

Gut Microbiome Provides A New Source of Variation to Improve Growth Efficiency in Crossbred Pigs

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Outline

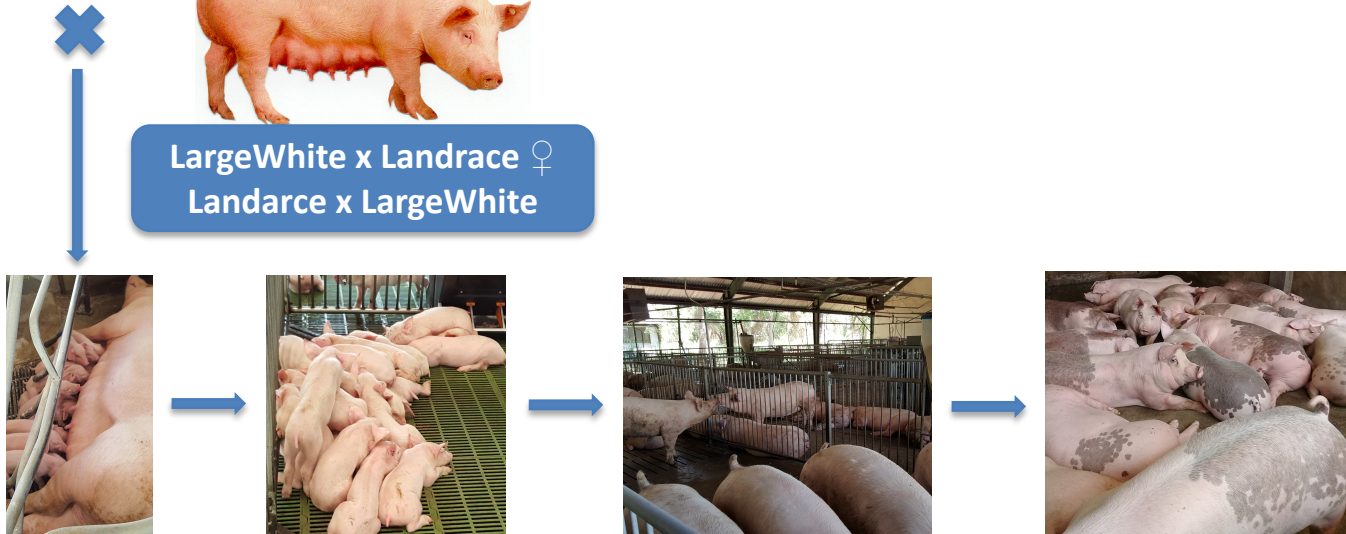
- 1. Does microbiome determine the phenotype?**
- 2. What shapes gut microbiome?**
- 3. Metagenomic predictions**



Duroc ♂
n = 28



LargeWhite x Landrace ♀
Landrace x LargeWhite



Weaning
15 – 24d

Fecal sample
n = 1205

Week 15
115 – 124d

Fecal sample
n = 1295

OffTest
180 – 217d

Fecal sample
n = 1283

Sample preparation → DNA extraction → Library construction

Sequencing → Data quality control

Operational taxonomic units (OTU)
n = 1755



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Statistical models:

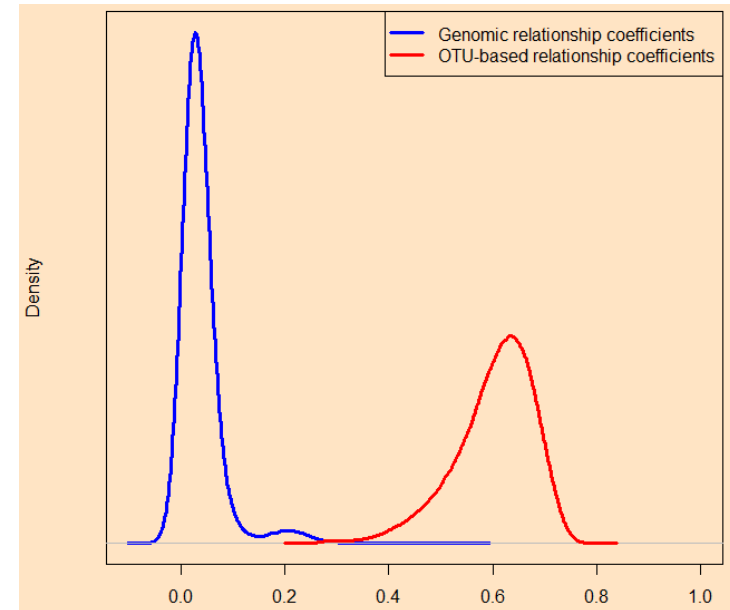
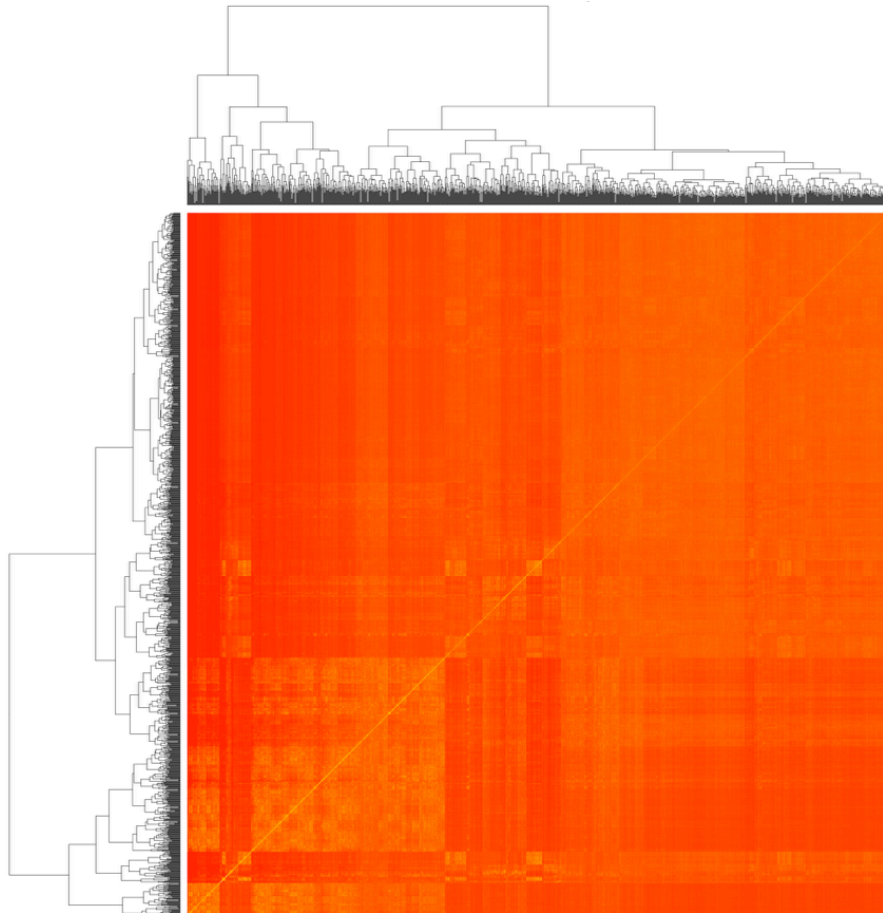
- Fixed effects: sex, contemporary group, age
- Random effects:
 - Cluster
 - Pen
 - Litter
 - Animal (GRM – VanRaden’s method 1)
 - **Microbiome (MRM)**



