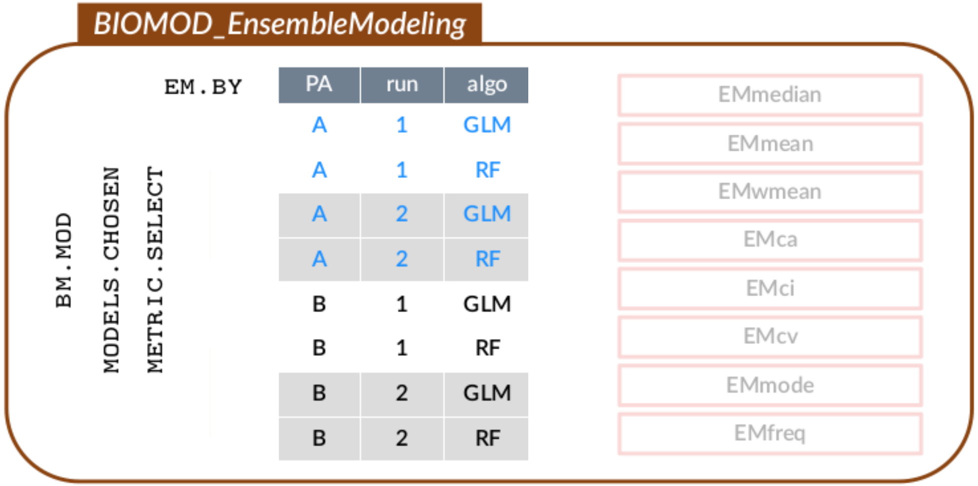
Different algo



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*

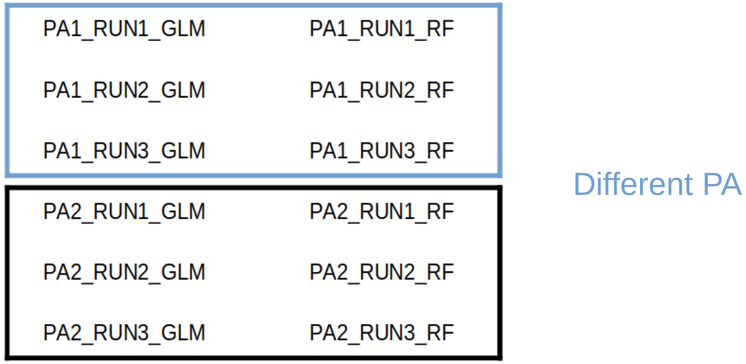


BIOMOD_EnsembleModeling

BM.MOD
MODELS.CHOSEN
METRIC.SELECT
EM.BY

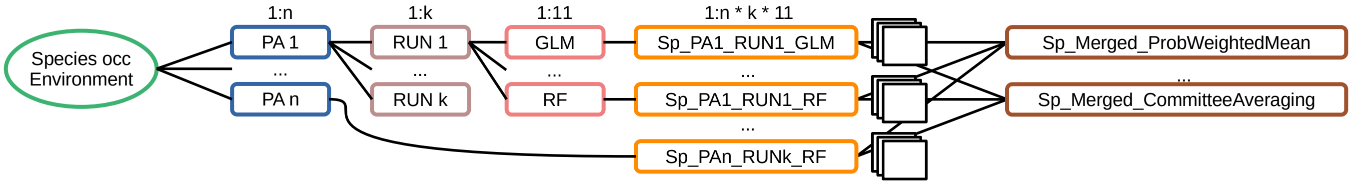
PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

- EMmedian
- EMmean
- EMwmean
- EMca
- EMci
- EMcv
- EMmode
- EMfreq



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

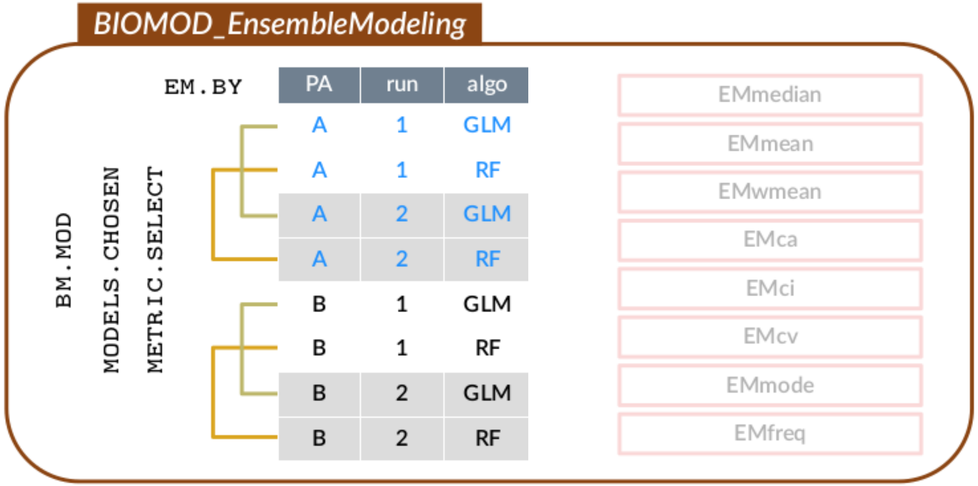
Different PA



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*



BIOMOD_EnsembleModeling

BM.MOD

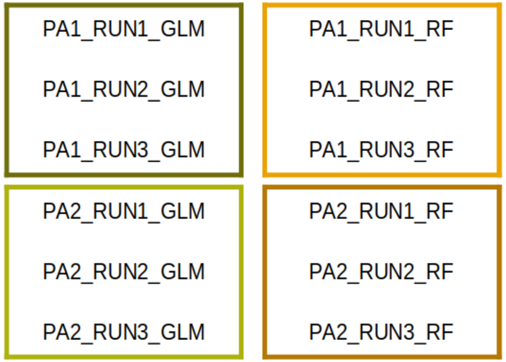
MODELS.CHOSEN

METRIC.SELECT

EM.BY

PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

EMmedian
EMmean
EMwmean
EMca
EMci
EMcv
EMmode
EMfreq



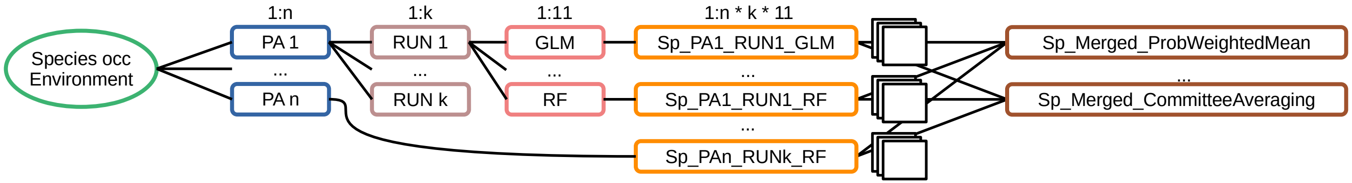
PA1_RUN1_GLM
PA1_RUN2_GLM
PA1_RUN3_GLM

PA1_RUN1_RF
PA1_RUN2_RF
PA1_RUN3_RF

PA2_RUN1_GLM
PA2_RUN2_GLM
PA2_RUN3_GLM

PA2_RUN1_RF
PA2_RUN2_RF
PA2_RUN3_RF

Different PA and algo

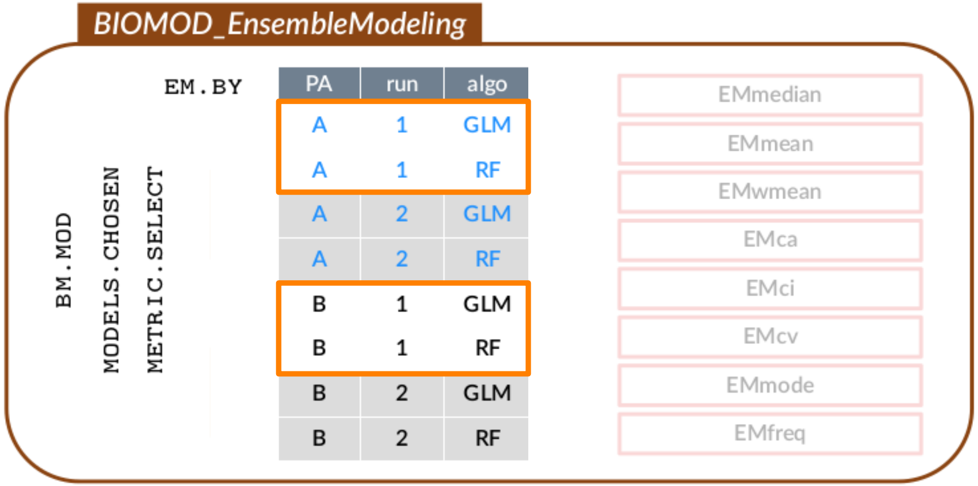


2.b Ensemble models

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

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

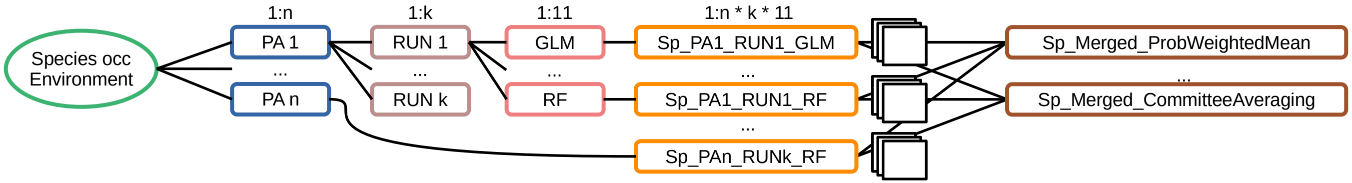
- *all*
- *algo*
- *PA*
- *PA+algo*
- *PA+run*



PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

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

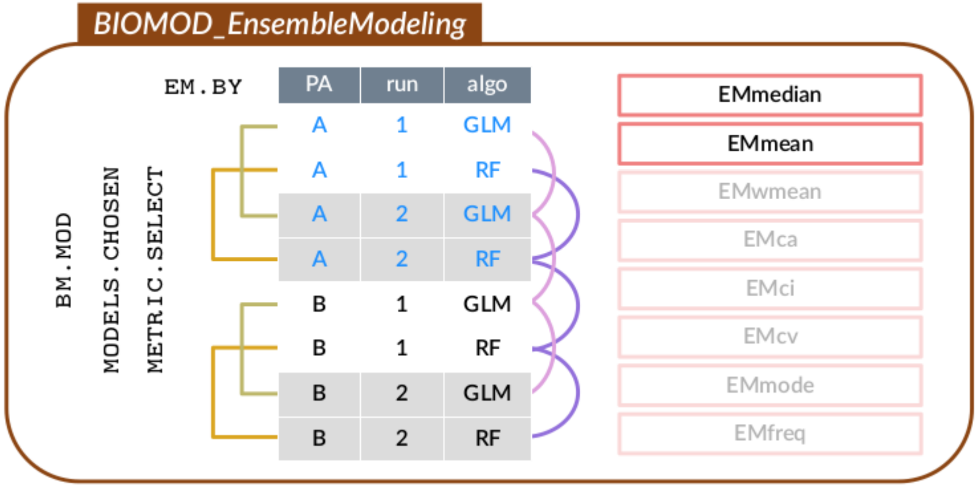
Different PA
and run



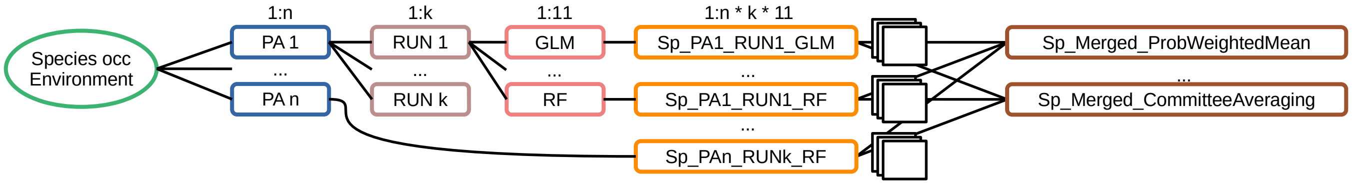
2.b Ensemble models

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

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



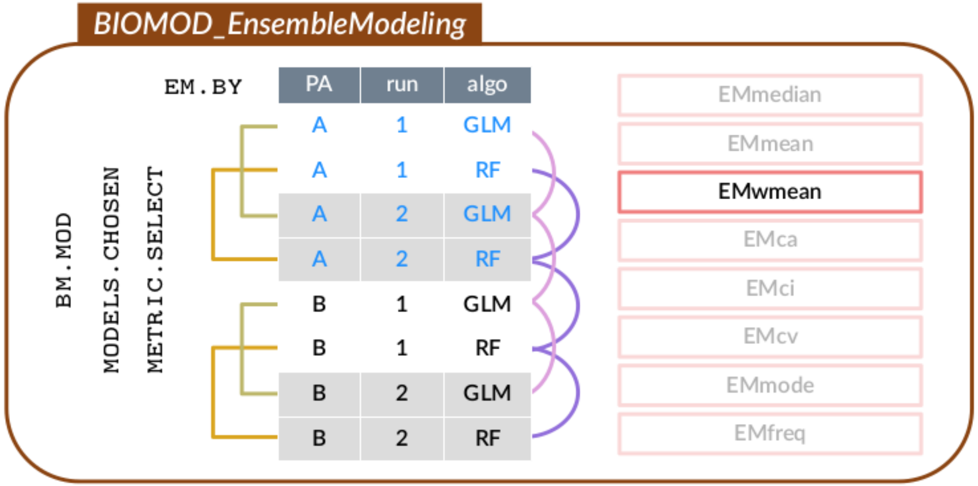
PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF



2.b Ensemble models

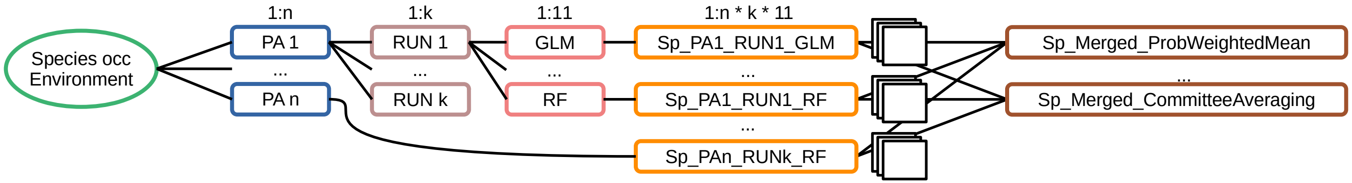
Step 1 : filter single models
Step 2 : gather single models
Step 3 : build ensemble models

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



PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

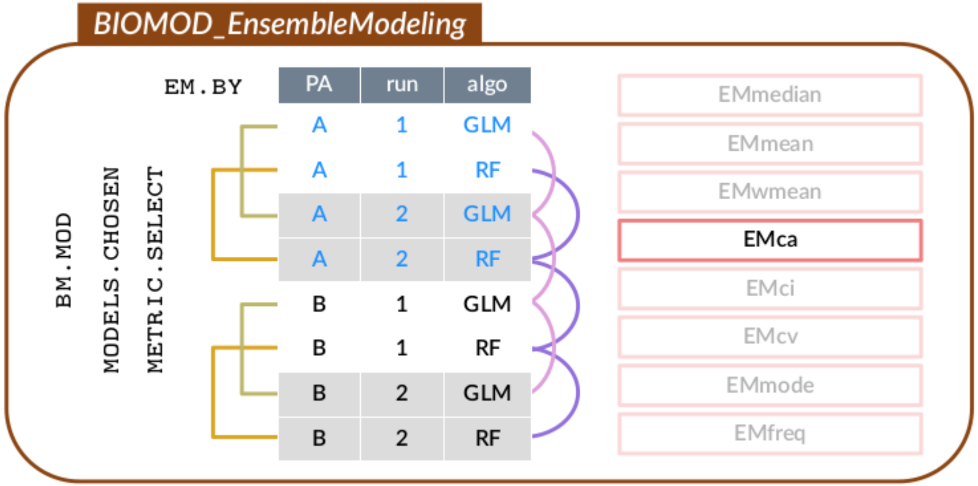
$$W1 * \begin{array}{|c|c|}\hline 0{,}45 & 0{,}01 \\ \hline 0{,}12 & 0{,}77 \\ \hline\end{array} + W2 * \begin{array}{|c|c|}\hline 0{,}30 & 0{,}5 \\ \hline 0{,}10 & 0{,}77 \\ \hline\end{array} + W3 * \begin{array}{|c|c|}\hline 0{,}15 & 0{,}23 \\ \hline 0{,}25 & 0{,}64 \\ \hline\end{array}$$

