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The relationship between gut microbiome and feed efficiency in Iberian pigs

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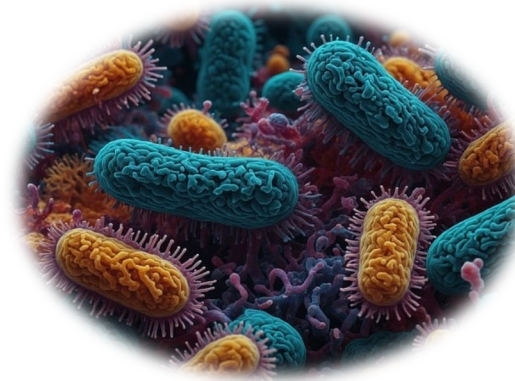


Ibergut project

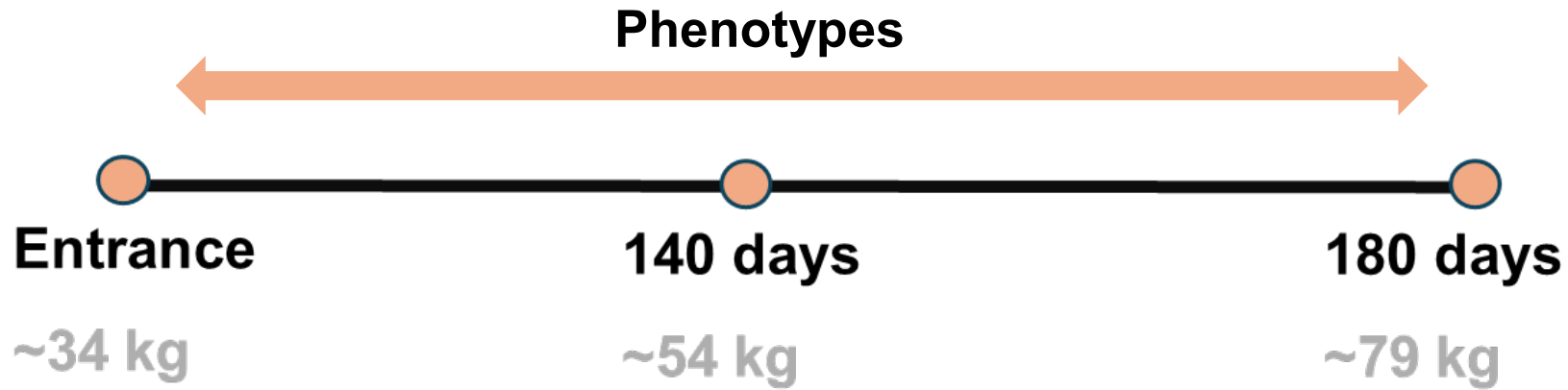
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Testing scheme



Phenotypes from 171 pigs

- Feed intake per visit
- Body weight

Microbiome data (fecal samples)

- 140 days
- 180 days

Objectives

- Estimate the **proportion of the phenotypic variance** of feed efficiency traits explained by the **microbiome**
- Evaluate the **microbiome at 140 days** as a **predictor** of the **phenotypes at 180 days**

Phenotypes



Feed efficiency traits

- Daily feed intake
- Average daily gain
- Feed conversion rate
- Body weight 180 days
- Residual feed intake

16S rRNA



Amplicon sequence variants

- 140 and 180 days
- >0.01% and >8 samples (5%)
- 588 and 598 ASV
- Centered log-ratio transformation

Variance components

G model

$$\mathbf{y} = \mu + \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$$



$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

M model

$$\mathbf{y} = \mu + \mathbf{Xb} + \mathbf{Wm} + \mathbf{e}$$



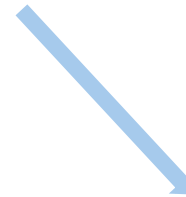
$$m^2 = \frac{\sigma_m^2}{\sigma_m^2 + \sigma_e^2}$$

