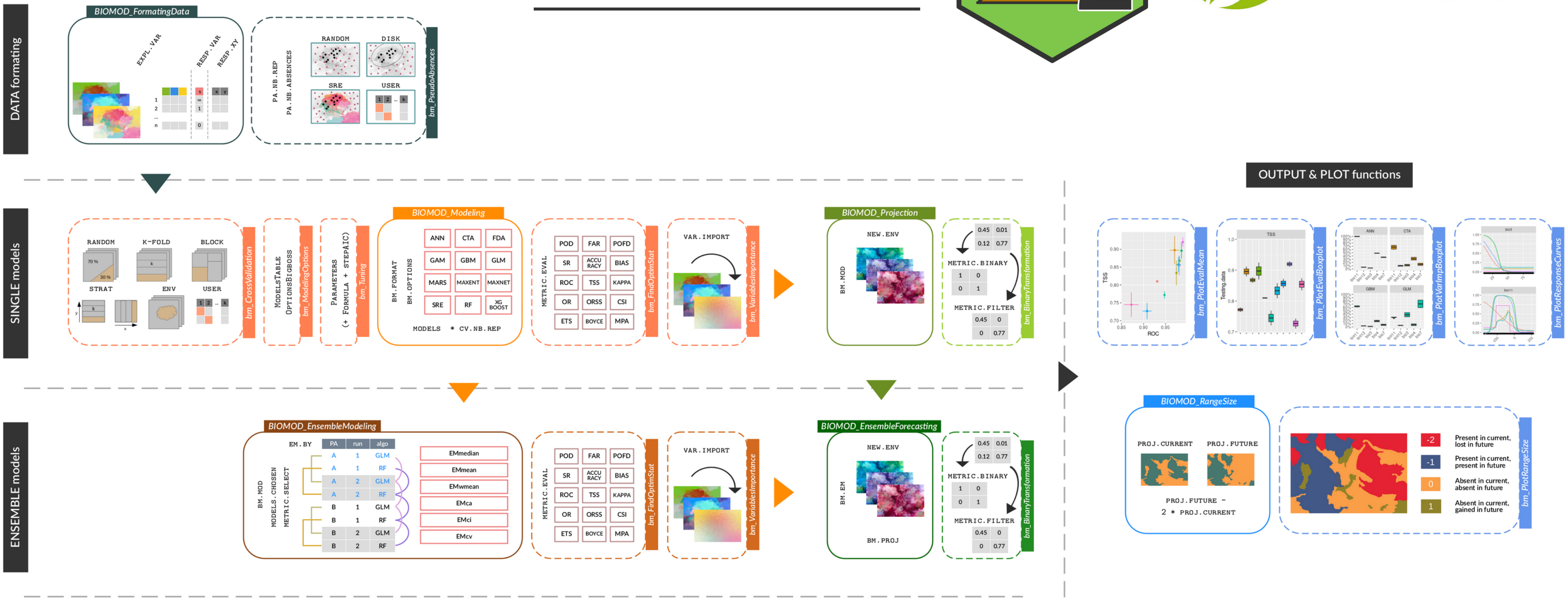
Species distribution modeling, calibration and evaluation, ensemble modeling

Laboratoire d'Ecologie Alpine



Species distribution modeling, calibration and evaluation, ensemble modeling

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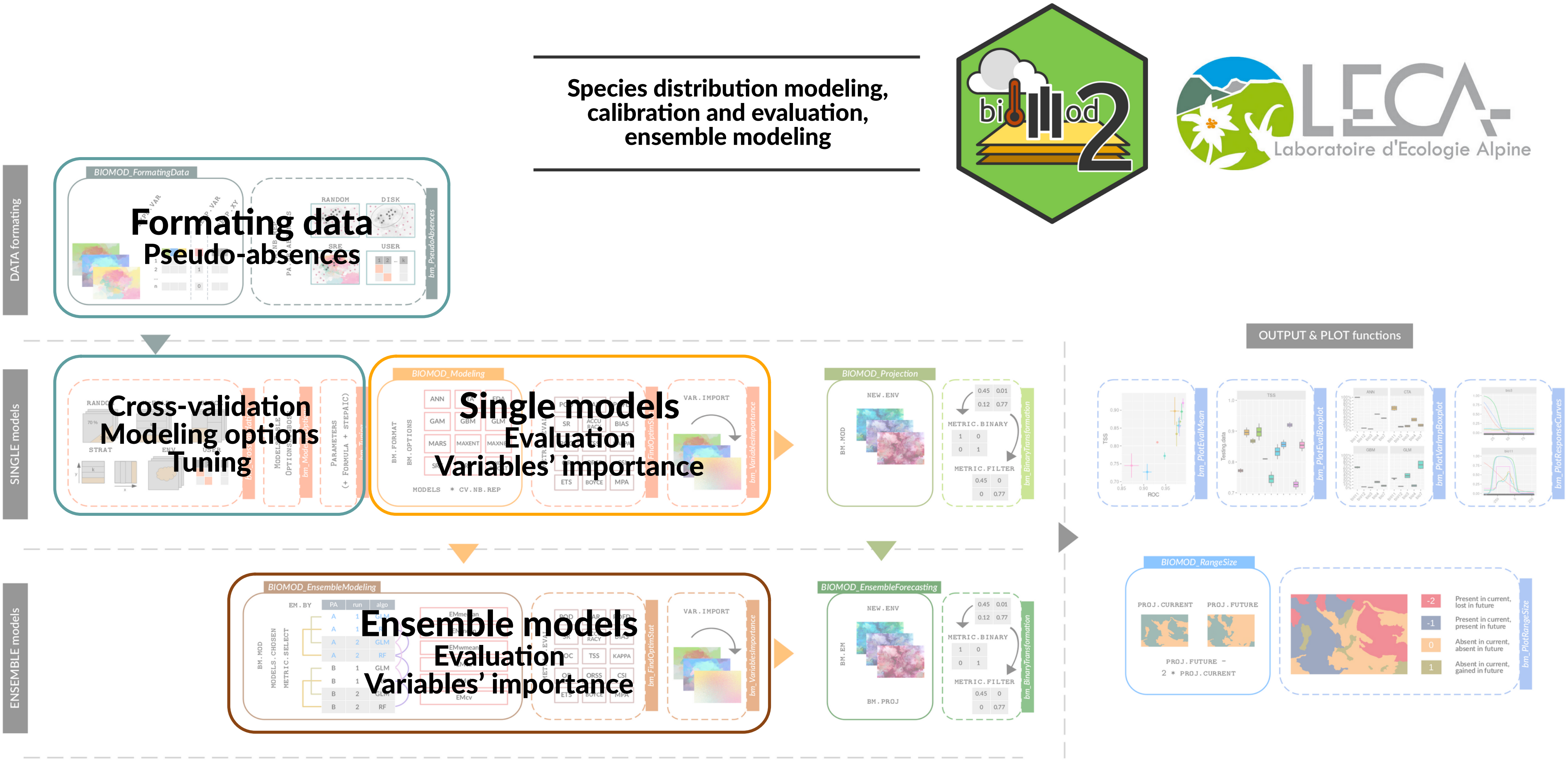
Species distribution modeling,
calibration and evaluation,
ensemble modeling
Laboratoire d'Ecologie Alpine
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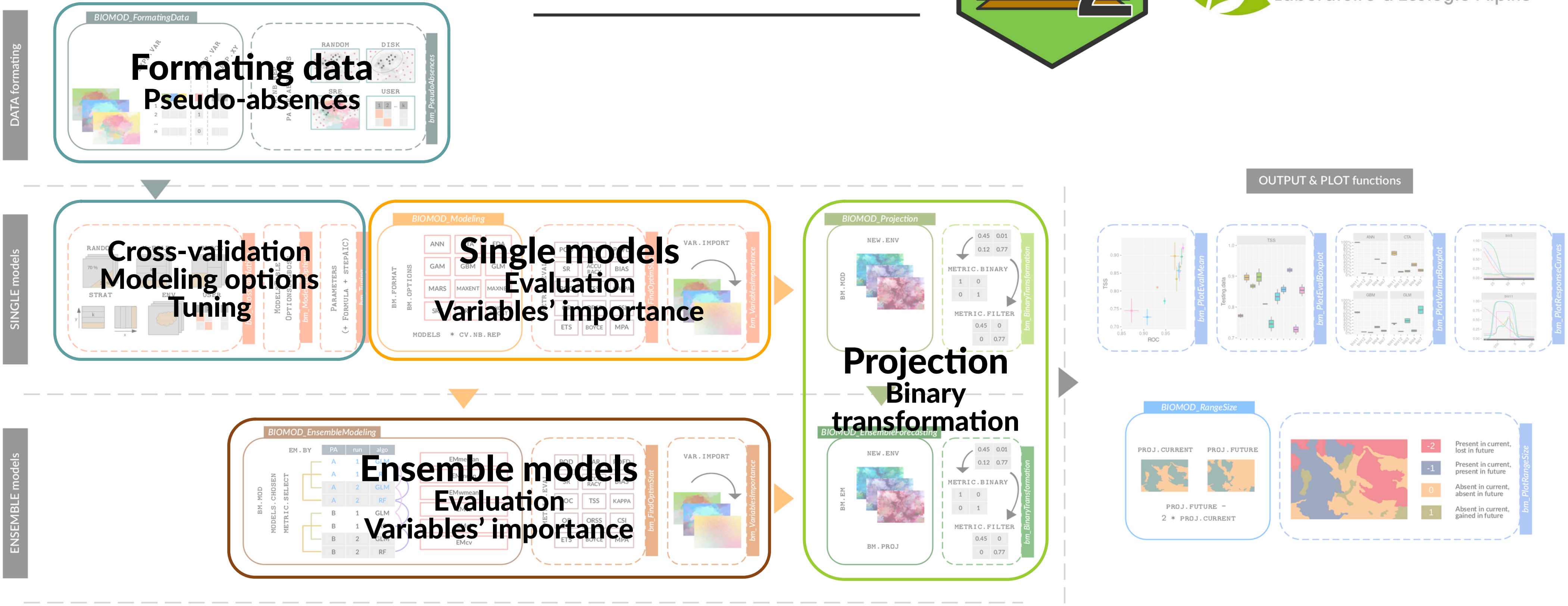
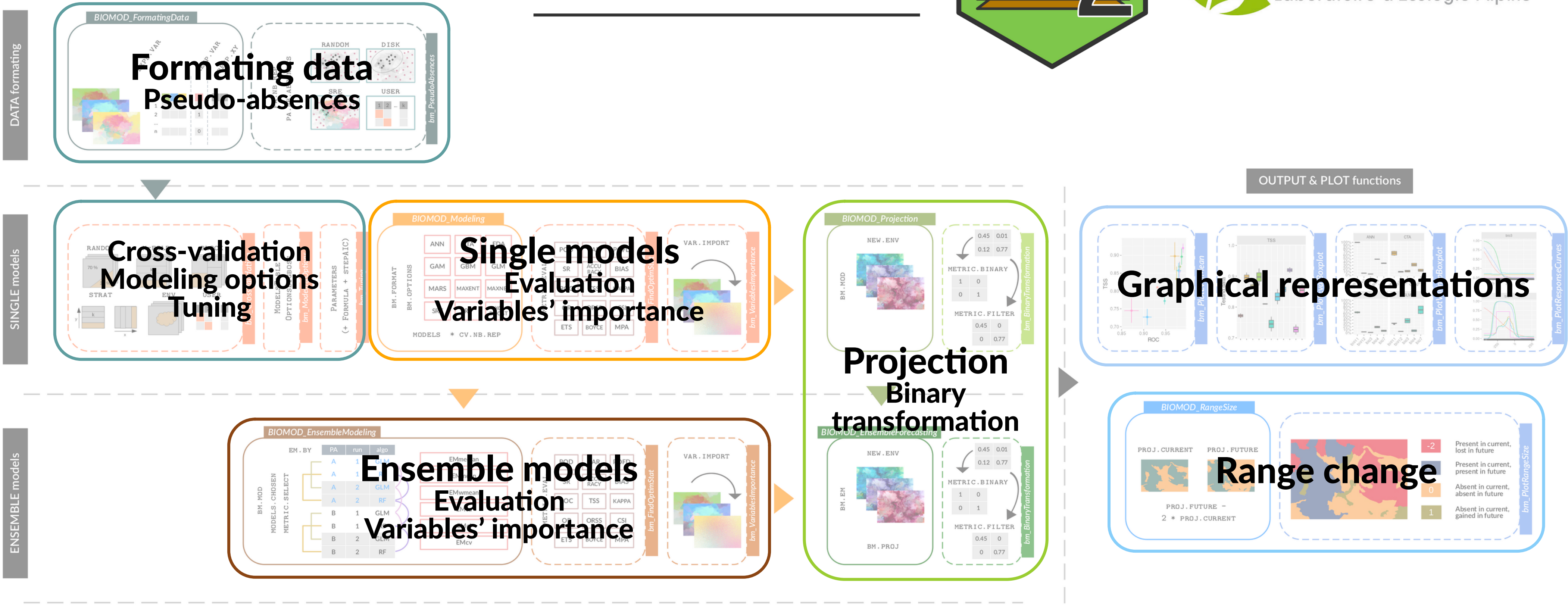
Present in current, present in future
Absent in current, absent in future
Absent in current, gained in future
bm_PlotRangeSize