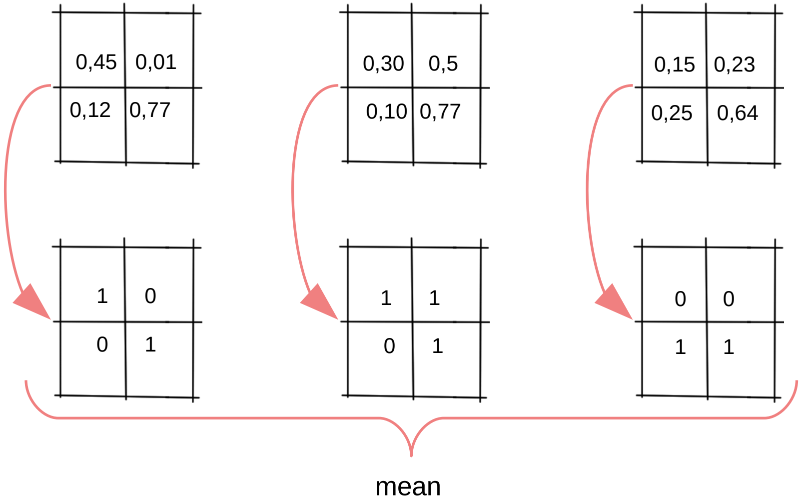


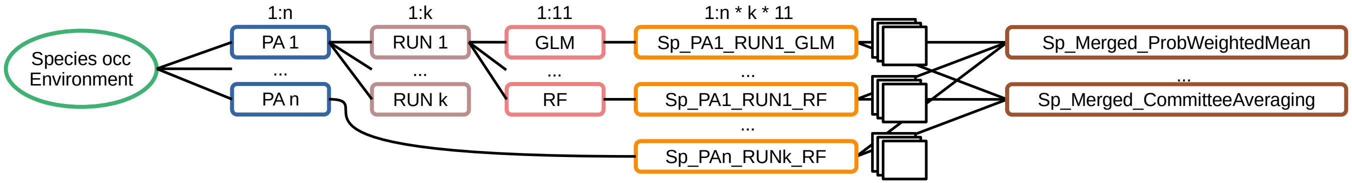
2.b Ensemble models

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**



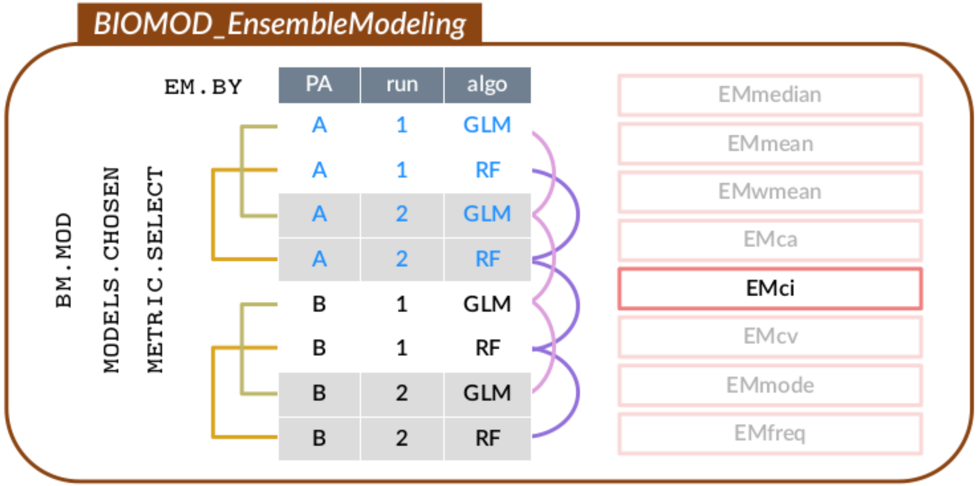


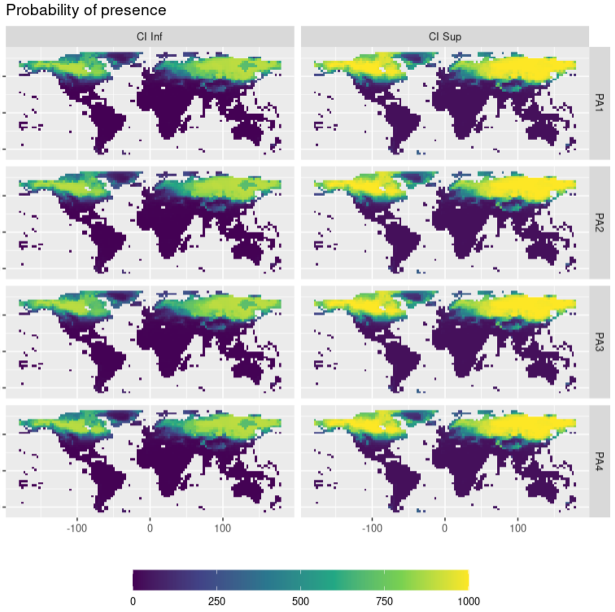


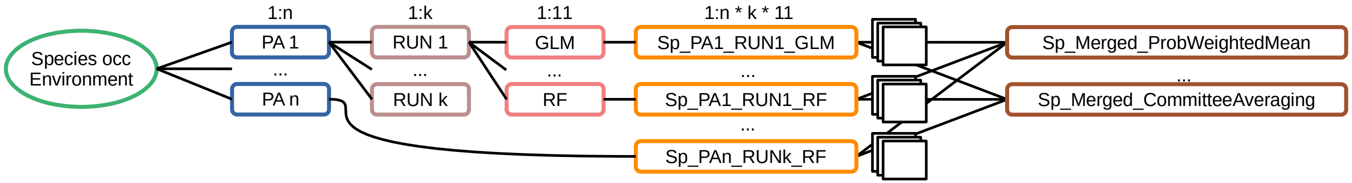
2.b Ensemble models

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
  - committe averaging
- « exploratory » ensemble models :
  - **confidence intervals** or **coefficient of variation**



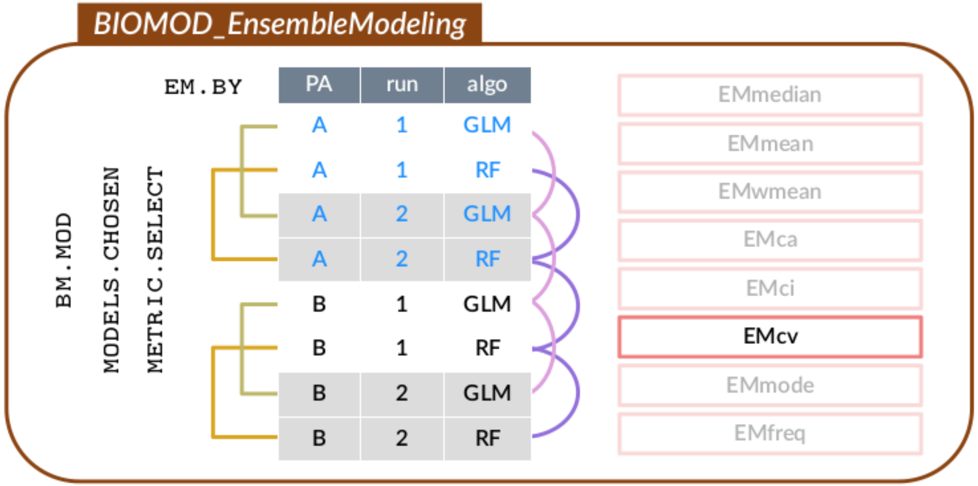


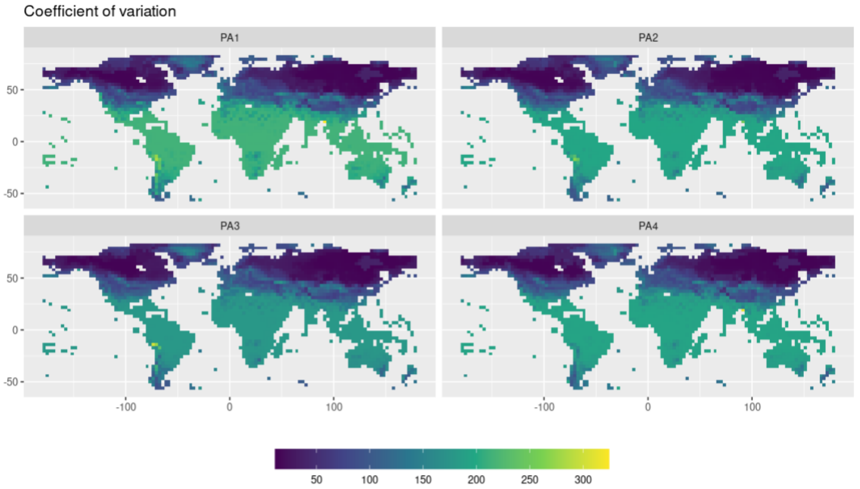

Species occ
Environment
1:n
PA 1
...
PA n
1:k
RUN 1
...
RUN k
1:11
GLM
...
RF
1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF
Sp_Merged_ProbWeightedMean
...
Sp_Merged_CommitteeAveraging

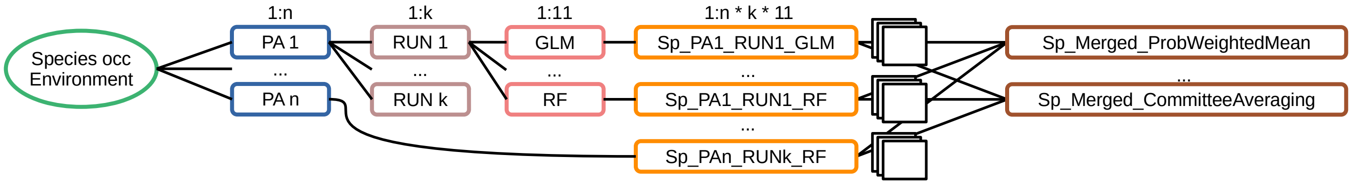
2.b Ensemble models

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
- « exploratory » ensemble models :
  - **confidence intervals** or **coefficient of variation**