G + M model

$$\mathbf{y} = \mu + \mathbf{Xb} + \mathbf{Za} + \mathbf{Wm} + \mathbf{e}$$

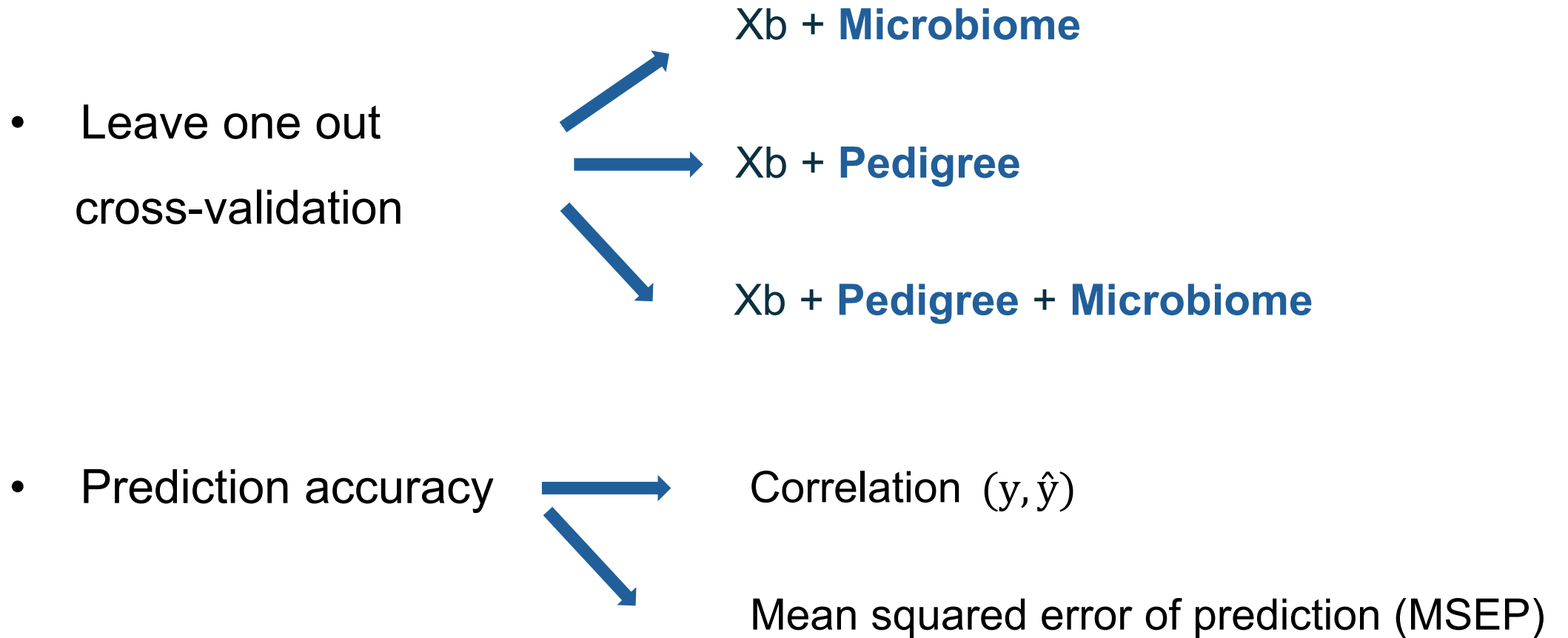