Species distribution modeling, calibration and evaluation, ensemble modeling

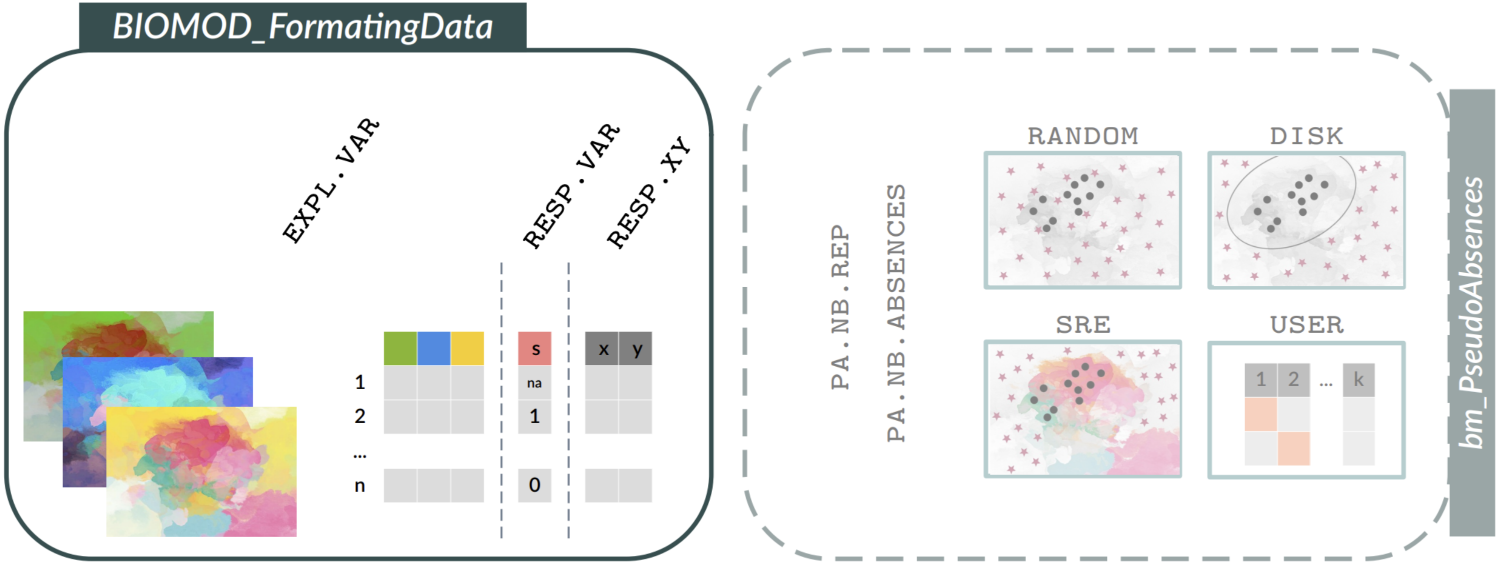


Species distribution modeling, calibration and evaluation, ensemble modeling



1. Formating data

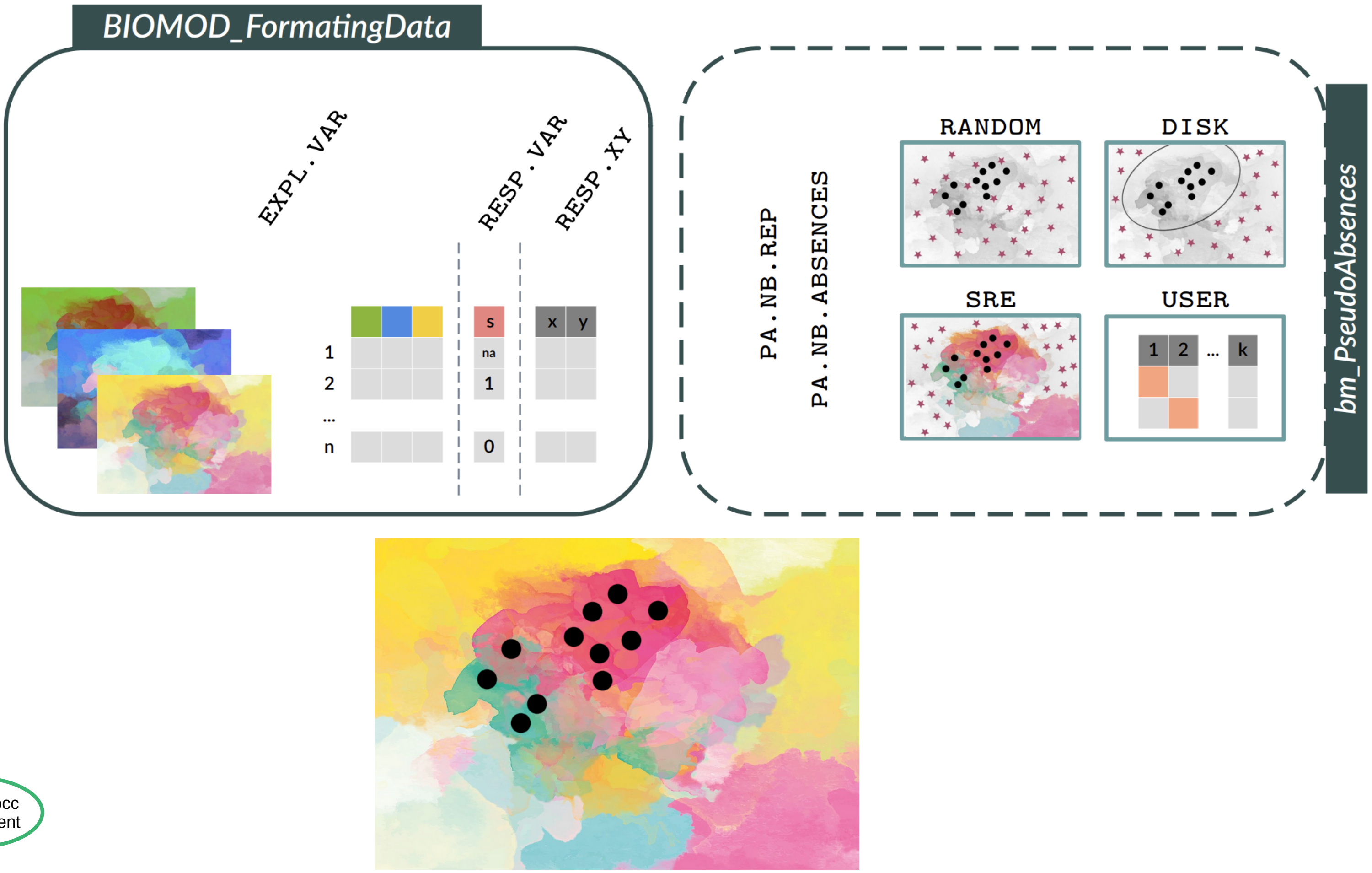
- **presences-absences**



Species occ
Environment

1. Formating data

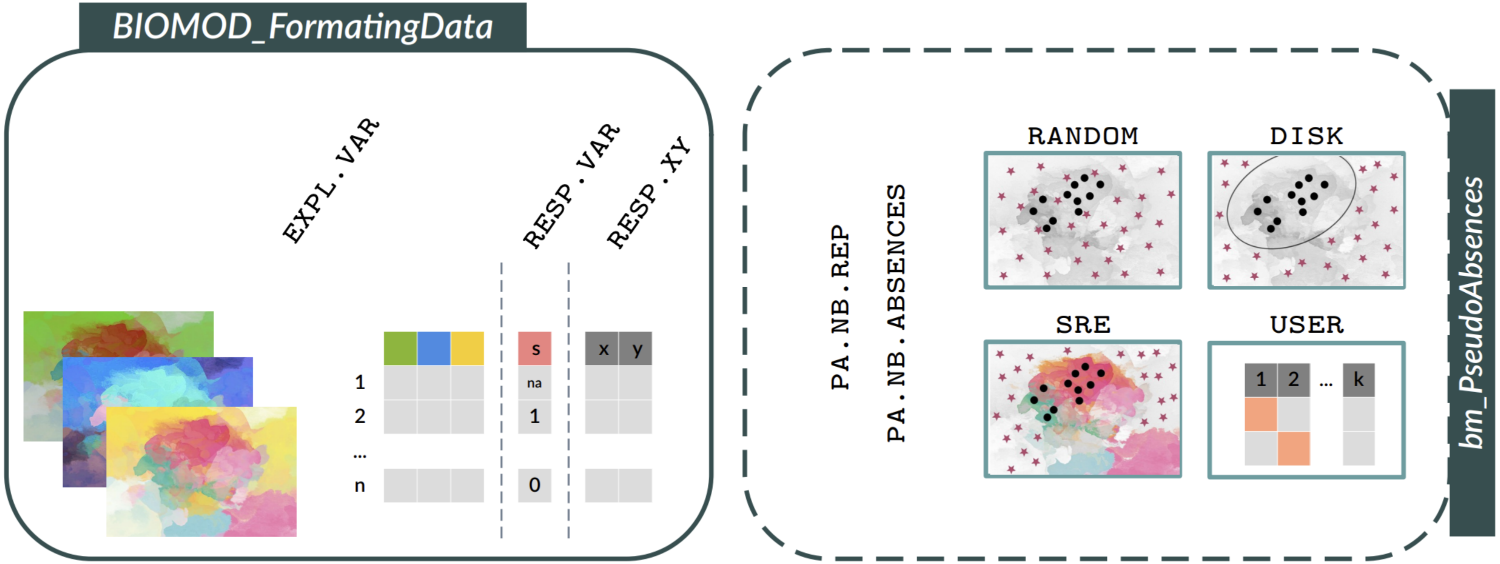
- **presence-only** data
- *avoid to mix with real absences*

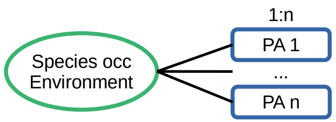


Species occ
Environment

1. Formating data

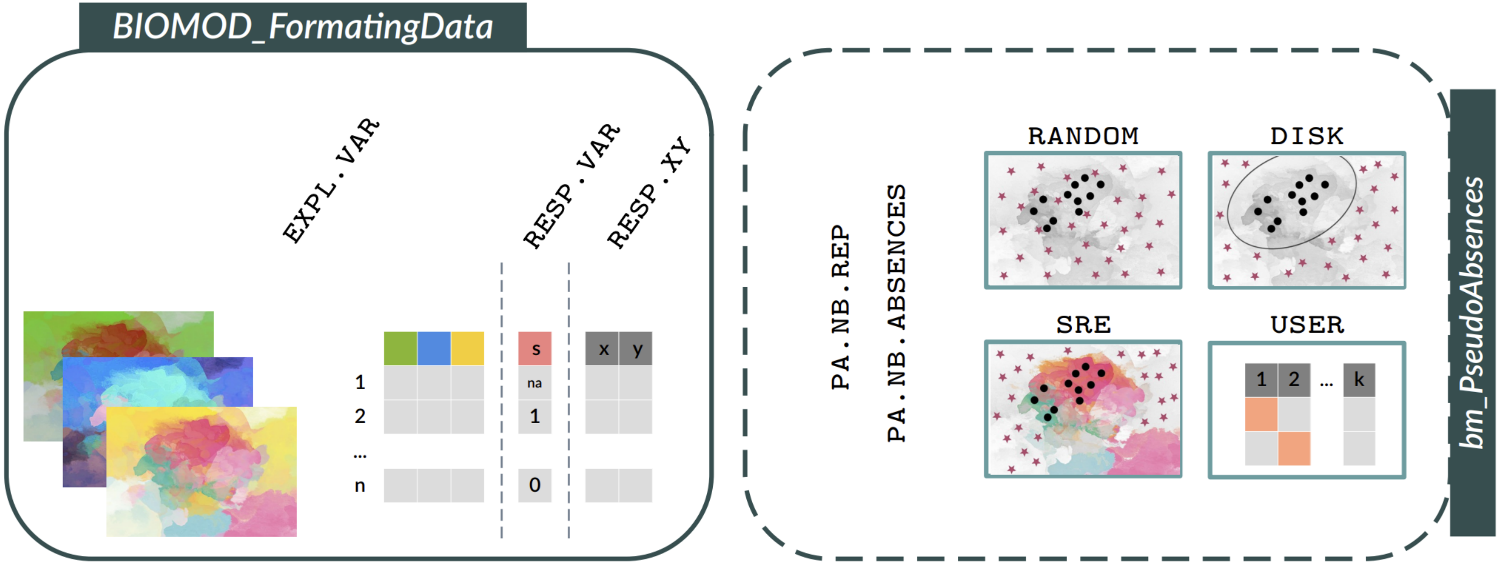
- **presence-only** data
- *avoid to mix with real absences*
- **random** : sampling potentially biased / non-exhaustive

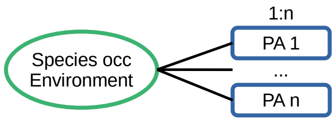


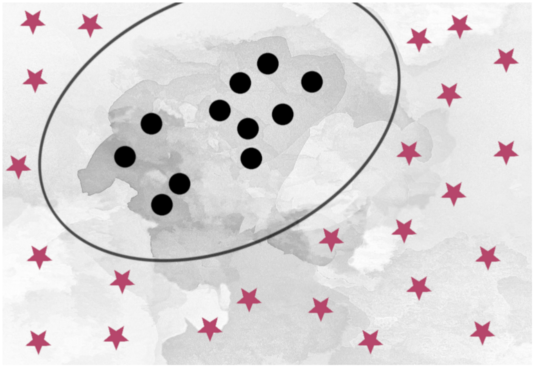


1. Formating data

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

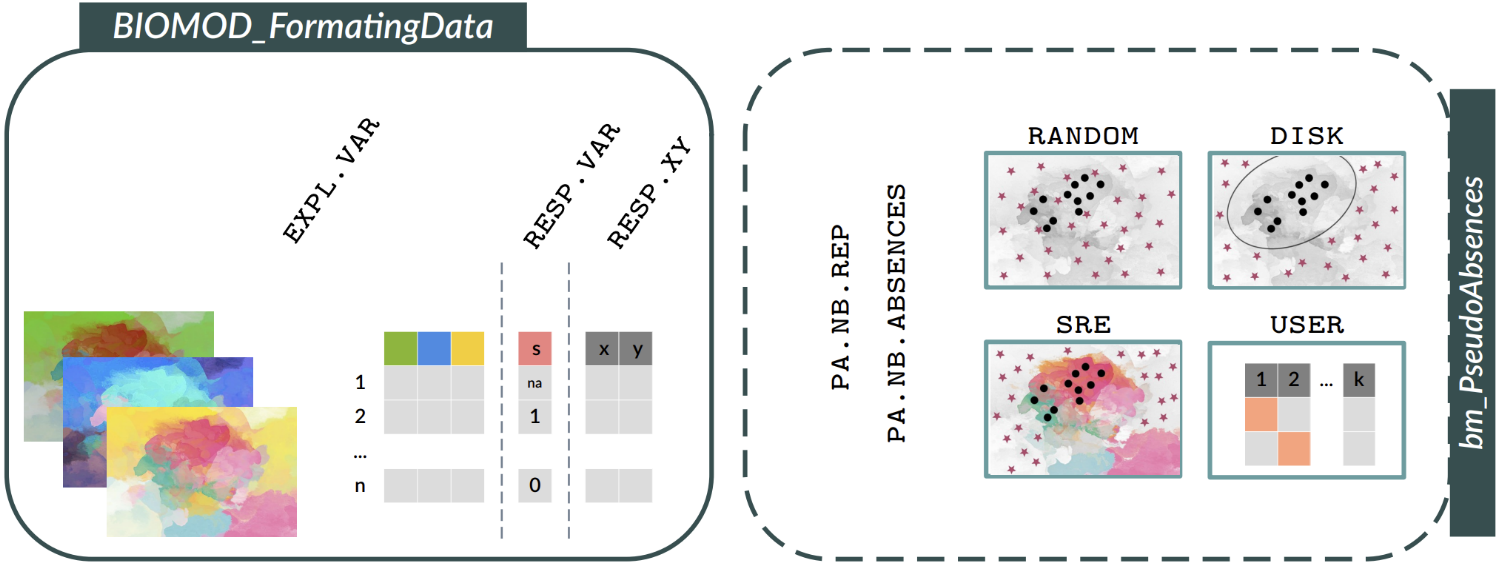


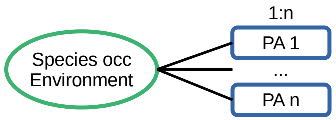




1. Formating data

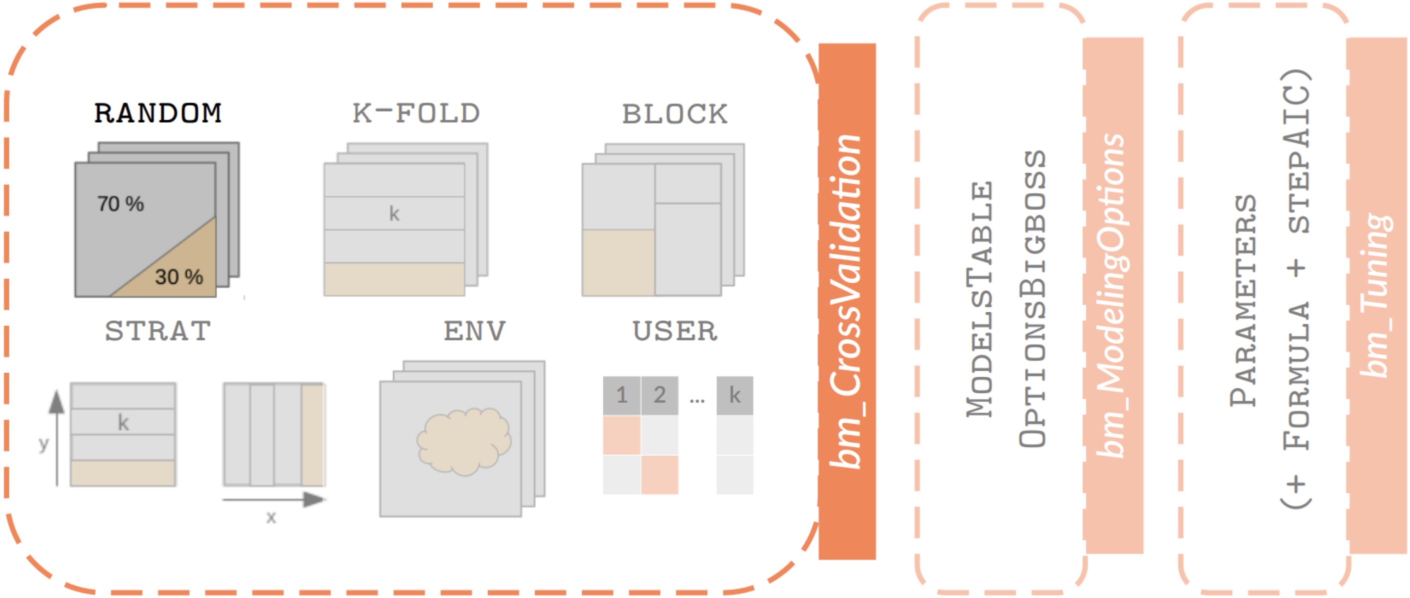
- **presence-only** data
- *avoid to mix with real absences*
- **random** : sampling potentially biased / non-exhaustive
- **disk** : geographic niche well sampled
- **SRE** : environmental niche well sampled

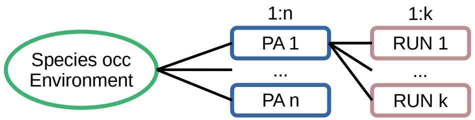




1. Formating data

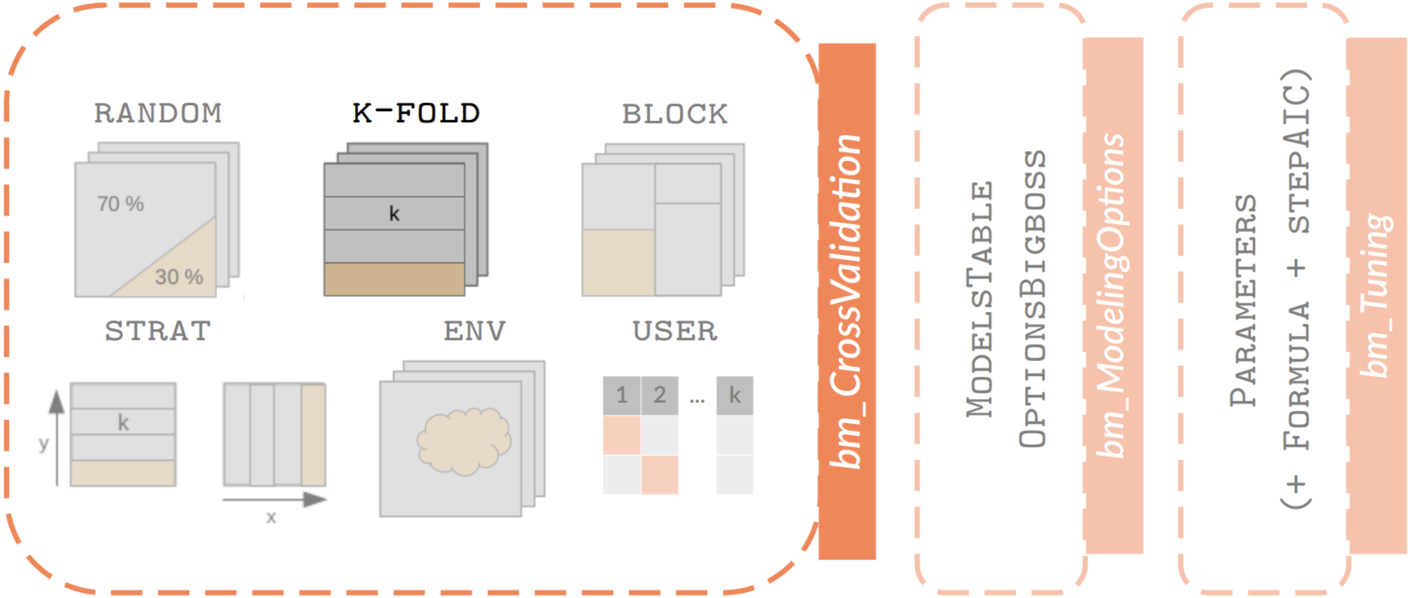
- simple calibration / validation split at the modeling step, and repeated nb.rep times

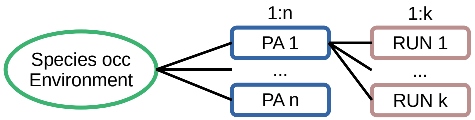




1. Formating data

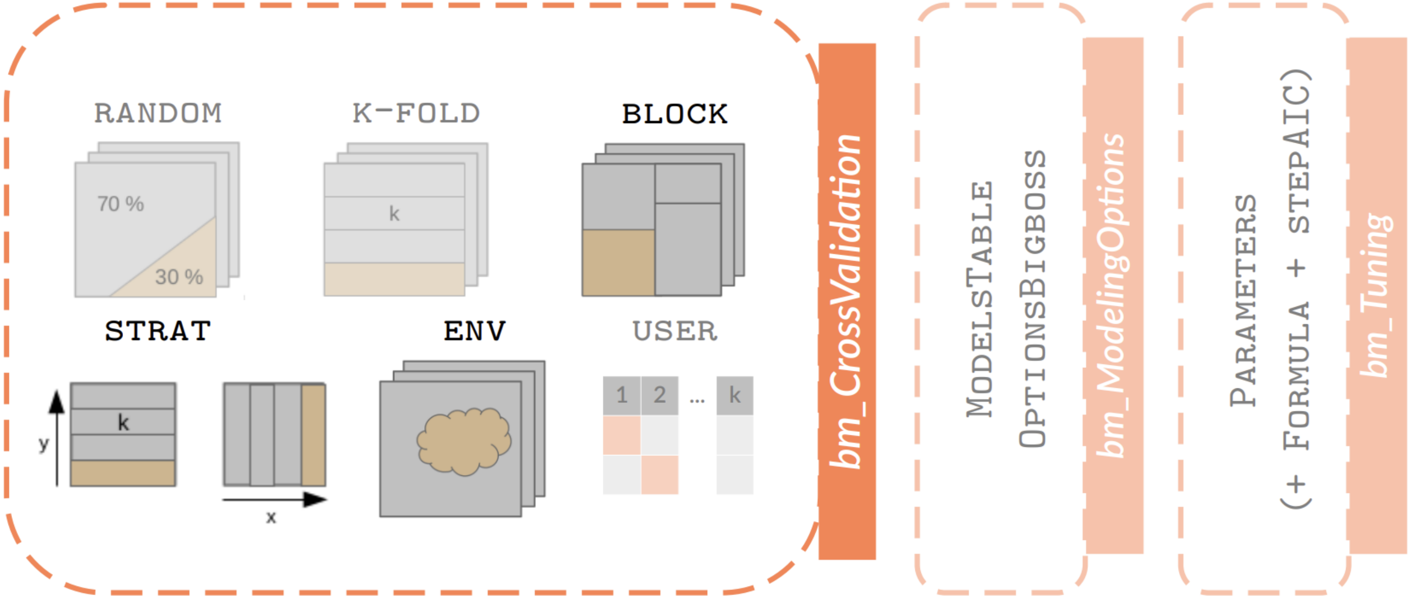
- simple calibration / validation split at the modeling step, and repeated nb.rep times
- **k-fold** : partition data into k sub-dataset, and repeated nb.rep times

