

Decoding the Genetic Dialogue: Rumen Microbiome and Host Genome Interaction in Enteric Methane Emission

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Rumen: A complex microbial ecosystem

- Importance in digesting fibrous plant material
- Key groups: Bacteria, Archaea, Protozoa, Fungi
- Archaea (methanogens) uses hydrogen, a byproduct, and produces methane
- Variability in Methane Emission
 - Feed composition: High fiber vs. low fiber
 - Microbial population
 - Animal factors: Age, health, and genetics

Co-evolution of cows and their rumen microbiome

- Cow-Microbiome interactions
 - Host systems (immune) shaping microbial populations
 - Genetic variants linked to microbiome structure and function
- Tools for studying rumen microbiome and host genetics
 - Metagenomics and 16S rRNA sequencing
 - Heritability of microbial traits
 - GWAS
- Selective breeding to optimize microbial composition
 - Reduce methane emission
 - Increase feed efficiency

Host (cow) genetics control rumen microbiome

- Results lack consistency
- Low sample sizes
- Large non-genetic variation

PLOS GENETICS

OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

Host genetics and the rumen microbiome jointly associate with methane emissions in dairy cows

Gareth Frank Difford , Damian Rafal Plichta, Peter Løvendahl, Jan Lassen, Samantha Joan Noel, Ole Højberg, André-Denis G. Wright, Zhigang Zhu, Lise Kristensen, Henrik Bjørn Nielsen, Bernt Guldbrandtsen, Goutam Sahana 

Version 2 Published: October 12, 2018 • <https://doi.org/10.1371/journal.pgen.1007580>



Volume 14, Issue 8

JOURNAL ARTICLE

Bayesian modeling reveals host genetics associated with rumen microbiota jointly influence methane emission in dairy cows

Qianqian Zhang , Gareth Difford , Goutam Sahana, Peter Løvendahl, Jan Lassen, Mogens Sandø Lund, Bernt Guldbrandtsen, Luc Janss

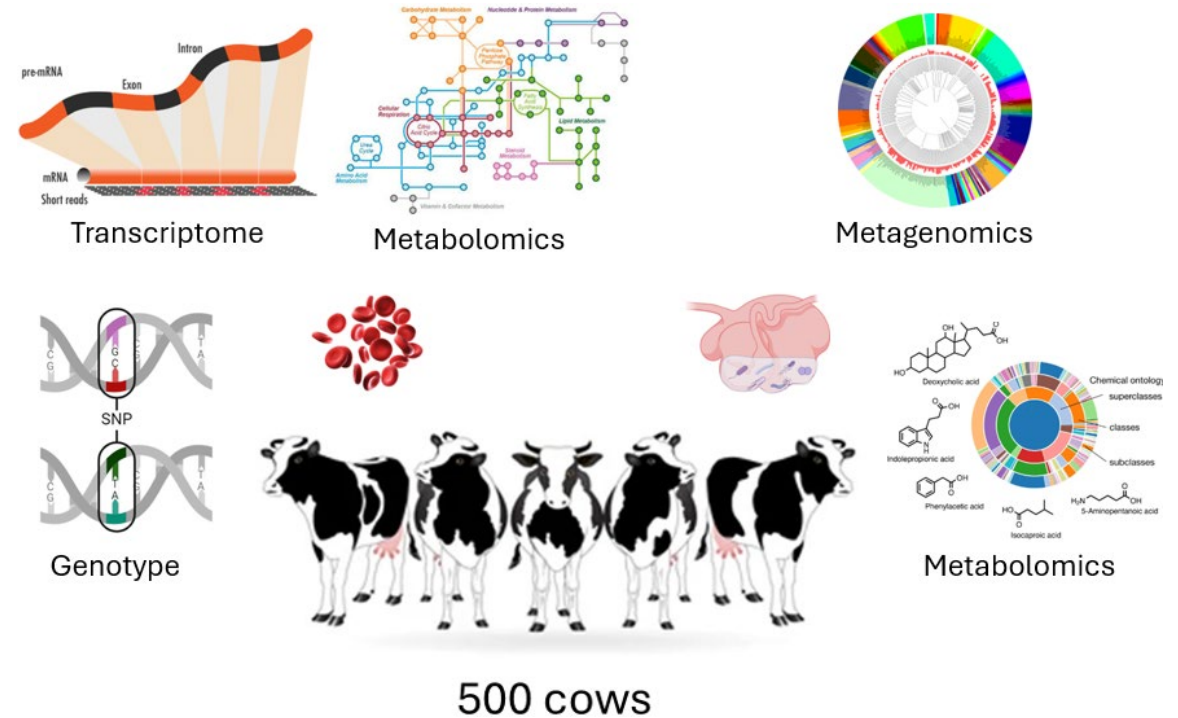
The ISME Journal, Volume 14, Issue 8, August 2020, Pages 2019–2033, <https://doi.org/10.1038/s41396-020-0663-0>