**Lu et al., 2018,
Microbiome**

Jensen-Shannon distance:

$$D(a, b) = \sqrt{\frac{1}{2} \left(\sum_{i=1}^n a_i \log \frac{a_i}{m_i} + \sum_{i=1}^n b_i \log \frac{b_i}{m_i} \right)}, \quad m_i = (a_i + b_i) / 2$$



Distribution of relationship coefficients

Proportion of total variance of **BF22 explained by random effects.**

	Model 1	Model 2
$\text{Var}_g (h^2)$	0.52 ± 0.05	0.33 ± 0.06
$\text{Var}_m (m^2)$	-	0.47 ± 0.09
Var_{pen}	0.01 ± 0.02	0.01 ± 0.01
Var_{litter}	0.03 ± 0.03	0.02 ± 0.02

Proportion of total variance of **ADG22 explained by random effects.**

	Model 1	Model 3
$\text{Var}_g (h^2)$	0.27 ± 0.06	0.12 ± 0.03
Var_m	-	0.76 ± 0.06
Var_{pen}	0	0
Var_{litter}	0.07 ± 0.04	0.04 ± 0.02

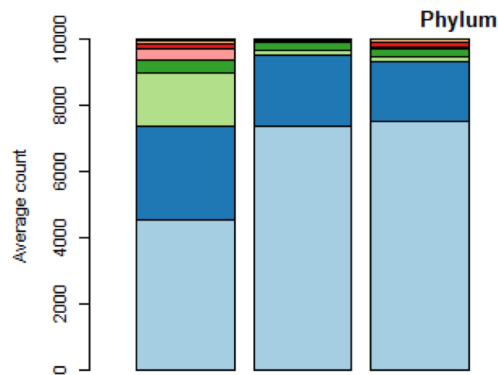
On Meat quality ...

- Microbiome at **off-test** affects **fat-related** traits
- Microbiome at **15 wks** affects **muscle-related** trait
- Microbiome at **weaning** doesn't affect anything

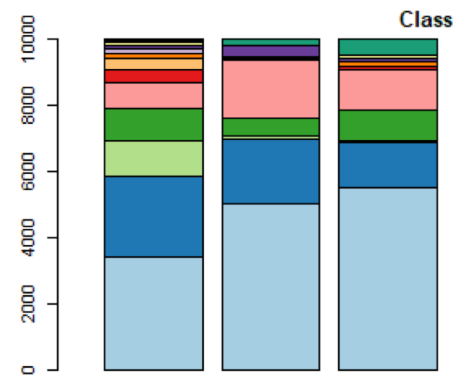
Work in progress

Outline

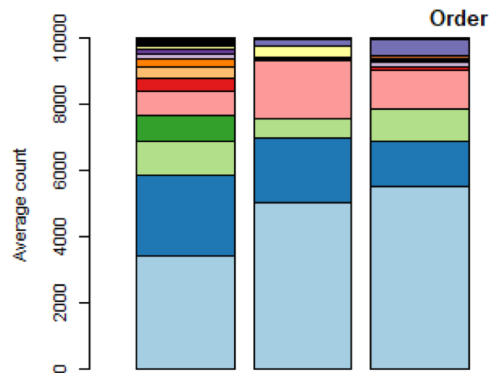
1. Does microbiome determine the phenotype?
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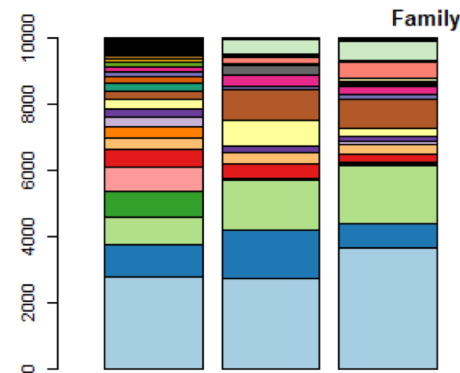
- 10 most abundant phyla
- firmicutes
 - bacteroidetes
 - proteobacteria
 - unassigned
 - fusobacteria
 - spirochaetes
 - actinobacteria
 - synergistetes
 - elusimicrobia
 - deferribacteres



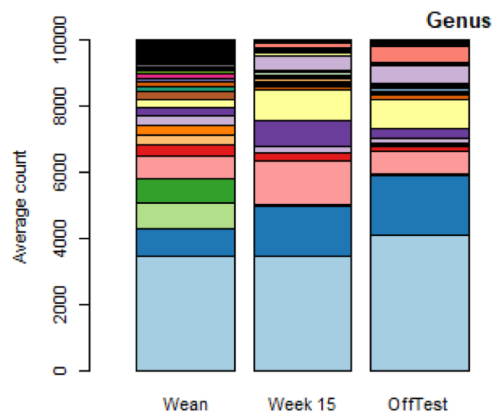
- 10 most abundant classes
- clostridia
 - bacteroidia
 - gammaproteobacteria
 - unassigned
 - bacilli
 - epsilonproteobacteria
 - fusobacteria
 - spirochaetia
 - deltaproteobacteria
 - negativicutes