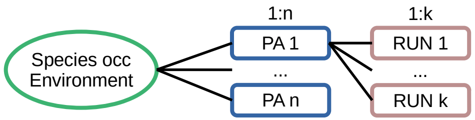




1. Formating data

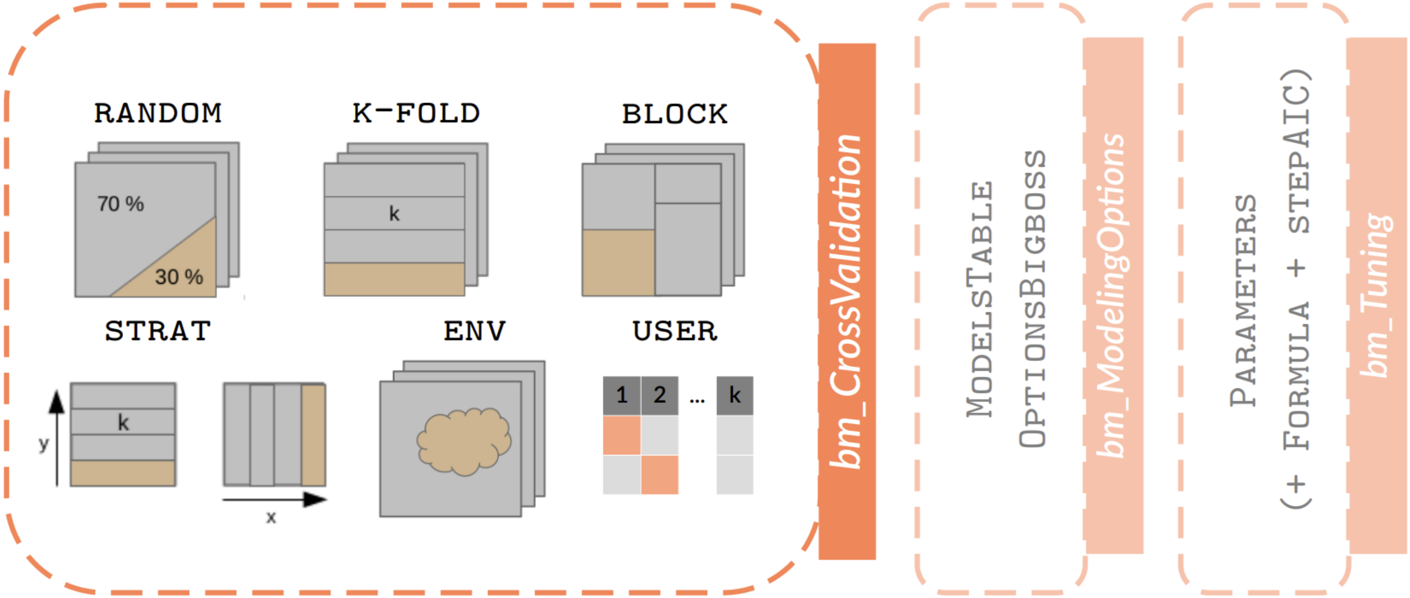
- simple calibration / validation split at the modeling step, and repeated nb.rep times
- **k-fold** : partition data into k sub-dataset, and repeated nb.rep times
- **stratified** : partition data into k sub-dataset (x, y, both, block)

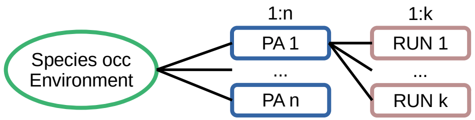


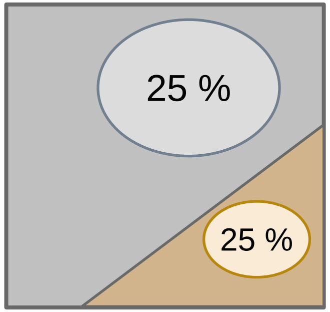


1. Formating data

- 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)
- **balance** : keep the prevalence of presences (*or absences*) in sub-dataset

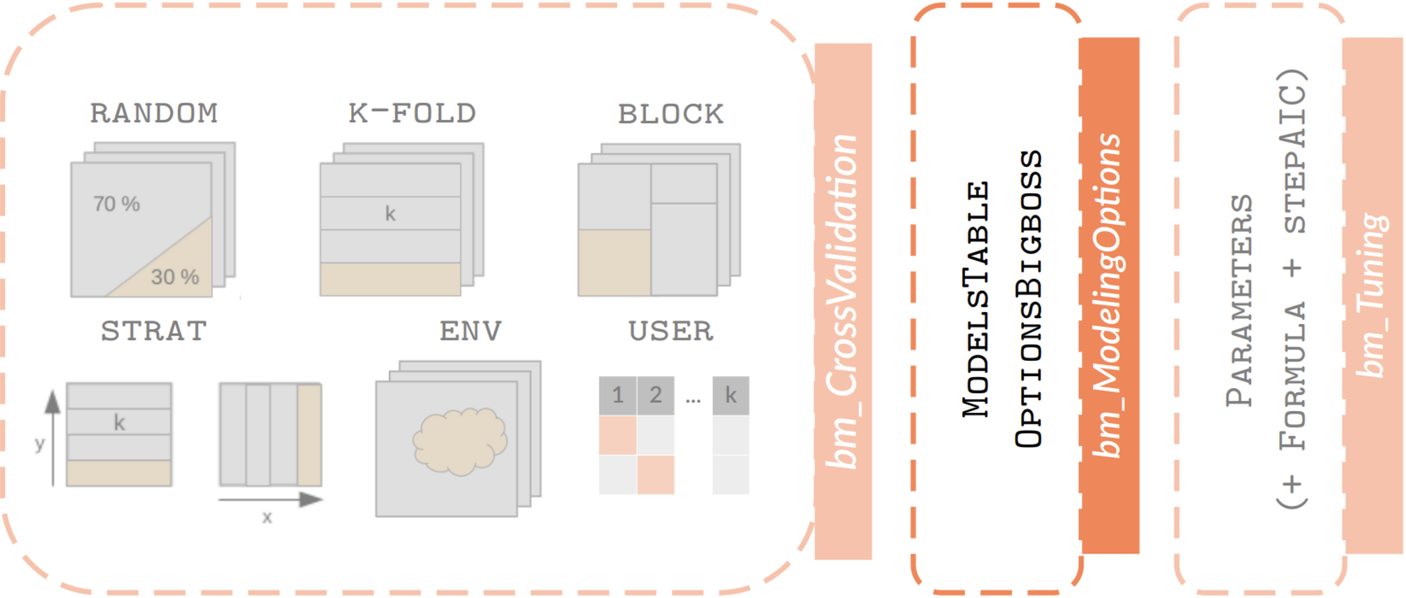


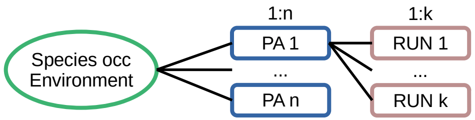




1. Formating data

- 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
```

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```
nnet                    package:nnet                    R Documentation

Fit Neural Networks

Description:

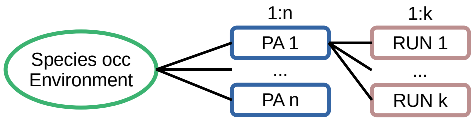
     Fit single-hidden-layer neural network, possibly with skip-layer
     connections.

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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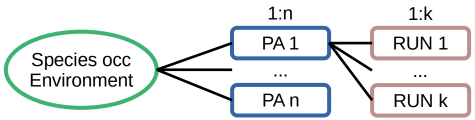
```

```
>  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	mgcv	bam	bam
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9	MARS	binary	earth	earth	earth
10	MAXENT	binary	MAXENT	MAXENT	ENMevaluate
11	MAXNET	binary	maxnet	maxnet	maxnet
12	RF	binary	randomForest	randomForest	rf
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- **default** : extracted from functions
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- **user-defined**

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nnet                    package:nnet                    R Documentation

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          censored = FALSE, skip = FALSE, rang = 0.7, decay = 0,
          maxit = 100, Hess = FALSE, trace = TRUE, MaxNWts = 1000,
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```
>  ANN options (datatype: binary , package: nnet , function: nnet ) :
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        - size = 5   (default: 2 )
        - decay = 5   (default: NULL )
        - trace = FALSE   (default: NULL )
        - rang = 0.1   (default: NULL )
        - maxit = 200   (default: NULL )
```

ModelsTable

OptionsBigBoss

bm_ModelingOptions

Parameters

(+ formula + stepAIC)

bm_Tuning

```
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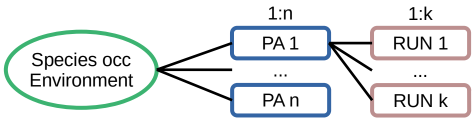
```

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



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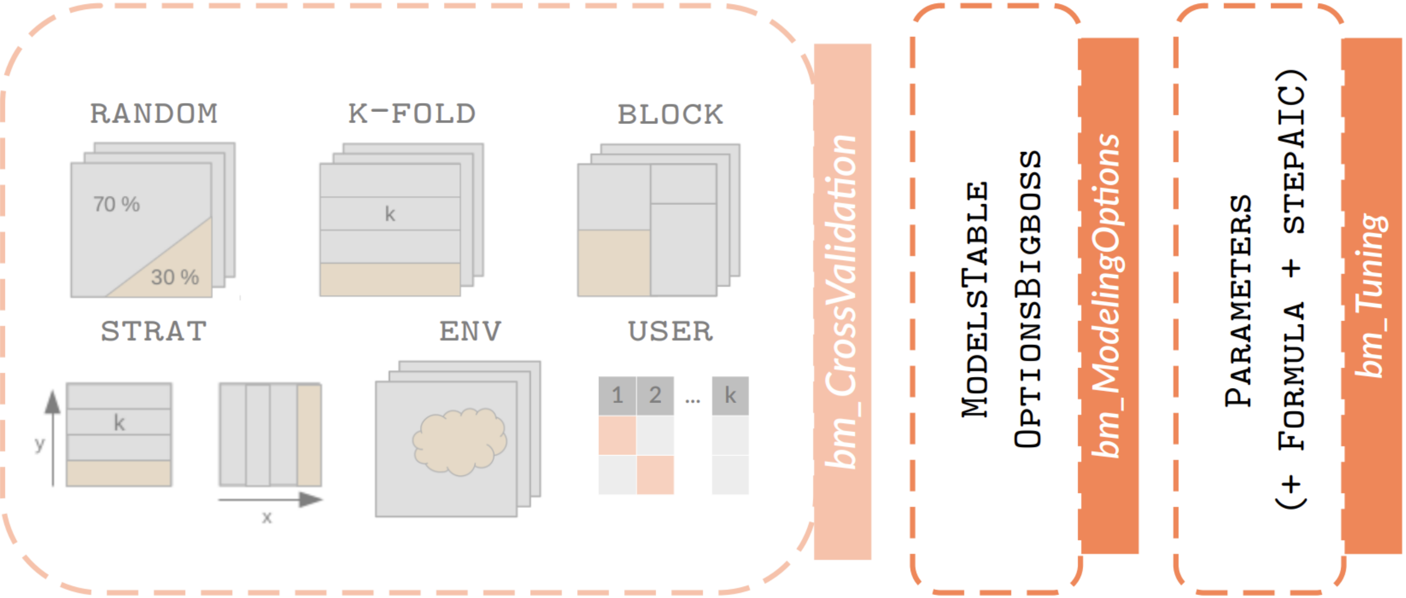
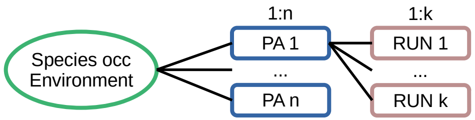
- **tuned** : with *train* function from *caret* package



