

Exploring the role of microbiota on phenotype expression under different biological assumptions

E. Mancin, C. Maltecca, F. Tiezzi

EAAP 2024, Firenze

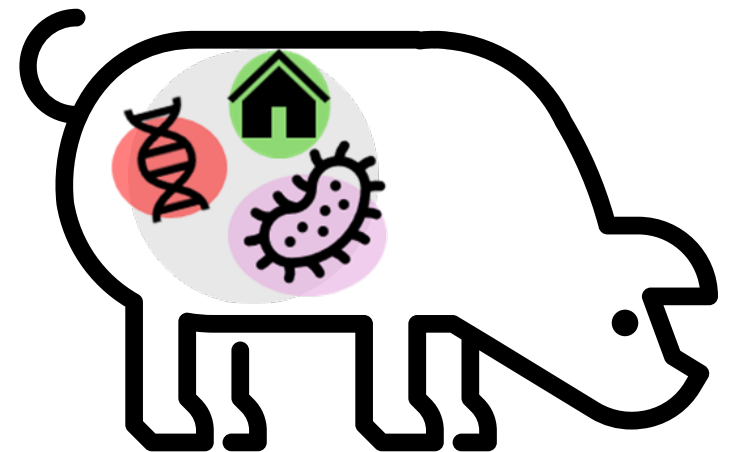
Tuesday 3 September 2024

Session 55. Host physiology/genetics and microbiome interactions – The holobiont concept

Why this study ?

Biological contribution of Microbiota on Phenotype

How can be use Microbiota in a prediction setting ?.. In pigs



In Particular ...

Weishaar et al., 2020; Christensen et al., 2021

led to prediction of BV (not of phenotypes) using intermediate data

They presented a method for EBV prediction based on 2 successive mixed model equations:

$$y = X\beta + \underbrace{Z\mu}_{\text{as pseudo-phenotype}} + (W\alpha) + e$$

$$\underbrace{\hat{\mu}} = X\beta_m + W\alpha_m + e_m$$

$$\hat{bv} = (W\alpha) + W\alpha_m$$

G	=	$W\alpha$
M	=	$Z\mu$
E	=	$X\beta$

Weishaar et al., 2020

$$y = X\beta + Z\mu + e \quad (1)$$

$$\hat{u} = X\beta_m + W\alpha_m + e_m \quad (2)$$

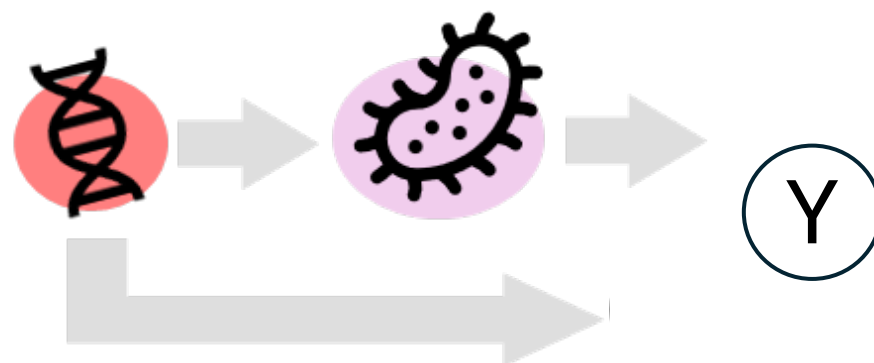


$$\hat{bv} = W\alpha_m$$

Christensen et al., 2021

$$y = X\beta + Z\mu + W\alpha + e \quad (1)$$

$$\hat{u} = X\beta_m + W\alpha_m + e_m \quad (2)$$



$$\hat{bv} = W\alpha + W\alpha_m$$

What we did

Regular Model

$$y_{corr} = y - X\beta$$

GB Model:

$$y = W\alpha + e$$

$$\text{Prediction: } \hat{y} = W\alpha$$

BASELINE

G

MB Model:

$$y = Z\mu + e$$

$$\text{Prediction: } \hat{y} = Z\mu$$

M

GMB Model:

$$y = W\alpha + Z\mu + e$$

$$\text{Prediction: } \hat{y} = Z\mu + W\alpha$$

G

M

Weishaar *et al.*, 2021 (alternative to MB):

$$y = W\mu + e$$

$$\hat{u} = W\alpha_m + e_m$$

Prediction: $\hat{y} = W\alpha_m$

Respecting MB, we are somehow ignoring e_m because:

Prediction with model MB = $Z\mu = W\alpha_m + e_m$

$$\text{M} = W\alpha_m + e_m$$



Same for GMB

Christensen *et al.*, 2020 (alternative to GMB):

$$y = Z\alpha + W\mu + e$$

$$\hat{u} = W\alpha_m + e_m$$

Prediction: $\hat{y} = W\alpha + W\alpha_m$

goal: Phenotype

**Different prediction
“challenges”**

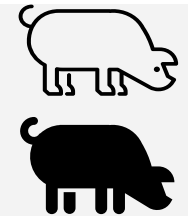
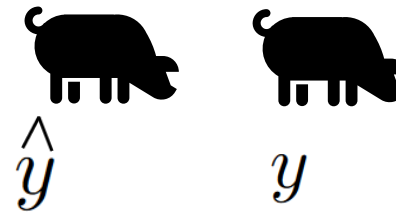
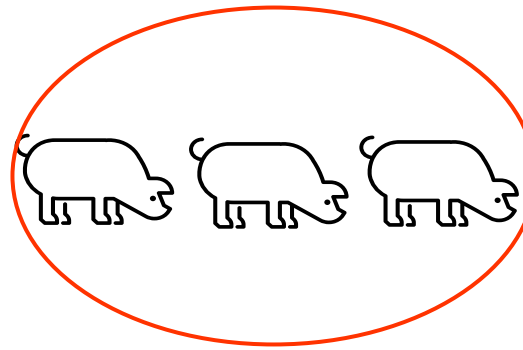
Different target traits

Different target traits

“goals”

ADG
BCKF
IMF

Phenotype:

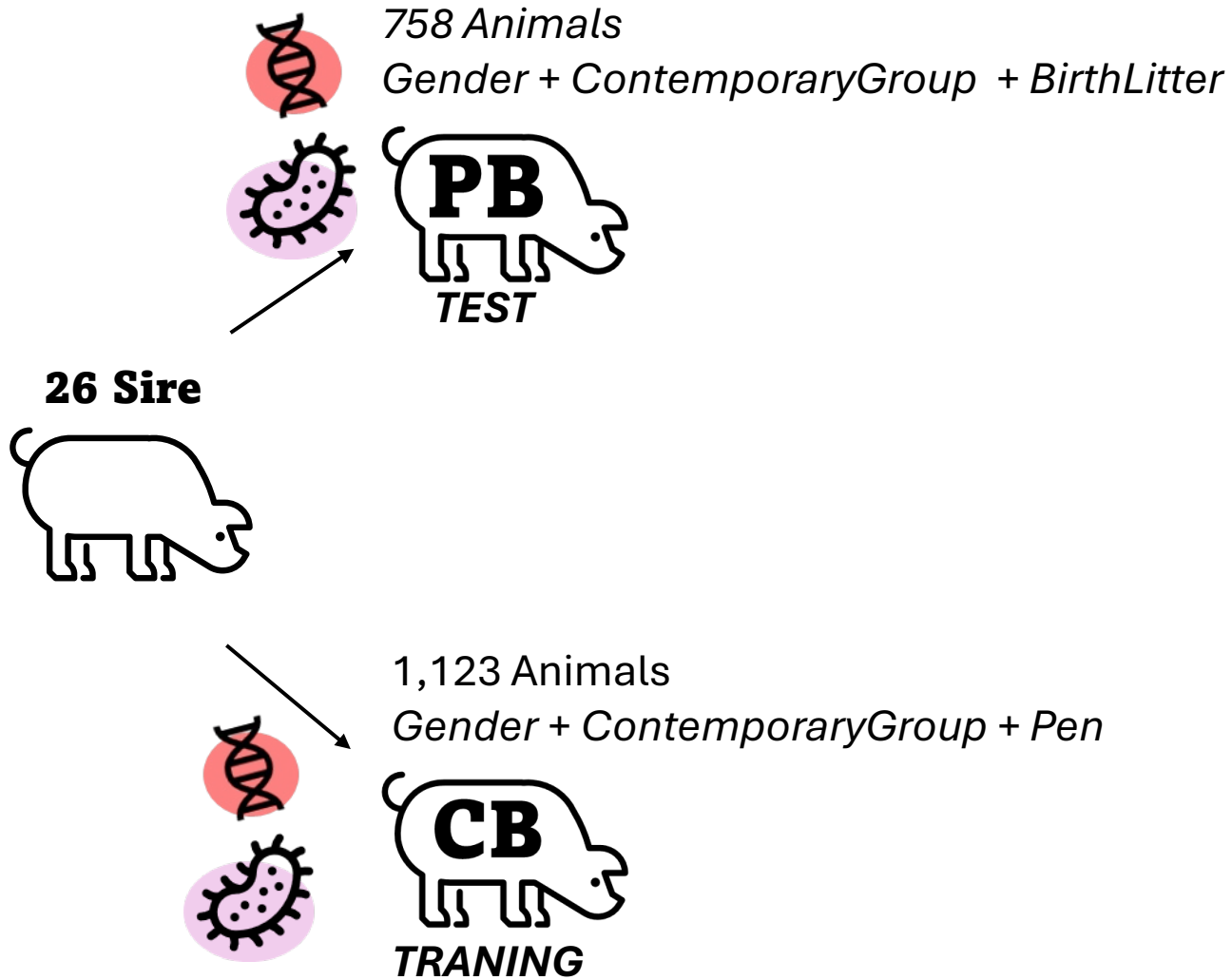


Training

Test

Metrics:
Correlation

DATA STRUCTURE



Different of prediction's "challenge"

1. Within Population

A. SIRE

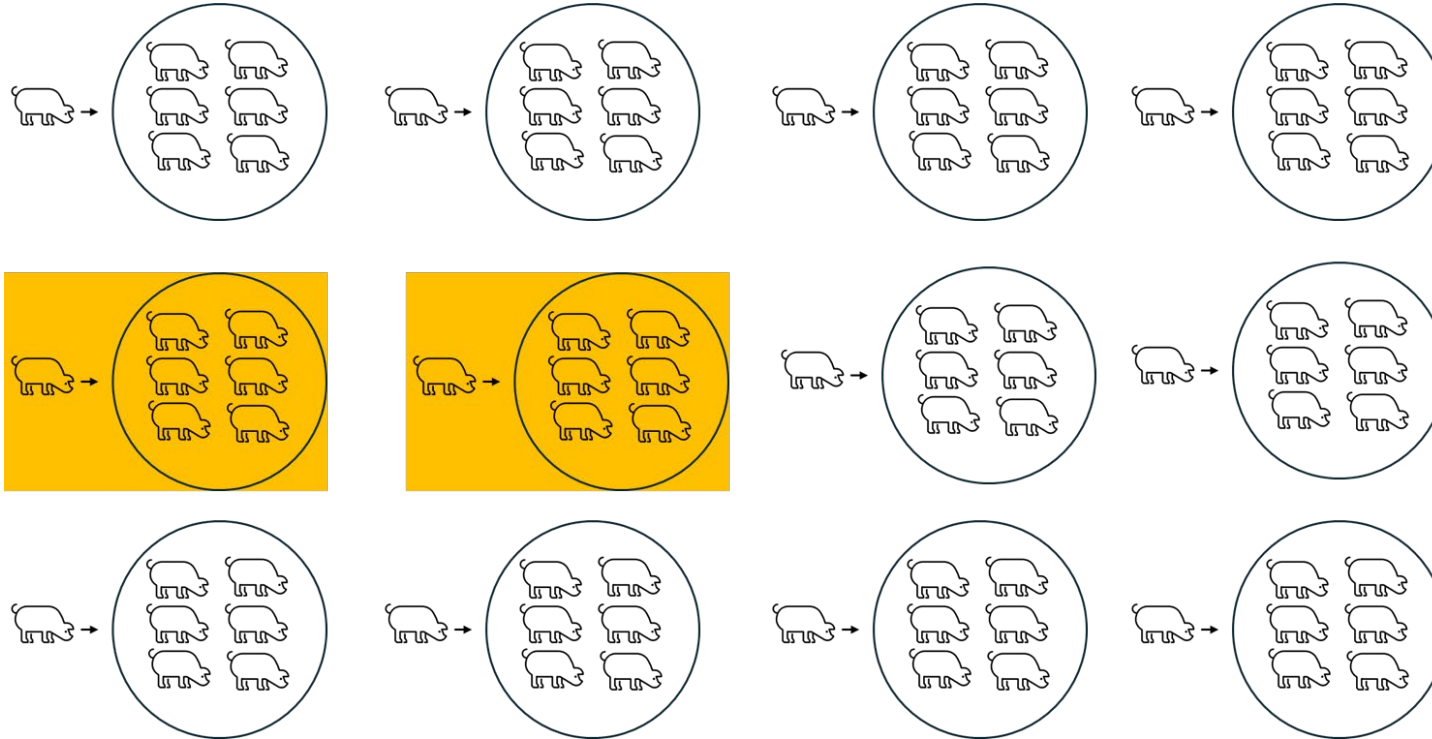
B. RND

2. Between Population

Sire CV x10:

Different of prediction's
“challenge”

1. Within Population

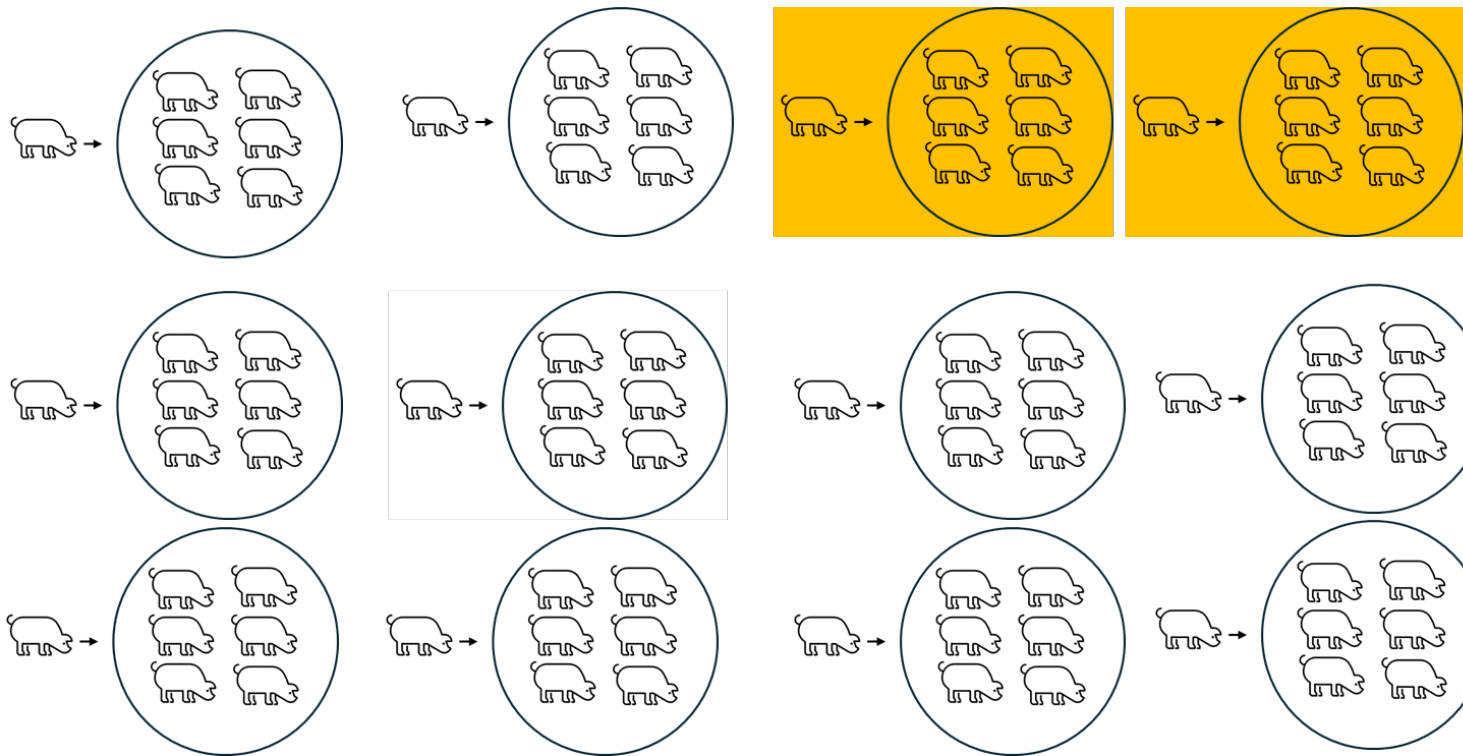


 test
 training

Sire CV x10:

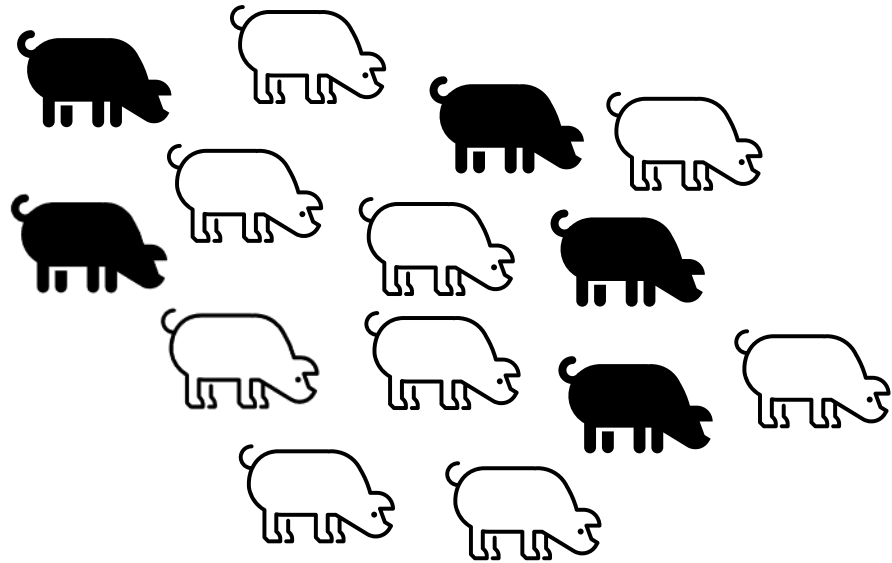
**Different of prediction's
“challenge”**

1. Within Population



 test
 training

RND CV:



**Different of prediction's
“challenge”**

1. Within Population

B.RND

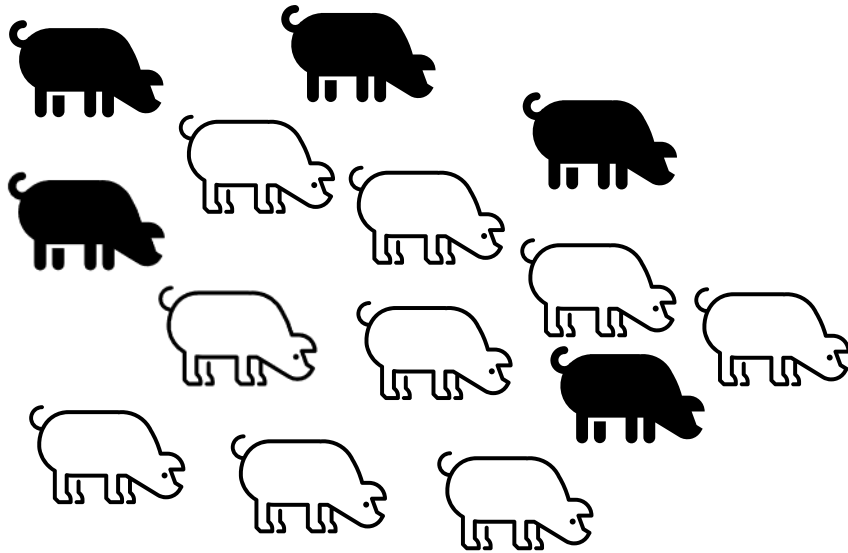


Different of prediction's “challenge”

1. Within Population

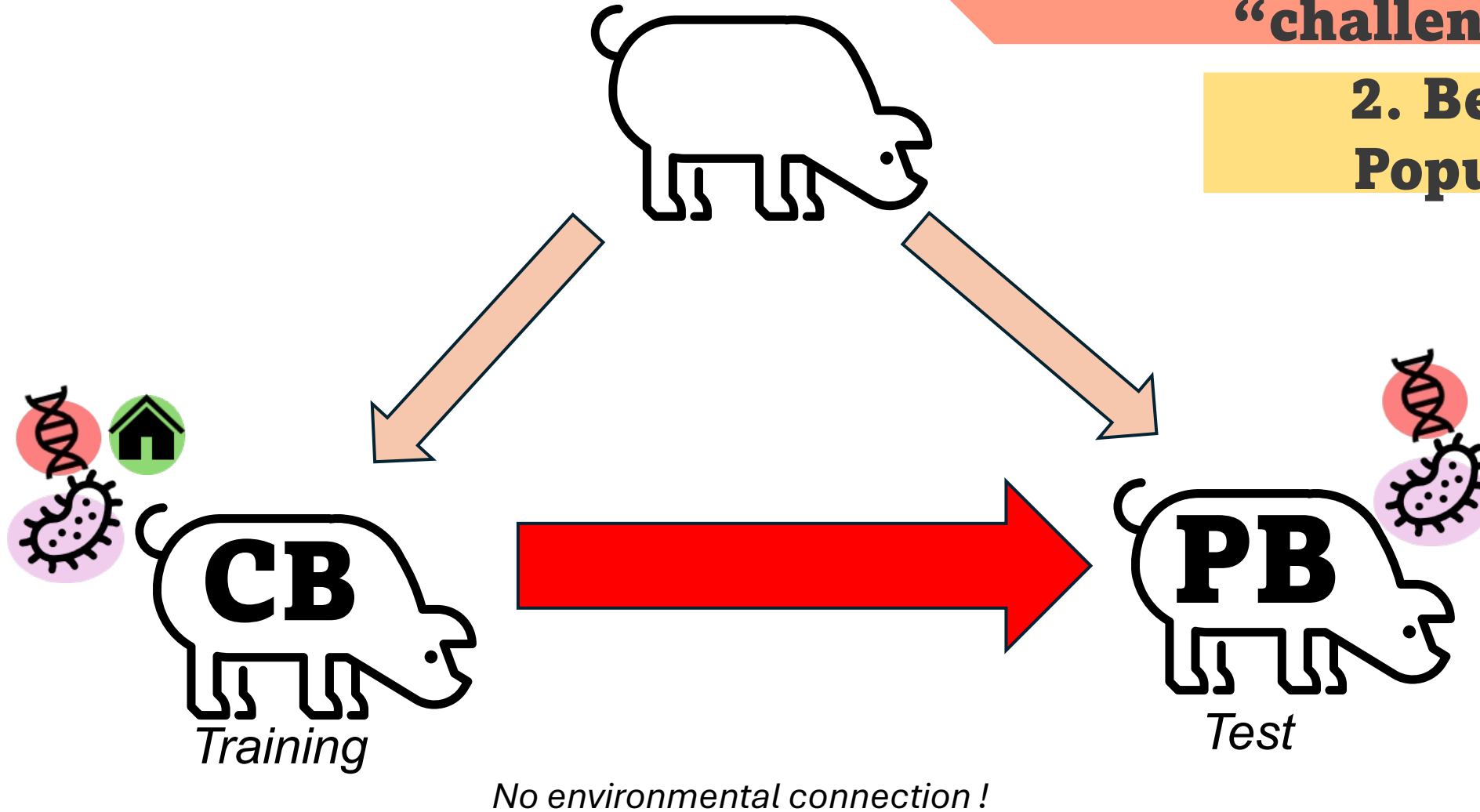
B. RND

RND CV x10:

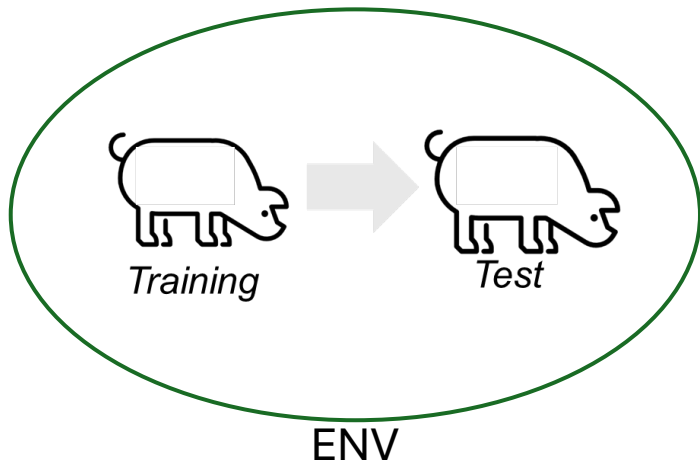


Different of prediction's “challenge”