$$h_d^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_m^2 + \sigma_e^2}$$

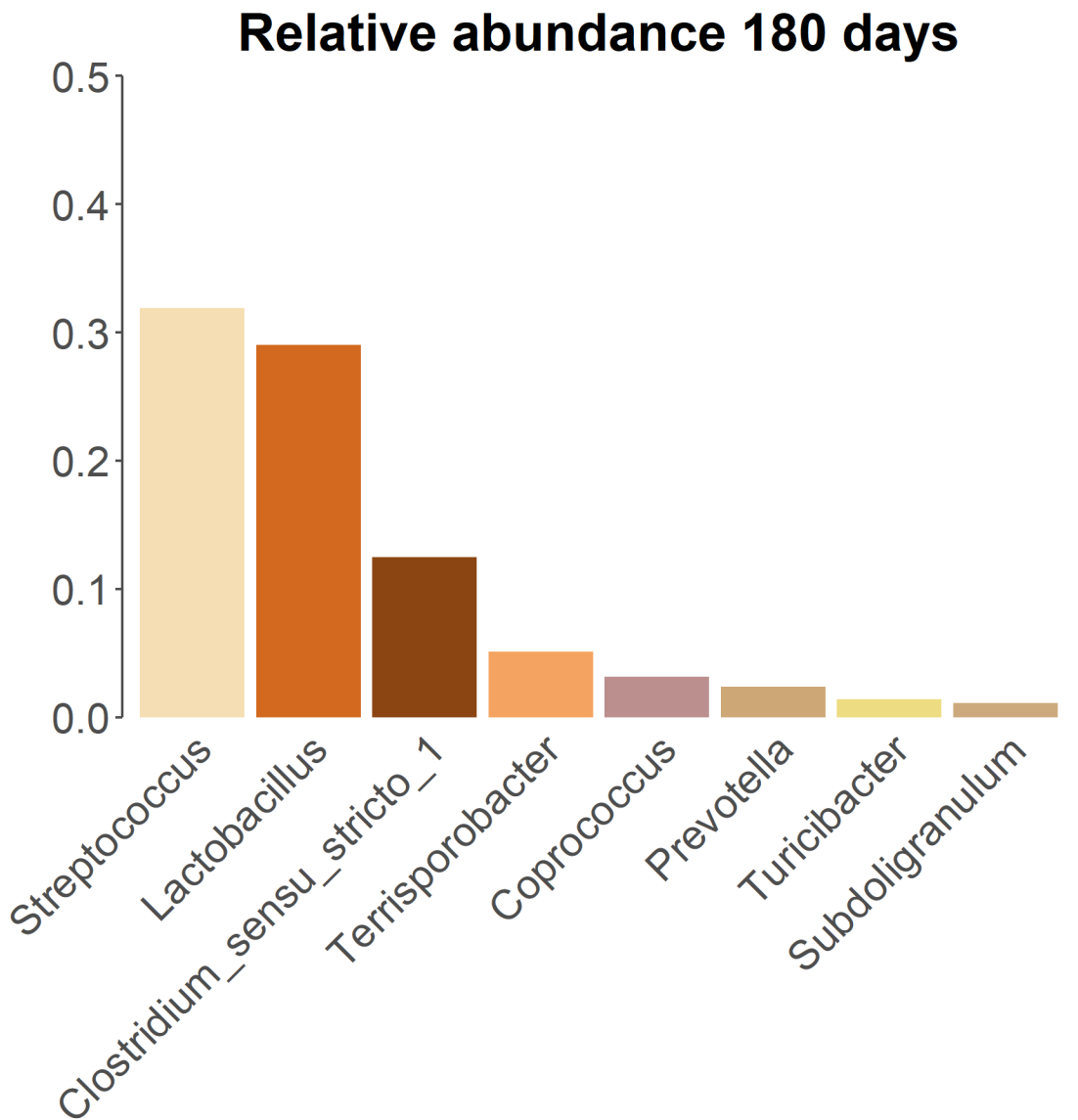
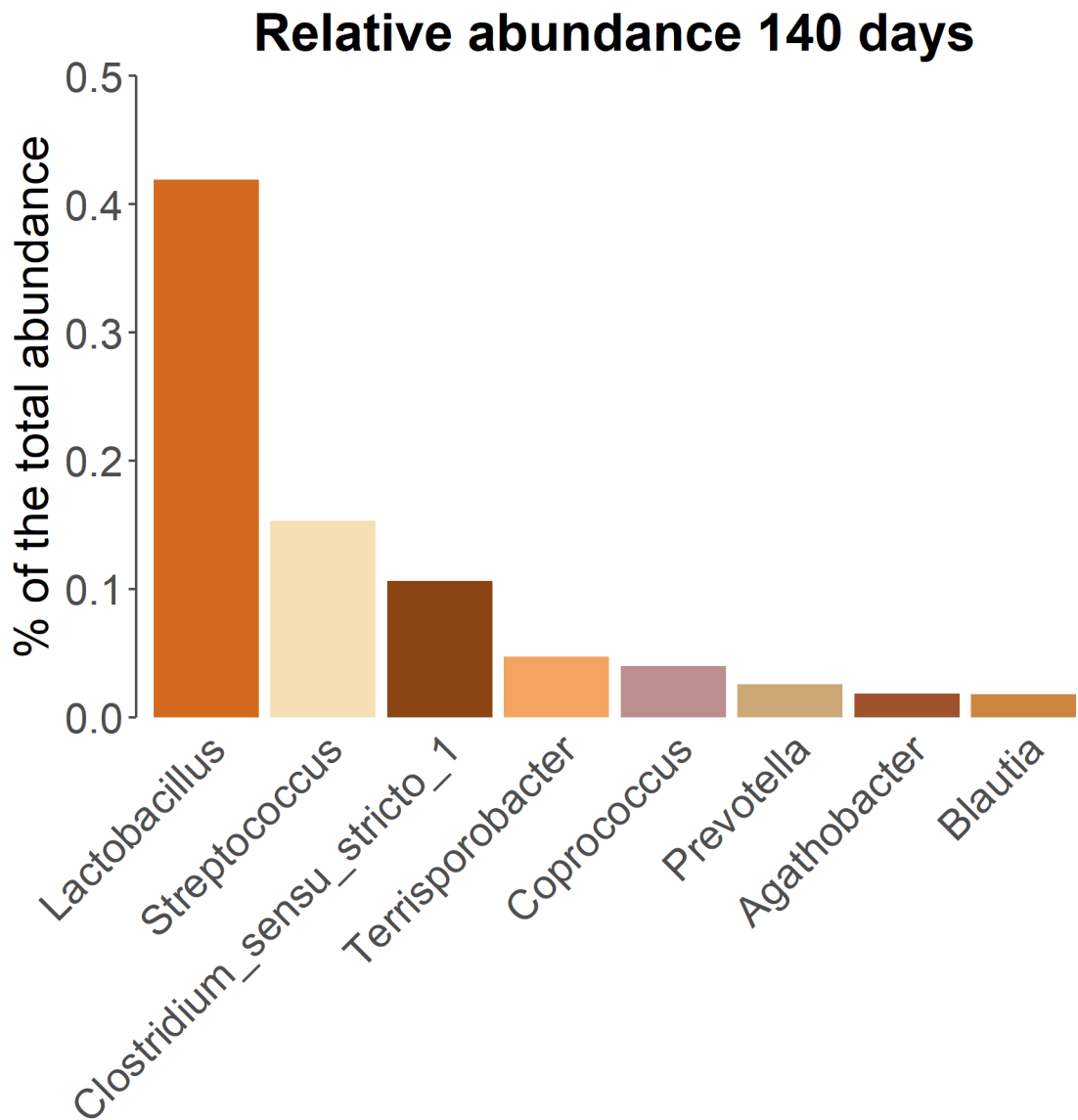