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6     GAM binary          mgcv         gam         gam
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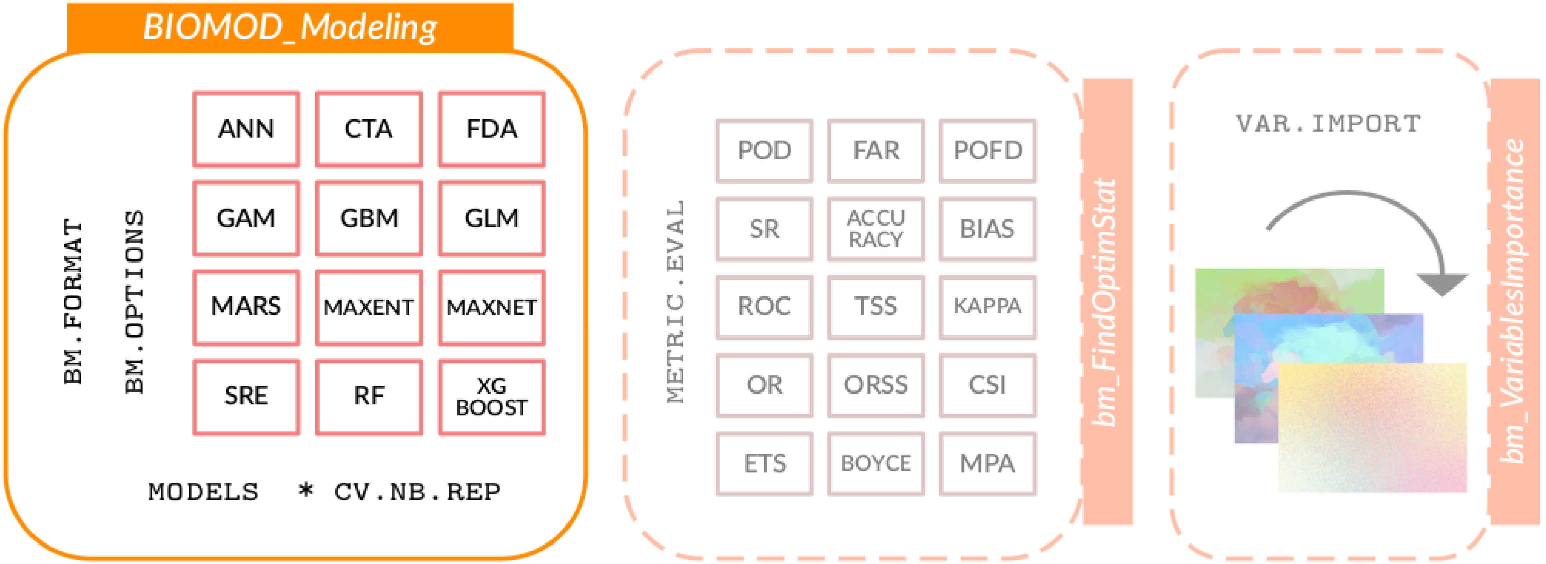
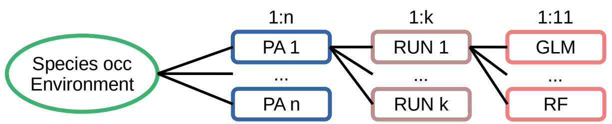
12     RF binary randomForest randomForest          rf
13    SRE binary       biomod2      bm_SRE      bm_SRE
14 XGBOOST binary      xgboost     xgboost     xgbTree
```

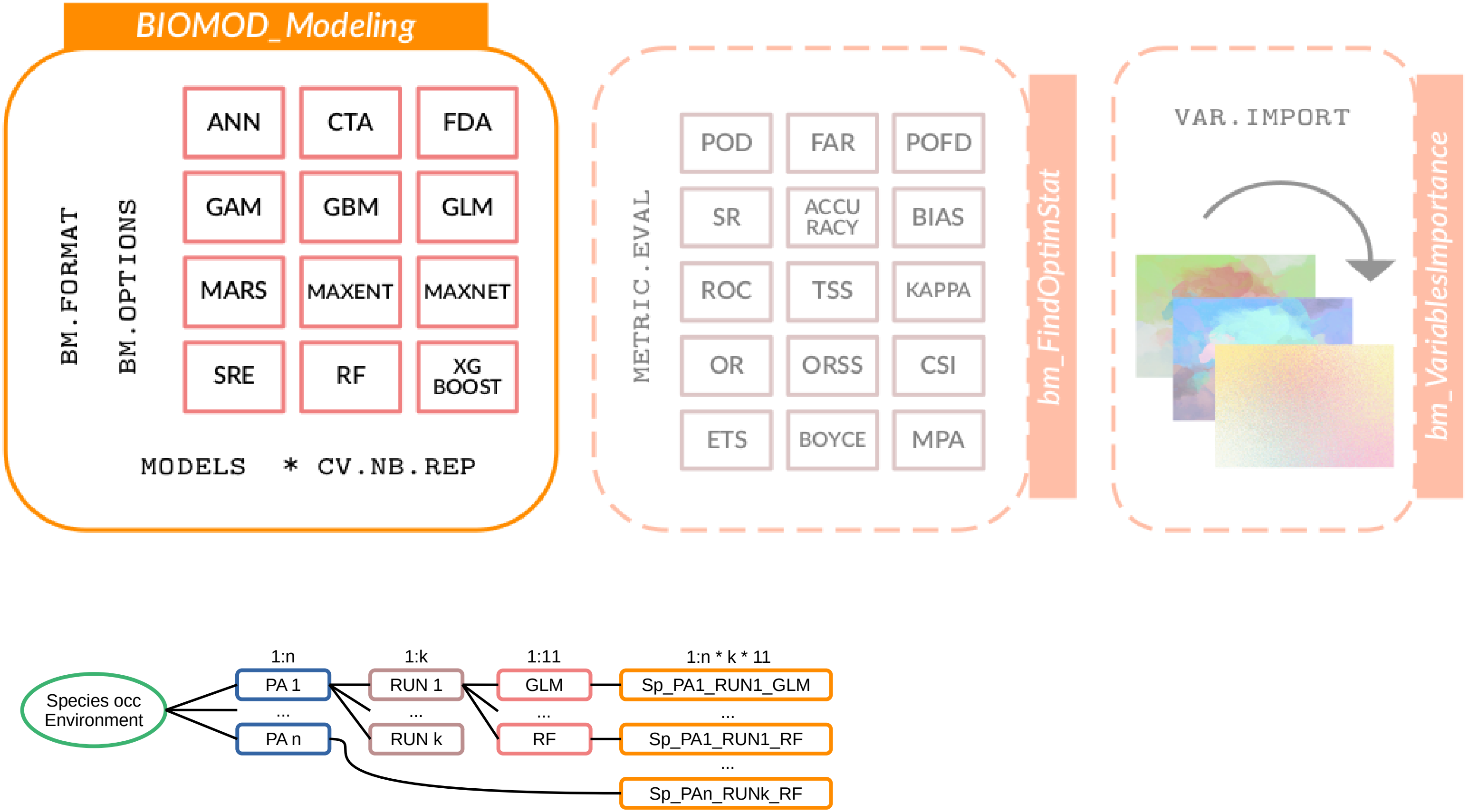
- test a bunch of parameters, and try to keep the « best » according to some evaluation metrics (TSS or ROC)

2.a Single models



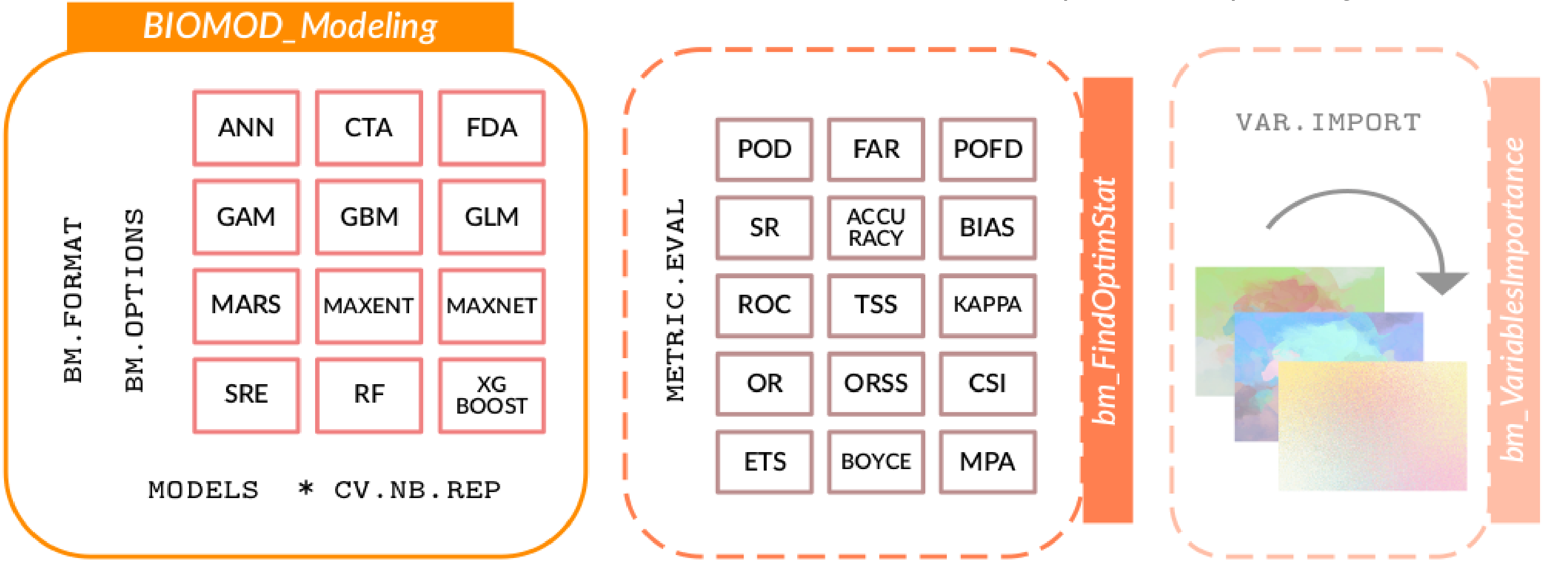


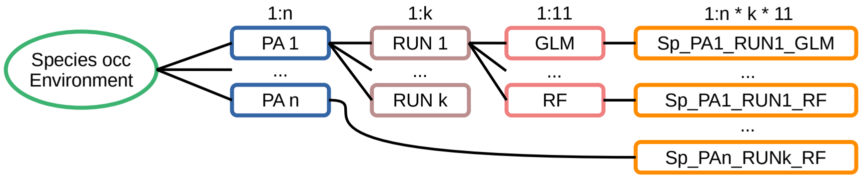
2.a Single models



2.a Single models

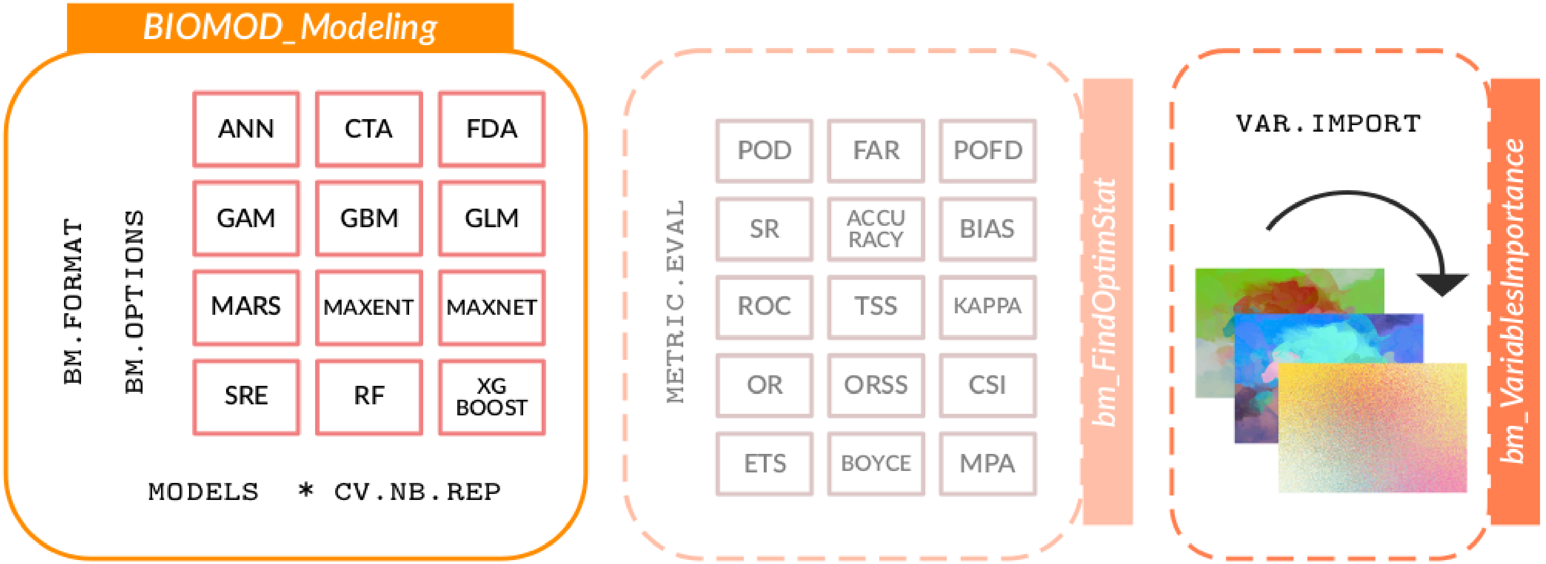
- except ROC, all evaluation metrics obtained from contingency table (*containing TP, FP, TN, FN*)
- require a **binary transformation** :
  - range of thresholds tested
  - keep thresold optimising the evaluation metric

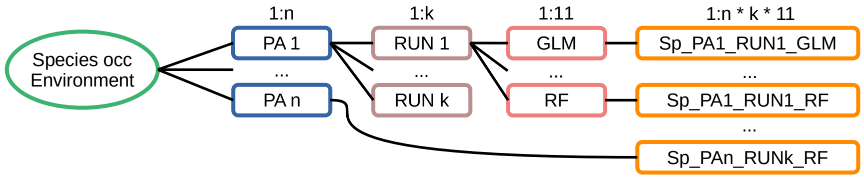




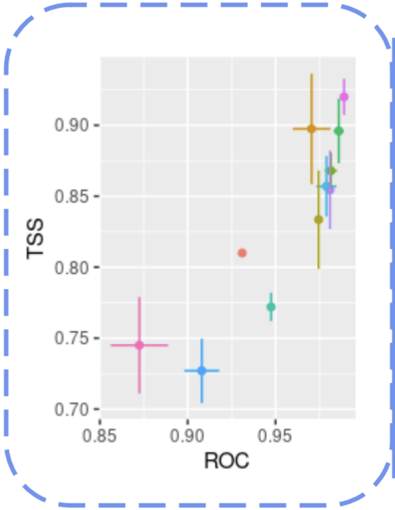
2.a Single models

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

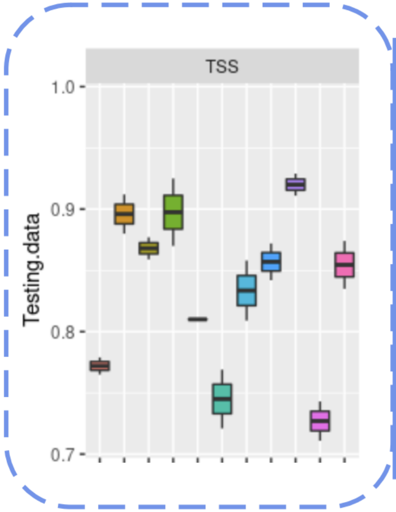




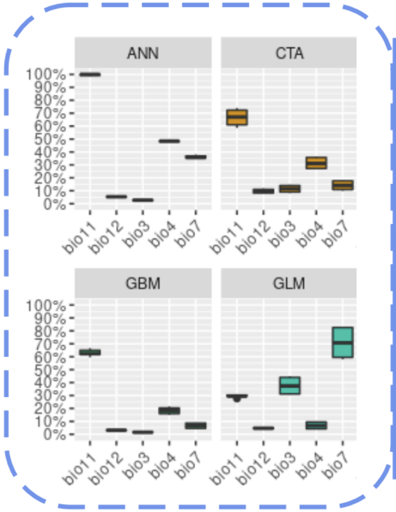
3.a Exploring single models



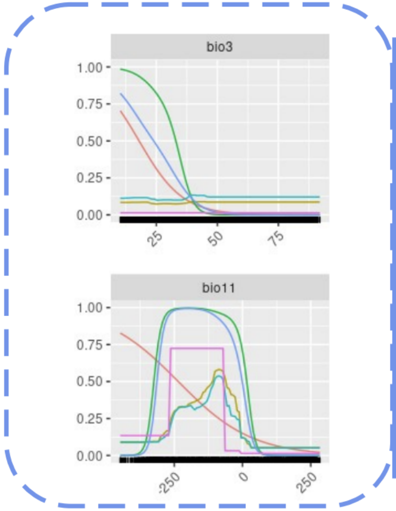
bm_PlotEvalMean



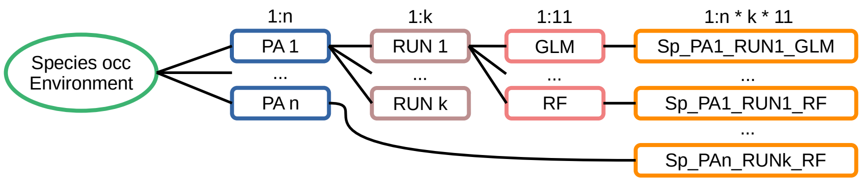
bm_PlotEvalBoxplot



bm_PlotVarImpBoxplot

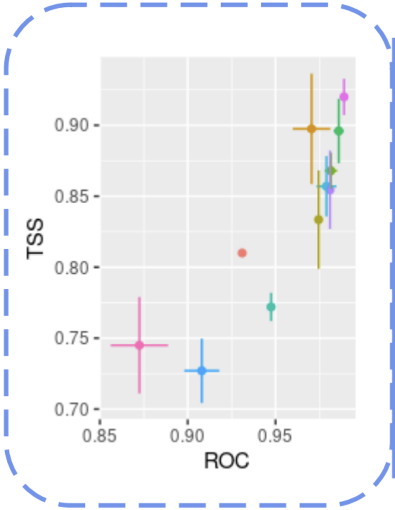


bm_PlotResponseCurves

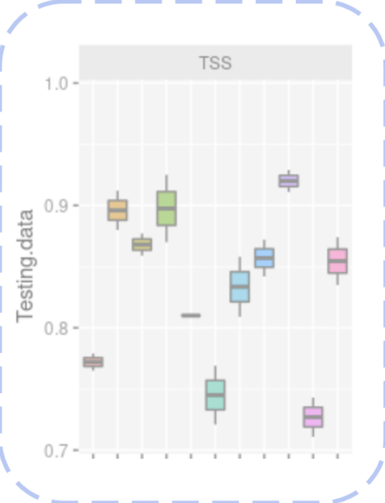


3.a Exploring single models

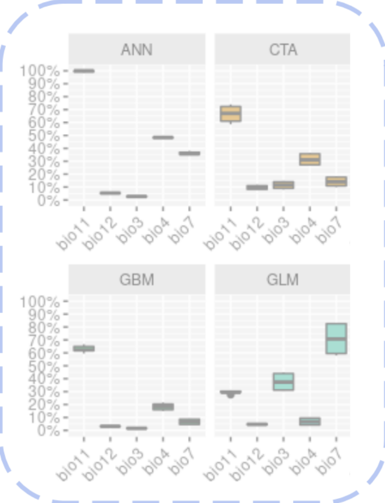
- « evaluation space »