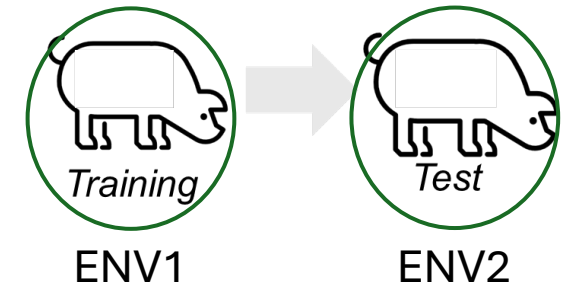
2. Between Population



1. Within Population

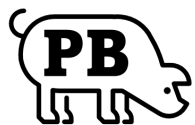


2. Between Population

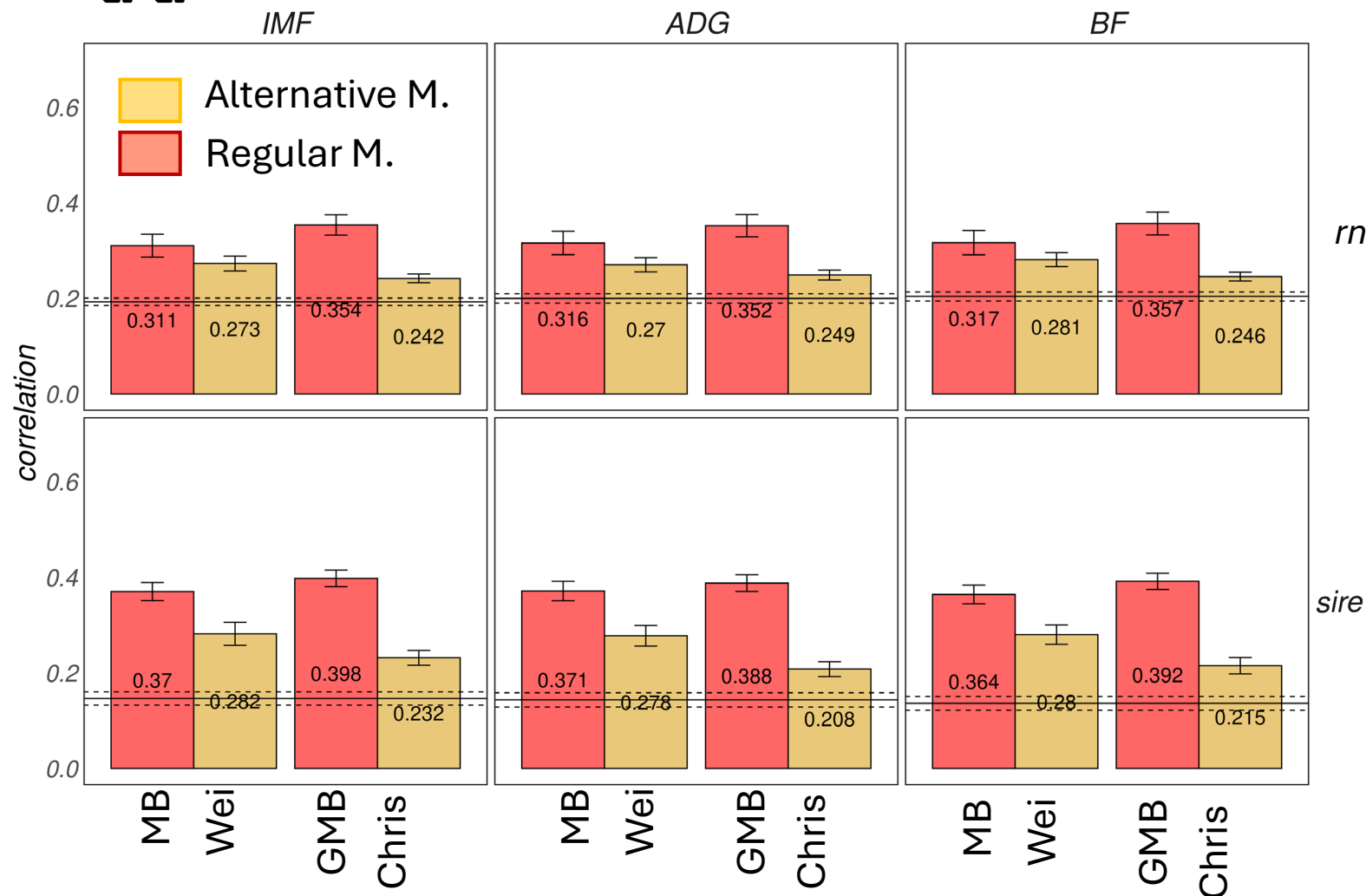


Results

Whitin Population Prediction



Highlights:



OBS: All model are better than GB (even decomposed one)

ASW: M bring more and different information respect **G**

OBS: Alternative predict worse than "Regular model"

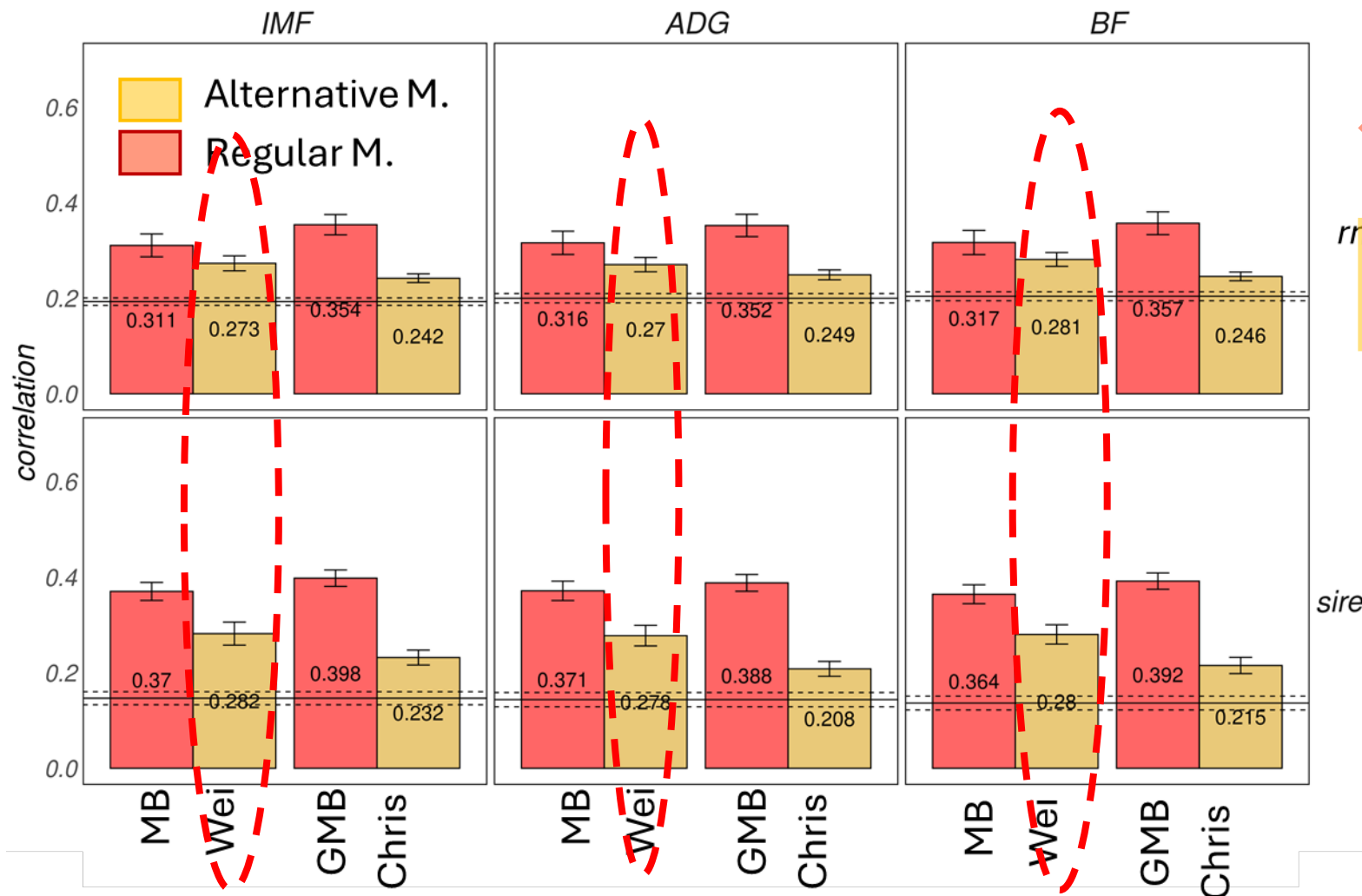
ASW: e_m still bring important information (when animal are in same enviroment)

$$W\alpha_m < W\alpha_m + e_m$$

Horizontal line: GB (baseline)

Whitin Population Prediction

Highlights:



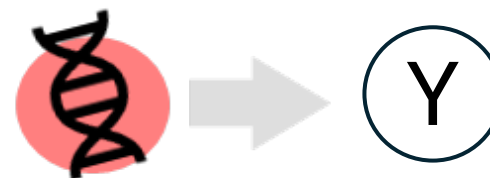
OBS: Whisharred predict better than GB

ASW: Effect of G Mediated by M
bring more info respect G

Weishaar *et al.*, 2021

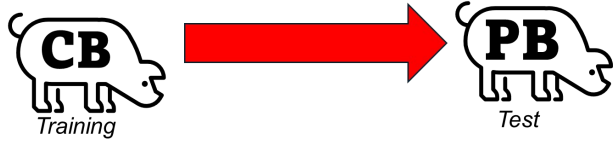


GB Model:

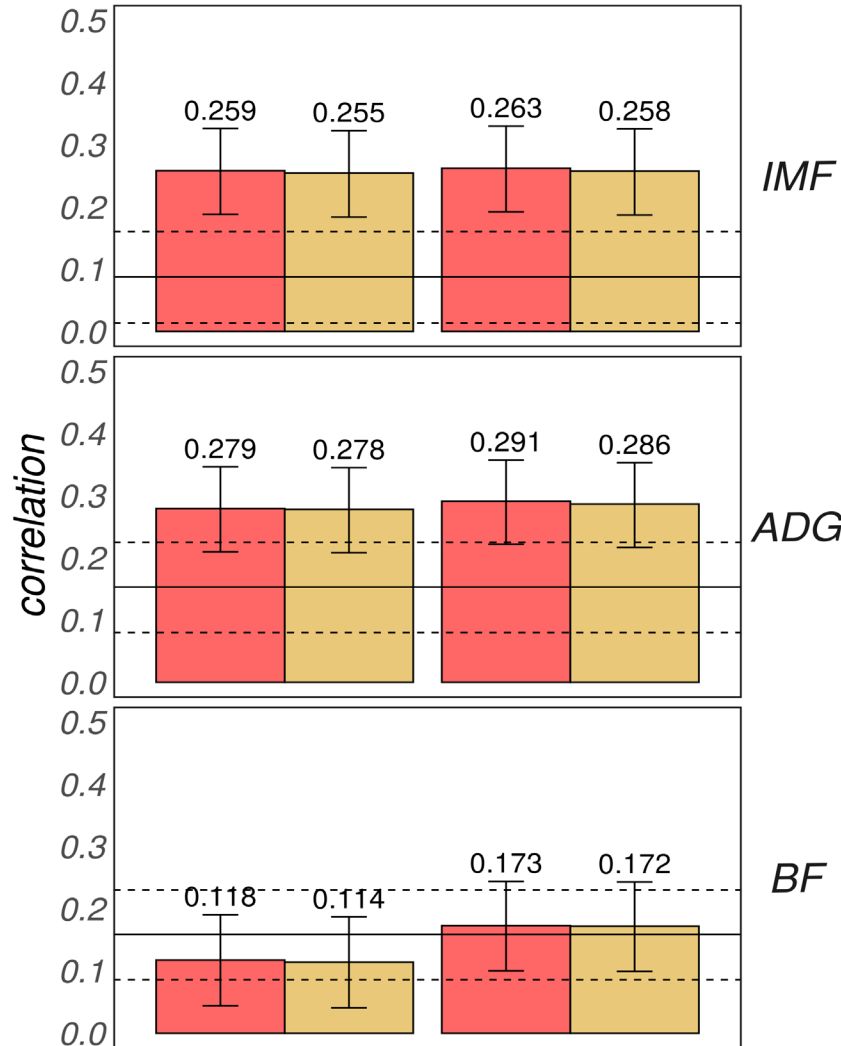


Between Population Prediction

Highlight:



Alternative
“Regular”



OBS: We can predict with microbiota in



ASW: ALL That “useful” information that can of microbiota come from mediated genetic effect mediated by M!!!!