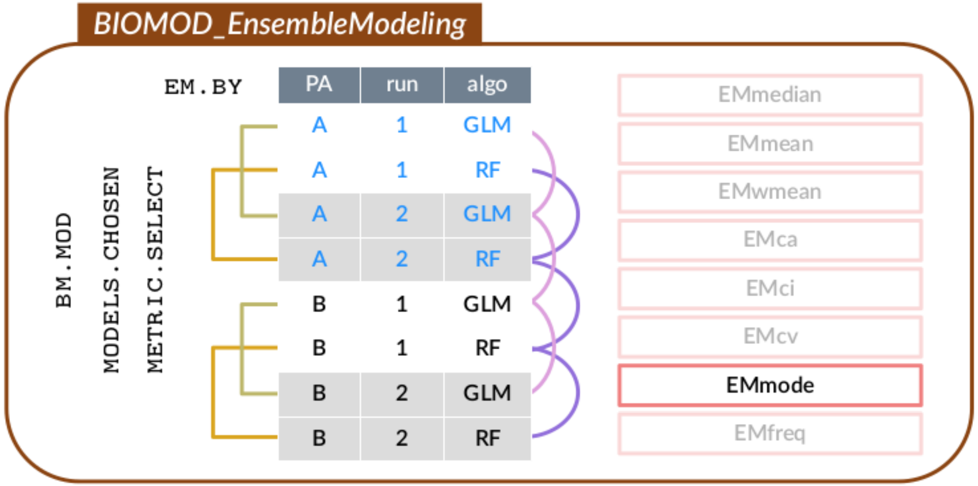




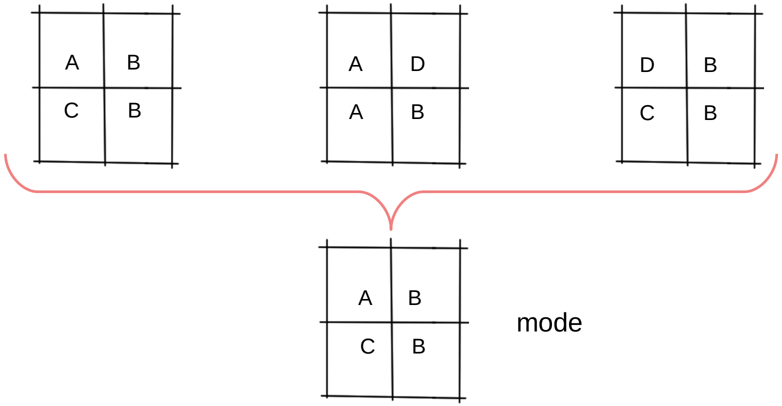


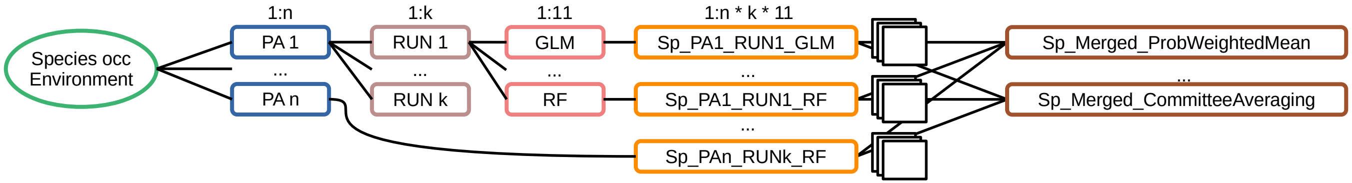
2.b Ensemble models

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



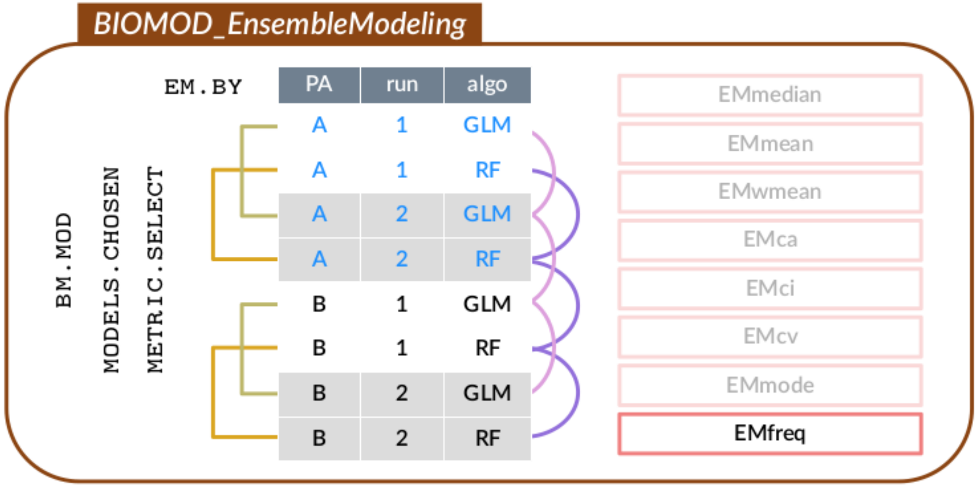
- « simple » ensemble models : mean or median
- « complex » ensemble models :
  - probability weighted mean
  - committe averaging
- « exploratory » ensemble models :
  - confidence intervals or coefficient of variation
- « multiclass » ensemble models :
  - **mode** or **frequency of the mode**



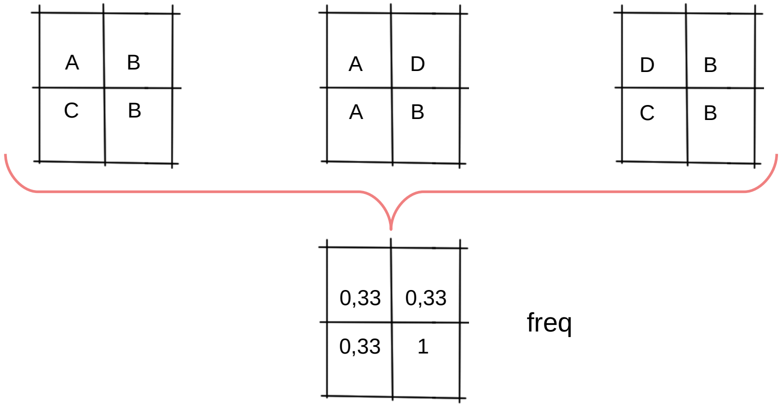


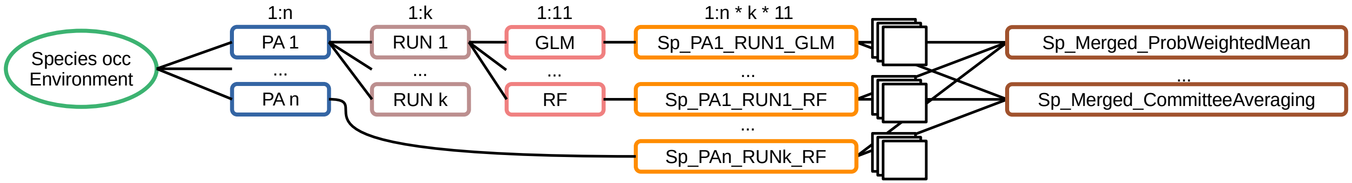
2.b Ensemble models

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



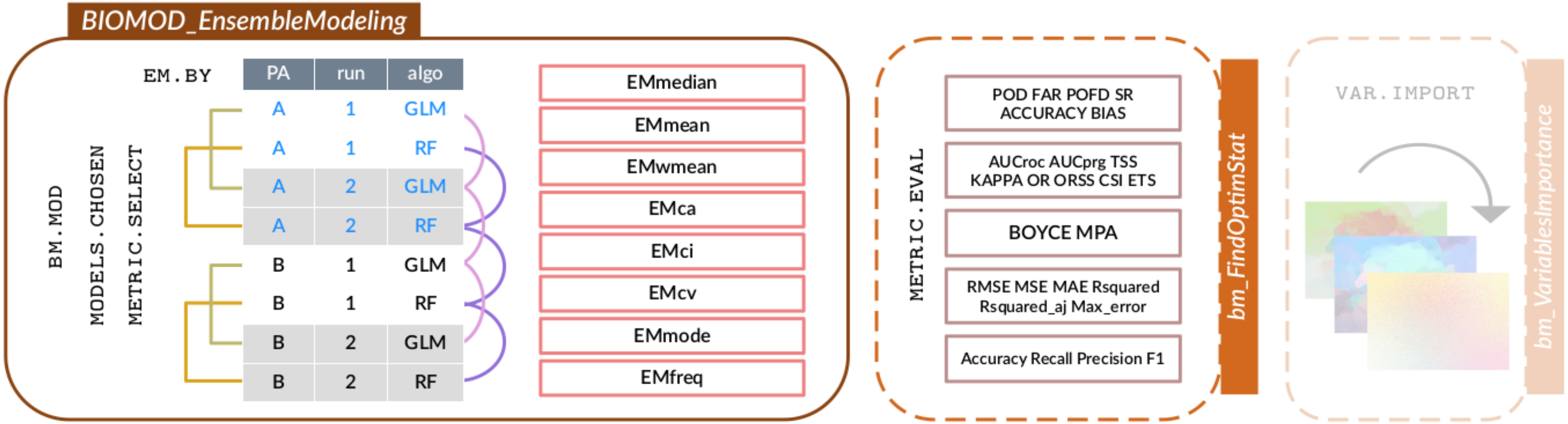
- « simple » ensemble models : mean or median
- « complex » ensemble models :
  - probability weighted mean
  - committe averaging
- « exploratory » ensemble models :
  - confidence intervals or coefficient of variation
- « multiclass » ensemble models :
  - **mode** or **frequency of the mode**





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 thresold optimising the evaluation metric



BIOMOD_EnsembleModeling

EM.BY

BM.MOD

MODELS.CHOSEN

METRIC.SELECT

PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

EMmedian
EMmean
EMwmean
EMca
EMci
EMcv
EMmode
EMfreq

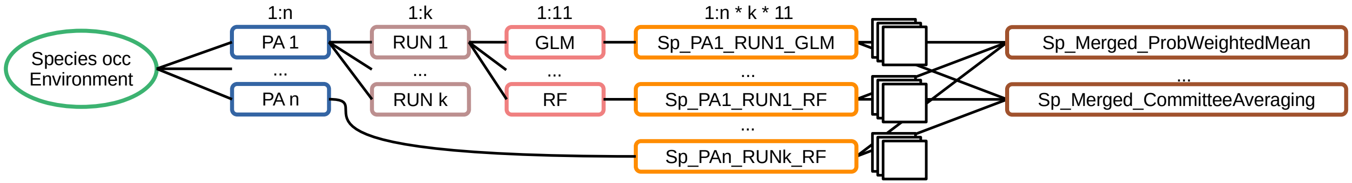
METRIC.EVAL

POD FAR POFD SR ACCURACY BIAS
AUCroc AUCprg TSS KAPPA OR ORSS CSI ETS
BOYCE MPA
RMSE MSE MAE Rsquared Rsquared_aj Max_error
Accuracy Recall Precision F1

bm_FindOptimStat

VAR.IMPORT

bm_VariablesImportance



Species occ Environment

1:n
PA 1
...
PA n

1:k
RUN 1
...
RUN k

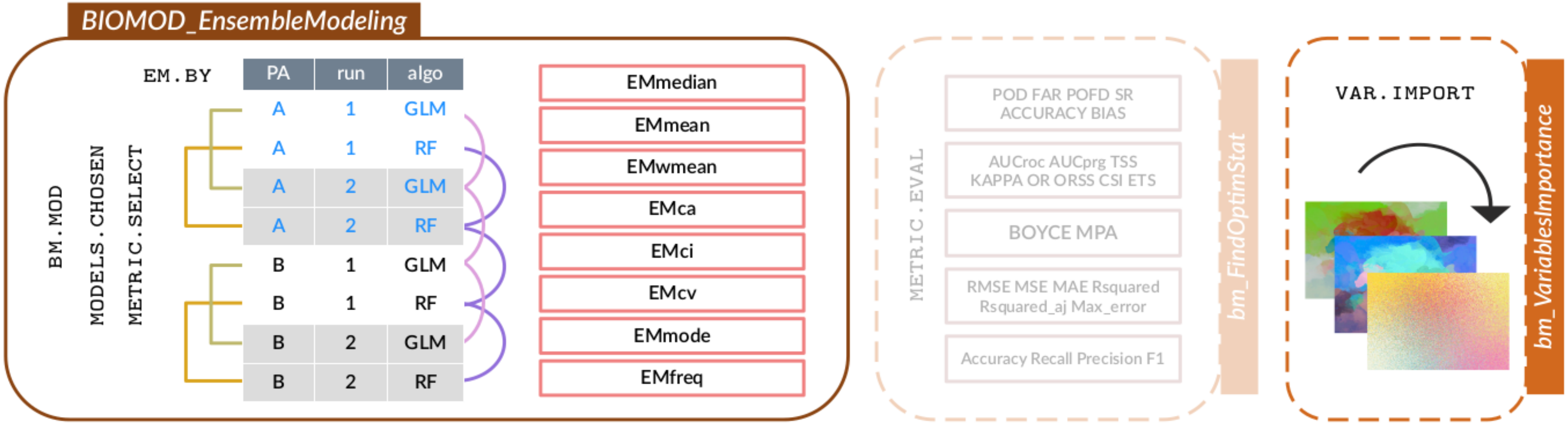
1:11
GLM
...
RF

1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

Sp_Merged_ProbWeightedMean
...
Sp_Merged_CommitteeAveraging

2.b Ensemble models

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



BIOMOD_EnsembleModeling

EM.BY

BM.MOD

MODELS.CHOSEN

METRIC.SELECT

PA	run	algo
A	1	GLM
A	1	RF
A	2	GLM
A	2	RF
B	1	GLM
B	1	RF
B	2	GLM
B	2	RF

EMmedian

EMmean

EMwmean

EMca

EMci

EMcv

EMmode

EMfreq

METRIC.EVAL

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AUCroc AUCprg TSS KAPPA OR ORSS CSI ETS