- visualize the metrics consistency between models



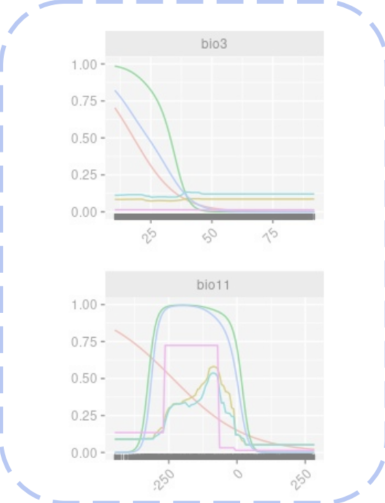
bm_PlotEvalMean



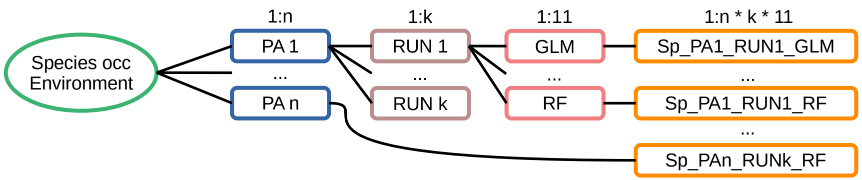
bm_PlotEvalBoxplot



bm_PlotVarImpBoxplot

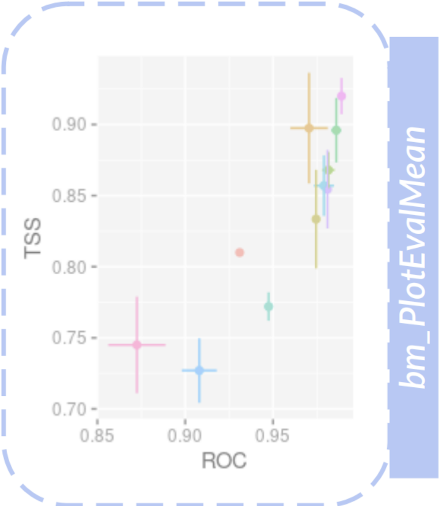


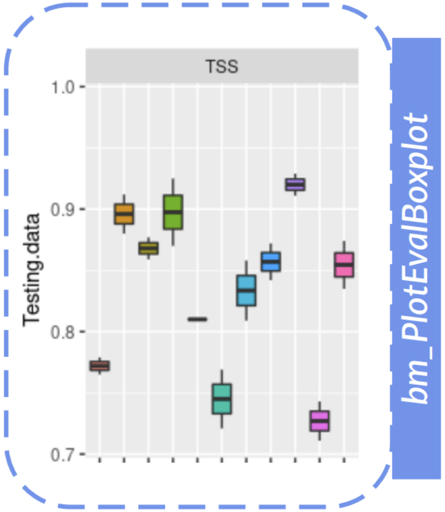
bm_PlotResponseCurves

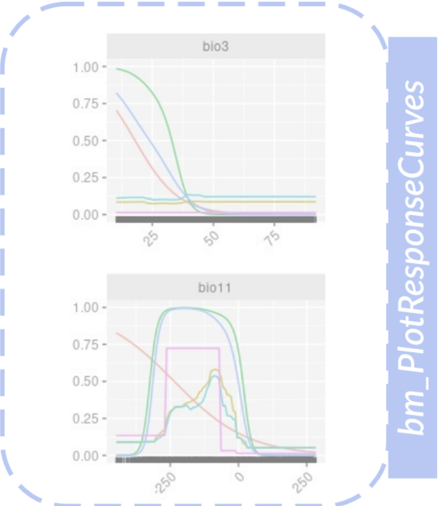


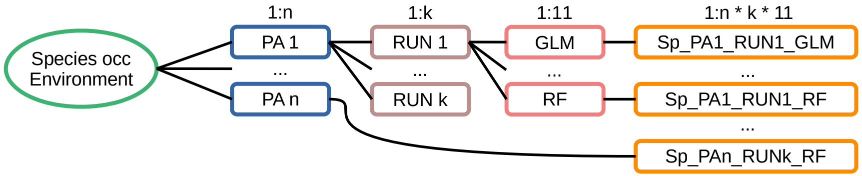
3.a Exploring single models

- more classical view
- visualize the metrics consistency between models



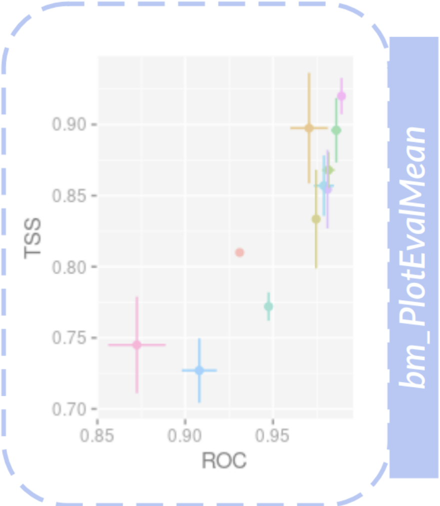


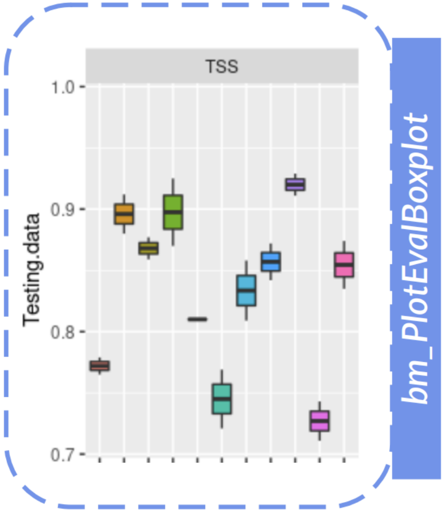


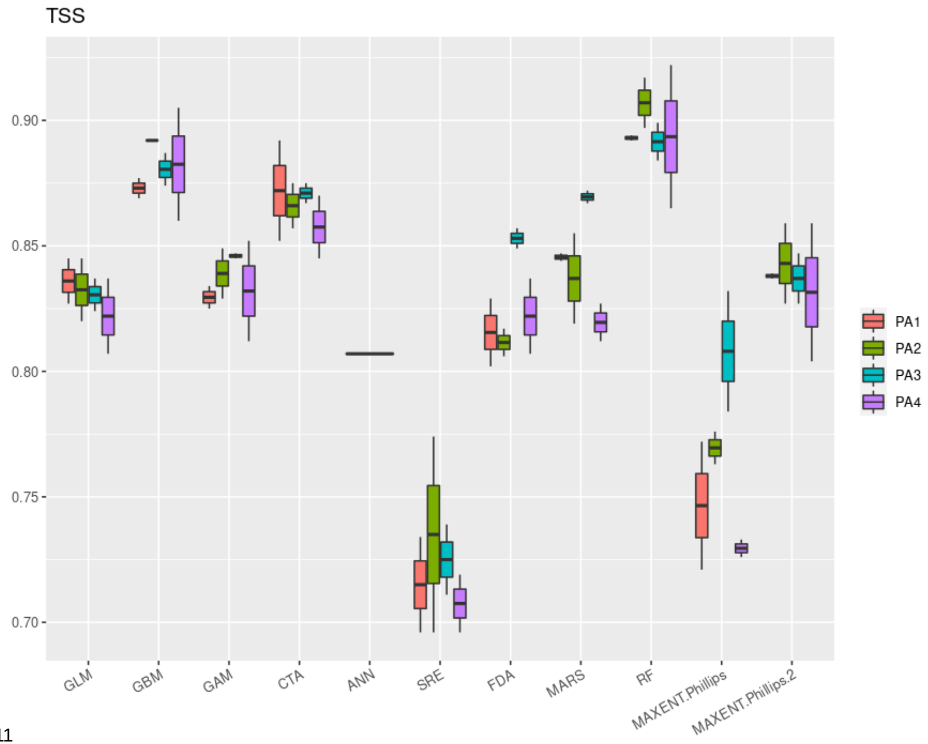


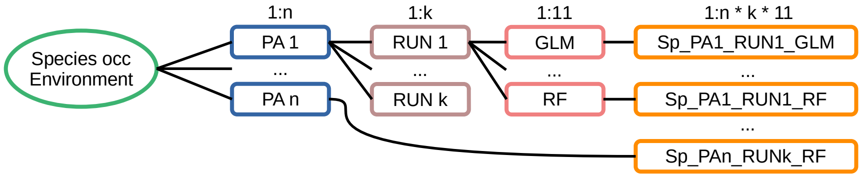
3.a Exploring single models

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



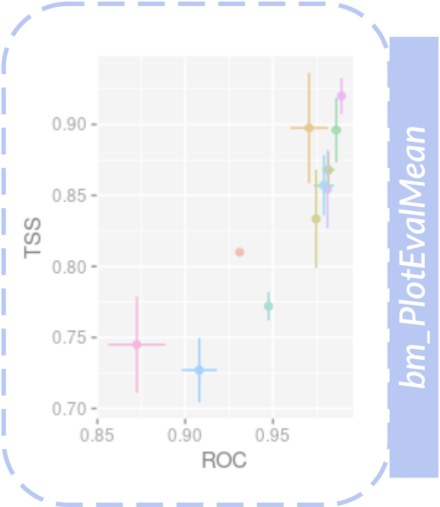


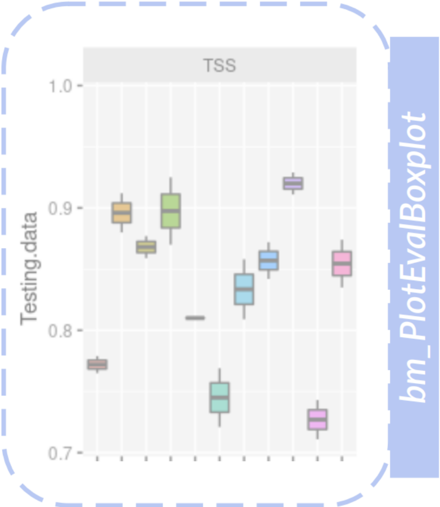


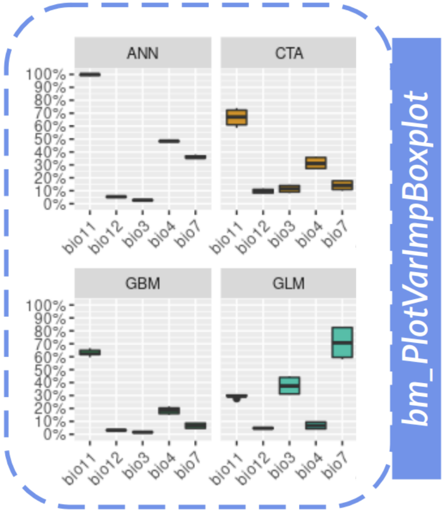


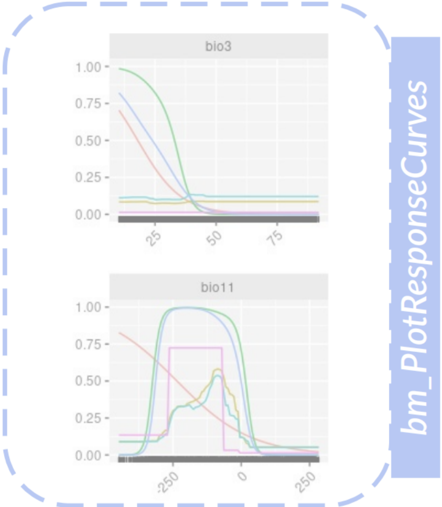
3.a Exploring single models

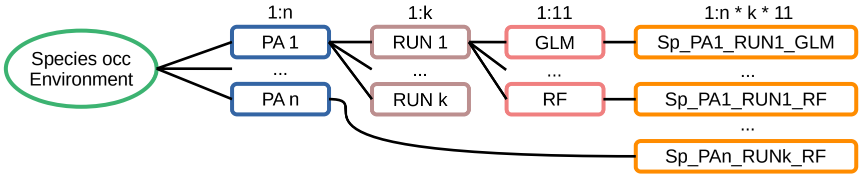
- compare importance of variables between models
- visualize the consistency between models
  (*and different types of models*)





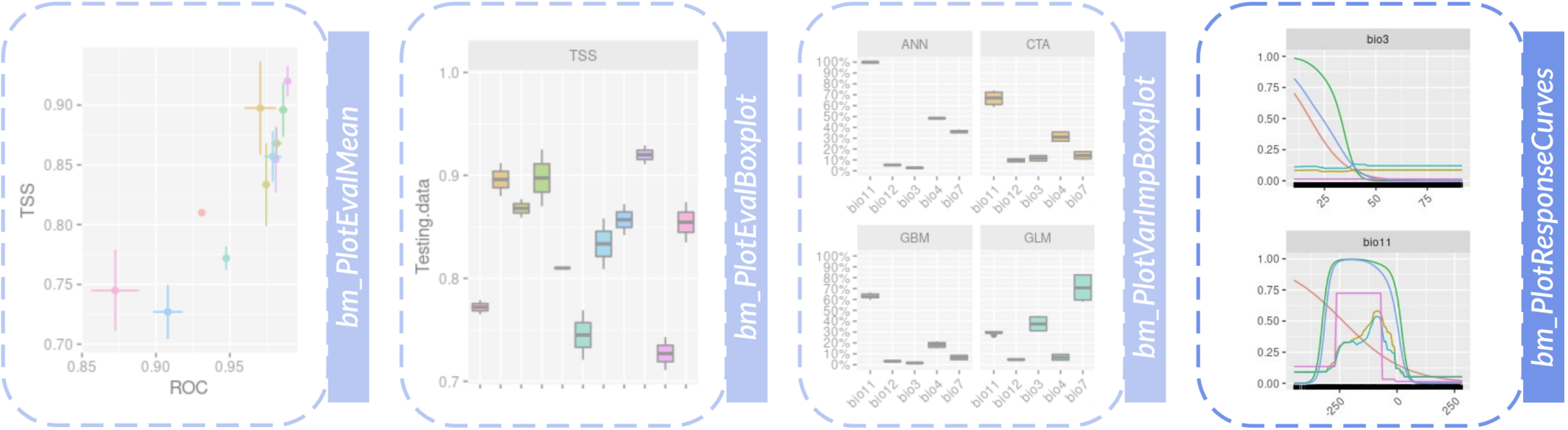


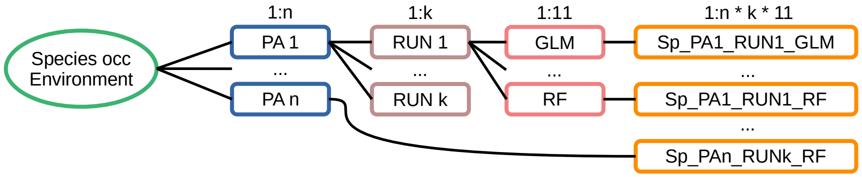




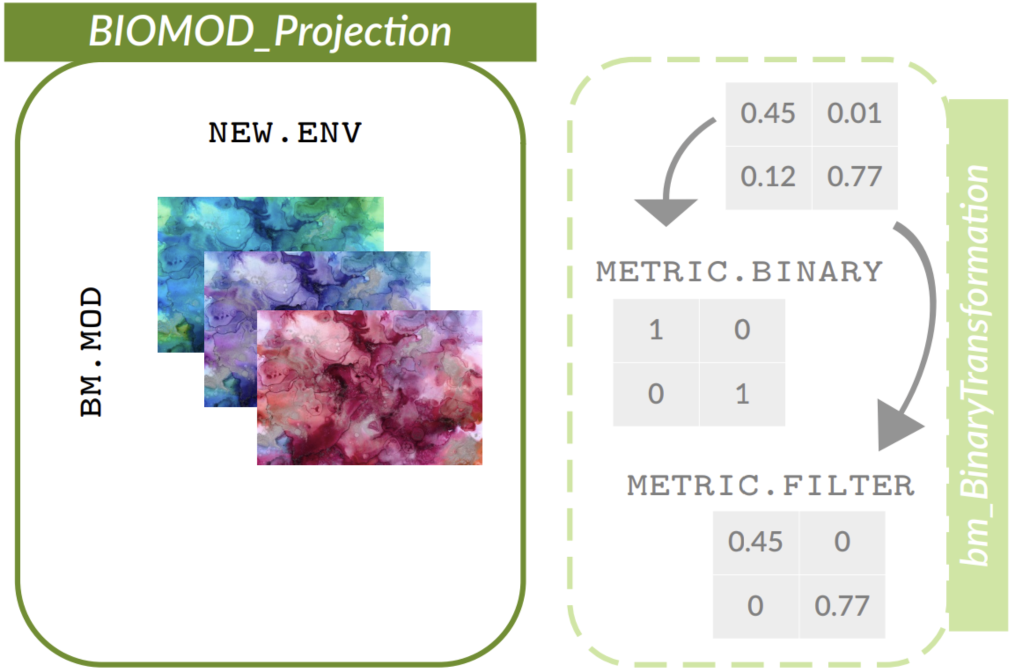
3.a Exploring single models

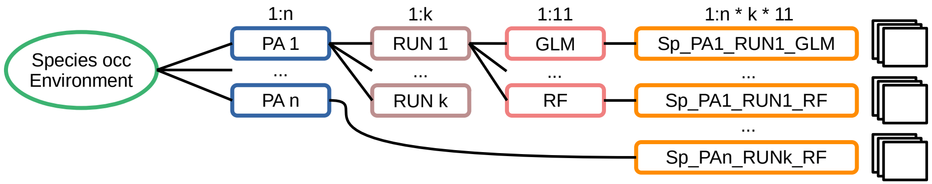
- better understand the effect of each variable along its gradient onto the probability of presence
- visualize the consistency between models (*and different types of models*)





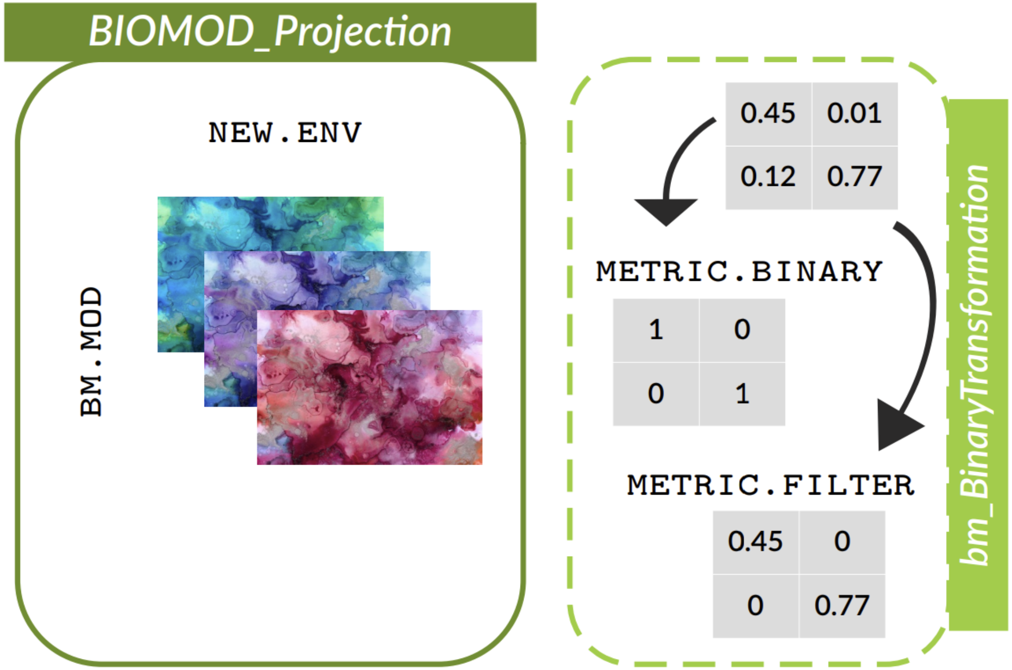
4.a Projecting single models

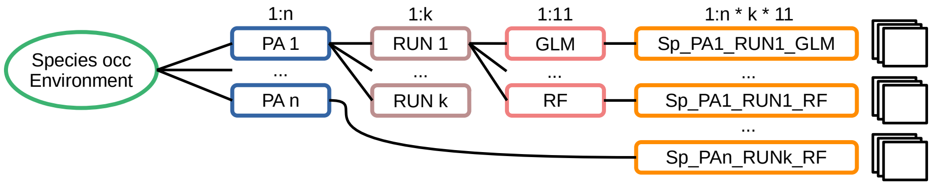