Horizontal line: GB (baseline)

Consideration



ASW: *ALL That "useful" information that can of microbiota come from mediated genetic effect mediated by M!!!!*

END

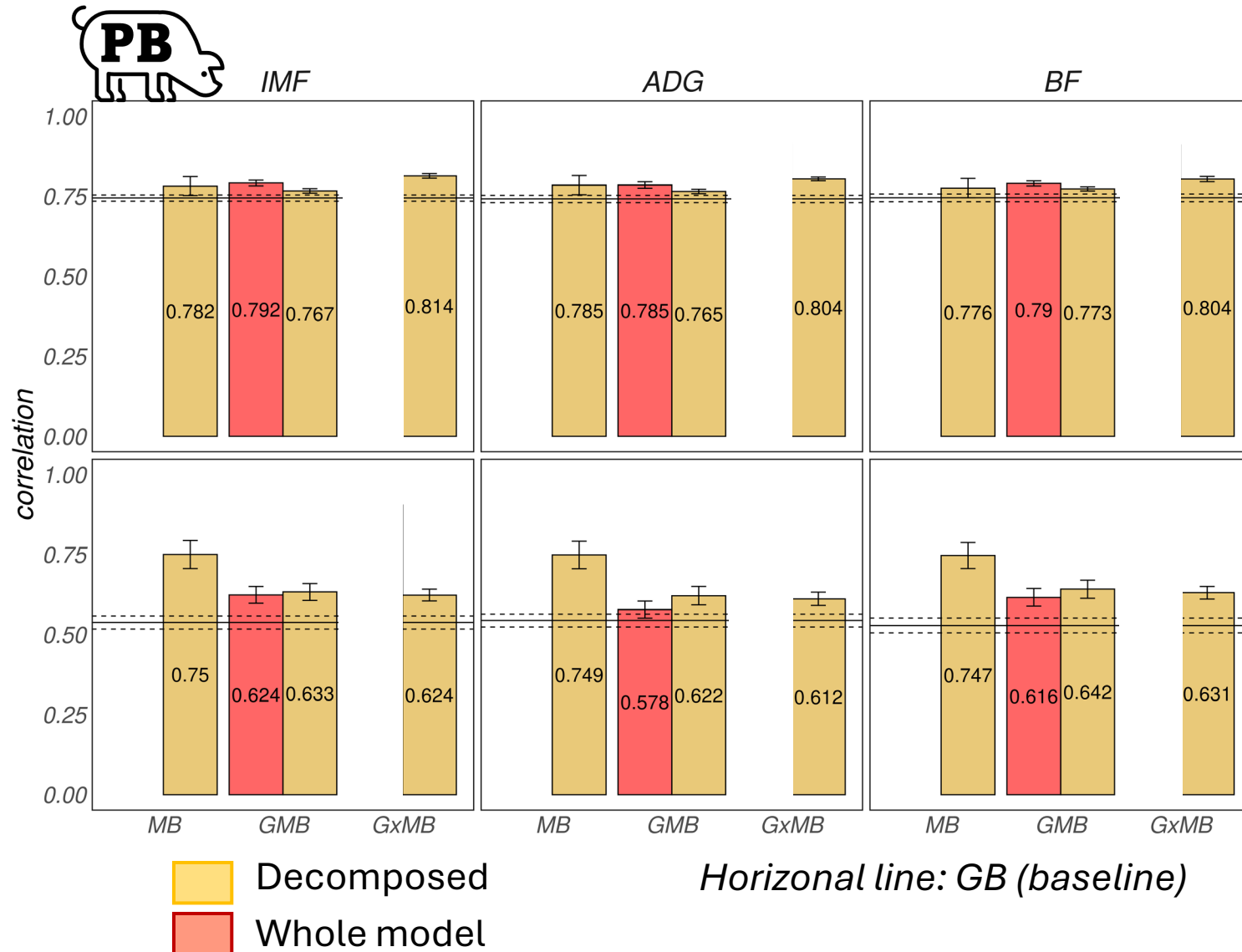
QUESTIONS to ASK:

enrico.mancin@unidp.it

**EXTRA STUFF
FOR THE QUESTION**

Genetic Value Prediction

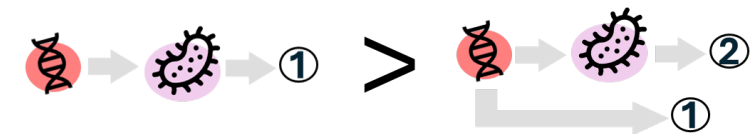
Whitin Breed Prediction

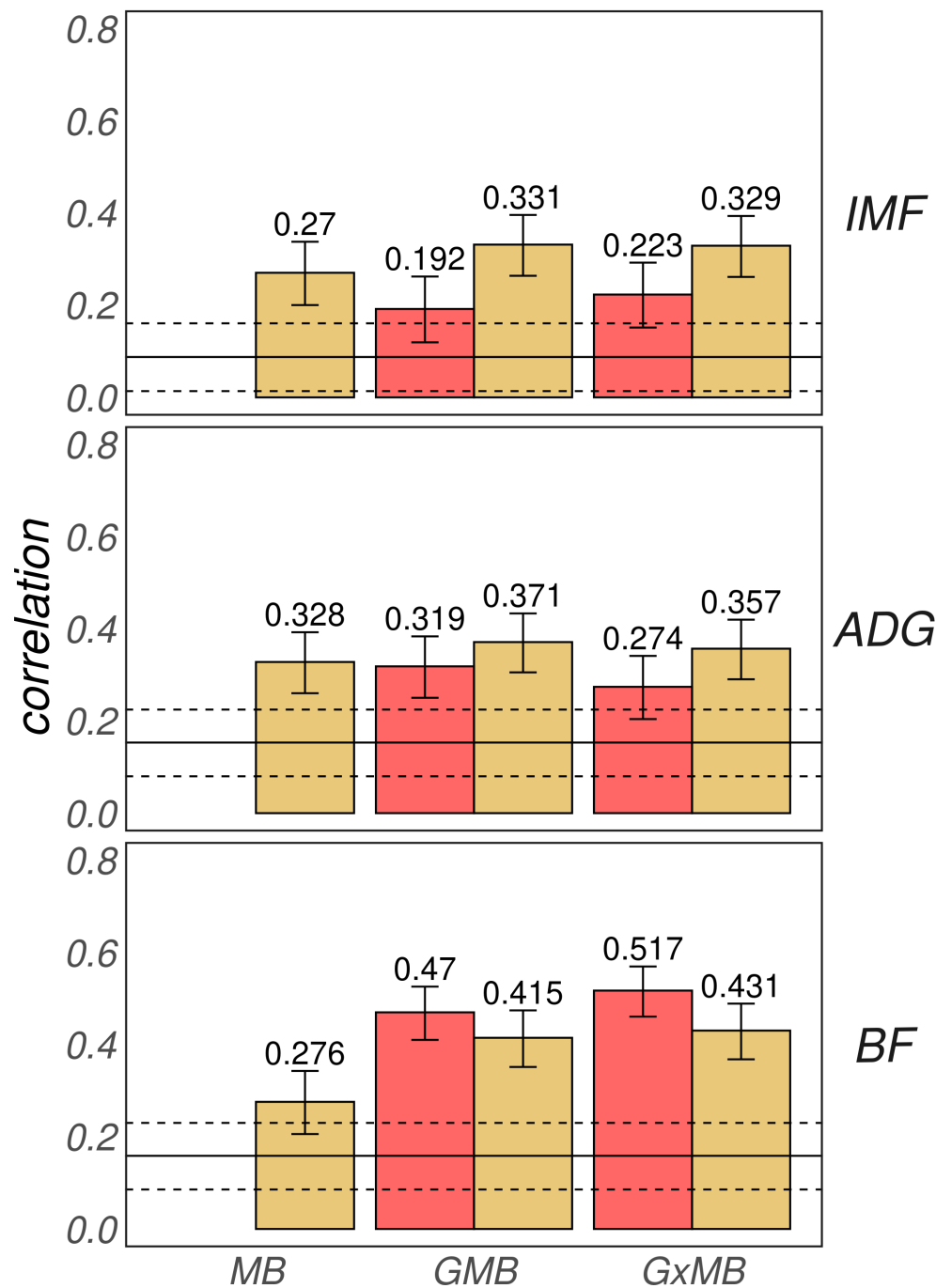


OBS: GxM predicted better

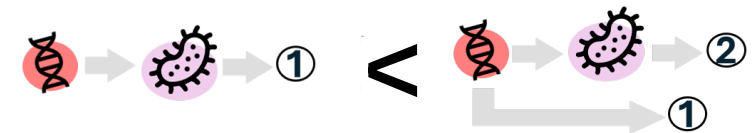
ASW: I Don't Know

OBS: Another model better than GB, especially MGB





OBS: Not in the case of between population prediction

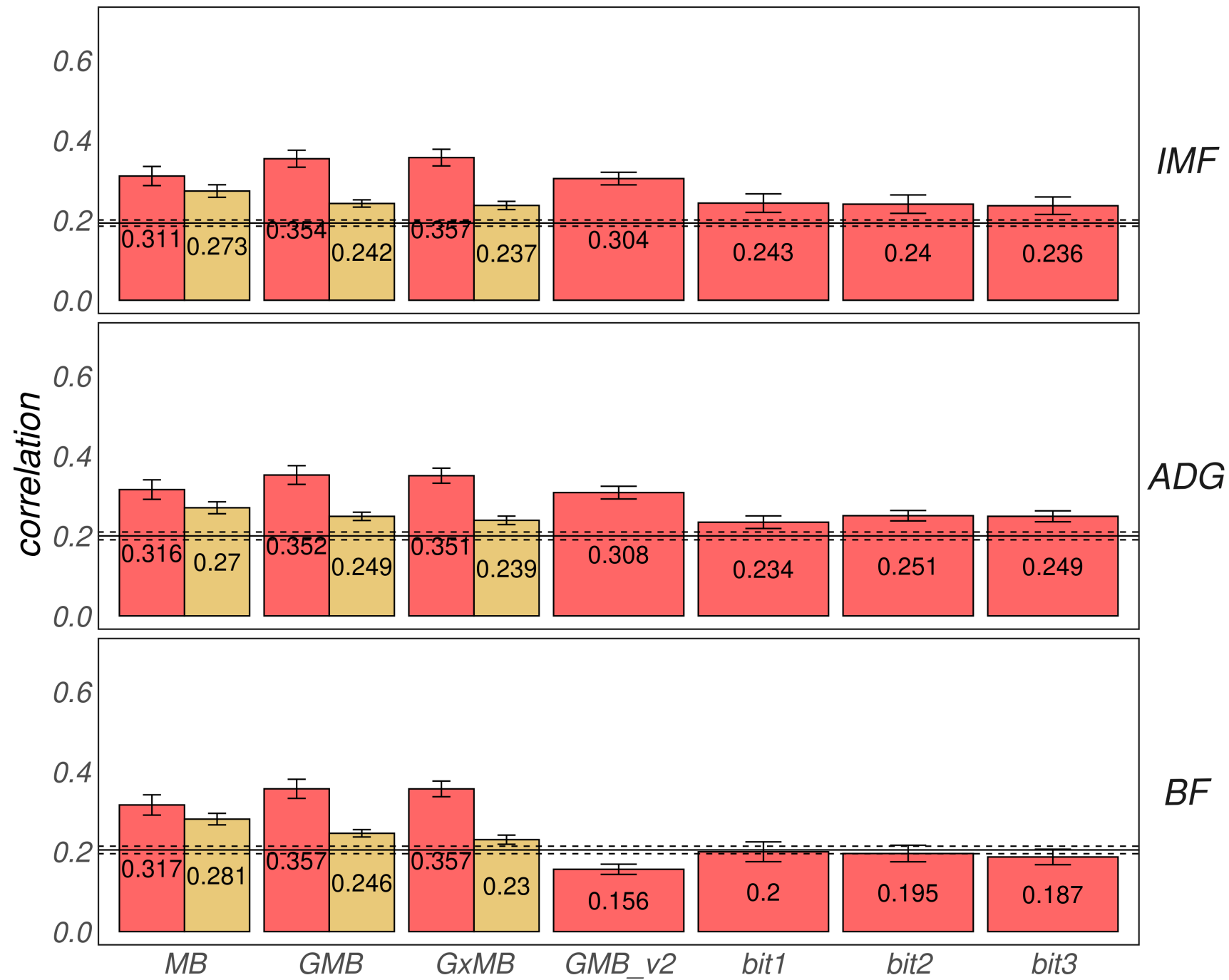


OBS: Decomposed predict better than "whole model"