BOYCE MPA

RMSE MSE MAE Rsquared Rsquared_aj Max_error

Accuracy Recall Precision F1

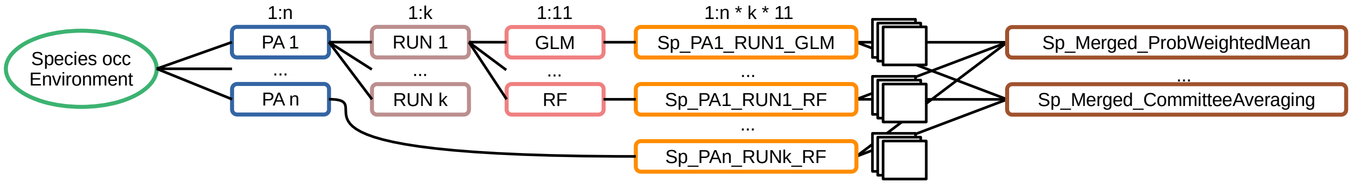
bm_FindOptimStat

VAR.IMPORT

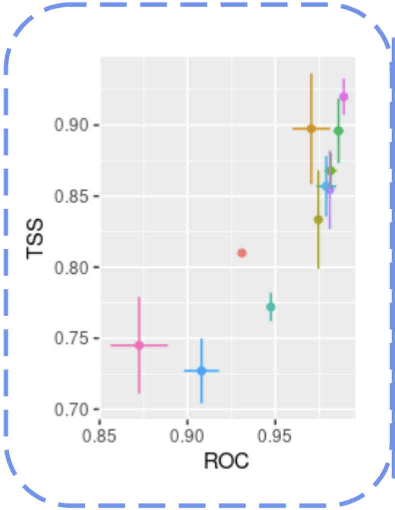
bm_VariablesImportance

IMPORTANT

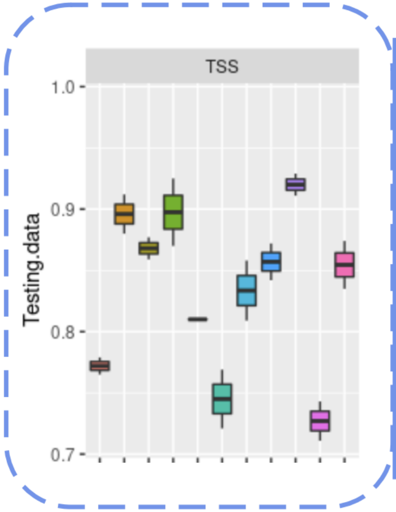
← Takes time ! Has to go through the whole workflow →