$$m^2 = \frac{\sigma_m^2}{\sigma_a^2 + \sigma_m^2 + \sigma_e^2}$$

Prediction of phenotypes



Descriptive results



Variance components

Trait	Pedigree	
	h^2	DIC
DFI	0.37	143
ADG	0.36	-359
FCR	0.39	269
BW180	0.47	1079
RFI	0.36	100

Variance components

Trait	Pedigree		Microbiome 140	
	h^2	DIC	m^2	DIC
DFI	0.37	143	0.33	150
ADG	0.36	-359	0.40	-367
FCR	0.39	269	0.38	271
BW180	0.47	1079	0.41	1095
RFI	0.36	100	0.37	97

Variance components

Trait	Pedigree		Microbiome 140		Pedigree + Microbiome 140		
	h^2	DIC	m^2	DIC	h_d^2	m^2	DIC
DFI	0.37	143	0.33	150	0.25	0.22	134
ADG	0.36	-359	0.40	-367	0.25	0.26	-383
FCR	0.39	269	0.38	271	0.26	0.25	253
BW180	0.47	1079	0.41	1095	0.31	0.25	1064
RFI	0.36	100	0.37	97	0.24	0.23	84

Variance components: comparison between points

Variance components: comparison between points

Trait	Pedigree + Microbiome 140			Pedigree + Microbiome 180		
	h_d^2	m^2	DIC	h_d^2	m^2	DIC
DFI	0.25	0.22	-383	0.26	0.20	-364
ADG	0.25	0.26	134	0.25	0.19	138
FCR	0.26	0.25	253	0.27	0.21	266
BW180	0.31	0.25	1064	0.33	0.21	1066
RFI	0.24	0.23	84	0.25	0.20	96

- Cosine similarity between matrices = 0.75

Phenotype prediction with microbiome 140 days

Phenotype prediction with microbiome 140 days

Trait	Unit	Xb + M	
		$\rho(y, \hat{y})$	MSEP
ADG	g	0.38	0.06
DFI	kg	0.52	0.17
FCR	kg/kg	0.61	0.39
BW180	kg	0.44	99.08
RFI	kg	0.64	0.12

Phenotype prediction with microbiome 140 days

Trait	Unit	Xb + M		Xb + P	
		$\rho(y, \hat{y})$	MSEP	$\rho(y, \hat{y})$	MSEP
ADG	g	0.38	0.06	0.42	0.05
DFI	kg	0.52	0.17	0.52	0.17
FCR	kg/kg	0.61	0.39	0.61	0.39
BW180	kg	0.44	99.08	0.50	92.37
RFI	kg	0.64	0.12	0.63	0.12