Objectives

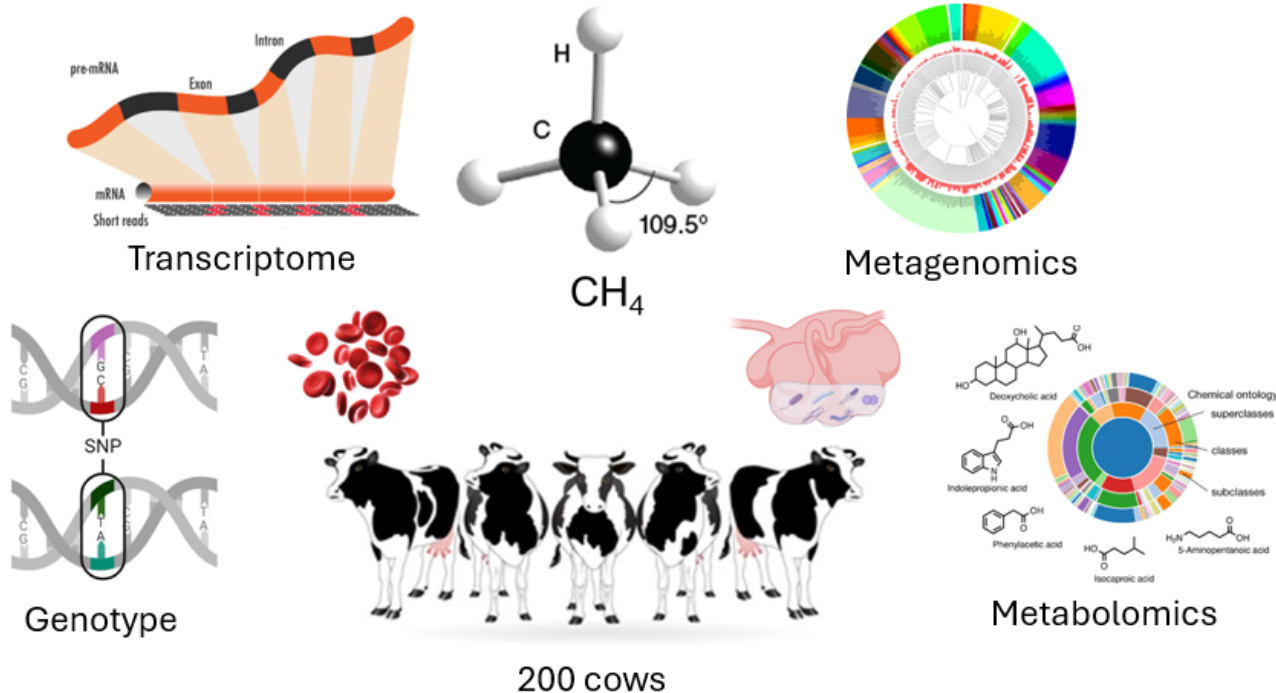
- Understanding on rumen microbiome and host genetics interaction
- Developing tools for microbiome study and routine use
- Developing genomic prediction model for methane and feed efficiency including metagenome and other omics data