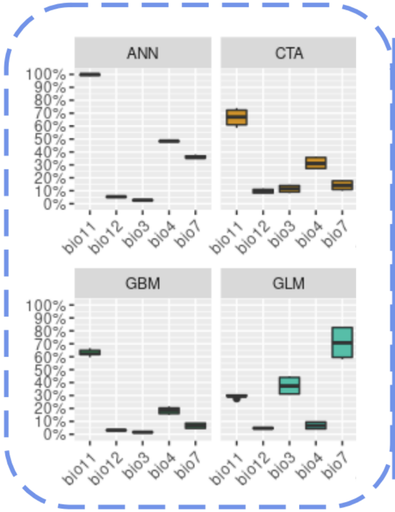
3.b Exploring ensemble models



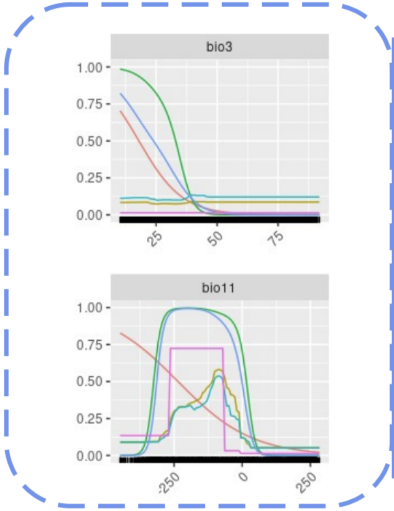
bm_PlotEvalMean



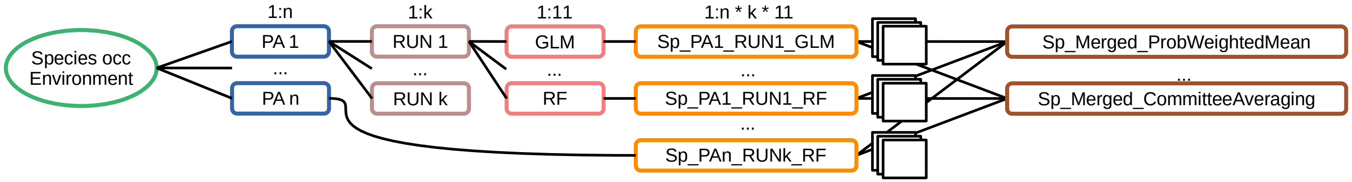
bm_PlotEvalBoxplot



bm_PlotVarImpBoxplot



bm_PlotResponseCurves



Species occ
Environment

1:n
PA 1
...
PA n

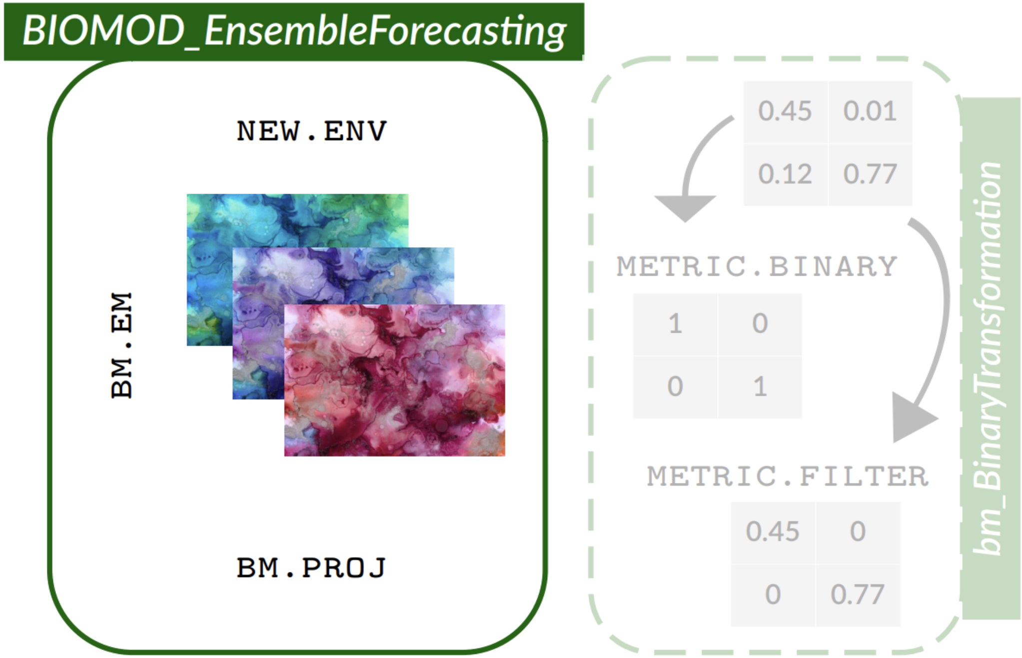
1:k
RUN 1
...
RUN k

1:11
GLM
...
RF

1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

Sp_Merged_ProbWeightedMean
...
Sp_Merged_CommitteeAveraging

4.b Projecting ensemble models



BIOMOD_EnsembleForecasting

NEW.ENV

BM.EM

BM.PROJ

bm_BinaryTransformation

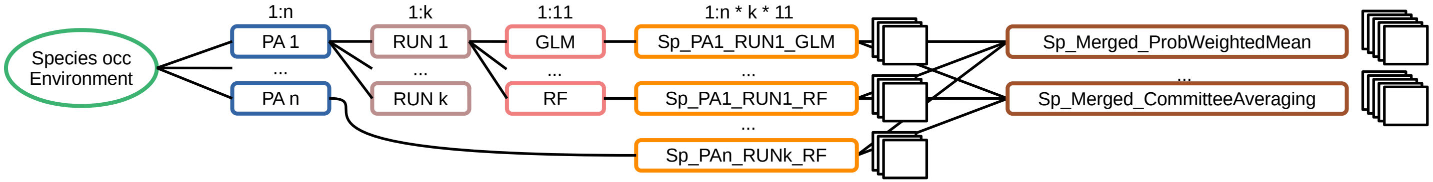
0.45	0.01
0.12	0.77

METRIC.BINARY

1	0
0	1

METRIC.FILTER

0.45	0
0	0.77



Species occ
Environment

1:n
PA 1
...
PA n

1:k
RUN 1
...
RUN k

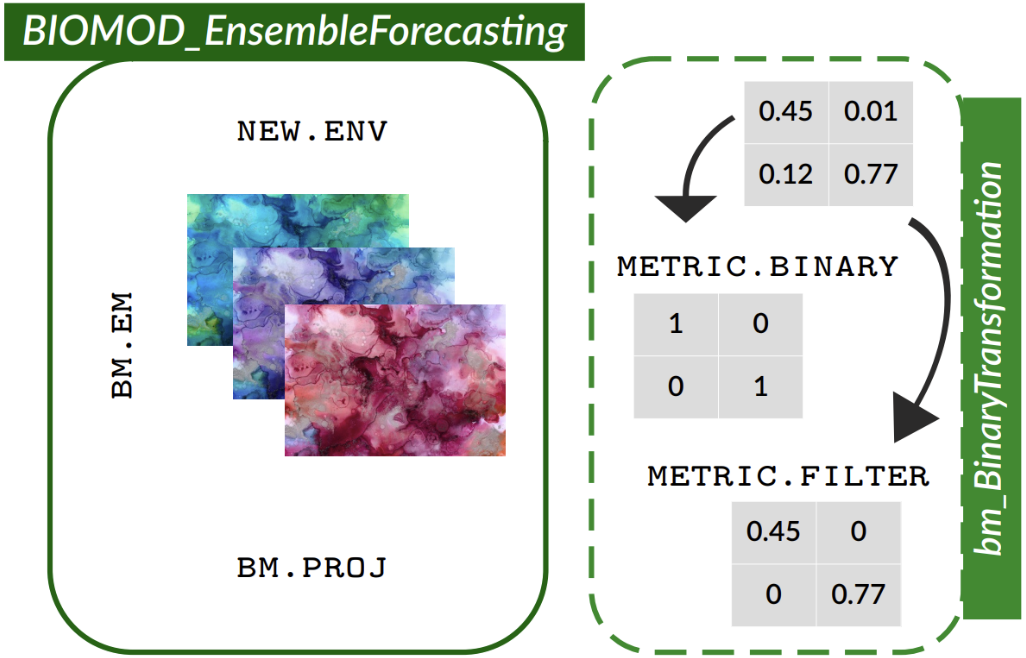
1:11
GLM
...
RF

1:n * k * 11
Sp_PA1_RUN1_GLM
...
Sp_PA1_RUN1_RF
...
Sp_PAn_RUNk_RF

Sp_Merged_ProbWeightedMean
...
Sp_Merged_CommitteeAveraging

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

NEW.ENV

BM.EM

BM.PROJ

0.45	0.01
0.12	0.77

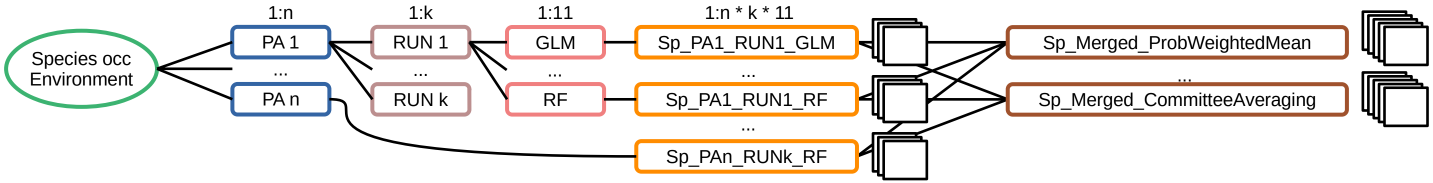
METRIC.BINARY

1	0
0	1

METRIC.FILTER

0.45	0
0	0.77

bm_BinaryTransformation



Species occ Environment

1:n

PA 1

...

PA n

1:k

RUN 1

...

RUN k

1:11

GLM

...

RF

1:n * k * 11

Sp_PA1_RUN1_GLM

...

Sp_PA1_RUN1_RF

...

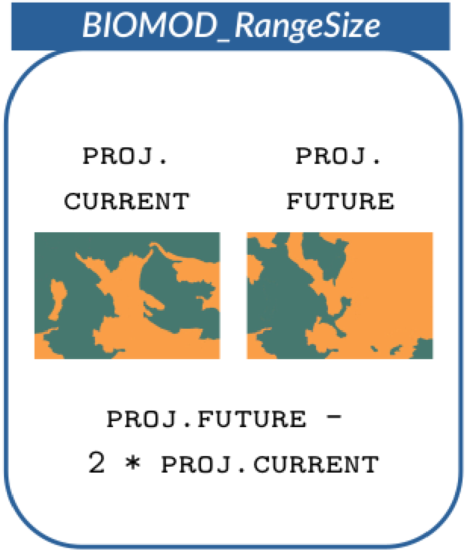
Sp_PAn_RUNk_RF

Sp_Merged_ProbWeightedMean

...

Sp_Merged_CommitteeAveraging

5. Species range change

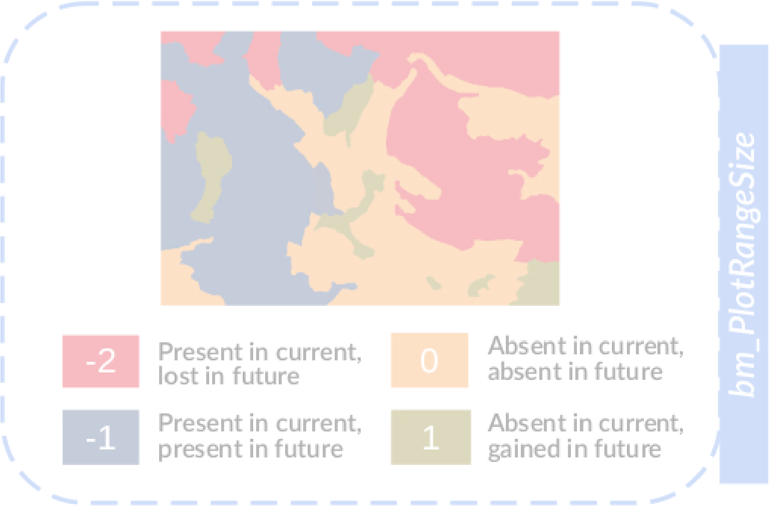


BIOMOD_RangeSize

PROJ. CURRENT

PROJ. FUTURE

PROJ.FUTURE − 2 * PROJ.CURRENT



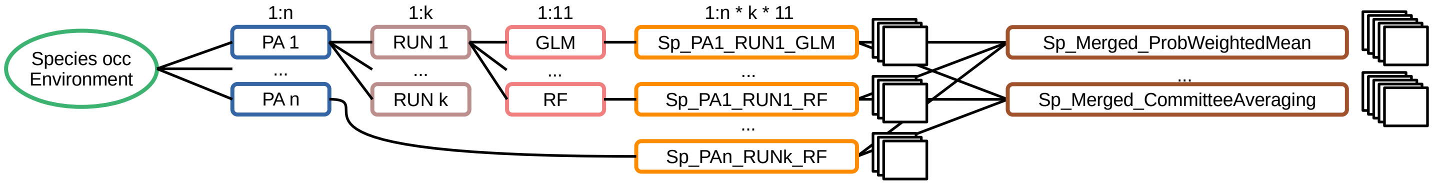
bm_PlotRangeSize

-2 Present in current, lost in future

0 Absent in current, absent in future

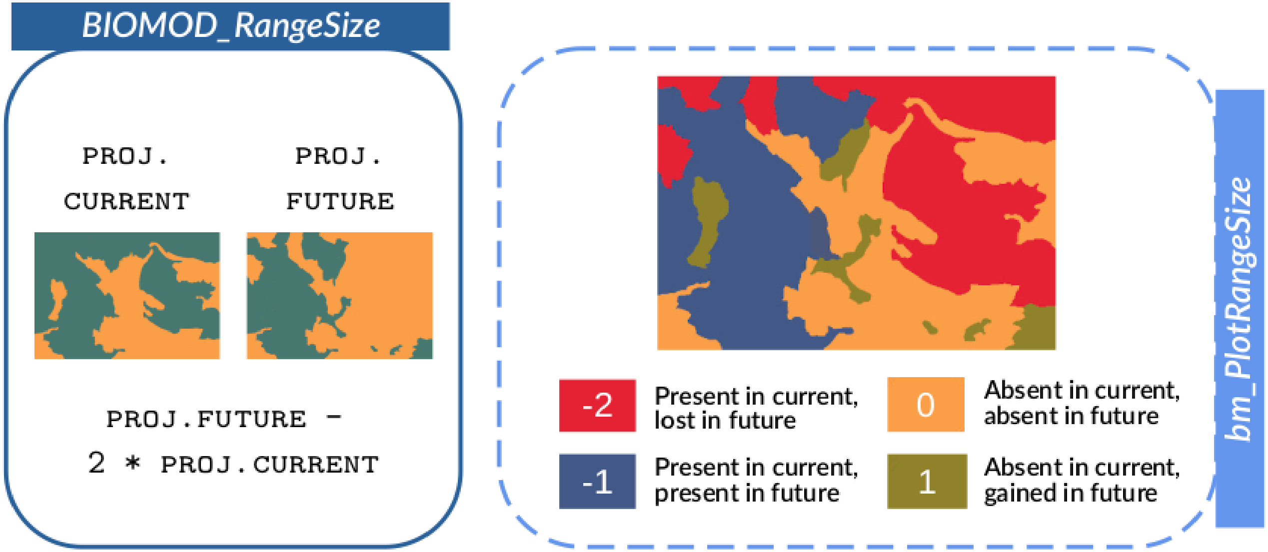
-1 Present in current, present in future

1 Absent in current, gained in future



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

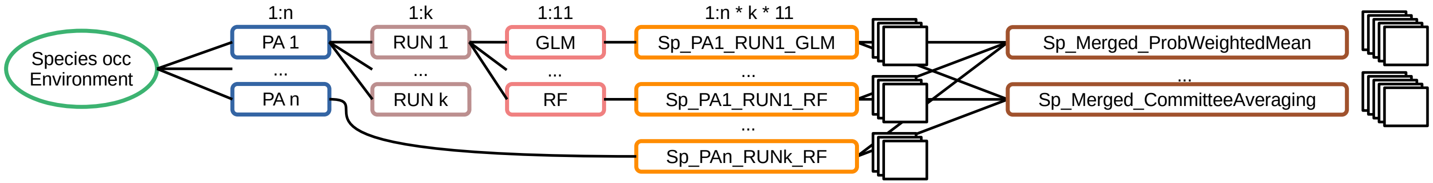
PROJ.FUTURE − 2 * PROJ.CURRENT

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

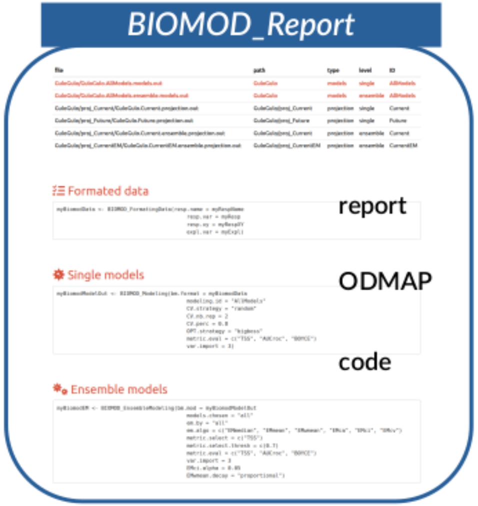
bm_PlotRangeSize

IMPORTANT

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



6. Report / ODMAP / code



BIOMOD_Report

file	path	type	level	ID
GuloGulo/GuloGulo.AllModels.models.out	GuloGulo	models	single	AllModels
GuloGulo/GuloGulo.AllModels.ensemble.models.out	GuloGulo	models	ensemble	AllModels
GuloGulo/proj_Current/GuloGulo.Current.projection.out	GuloGulo/proj_Current	projection	single	Current
GuloGulo/proj_Future/GuloGulo.Future.projection.out	GuloGulo/proj_Future	projection	single	Future
GuloGulo/proj_Current/GuloGulo.Current.ensemble.projection.out	GuloGulo/proj_Current	projection	ensemble	Current
GuloGulo/proj_CurrentEM/GuloGulo.CurrentEM.ensemble.projection.out	GuloGulo/proj_CurrentEM	projection	ensemble	CurrentEM