Phenotype prediction with microbiome 140 days

Trait	Unit	Xb + M		Xb + P		Xb + M + P	
		$\rho(y, \hat{y})$	MSEP	$\rho(y, \hat{y})$	MSEP	$\rho(y, \hat{y})$	MSEP
ADG	g	0.38	0.06	0.42	0.05	0.42	0.05
DFI	kg	0.52	0.17	0.52	0.17	0.52	0.17
FCR	kg/kg	0.61	0.39	0.61	0.39	0.62	0.38
BW180	kg	0.44	99.08	0.50	92.37	0.51	90.94
RFI	kg	0.64	0.12	0.63	0.12	0.64	0.12

Microbiome 140 vs 180

Trait	Unit	Xb + M140		Xb + M180	
		$\rho(y, \hat{y})$	MSEP	$\rho(y, \hat{y})$	MSEP
ADG	g	0.38	0.06	0.37	0.06
DFI	kg	0.52	0.17	0.52	0.18
FCR	kg/kg	0.61	0.39	0.62	0.39
BW180	kg	0.44	99.08	0.41	110.32
RFI	kg	0.64	0.12	0.66	0.12

Conclusions

- The microbiome composition explained a moderate proportion of the phenotypic variance (~20%)
- The gut microbiome at 140 and 180 days provided very similar information
- The microbiome-only model achieved prediction accuracy comparable to the genetic model, but combining both did not enhance accuracy



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Variance components

Trait	Genetic		Microbiome		Genetic + Microbiome		
	h^2	DIC	m^2	DIC	h_d^2	m^2	DIC
ADG	0.37 [0.15, 0.61]	143	0.33 [0.14, 0.54]	150	0.25 [0.09, 0.44]	0.22 [0.08, 0.38]	134
DFI	0.36 [0.14, 0.59]	-359	0.40 [0.17, 0.65]	-367	0.25 [0.09, 0.44]	0.26 [0.09, 0.45]	-383
FCR	0.39 [0.17, 0.62]	269	0.38 [0.17, 0.59]	271	0.26 [0.10, 0.44]	0.25 [0.10, 0.43]	253
BW180	0.47 [0.22, 0.73]	1079	0.41 [0.18, 0.64]	1095	0.31 [0.11, 0.52]	0.25 [0.09, 0.43]	1064
RFI	0.36 [0.16, 0.58]	100	0.37 [0.17, 0.58]	97	0.24 [0.10, 0.41]	0.25 [0.10, 0.42]	84

Variance components: comparison between points

Trait	Pedigree + Microbiome 140			Pedigree + Microbiome 180		
	h_d^2	m^2	DIC	h_d^2	m^2	DIC
DFI	0.25 [0.09, 0.44]	0.22 [0.08, 0.38]	-383	0.26 [0.09, 0.44]	0.20 [0.07, 0.36]	-364
ADG	0.25 [0.09, 0.45]	0.26 [0.09, 0.45]	134	0.25 [0.09, 0.44]	0.19 [0.08, 0.35]	138
FCR	0.26 [0.10, 0.44]	0.25 [0.10, 0.43]	253	0.27 [0.10, 0.46]	0.21 [0.08, 0.34]	266
BW180	0.31 [0.11, 0.52]	0.25 [0.09, 0.43]	1064	0.33 [0.13, 0.55]	0.21 [0.08, 0.36]	1066
RFI	0.24 [0.10, 0.41]	0.23 [0.10, 0.42]	84	0.25 [0.10, 0.43]	0.20 [0.09, 0.34]	96

- Cosine similarity between matrices = 0.75

Leave-one-out **vs** 10% holdout validation

Trait	Xb + M (LOO)		Xb + M (10% HV)		Xb + P + M (LOO)		Xb + P + M (10% HV)	
	$\rho(y, \hat{y})$	MSEP	$\rho(y, \hat{y})$	MSEP	$\rho(y, \hat{y})$	MSEP	$\rho(y, \hat{y})$	MSEP
ADG	0.38	0.06	0.39±0.21	0.06±0.03	0.42	0.05	0.43±0.21	0.06±0.03
DFI	0.52	0.17	0.51±0.22	0.16±0.08	0.52	61.23	0.52±0.21	0.16±0.08
FCR	0.61	0.39	0.61±0.20	0.37±0.20	0.62	0.38	0.62±0.19	0.37±0.19
BW180	0.44	99.08	0.47±0.21	93± 36	0.51	90.94	0.52±0.20	85± 34
RFI	0.64	0.12	0.65±0.20	0.12±0.07	0.64	0.12	0.65±0.20	0.12±0.07