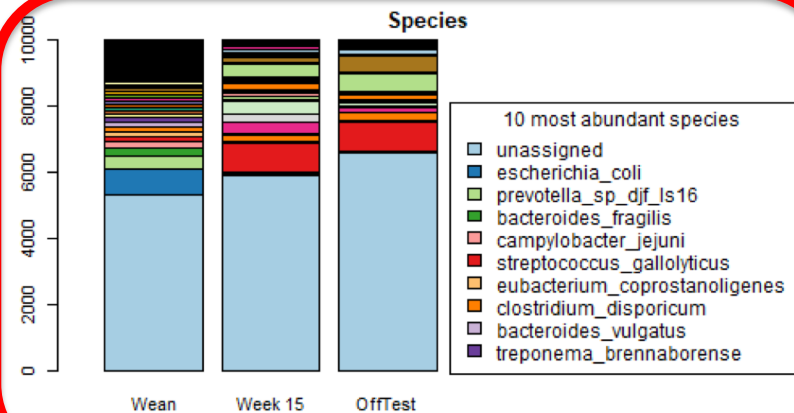
- 10 most abundant orders
- clostridiales
 - bacteroidales
 - unassigned
 - enterobacteriales
 - lactobacillales
 - campylobacteriales
 - fusobacteriales
 - pasteuriales
 - spirochaetales
 - desulfovibrionales



- 10 most abundant families
- unassigned
 - prevotellaceae
 - clostridiaceae
 - enterobacteriaceae
 - bacteroidaceae
 - ruminococcaceae
 - porphyromonadaceae
 - fusobacteriaceae
 - campylobacteraceae
 - eubacteriaceae



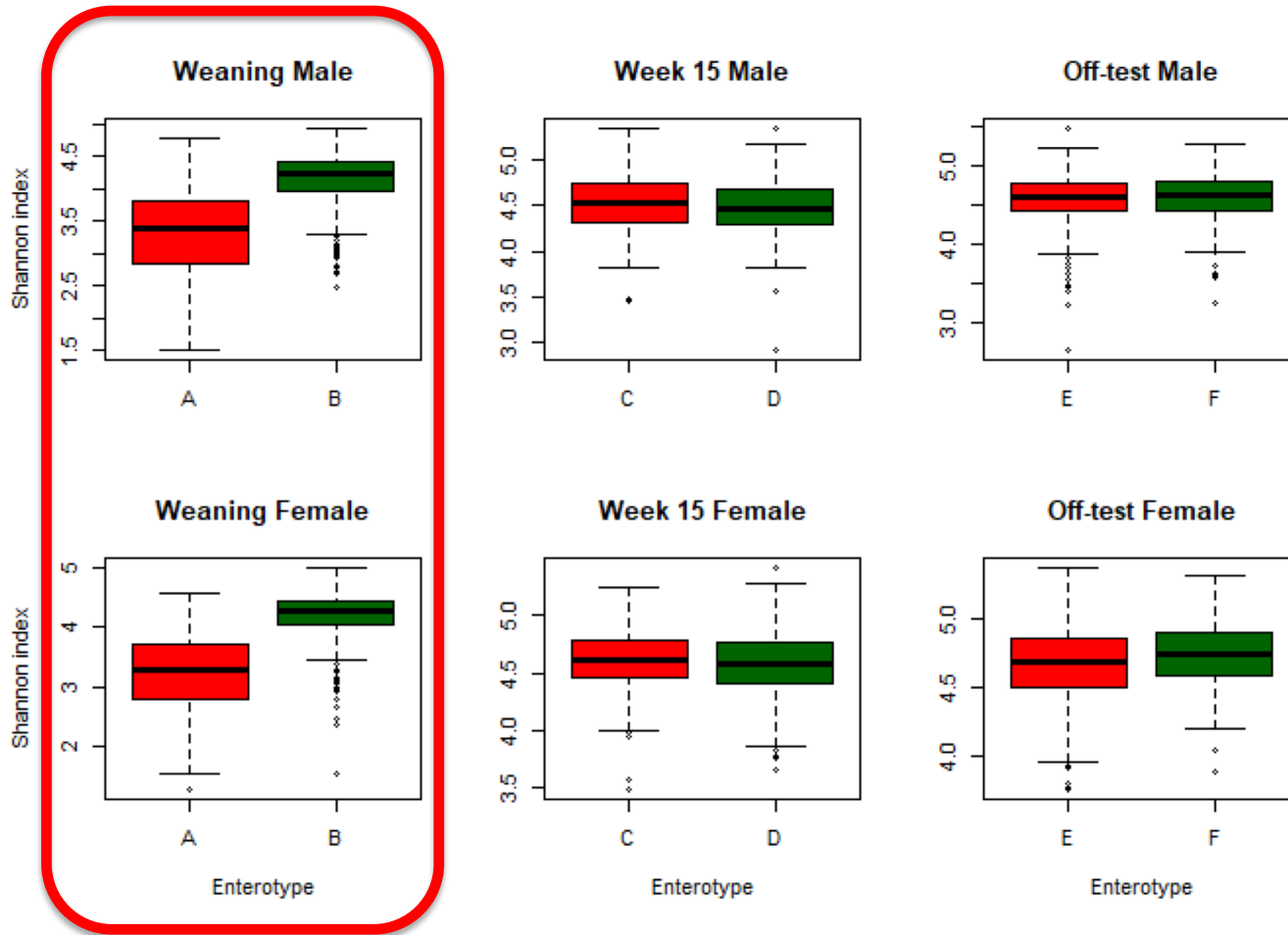
- 10 most abundant genera
- unassigned
 - clostridium
 - escherichia
 - bacteroides
 - prevotella
 - ruminococcus
 - fusobacterium
 - campylobacter
 - eubacterium
 - lactobacillus