Formated data

```
myBiomodData <- BIOMOD_FormatingData(resp.name = myRespName
                                     resp.var = myResp
                                     resp.xy = myRespXY
                                     expl.var = myExpl)
```

Single models

```
myBiomodModelOut <- BIOMOD_Modeling(bm.format = myBiomodData
                                    modeling.id = 'AllModels'
                                    CV.strategy = 'random'
                                    CV.nb.rep = 2
                                    CV.perc = 0.8
                                    OPT.strategy = 'bigboss'
                                    metric.eval = c('TSS', 'AUCroc', 'BOYCE')
                                    var.import = 3)
```

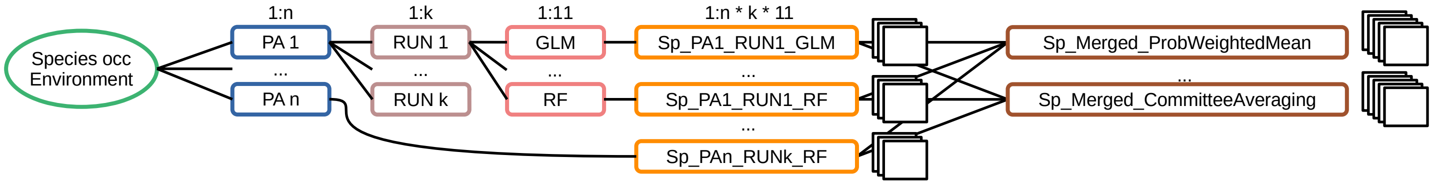
Ensemble models

```
myBiomodEM <- BIOMOD_EnsembleModeling(bm.mod = myBiomodModelOut
                                      models.chosen = 'all'
                                      em.by = 'all'
                                      em.algo = c('EMmedian', 'EMmean', 'EMwmean', 'EMca', 'EMci', 'EMcv')
                                      metric.select = c('TSS')
                                      metric.select.thresh = c(0.7)
                                      metric.eval = c('TSS', 'AUCroc', 'BOYCE')
                                      var.import = 3
                                      EMci.alpha = 0.05
                                      EMwmean.decay = 'proportional')
```

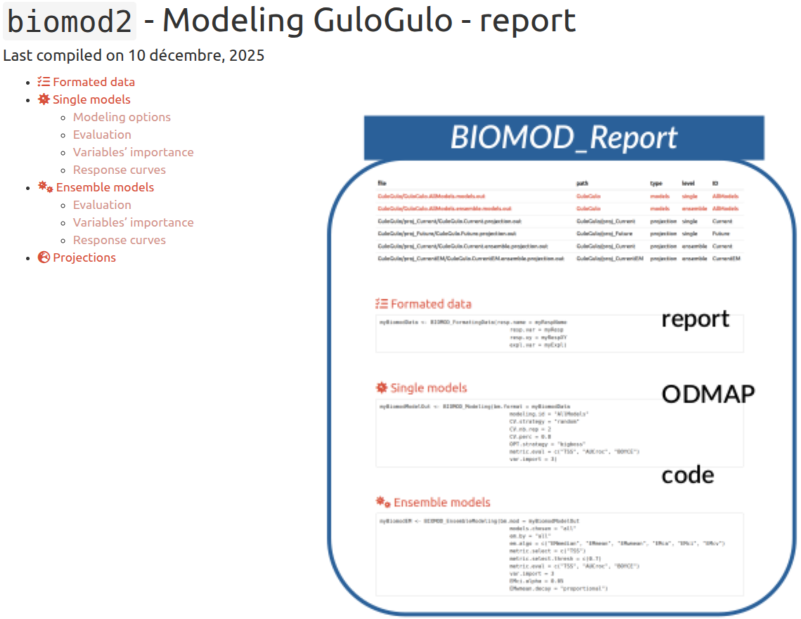
report

ODMAP

code



6. Report / ODMAP / code

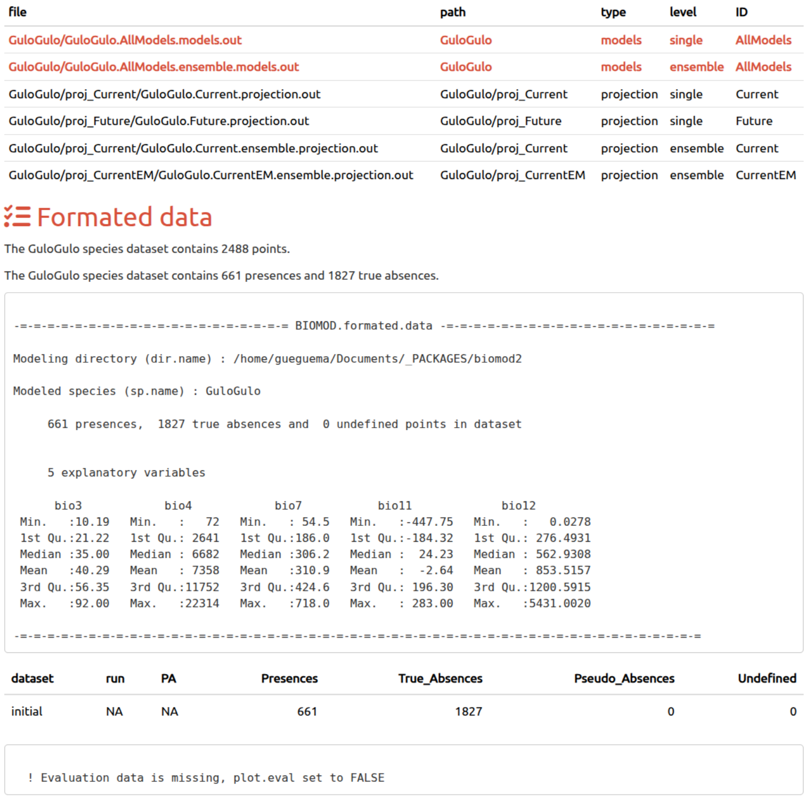


`biomod2` - Modeling GuloGulo - report

Last compiled on 10 décembre, 2025

- Formated data
- Single models
    - Modeling options
    - Evaluation
    - Variables' importance
    - Response curves
- Ensemble models
    - Evaluation
    - Variables' importance
    - Response curves
- Projections

- **report** : provide all possible prints, summaries, results and plots from a biomod2 object



file	path	type	level	ID
GuloGulo/GuloGulo.AllModels.models.out	GuloGulo	models	single	AllModels
GuloGulo/GuloGulo.AllModels.ensemble.models.out	GuloGulo	models	ensemble	AllModels
GuloGulo/proj_Current/GuloGulo.Current.projection.out	GuloGulo/proj_Current	projection	single	Current
GuloGulo/proj_Future/GuloGulo.Future.projection.out	GuloGulo/proj_Future	projection	single	Future
GuloGulo/proj_Current/GuloGulo.Current.ensemble.projection.out	GuloGulo/proj_Current	projection	ensemble	Current
GuloGulo/proj_CurrentEM/GuloGulo.CurrentEM.ensemble.projection.out	GuloGulo/proj_CurrentEM	projection	ensemble	CurrentEM

Formated data

The GuloGulo species dataset contains 2488 points.

The GuloGulo species dataset contains 661 presences and 1827 true absences.

```
-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= BIOMOD.formated.data -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=

Modeling directory (dir.name) : /home/gueguema/Documents/_PACKAGES/biomod2

Modeled species (sp.name) : GuloGulo

     661 presences,  1827 true absences and  0 undefined points in dataset

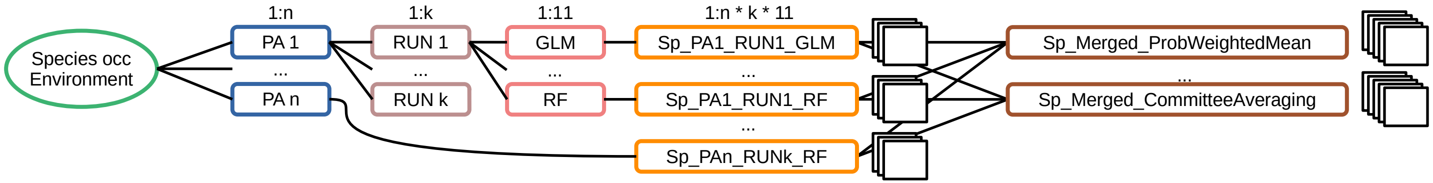

     5 explanatory variables

      bio3            bio4            bio7           bio11             bio12        
 Min.   :10.19   Min.   :   72   Min.   : 54.5   Min.   :-447.75   Min.   :   0.0278  
 1st Qu.:21.22   1st Qu.: 2641   1st Qu.:186.0   1st Qu.:-184.32   1st Qu.: 276.4931  
 Median :35.00   Median : 6682   Median :306.2   Median :  24.23   Median : 562.9308  
 Mean   :40.29   Mean   : 7358   Mean   :310.9   Mean   :  -2.64   Mean   : 853.5157  
 3rd Qu.:56.35   3rd Qu.:11752   3rd Qu.:424.6   3rd Qu.: 196.30   3rd Qu.:1200.5915  
 Max.   :92.00   Max.   :22314   Max.   :718.0   Max.   : 283.00   Max.   :5431.0020  

-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

dataset	run	PA	Presences	True_Absences	Pseudo_Absences	Undefined
initial	NA	NA	661	1827	0	0