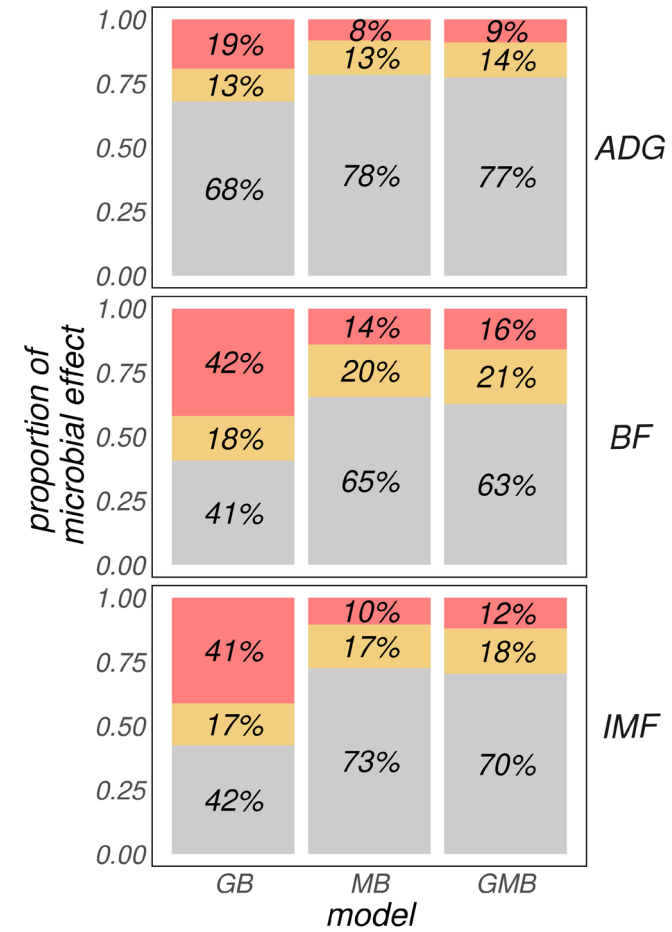
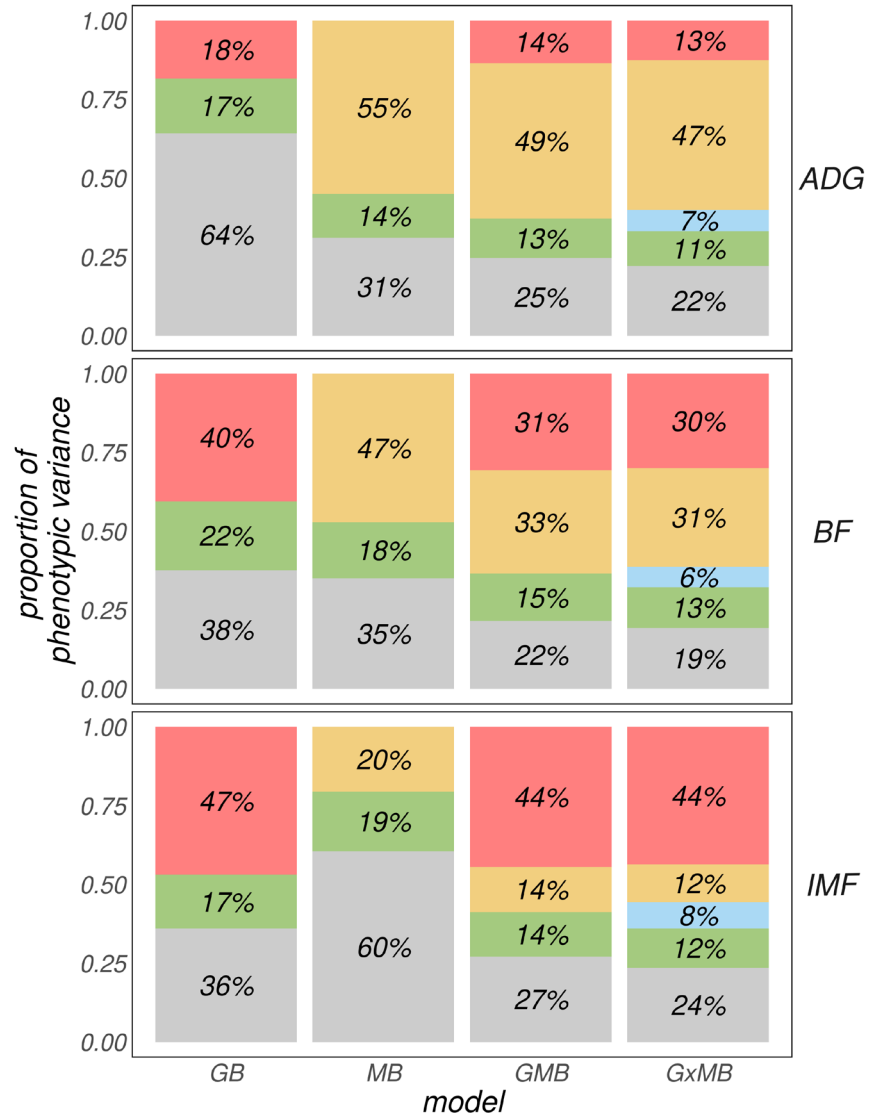
ASW: $G|M$ bring more information and additional than G direct



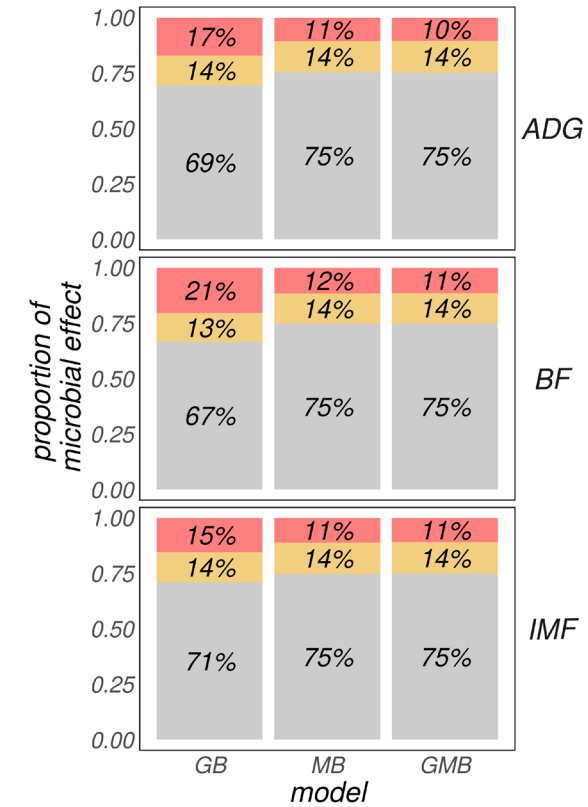
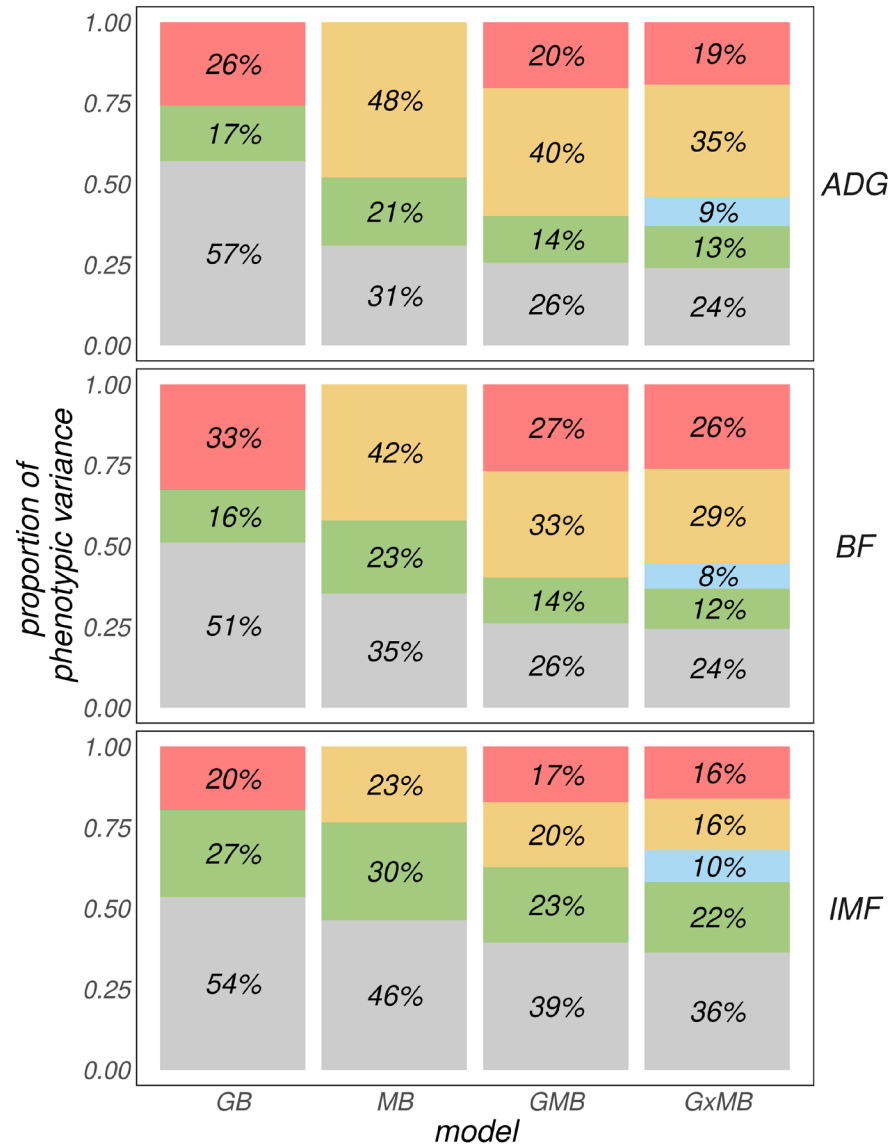
ASW: even for different population and in different environment !!!!!



VCE CB



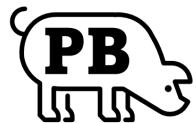
VCE PB



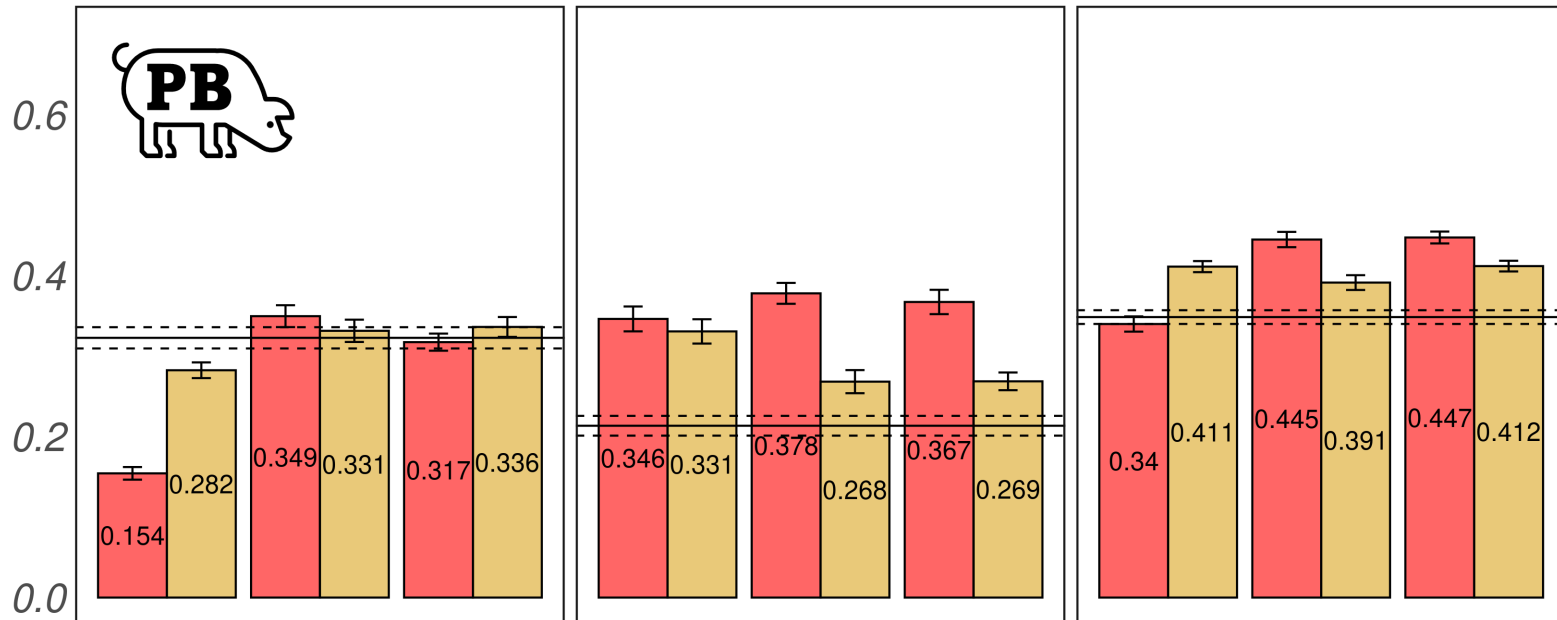
IMF

ADG

BF



correlation



Extra Higligh
(Comparison CV)

box

OBS: Sire C.V. large gap respect
GB to Box

ASW: CV broke genetic
relationship and M fill

OBS: Box C.V. less different
between Decomposed and "whole"