- 10 most abundant species
- unassigned
 - escherichia_coli
 - prevotella_sp_djf_Is16
 - bacteroides_fragilis
 - campylobacter_jejuni
 - streptococcus_gallolyticus
 - eubacterium_coprostanoligenes
 - clostridium_disporicum
 - bacteroides_vulgatus
 - treponema_brennaborensis

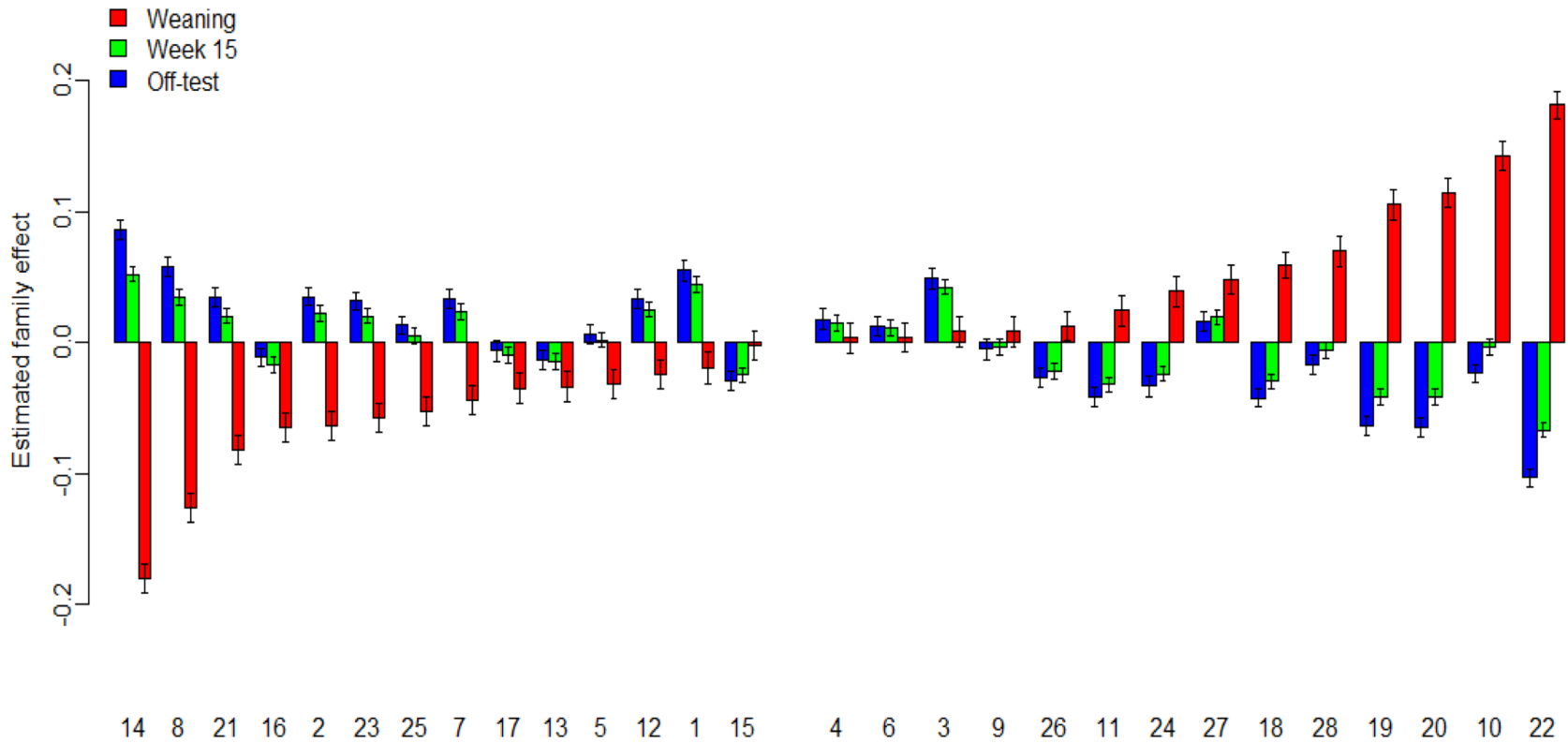
Shannon diversity index

$$d = - \sum_{i=1}^n p_i \ln(p_i)$$



Shannon diversity index

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Estimated genetic parameters of the Shannon index and their standard errors.