```
 ! Evaluation data is missing, plot.eval set to FALSE
```



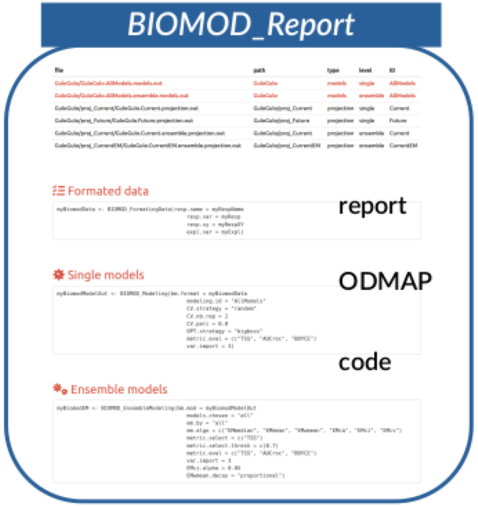
6. Report / ODMAP / code

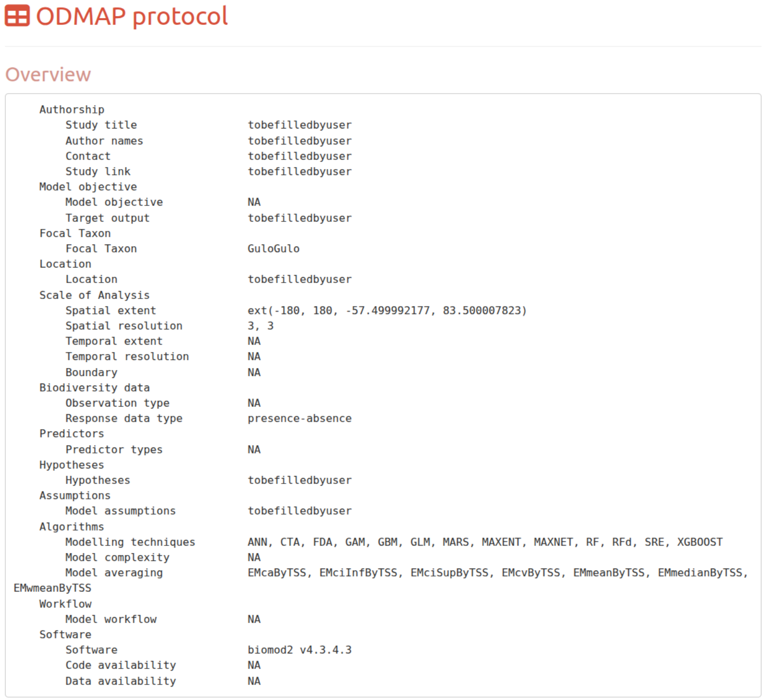
- **report** : provide all possible prints, summaries, results and plots from a biomod2 object
- **ODMAP** : pre-fill ODMAP protocol following Zurell et al. 2020 with biomod2 modelling elements

`biomod2` - Modeling GuloGulo - ODMAP

Last compiled on 08 décembre, 2025

- ODMAP protocol
  - Overview
  - Data
  - Model
  - Assessment
  - Prediction





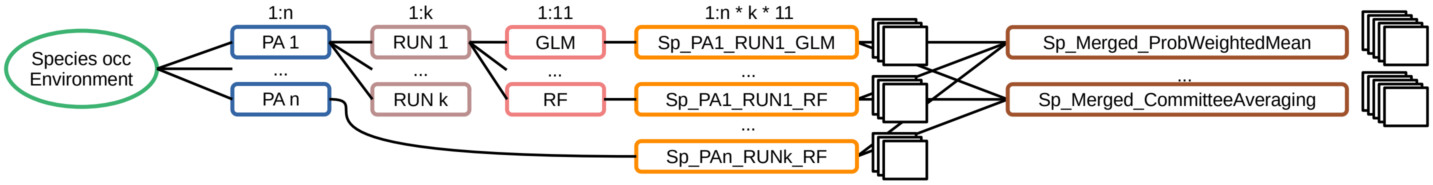
ODMAP protocol

Overview

```
    Authorship
        Study title                 tobefilledbyuser
        Author names                tobefilledbyuser
        Contact                     tobefilledbyuser
        Study link                  tobefilledbyuser
    Model objective
        Model objective             NA
        Target output               tobefilledbyuser
    Focal Taxon
        Focal Taxon                 GuloGulo
    Location
        Location                    tobefilledbyuser
    Scale of Analysis
        Spatial extent              ext(-180, 180, -57.499992177, 83.500007823)
        Spatial resolution          3, 3
        Temporal extent             NA
        Temporal resolution         NA
        Boundary                    NA
    Biodiversity data
        Observation type            NA
        Response data type          presence-absence
    Predictors
        Predictor types             NA
    Hypotheses
        Hypotheses                  tobefilledbyuser
    Assumptions
        Model assumptions           tobefilledbyuser
    Algorithms
        Modelling techniques        ANN, CTA, FDA, GAM, GBM, GLM, MARS, MAXENT, MAXNET, RF, RFd, SRE, XGBOOST
        Model complexity            NA
        Model averaging             EMcaByTSS, EMciInfByTSS, EMciSupByTSS, EMcvByTSS, EMmeanByTSS, EMmedianByTSS,
EMwmeanByTSS
    Workflow
        Model workflow              NA
    Software
        Software                    biomod2 v4.3.4.3
        Code availability           NA
        Data availability           NA
```

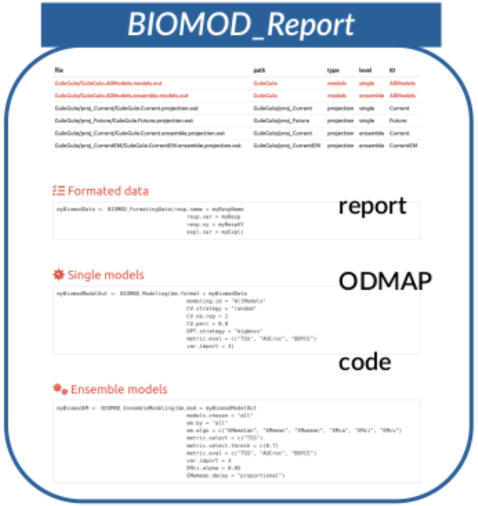
IMPORTANT

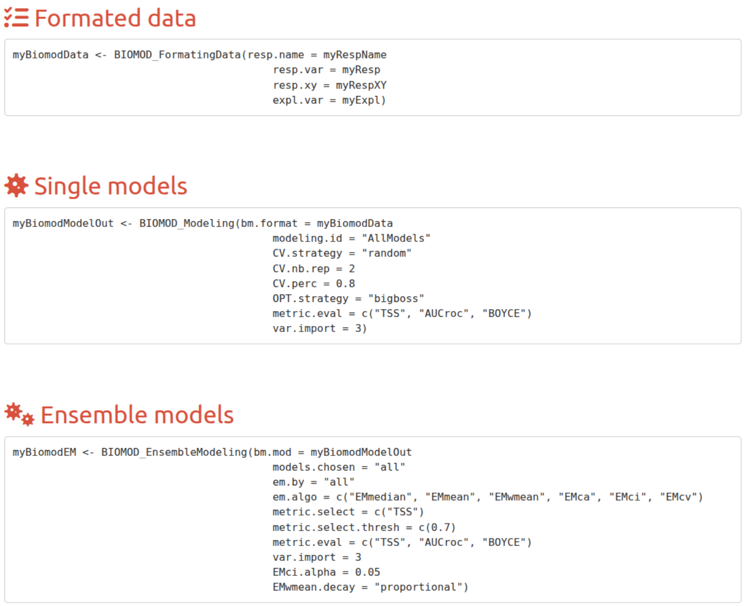
Overview, Data, Model, Assessment and Prediction



6. Report / ODMAP / code

- **report** : provide all possible prints, summaries, results and plots from a biomod2 object
- **ODMAP** : pre-fill ODMAP protocol following Zurell et al. 2020 with biomod2 modelling elements
- **code** : provide command lines used to call main functions





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                                         resp.var = myResp
                                         resp.xy = myRespXY
                                         expl.var = myExpl)
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Single models

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                                         modeling.id = "AllModels"
                                         CV.strategy = "random"
                                         CV.nb.rep = 2
                                         CV.perc = 0.8
                                         OPT.strategy = "bigboss"
                                         metric.eval = c("TSS", "AUCroc", "BOYCE")
                                         var.import = 3)
```

Ensemble models

```
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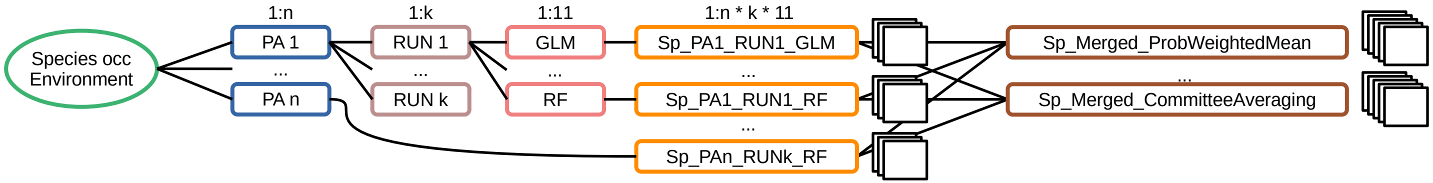
                                         models.chosen = "all"
                                         em.by = "all"
                                         em.algo = c("EMmedian", "EMmean", "EMwmean", "EMca", "EMci", "EMcv")
                                         metric.select = c("TSS")
                                         metric.select.thresh = c(0.7)
                                         metric.eval = c("TSS", "AUCroc", "BOYCE")
                                         var.import = 3
                                         EMci.alpha = 0.05
                                         EMwmean.decay = "proportional")
```



Species distribution modeling,
calibration and evaluation,
ensemble modeling

Laboratoire d'Ecologie Alpine

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/