Data-1: 500 Holstein cow from one farm

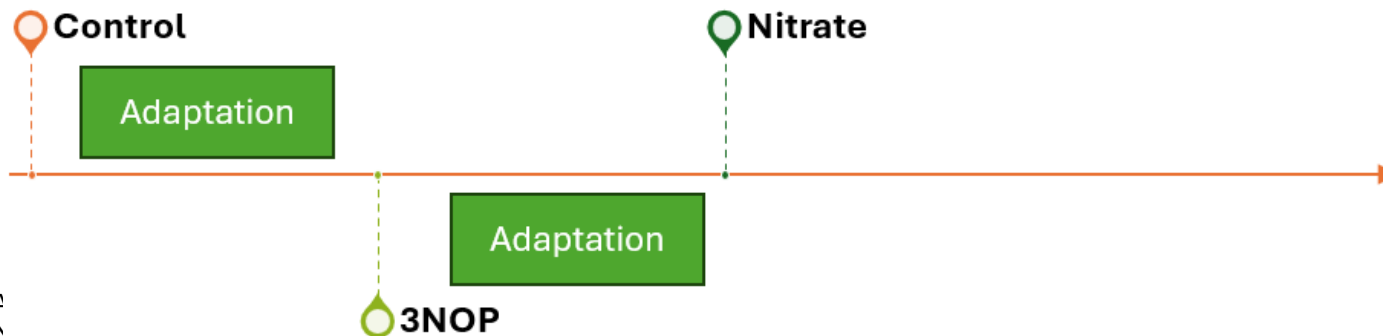
- Rumen samples
 - Metagenome sequenced
 - 16S rRNA
 - Rumen metabolites
- Blood
 - Metabolites
 - Transcriptome
- Phenotypes
 - Methane – sniffer
 - Feed intake – CFIT
 - All 'routine' phenotypes
- Genotypes imputed to WGS



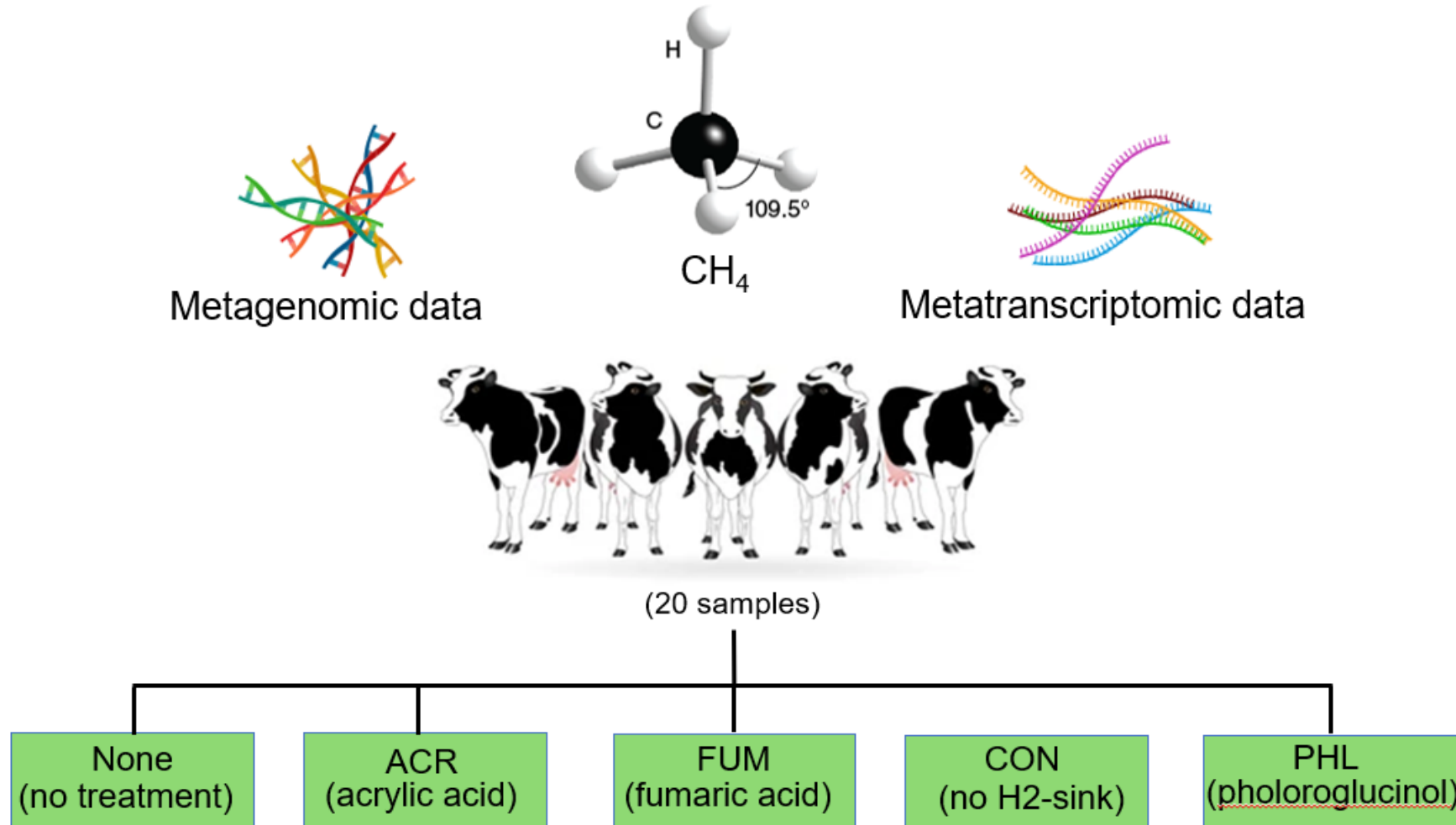
Data-2: 200 cows on feed additive treatments