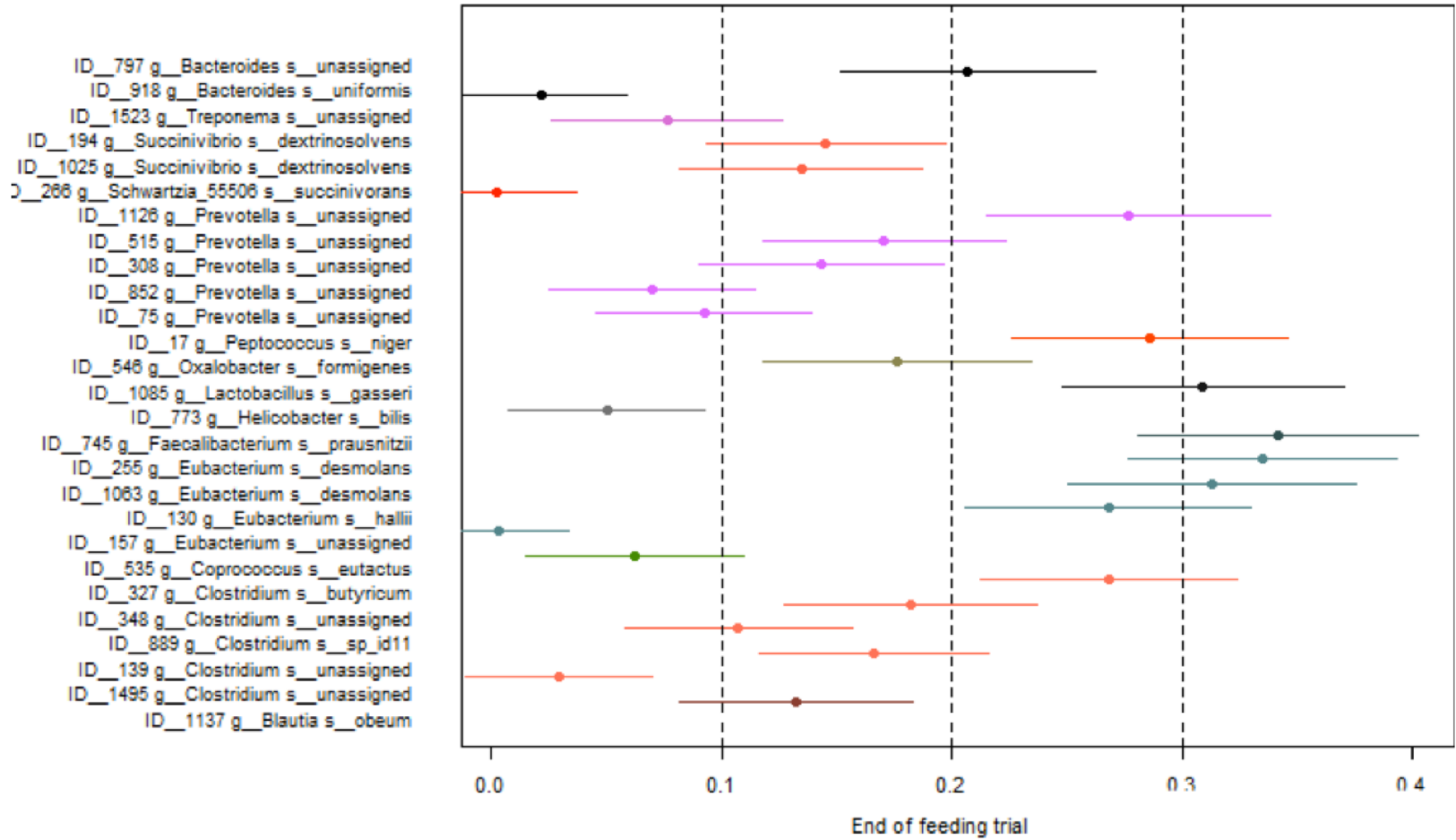
	Weaning	Week 15	Off-test
Weaning	0.04 ± 0.04	-0.01 ± 0.03	-0.04 ± 0.03
Week 15	-0.17 ± 0.48	0.15 ± 0.06	0.15 ± 0.03
Off-test	-0.34 ± 0.47	0.44 ± 0.25	0.33 ± 0.10

Genomic/phenotypic correlations between BF, ADG, and Shannon index at weaning and week 15

	Sha_w	Sha_15	BF_18	BF_22	ADGw_14	ADG14_22
Sha_w	-	-	0.05±0.03	0.06±0.03	0.04±0.03	0.07±0.03
Sha_15	-	-	-0.10±0.03	-0.08±0.03	-0.09±0.03	-0.09±0.03
BF_18	0.42±0.50	-0.53±0.23	-	-	0.43±0.03	0.31±0.03
BF_22	0.52±0.49	-0.45±0.25	-	-	-	0.45±0.03
ADGw_14	-0.73±0.51	-0.53±0.32	0.29±0.32	-	-	-
ADG14_22	0.44±0.48	-0.53±0.29	0.10±0.29	0.24±0.28	-	-

What about single-OTU heritabilities?

Heritability for significant OTUs



Metagenomic predictions

Objectives:

Can Machine Learning help in understanding microbiome-phenotype relationships?



Submitted to Scientific Reports

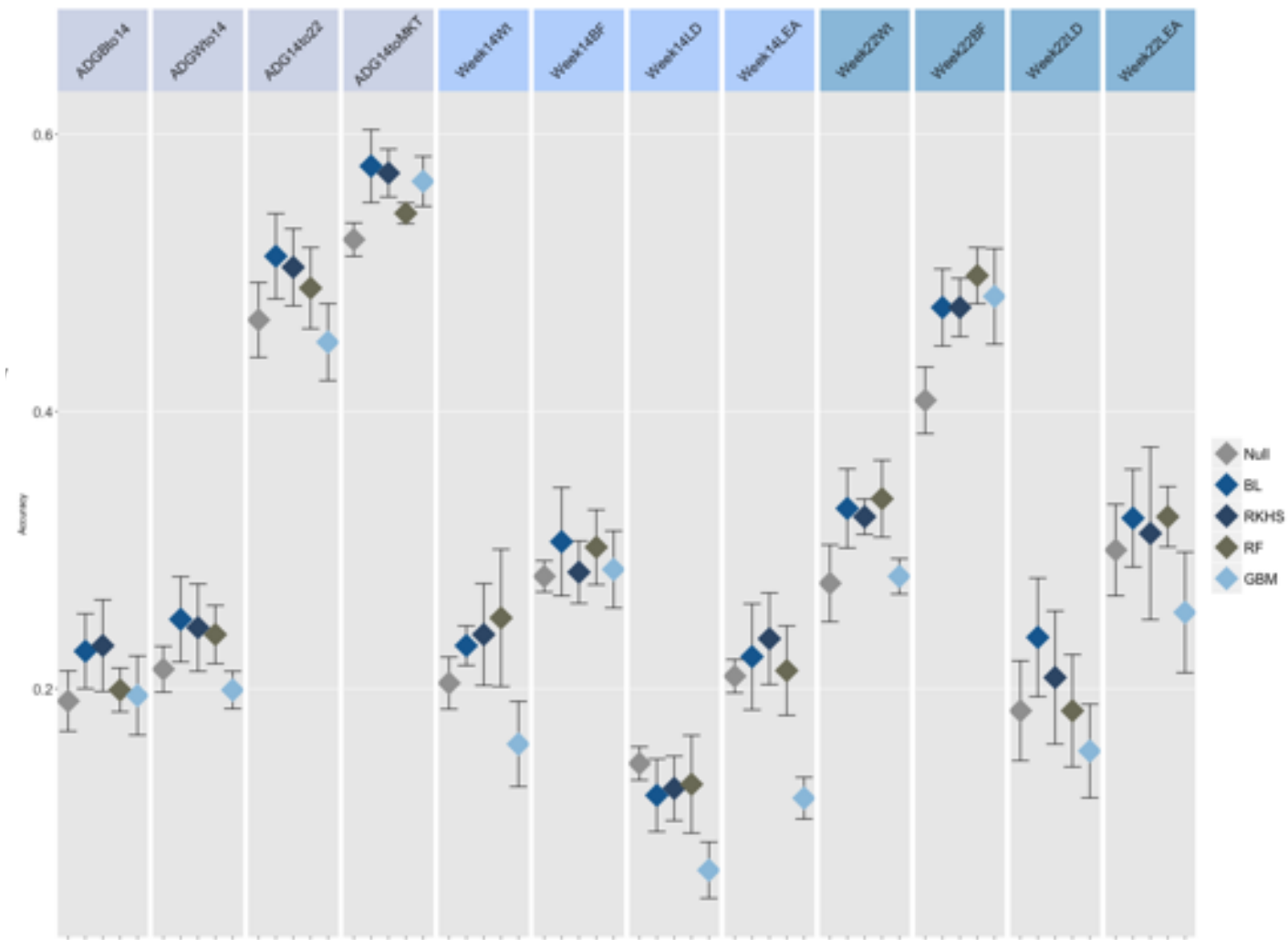
Prediction:

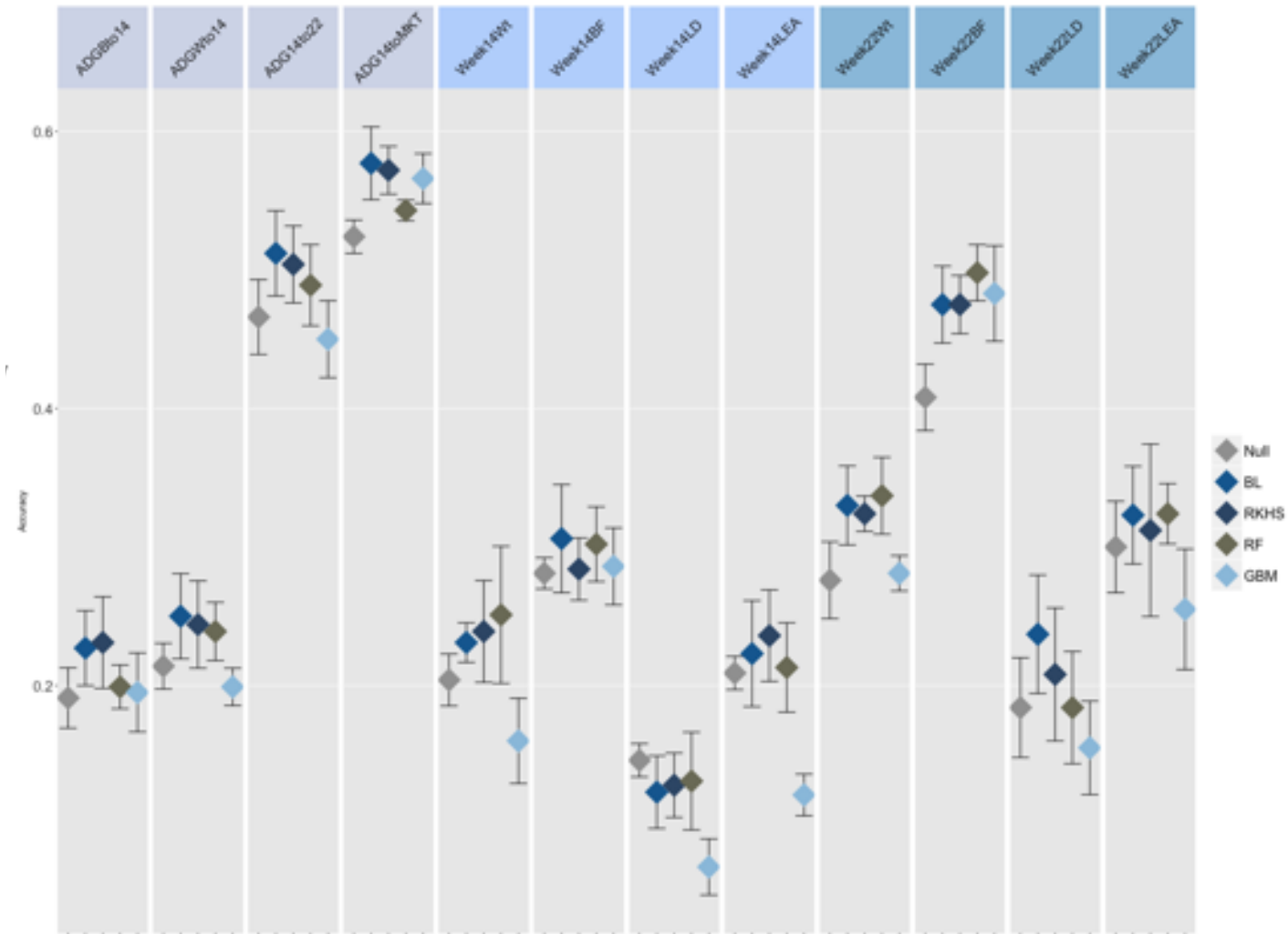
- Reproducing Kernel Hilbert Spaces regression
- Bayesian LASSO
- Random Forest
- Gradient Boosting

Classification:

- Random Forest
- Recurrent Neural Network



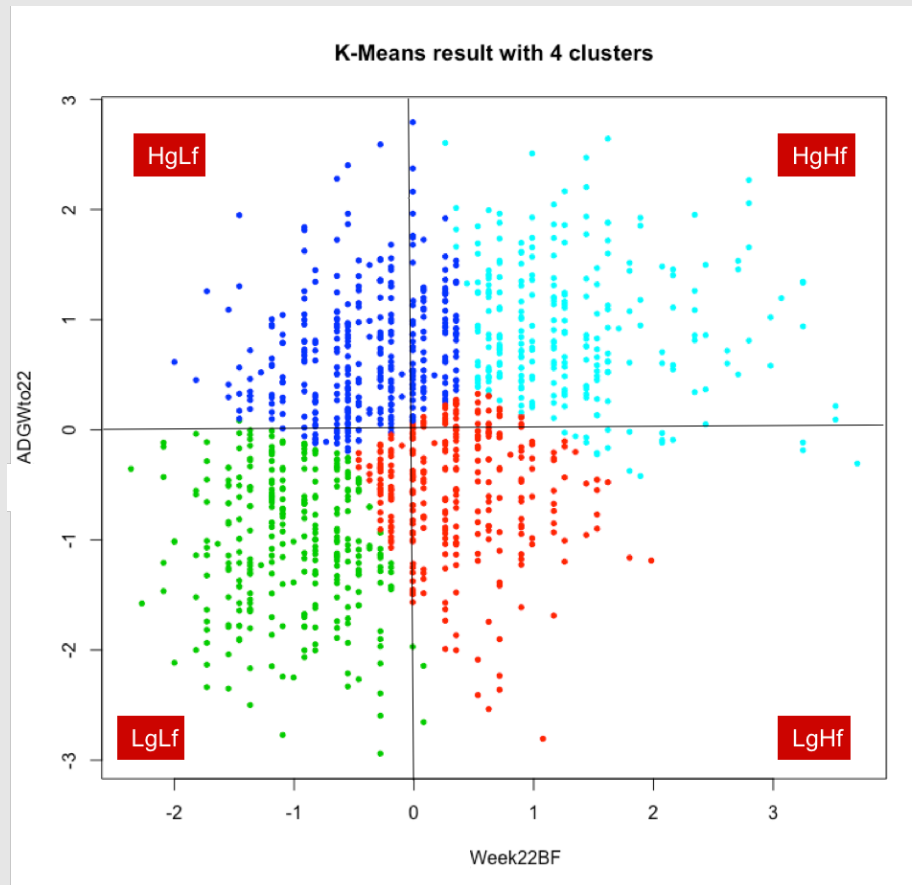




RKHS > BL > RF > GBM

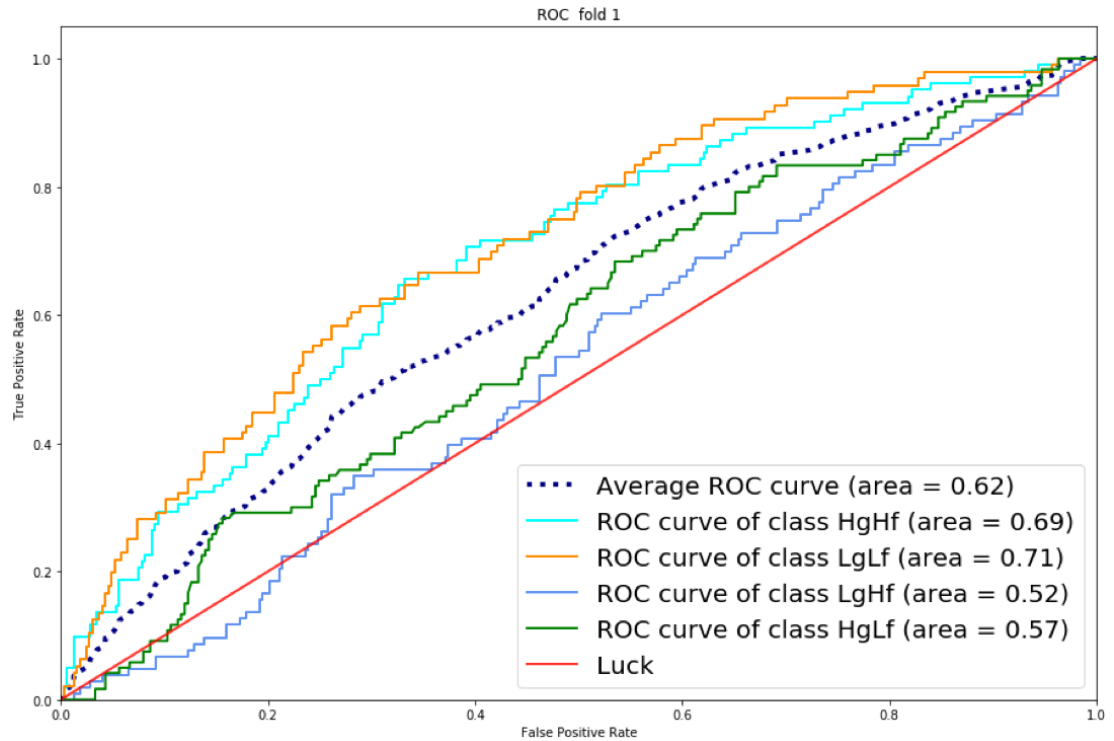
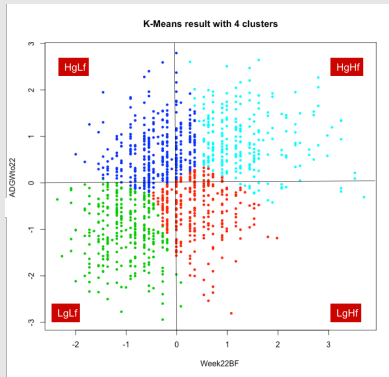
Classification

- ▶ k-means groups at 22wk based on **adg** and **bf** (all microbiome timepoints) **HgHf**, **LgLf**, **LgHf**, **HgLf**