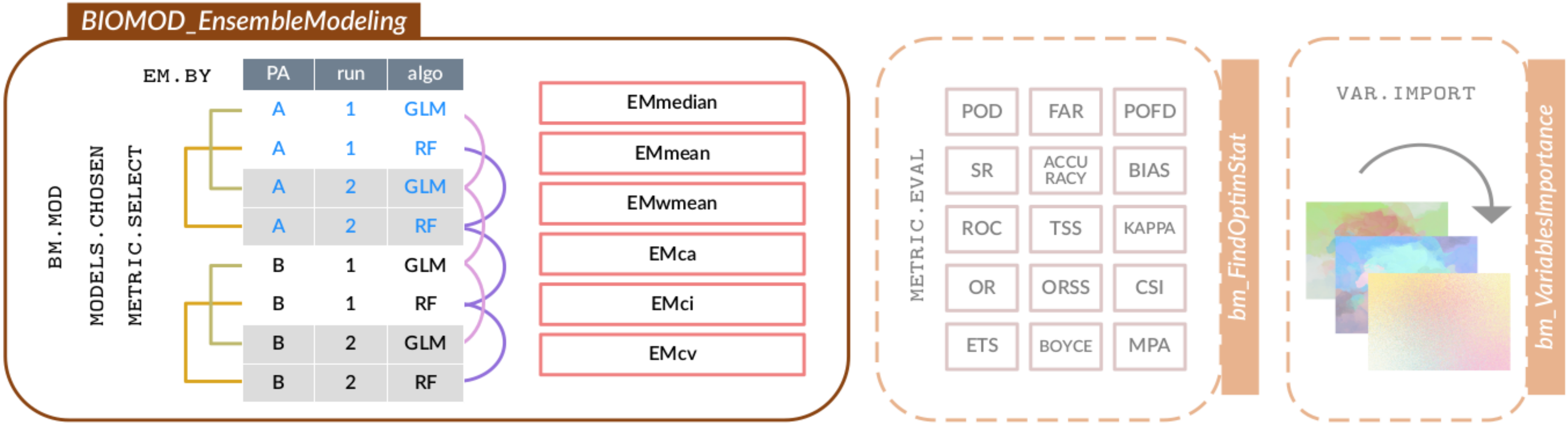
4.a Projecting single models

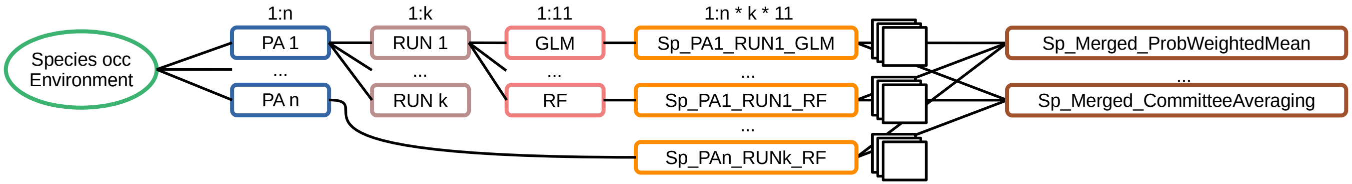
- transformation associated to one evaluation metric (*one map created for each metric selected*)
- use the threshold maximising the chosen metric





2.b Ensemble models

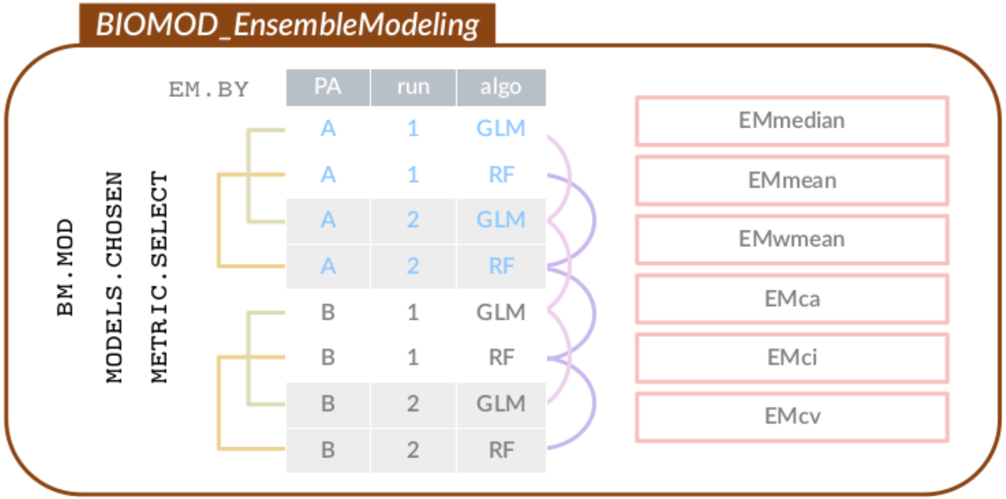


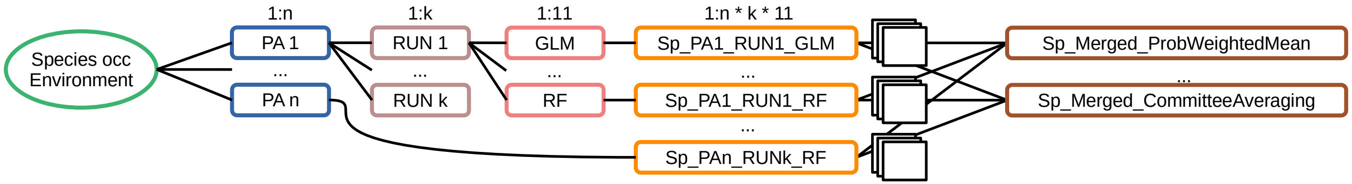


2.b Ensemble models

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

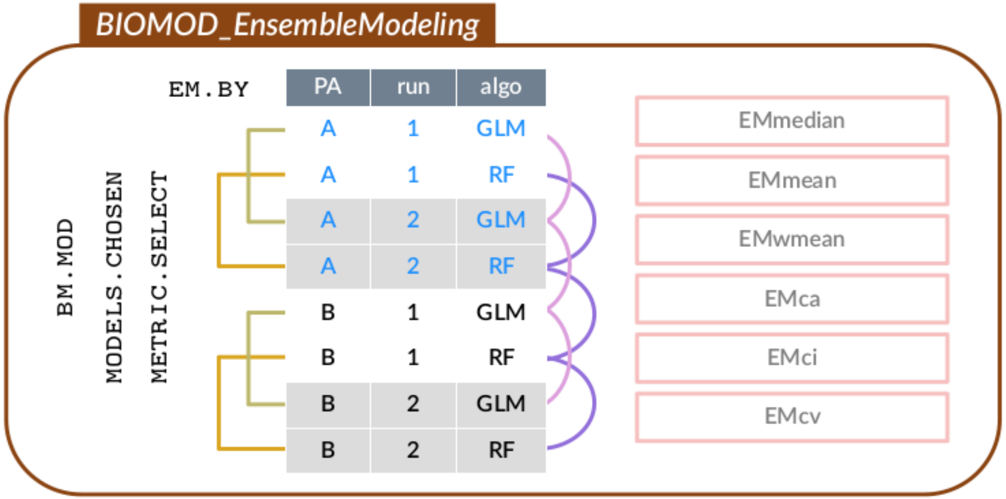




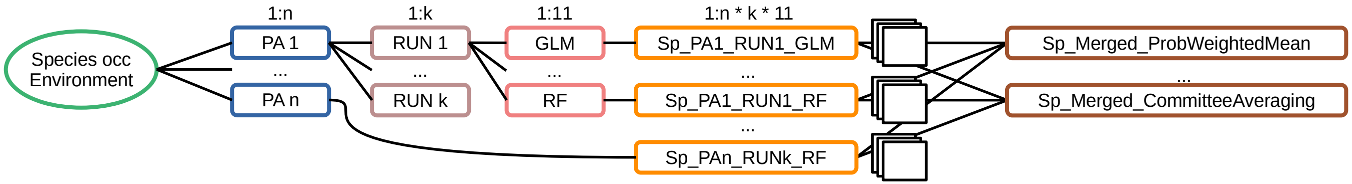
2.b Ensemble models

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



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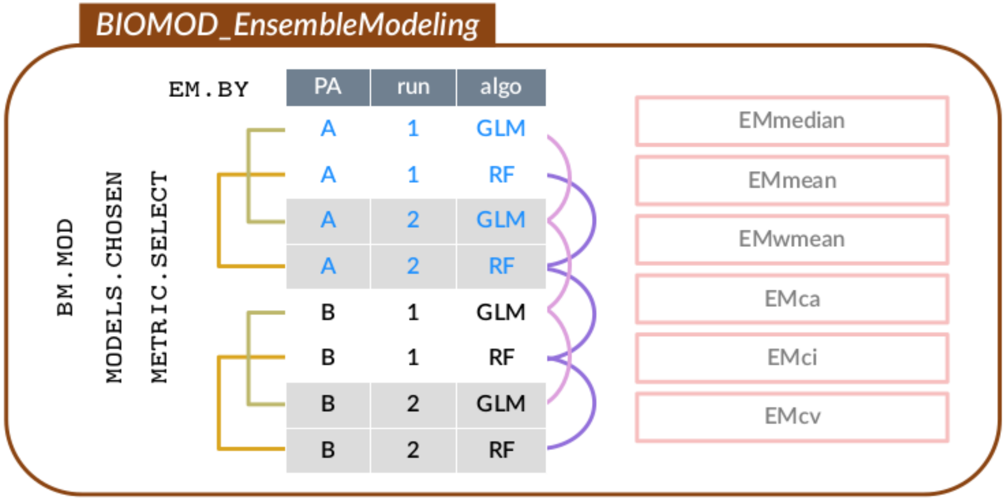
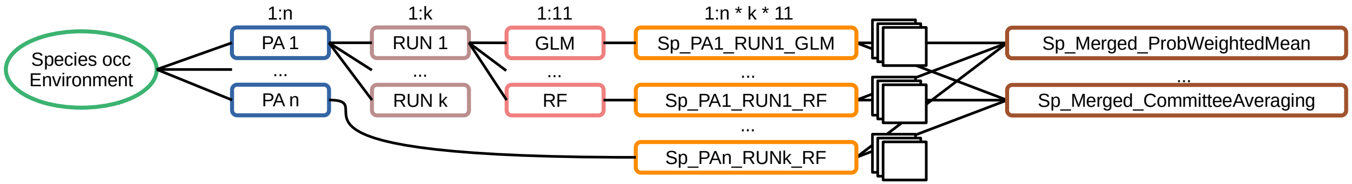


PA1_RUN1_GLM	PA1_RUN1_RF
PA1_RUN2_GLM	PA1_RUN2_RF
PA1_RUN3_GLM	PA1_RUN3_RF
PA2_RUN1_GLM	PA2_RUN1_RF
PA2_RUN2_GLM	PA2_RUN2_RF
PA2_RUN3_GLM	PA2_RUN3_RF

All models



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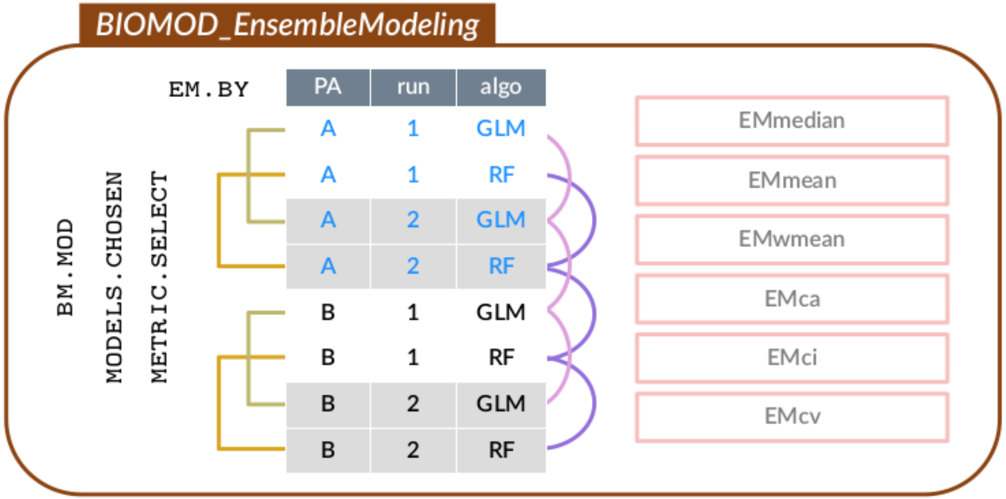

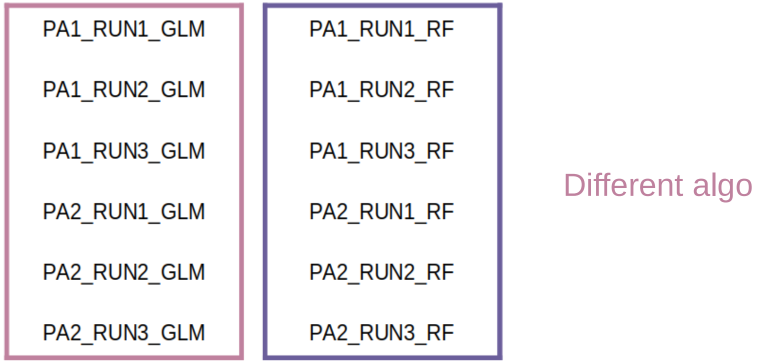

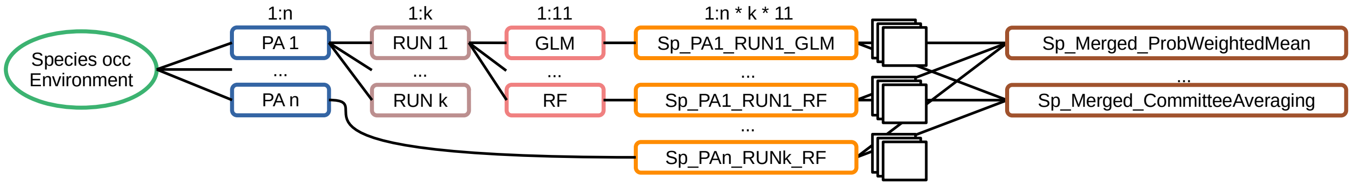

2.b Ensemble models

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Step 2 : gather single models

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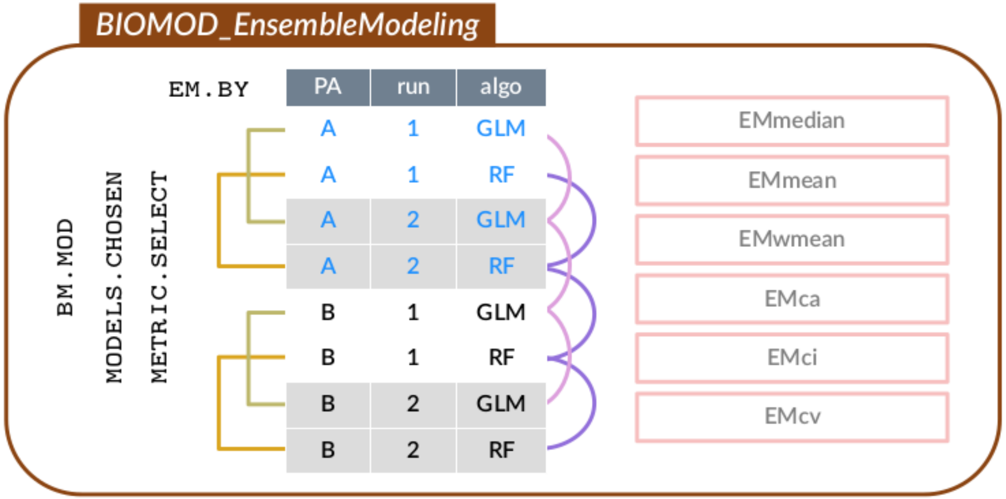

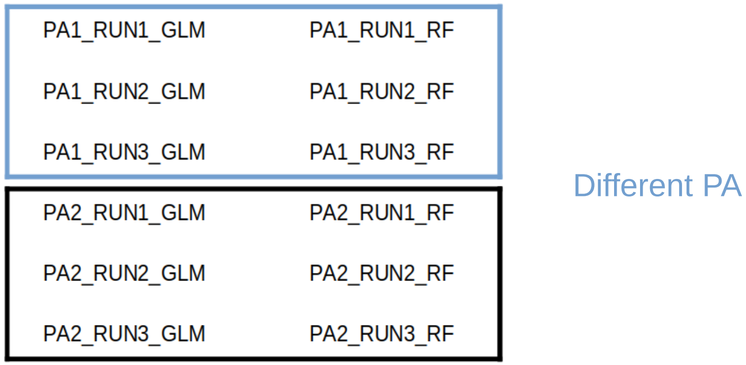

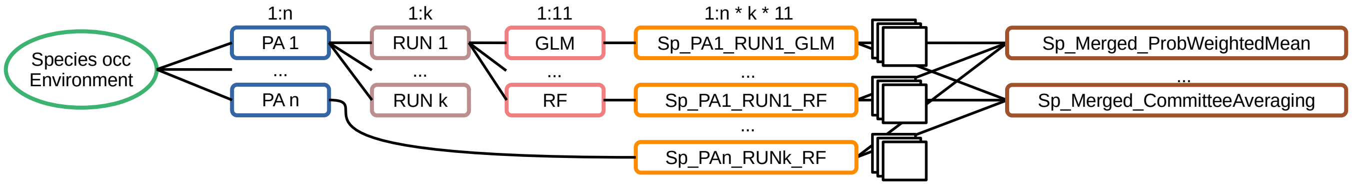

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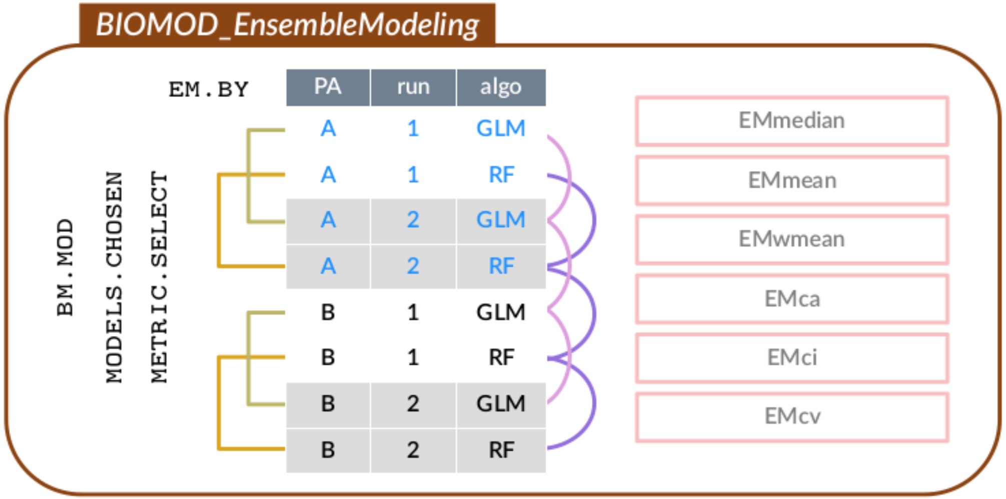
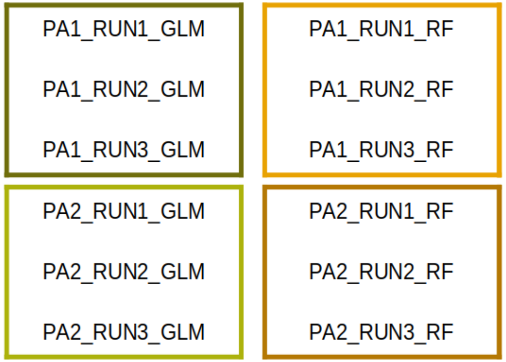
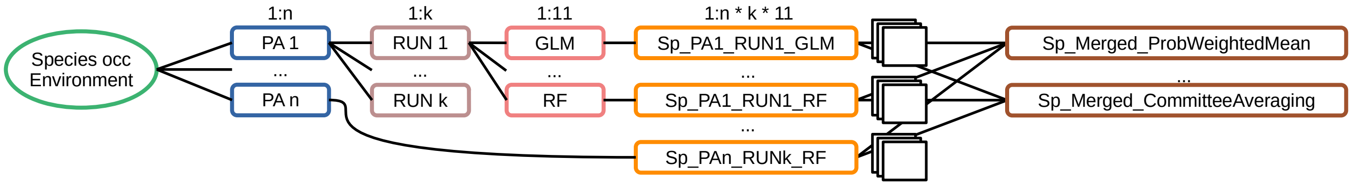




Different PA and algo



2.b Ensemble models