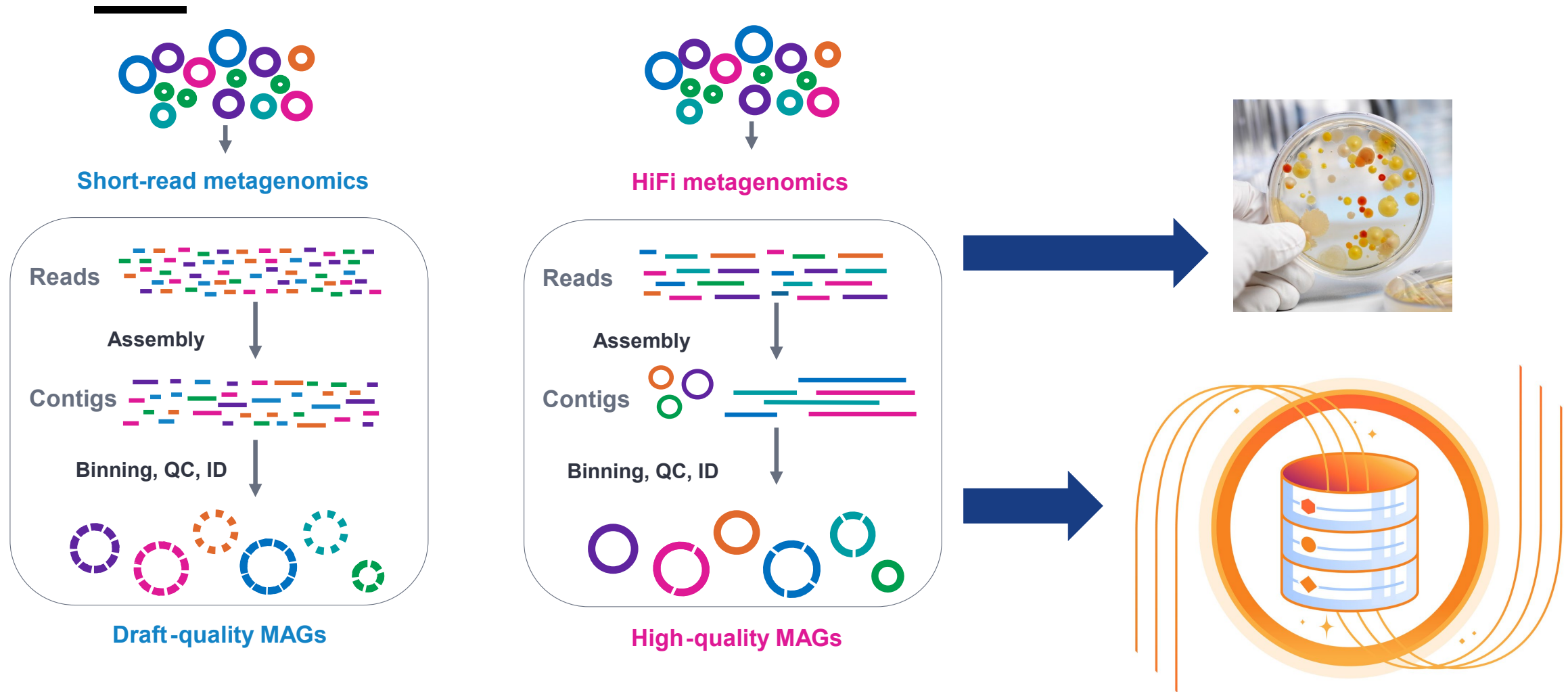
- 200 first lactation cows
- 50 each will be followed in 2nd and 3rd lactation