ASW: we partially remove E.
information but still present

sire

 $E|M$

SIRE

>

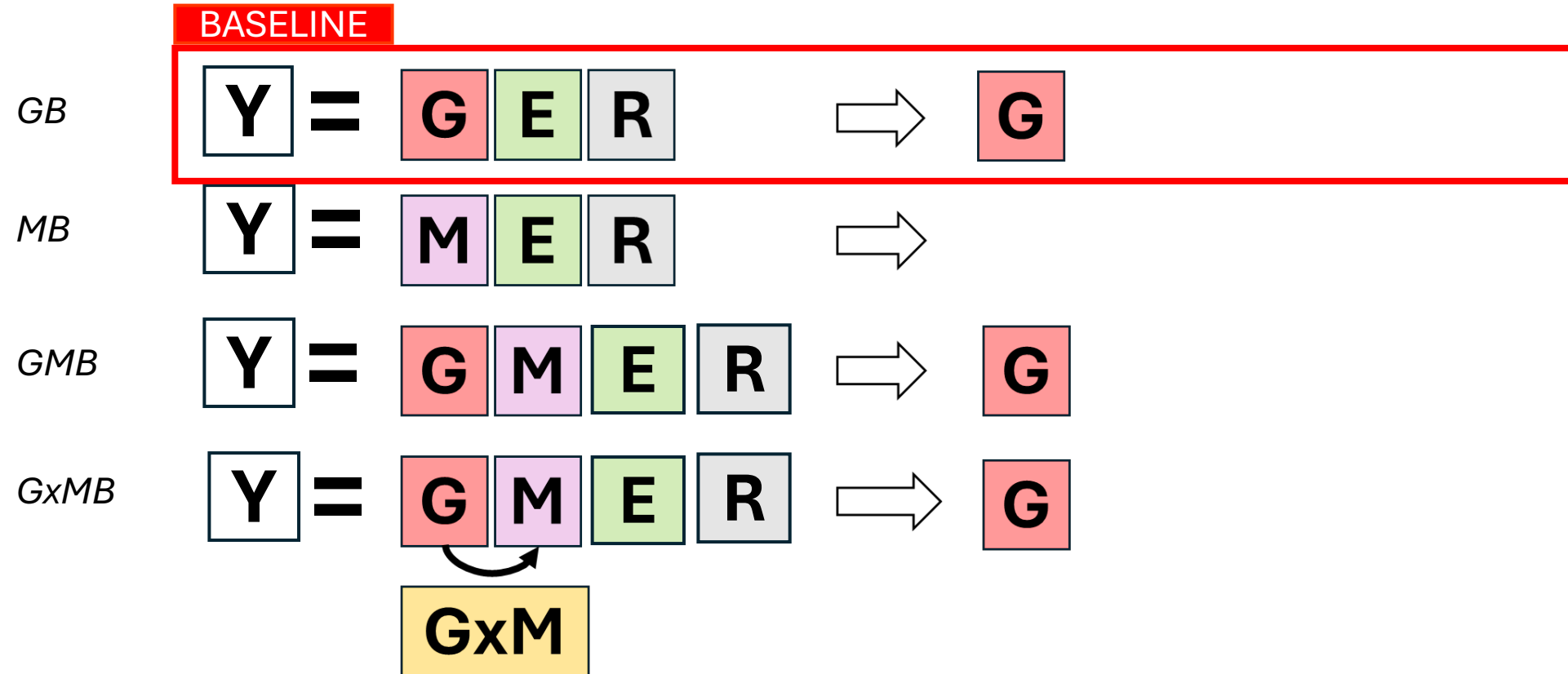
 $E|M$

BOX

Different assumption

“whole model”

EBV

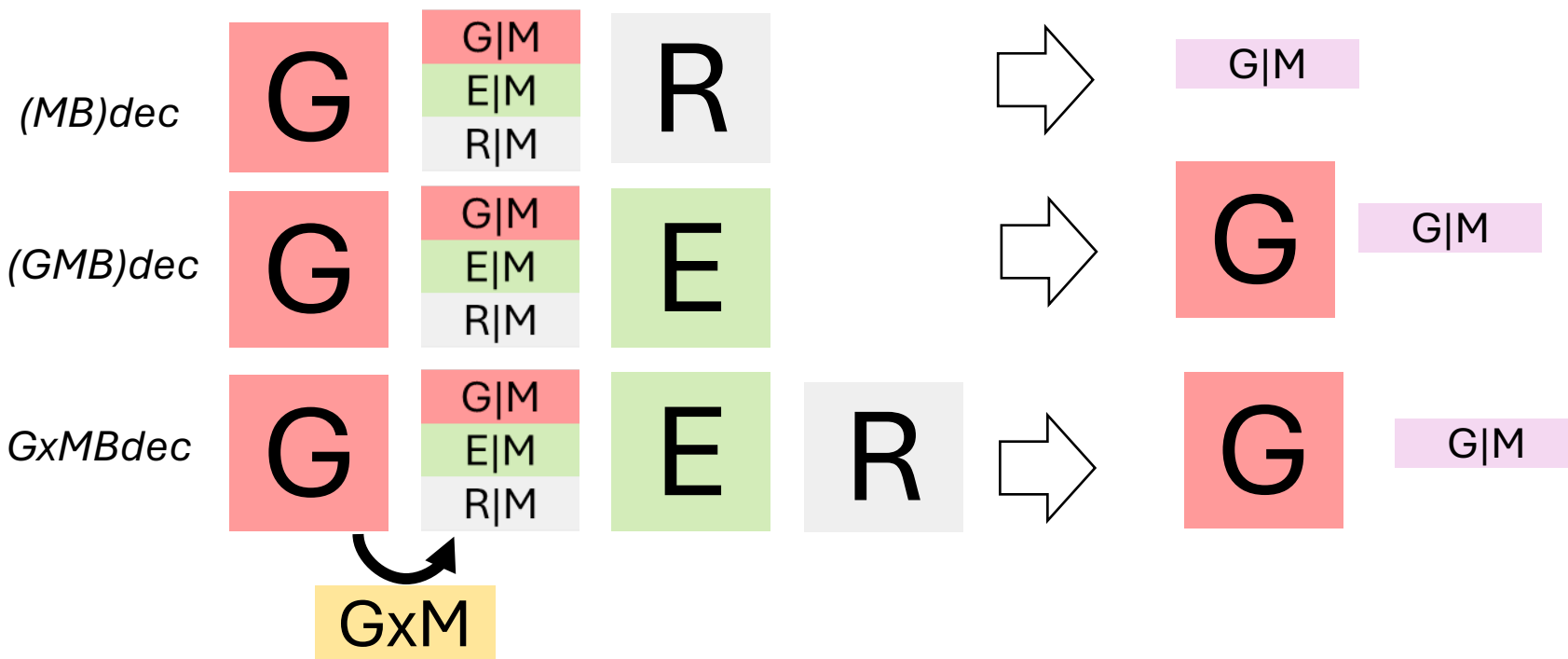


Different assumption

...

“Decomposed model”

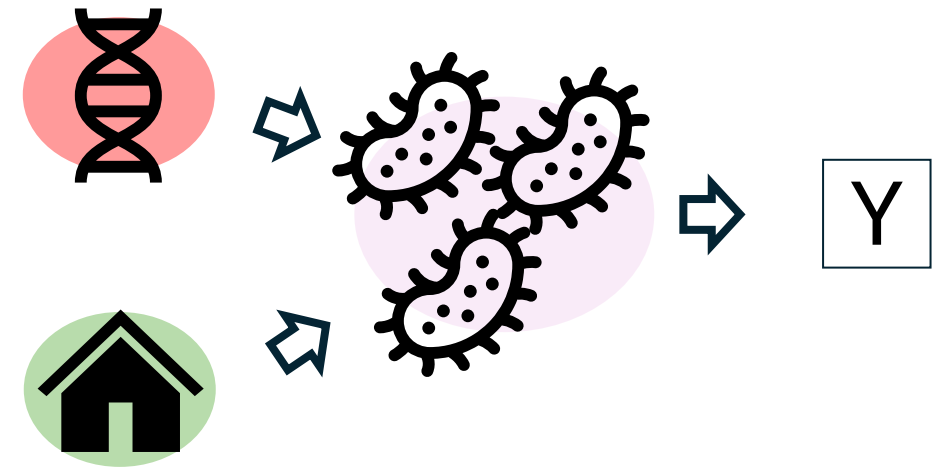
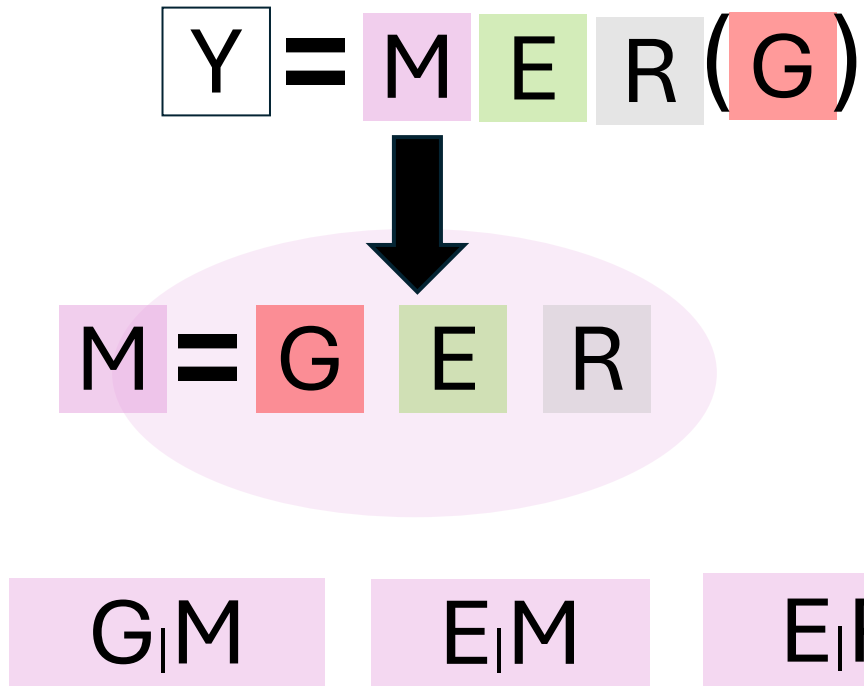
EBV



$$M = \begin{matrix} G|M \\ E|M \\ R|M \end{matrix}$$

Considering not the whole M but the M driven by Genetics !!

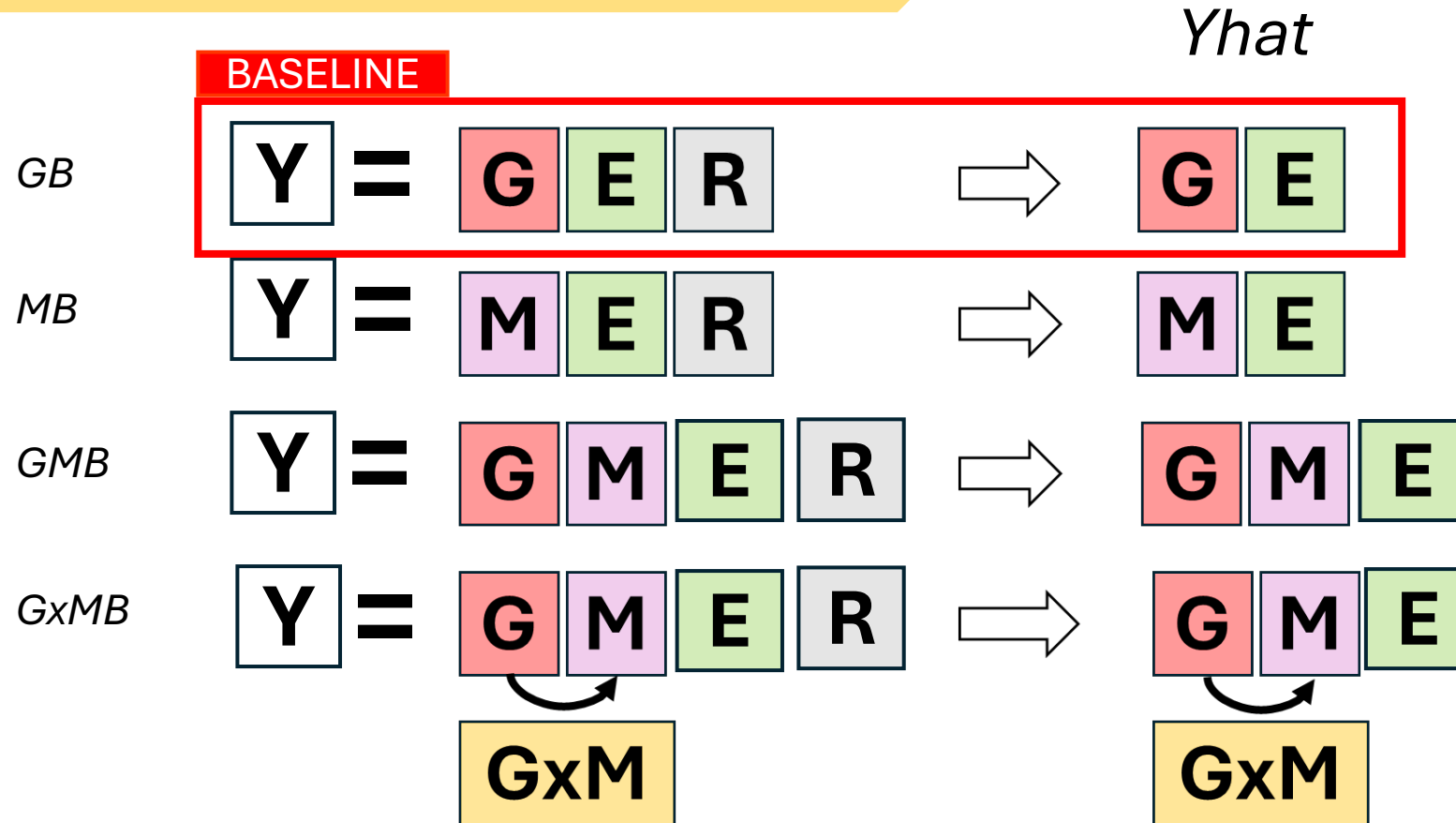
Different assumption



After knowing
that

Different assumption

“whole model”