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Step 2 : gather single models

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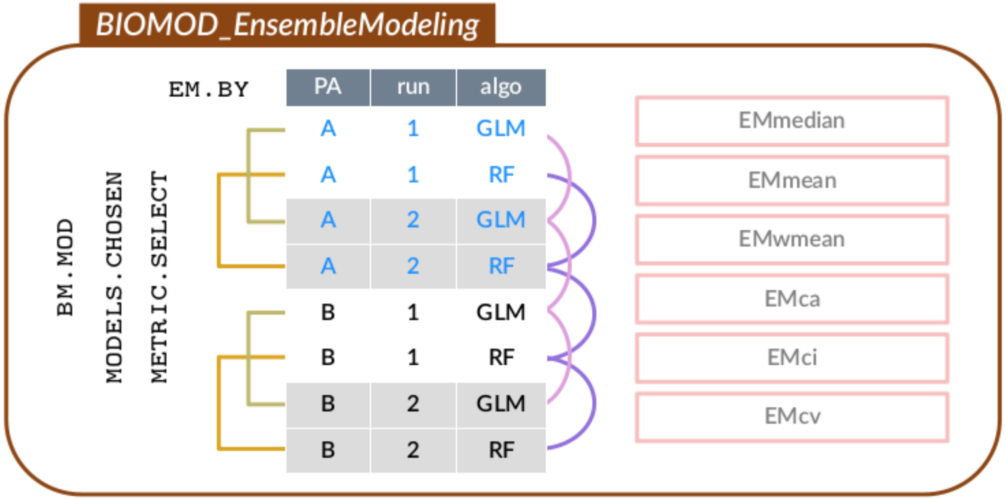
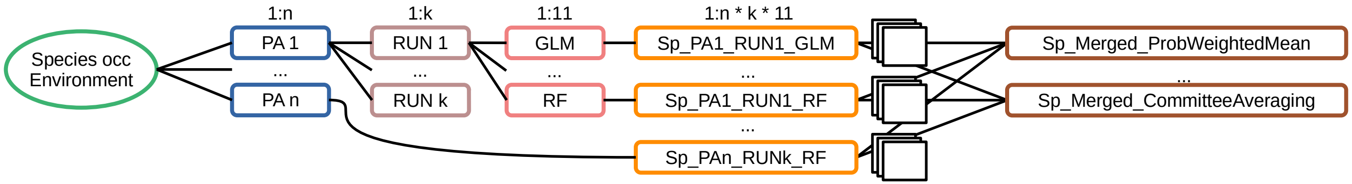
  - *PA+run*



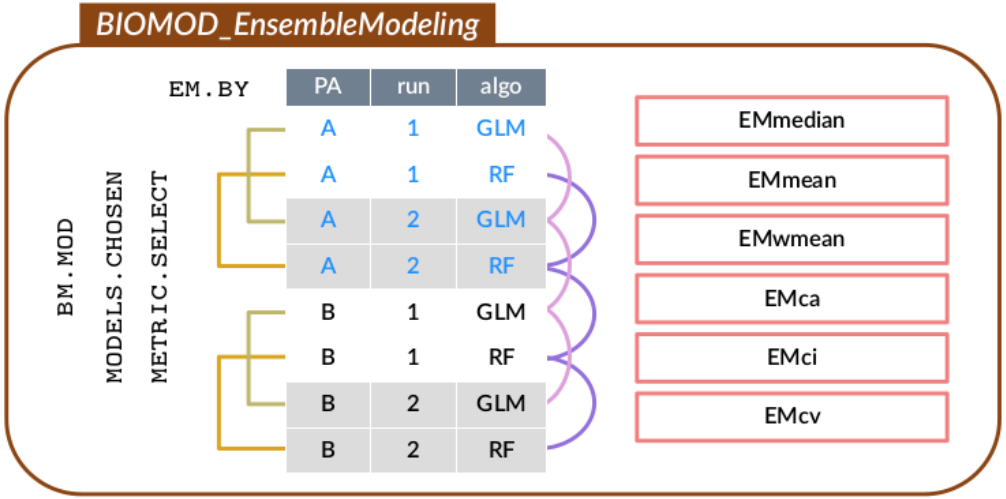
Different PA and run

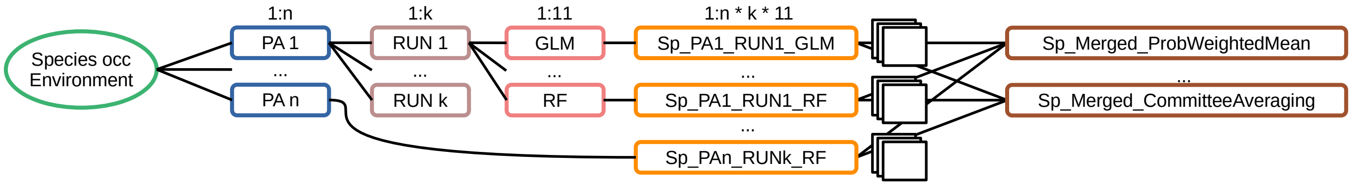


2.b Ensemble models

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

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

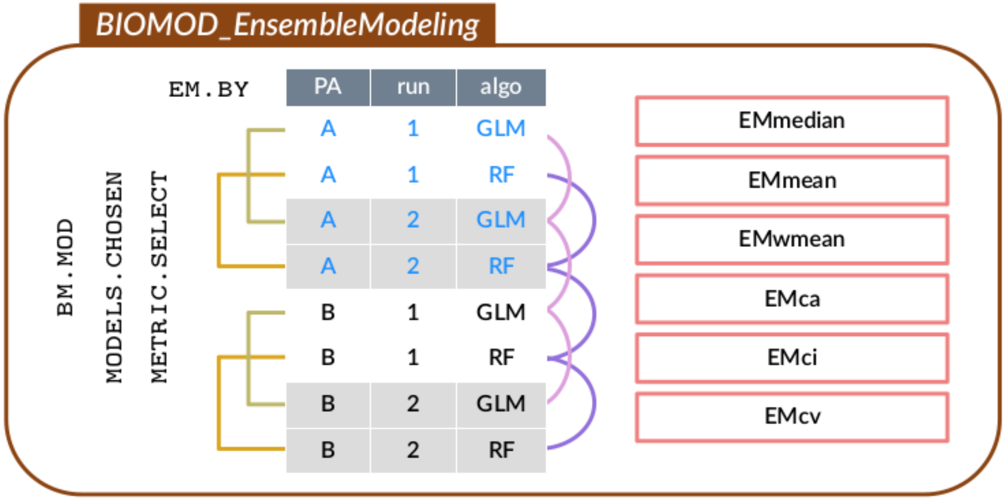


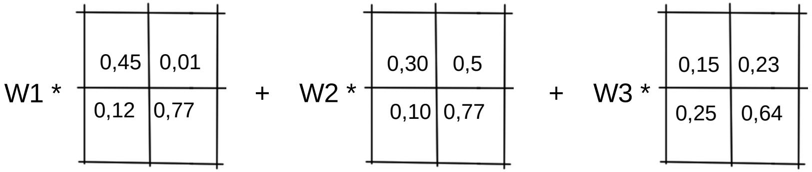


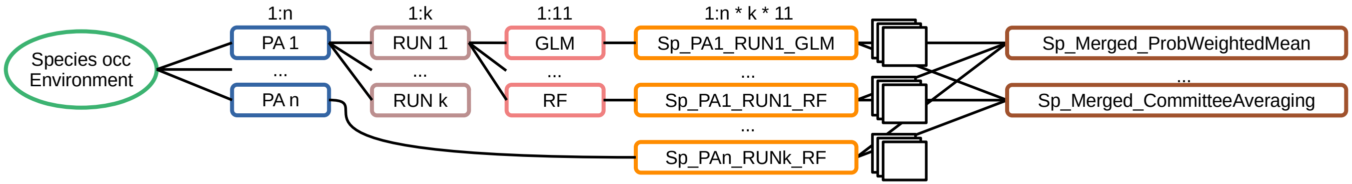
2.b Ensemble models

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**



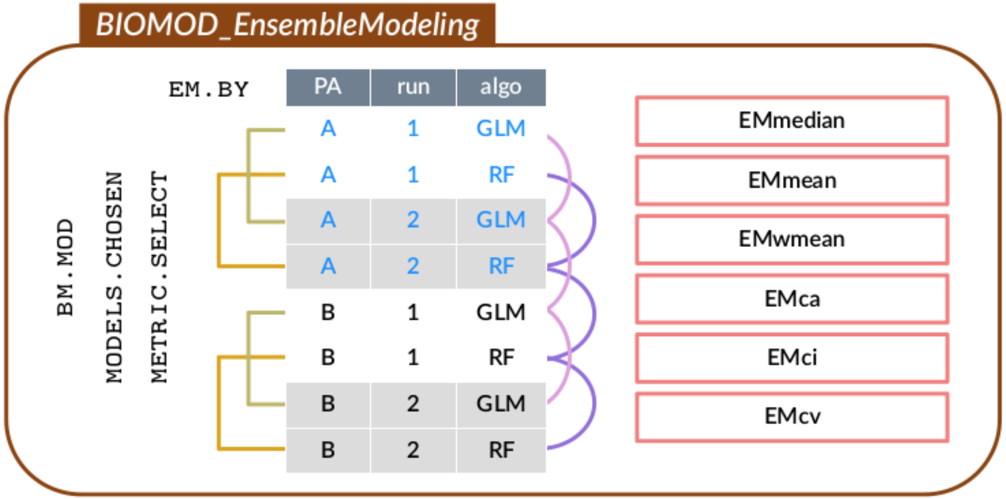


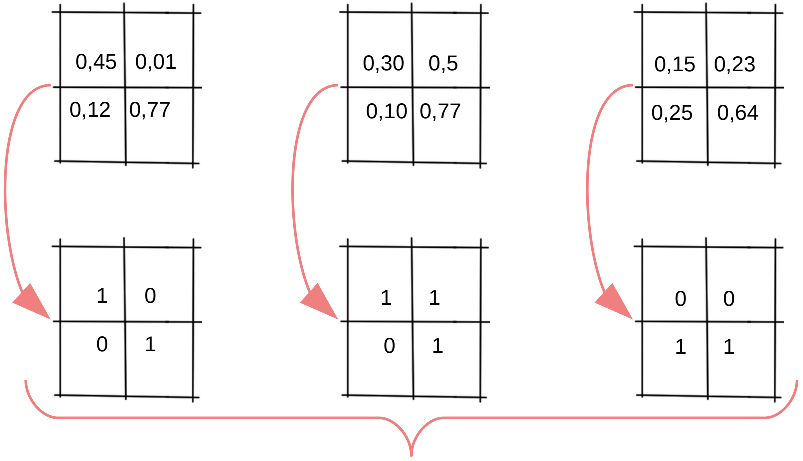


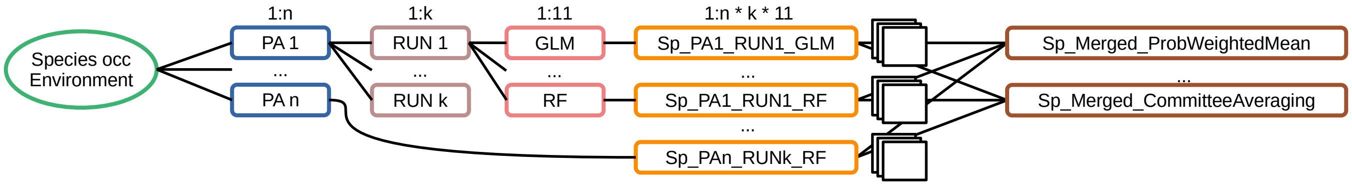
2.b Ensemble models

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**

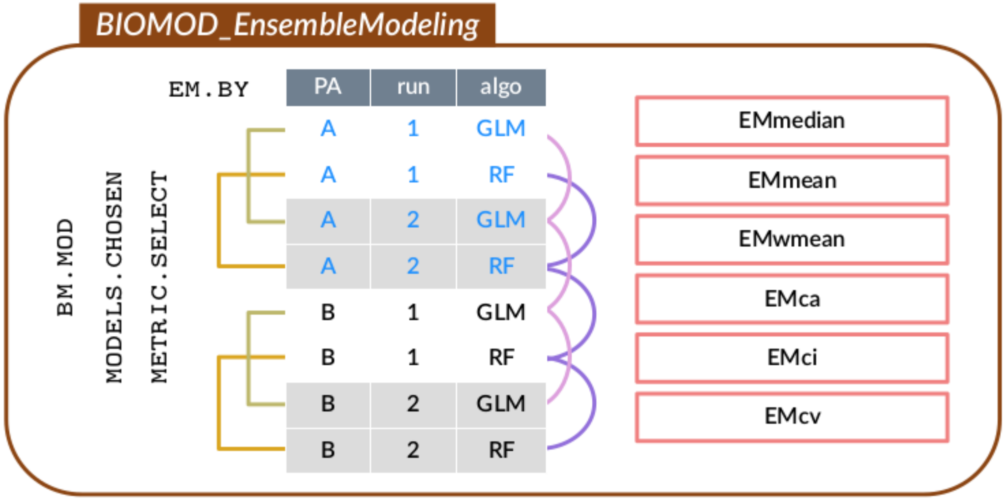




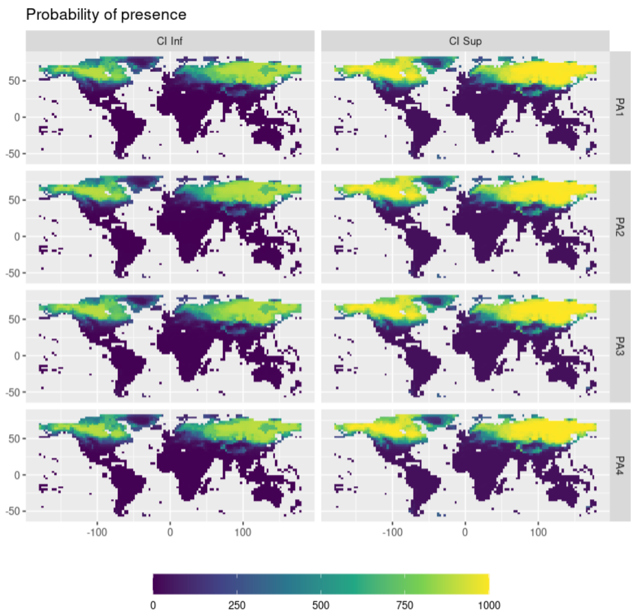


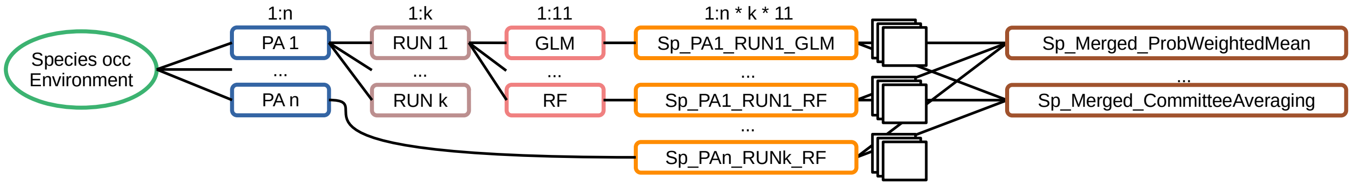
2.b Ensemble models

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**





2.b Ensemble models

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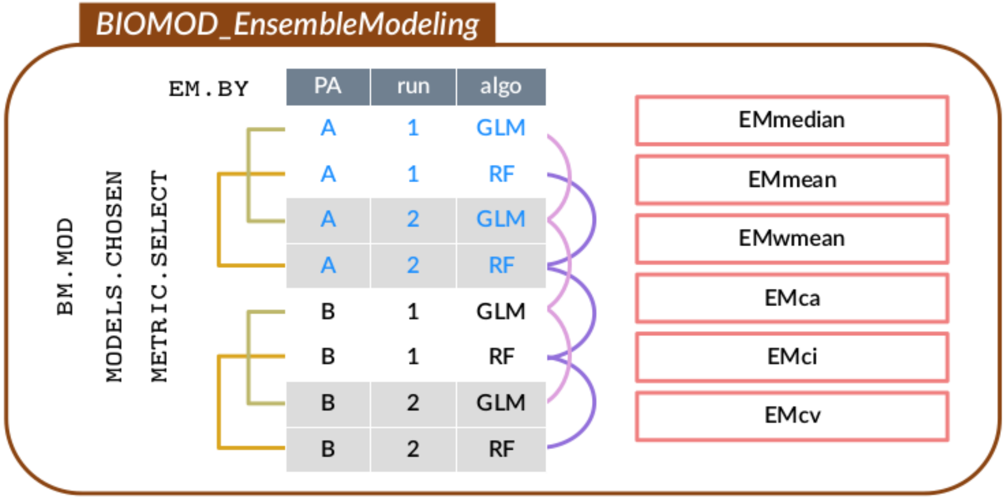
Step 3 : build ensemble models



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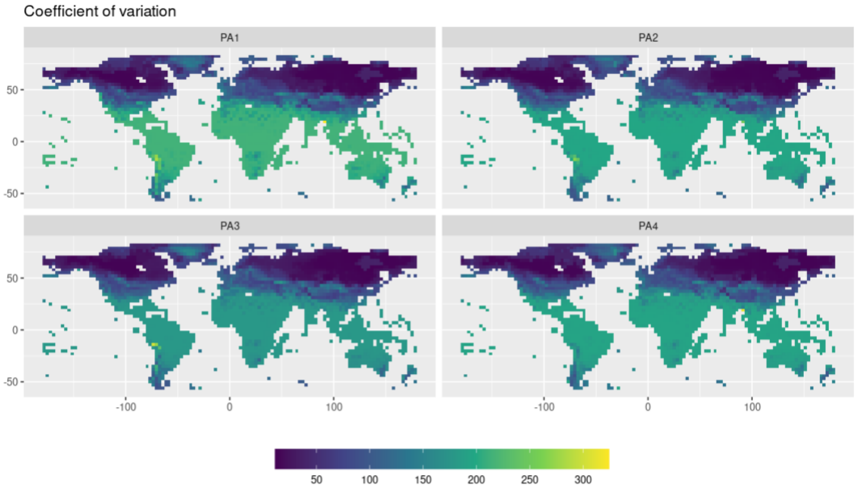
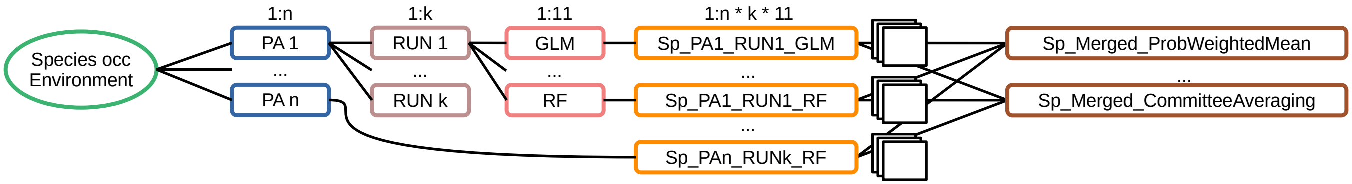
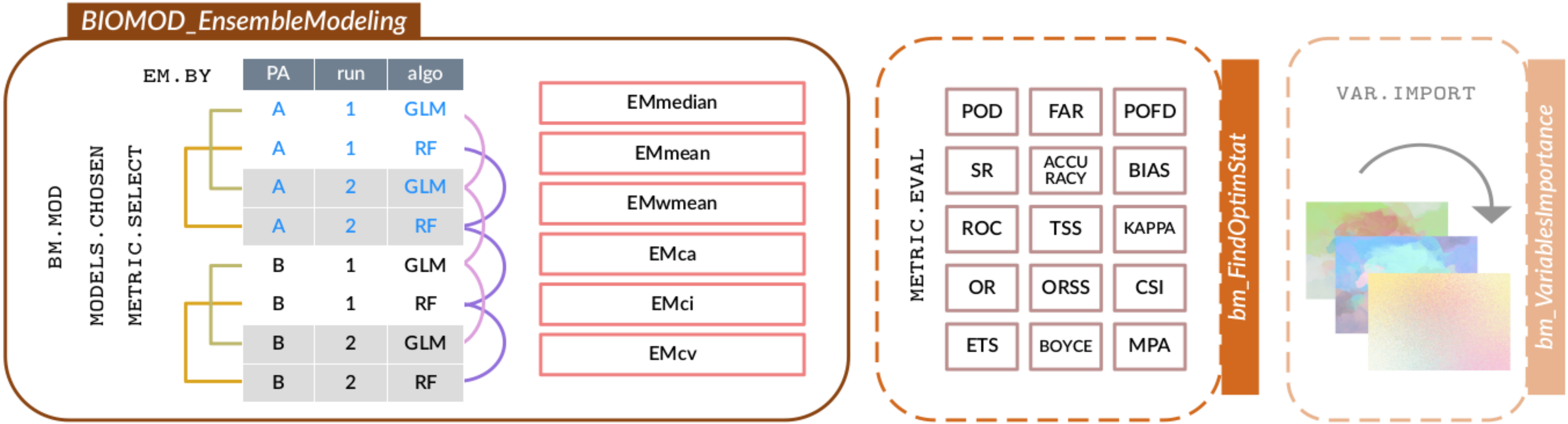
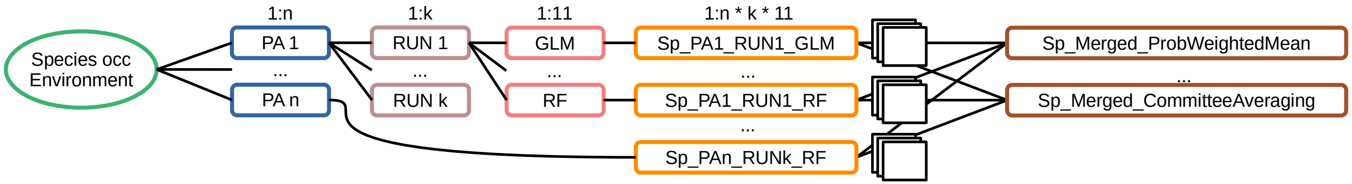




2.b Ensemble models

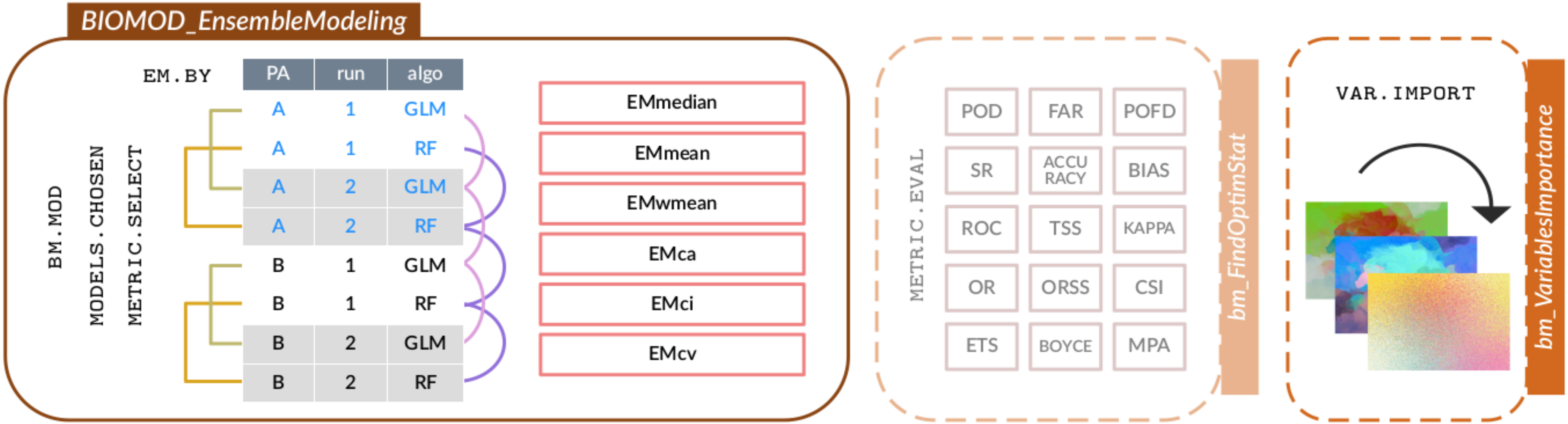
- except ROC, all evaluation metrics obtained from contingency table (*containing TP, FP, TN, FN*)