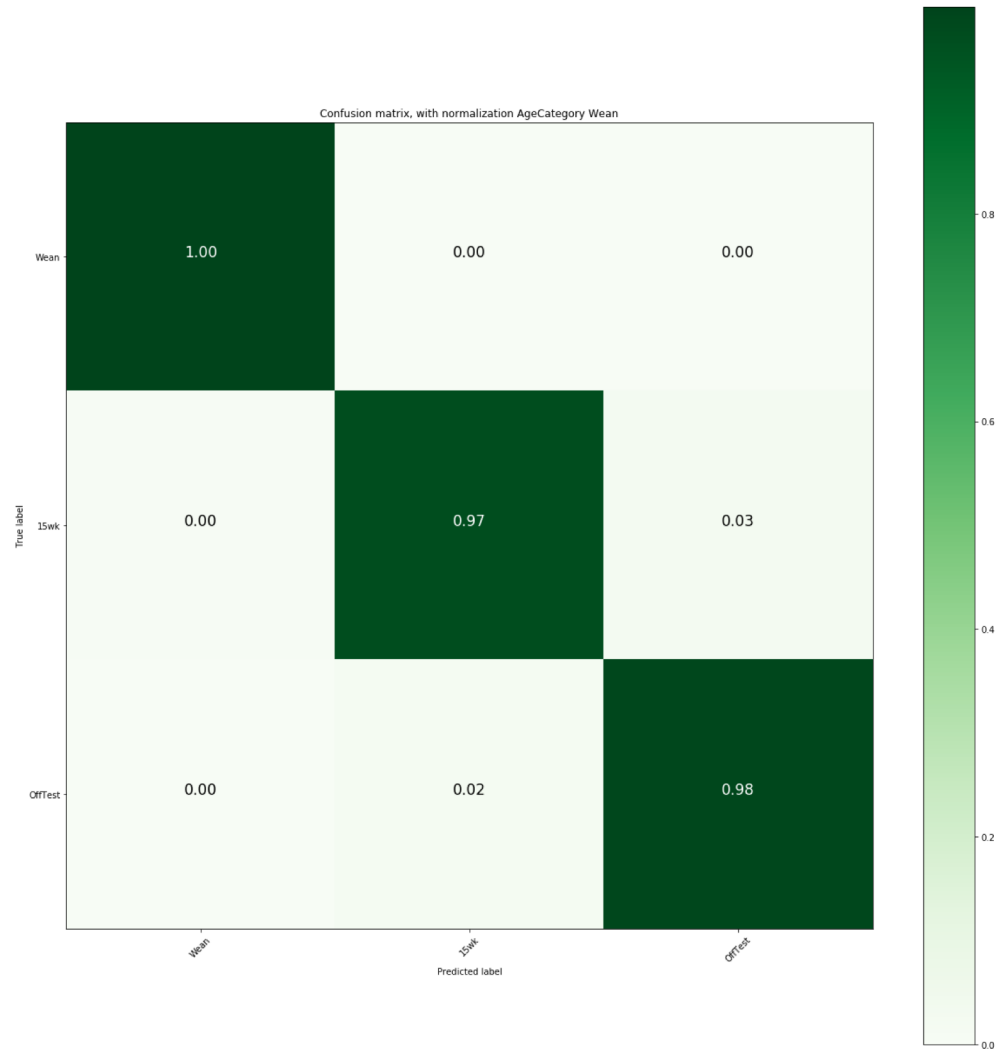
Classification

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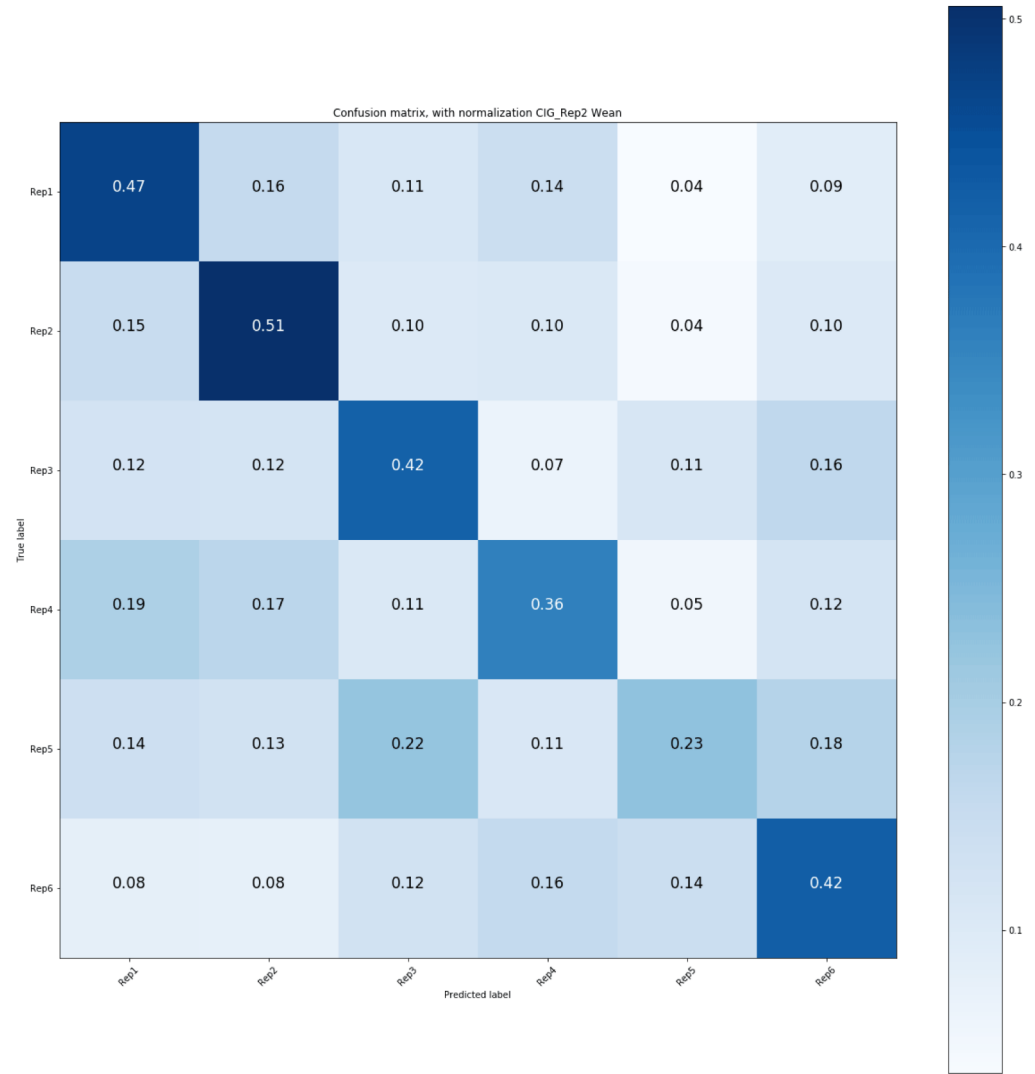
**Further
classification:
timepoint**

Further classification: timepoint



**Further
classification:
contemporary
group**

Further classification: contemporary group



Conclusions

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Acknowledgements

- North Carolina Pork Council
- National Pork Board
- North Carolina Agricultural Foundation

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Thank you for your attention!