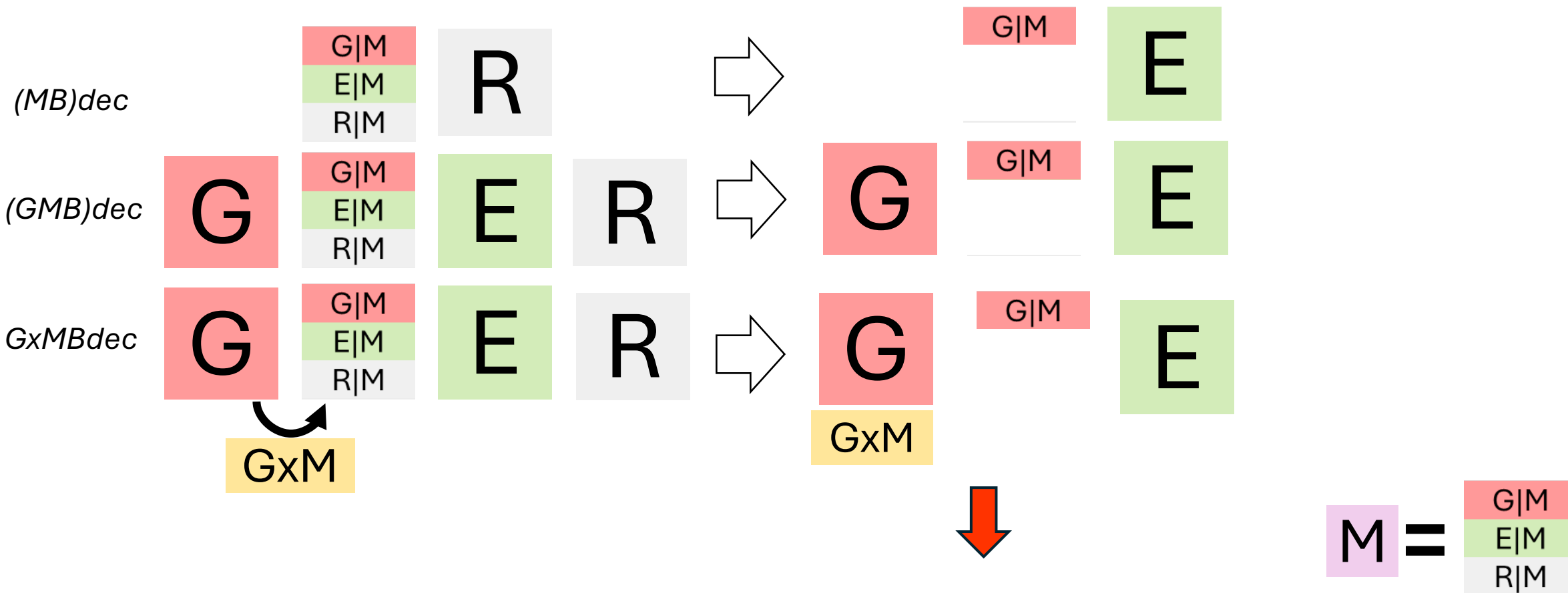


• • • •

Different assumption

“Decomposed model”

Y_{hat}



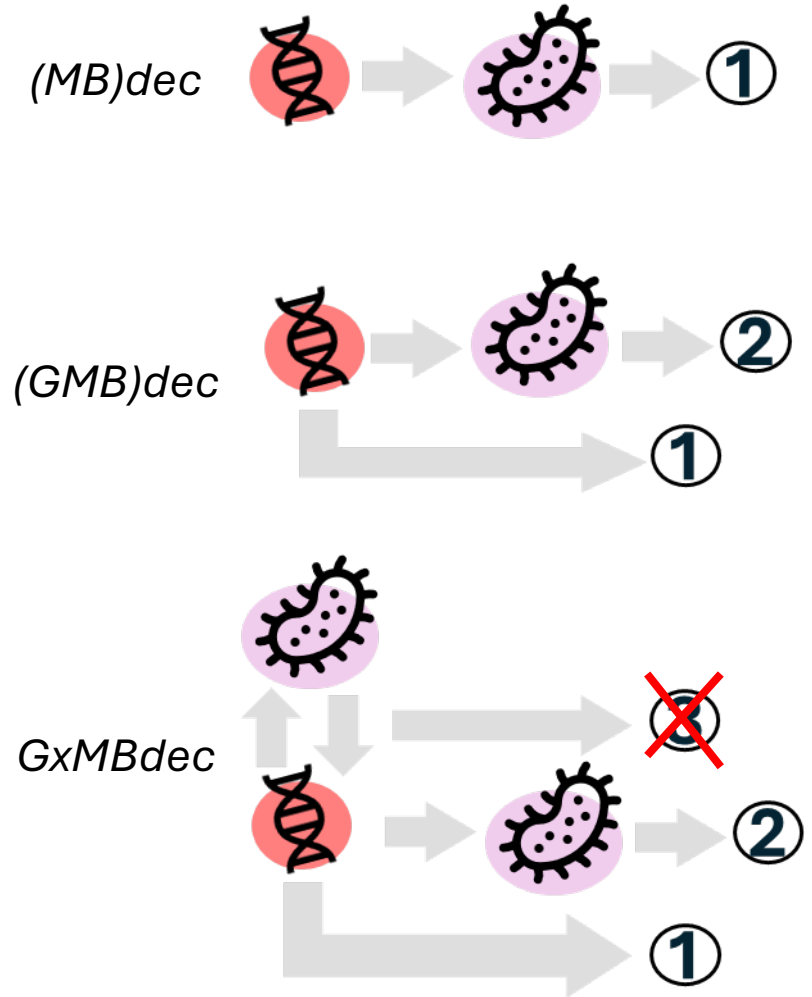
Considering not the whole M but the M driven by Genetics !!