- require a **binary transformation** :
  - range of thresholds tested
  - keep thresold optimising the evaluation metric





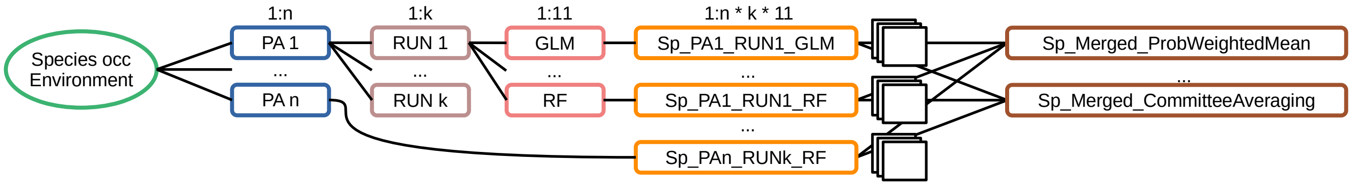
2.b Ensemble models

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

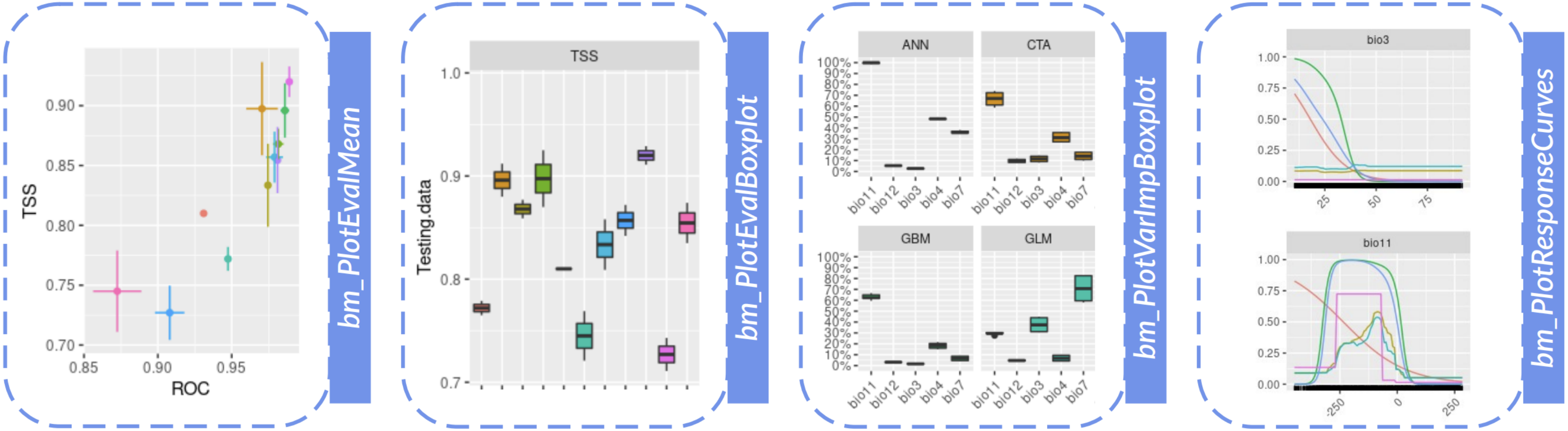


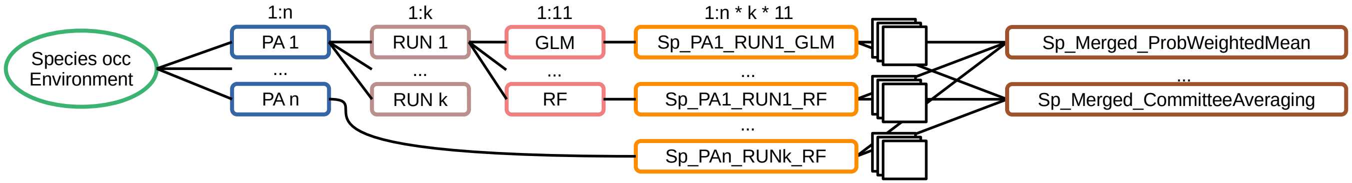
IMPORTANT

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

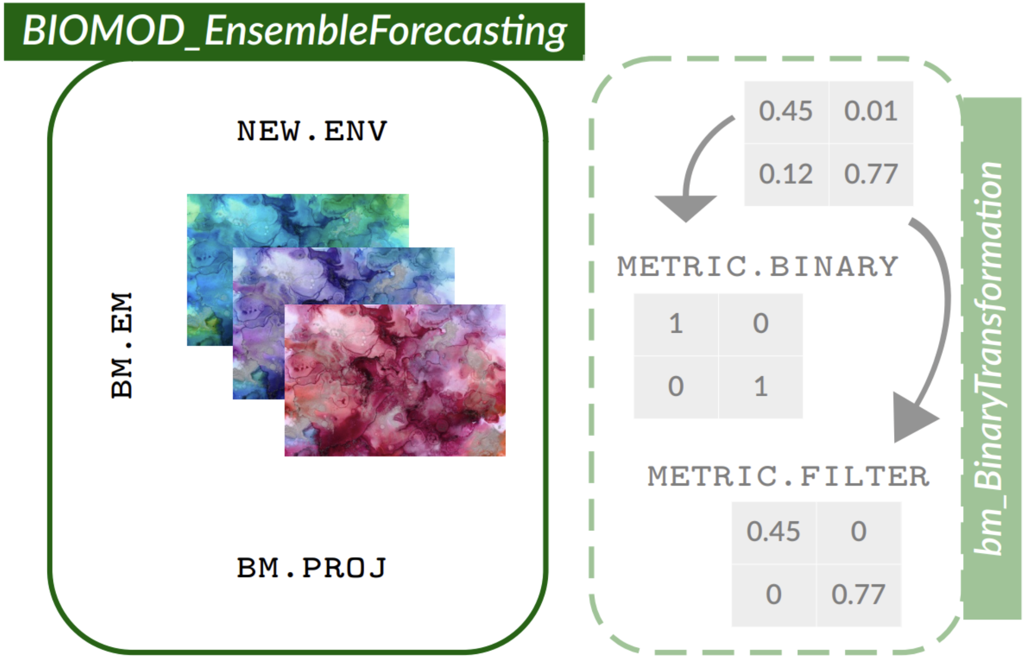


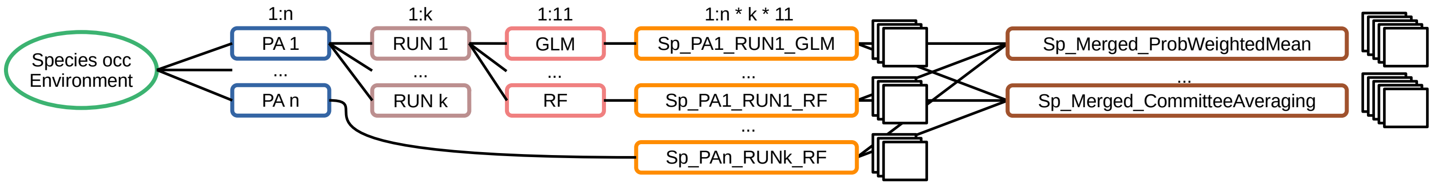
3.b Exploring ensemble models





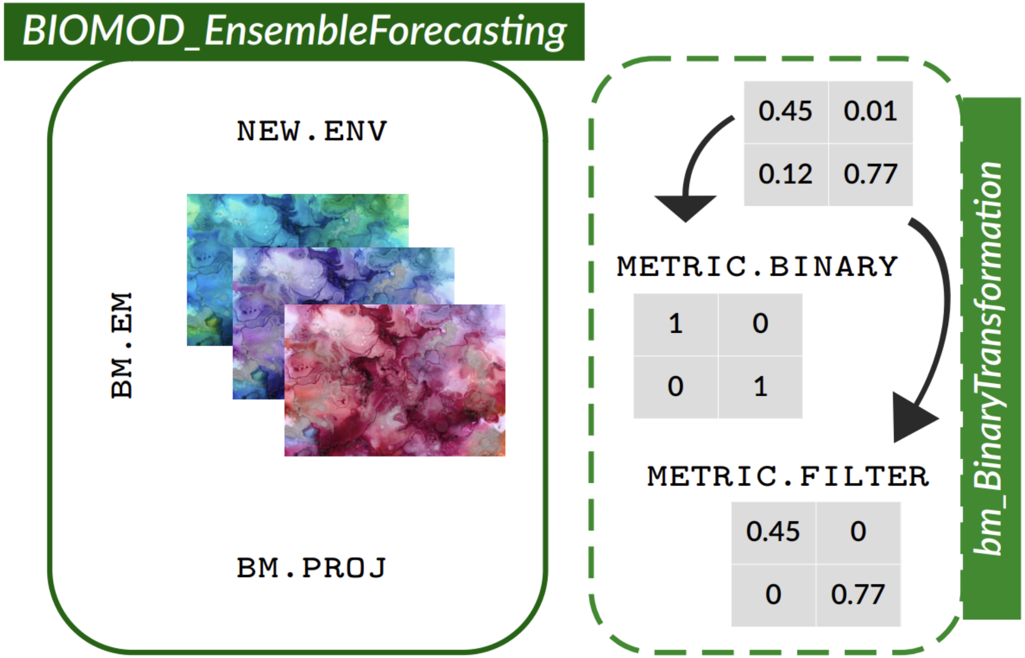
4.b Projecting ensemble models

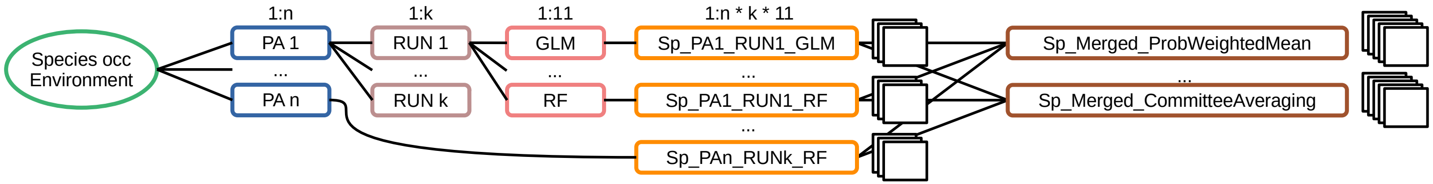




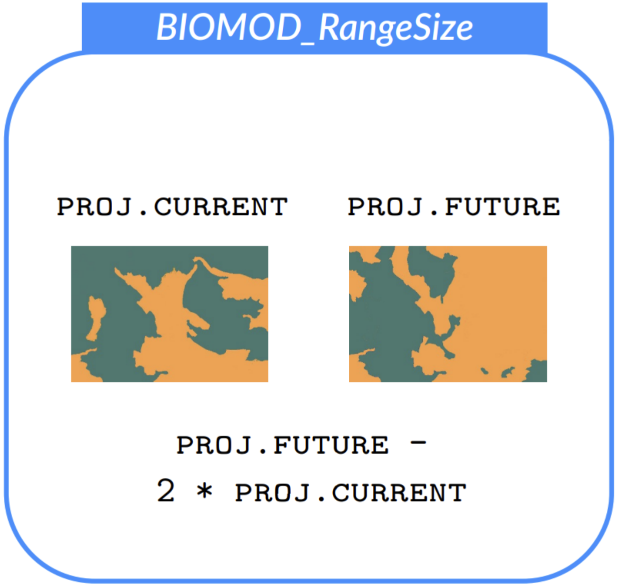
4.b Projecting ensemble models

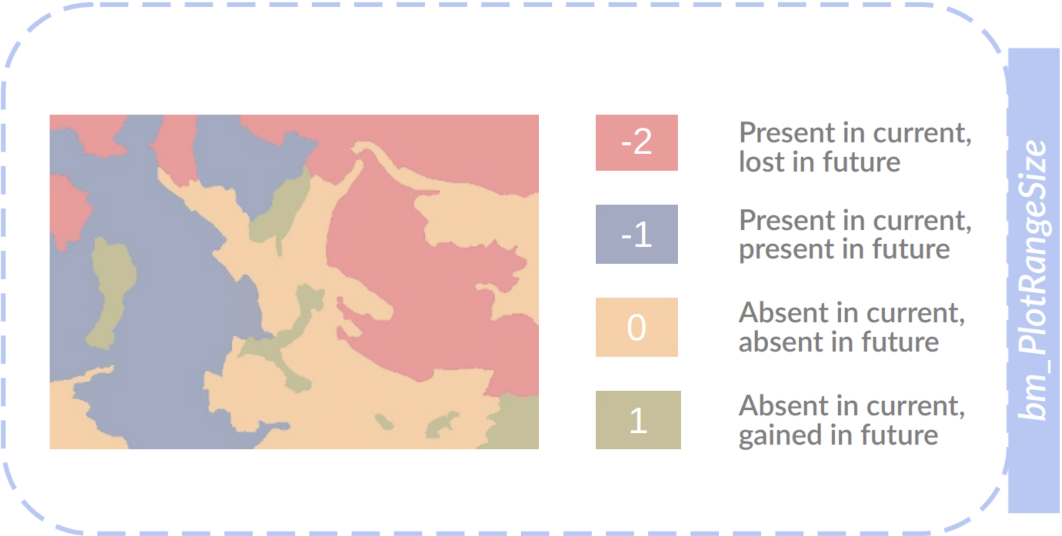
- transformation associated to one evaluation metric (*one map created for each metric selected*)
- use the threshold maximising the chosen metric

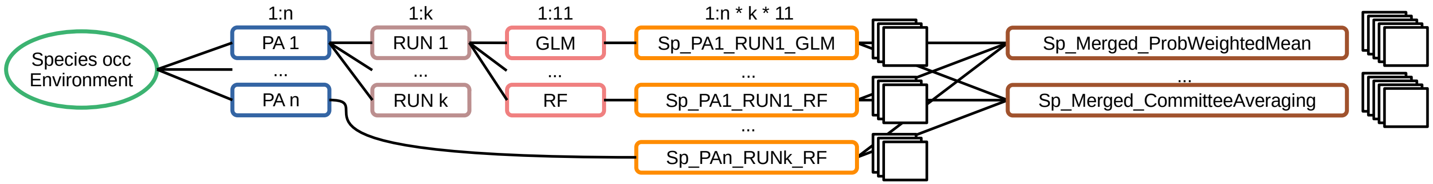




5. Species range change

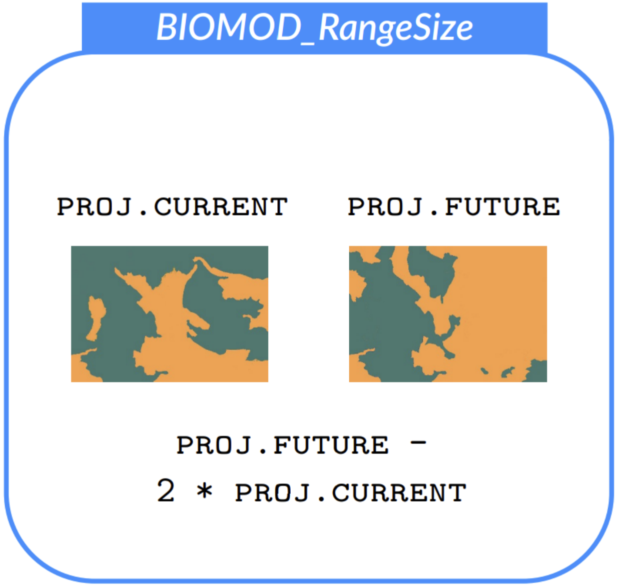


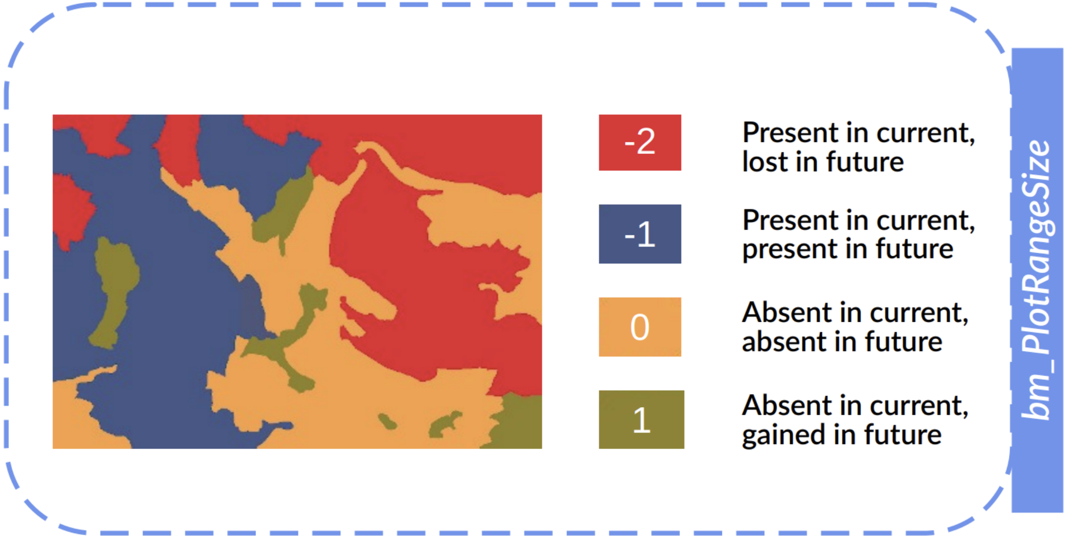


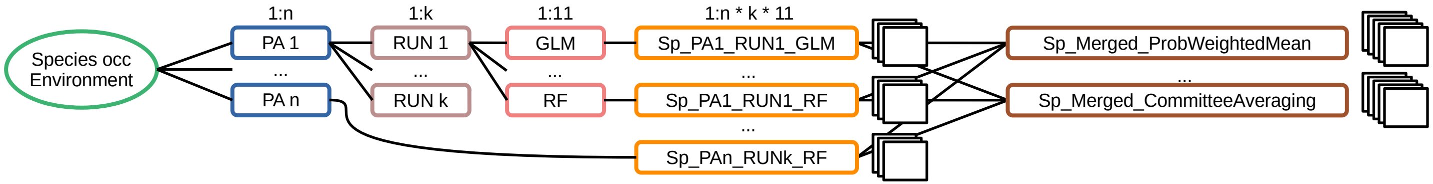


5. Species range change

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







5. Species range change

- explore **spatially** the difference in predictions
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  - species range change

BIOMOD_RangeSize

PROJ.CURRENT

PROJ.FUTURE

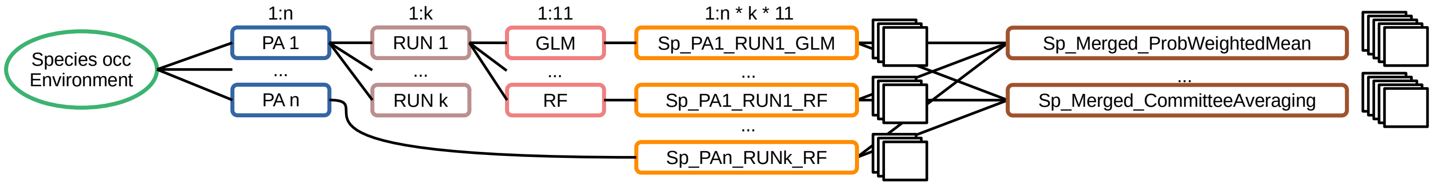
PROJ.FUTURE - 2 * PROJ.CURRENT

-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

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/

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