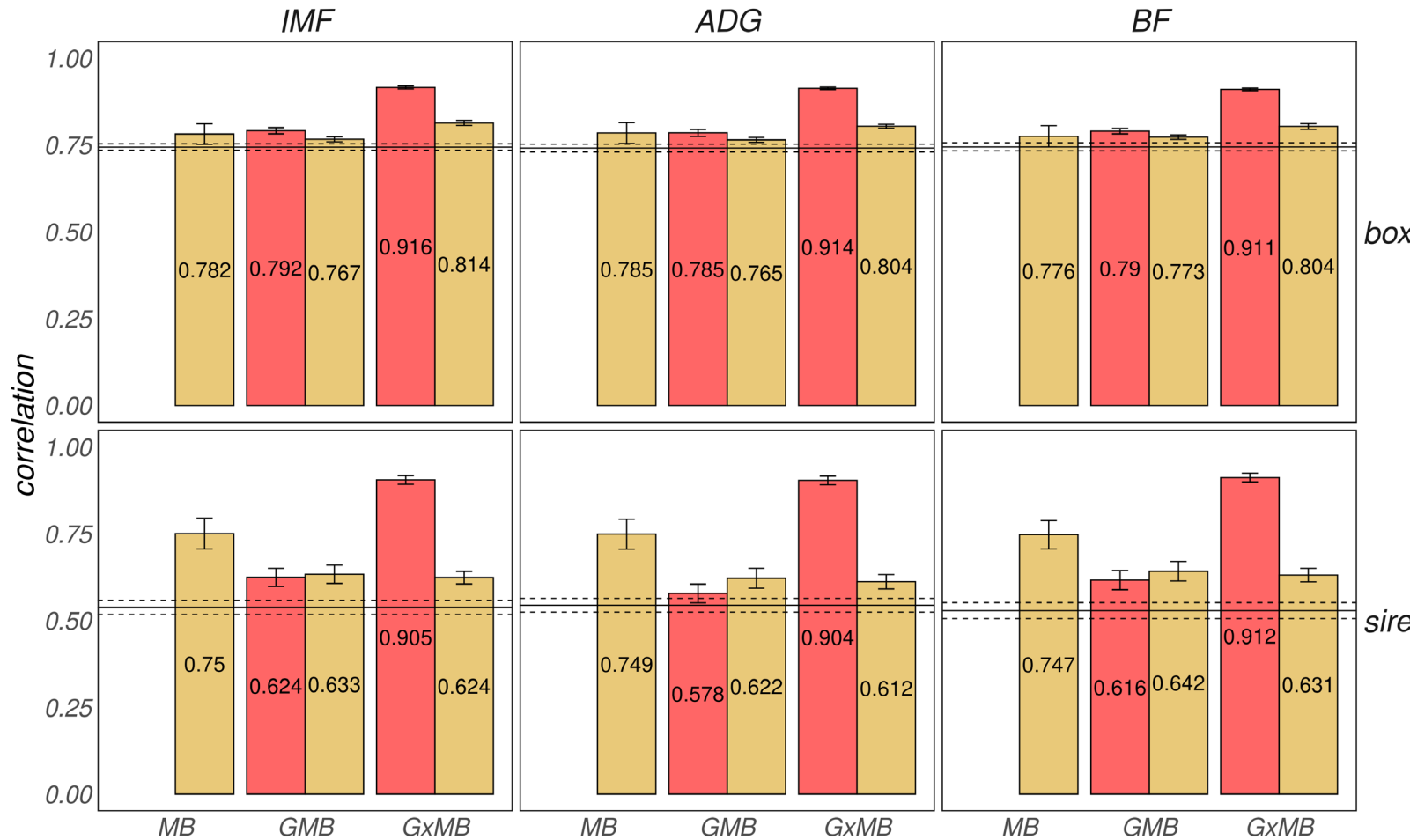
Different assumption

EBV



Interaction between G and M



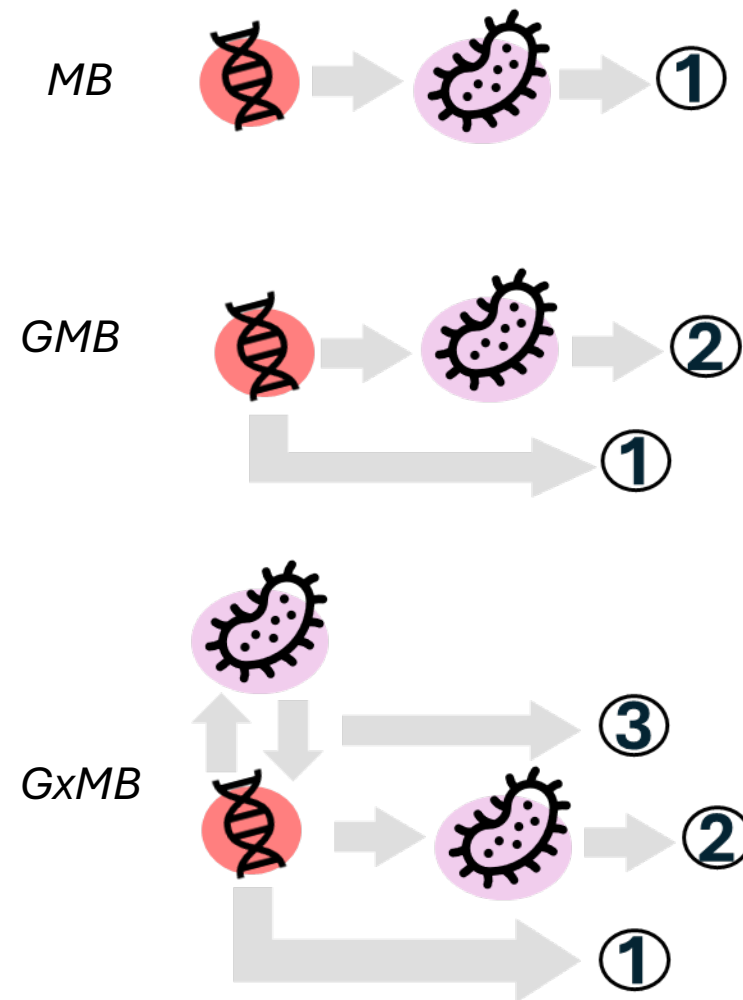
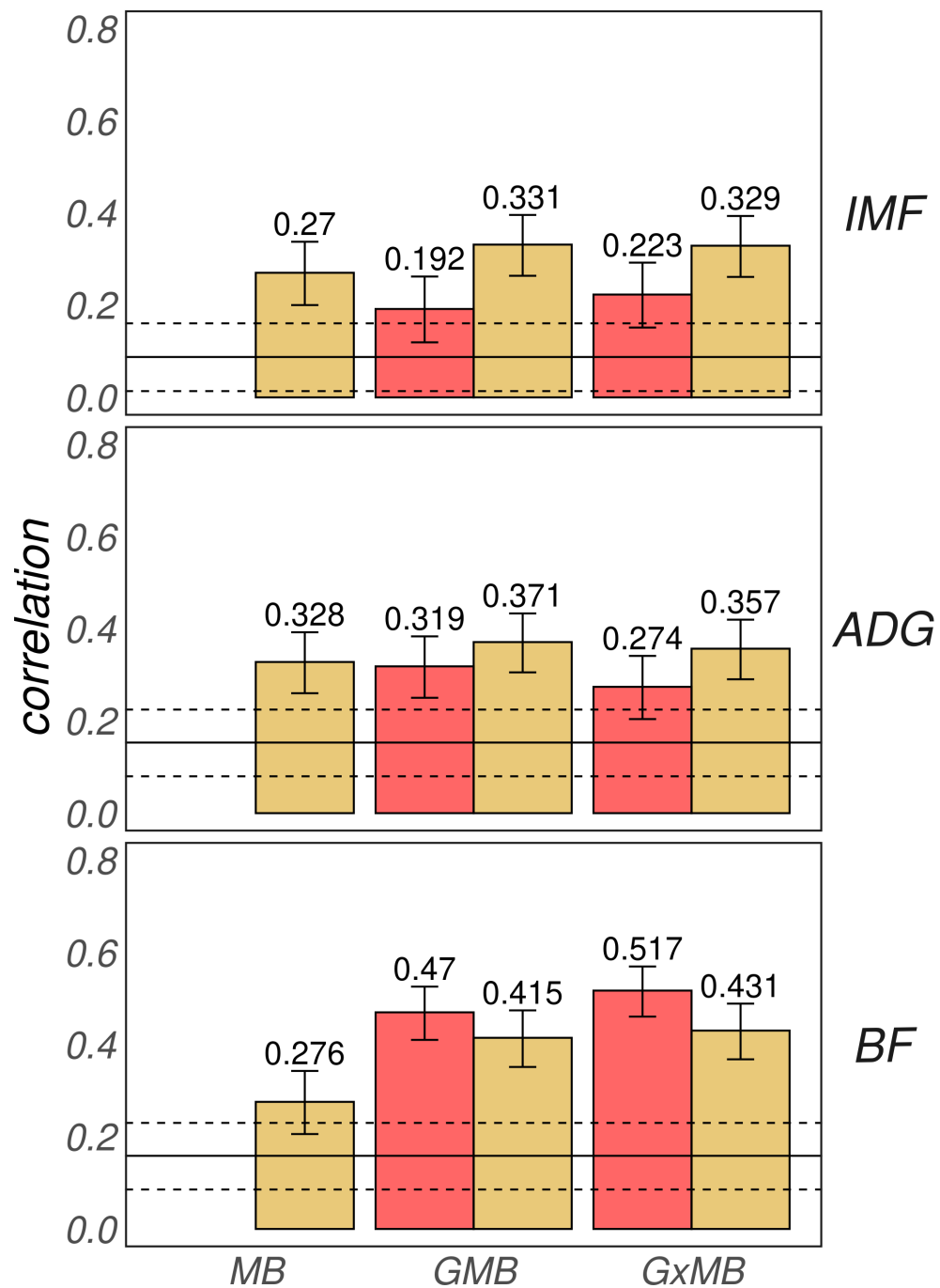


box

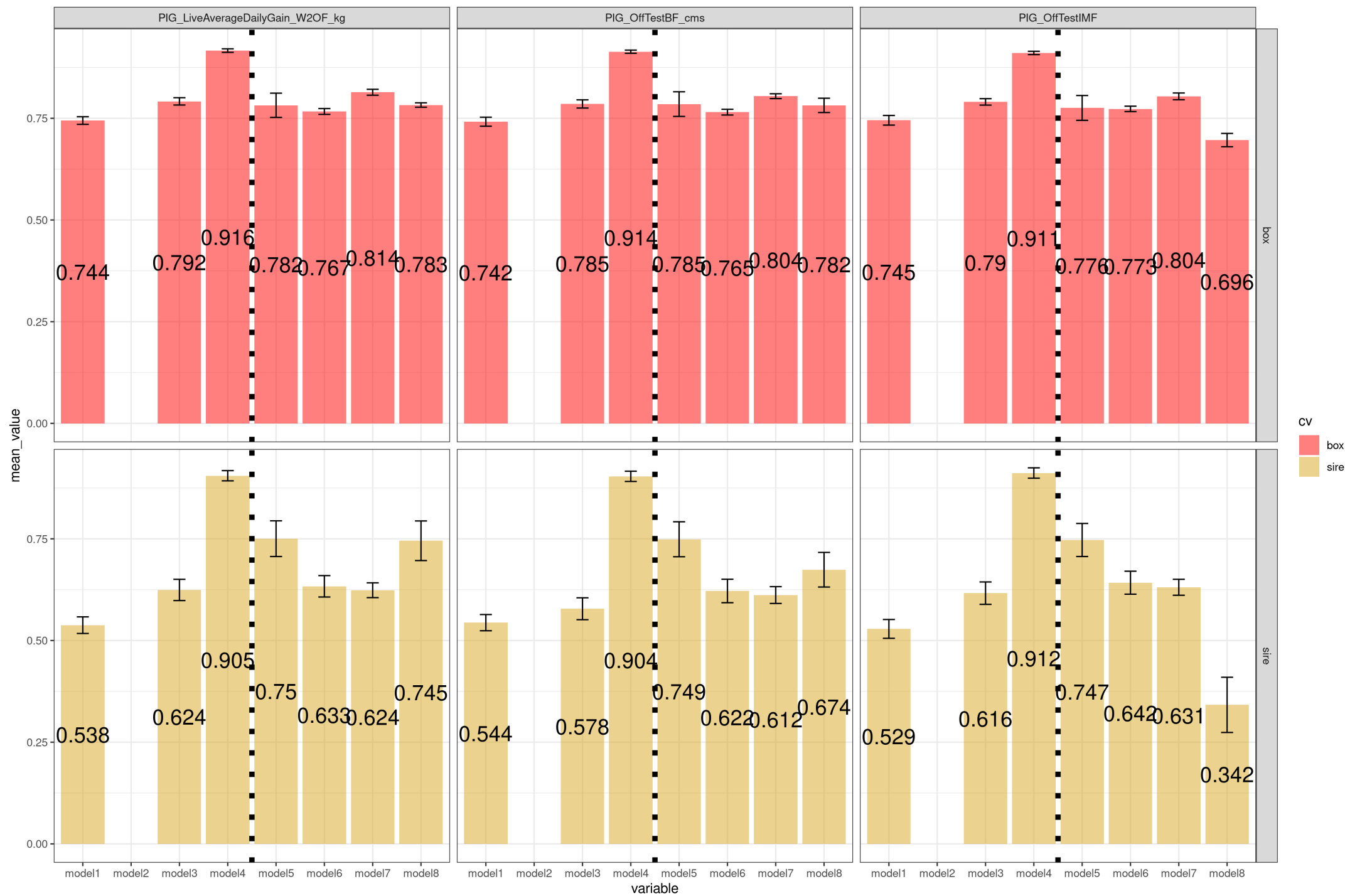
USE MODEL BETTER IN

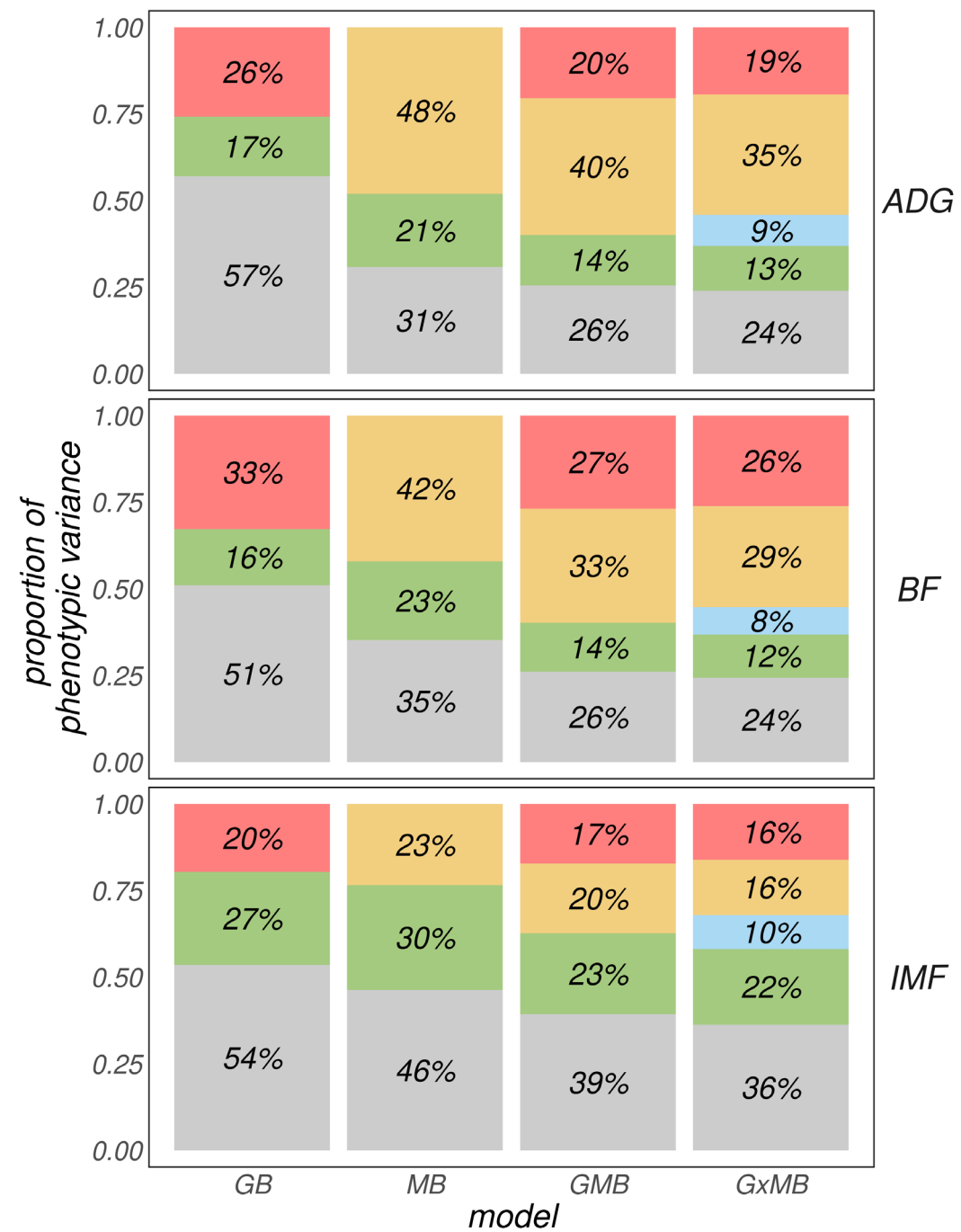
sire

d" model ALL G=>mM better
IS COMPONENTS



1. CONCRETO DRETTO CHEE MEGLIO DEL DIRETTO (TRANNE I
2. AIUTA ANCHE LA ECONDA ASSUNZIONE
3. BF PIU ITERAZIONE





G E R →

M E R

G M E R

G M E

GxM

G=>M

E=>M

E=>R

R

→

→

→

.....

G E

M E

G M R

G M R

GxM
M

G

G

G