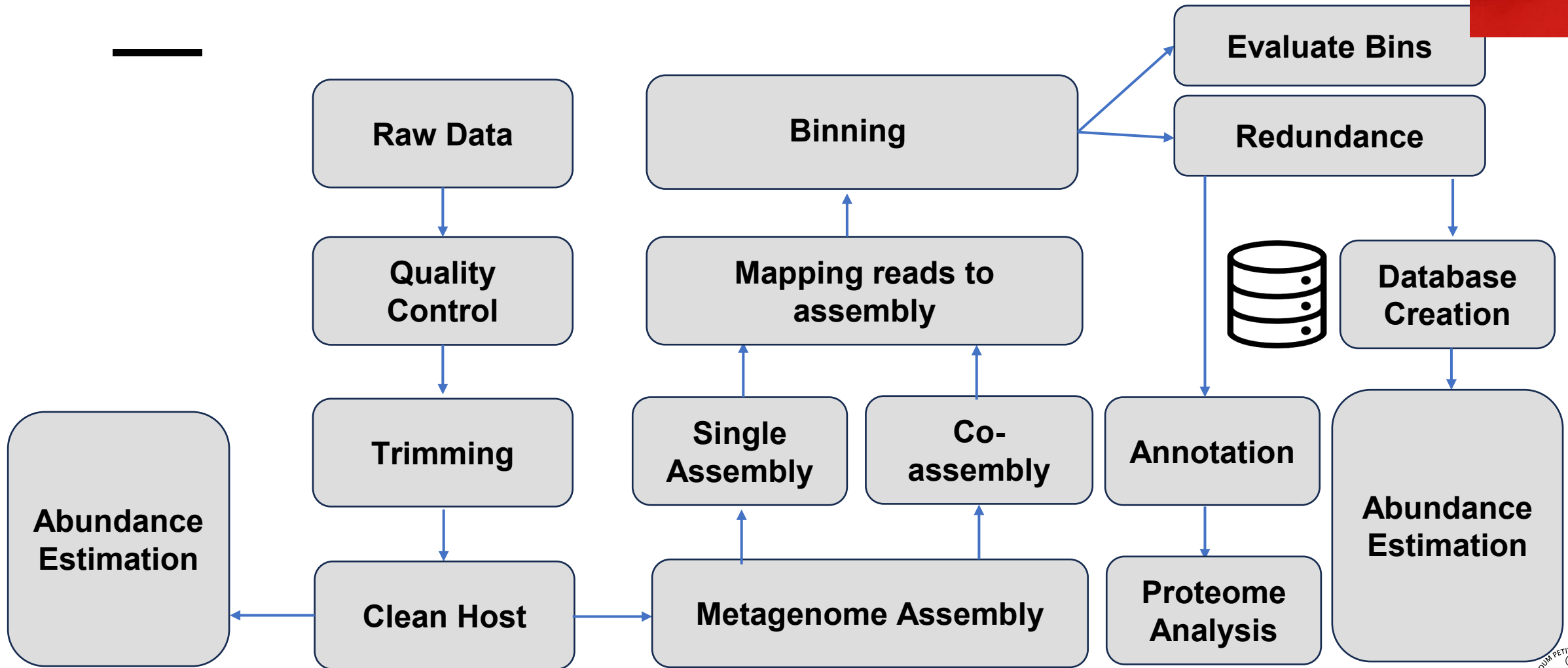
Data-3: Intensive study



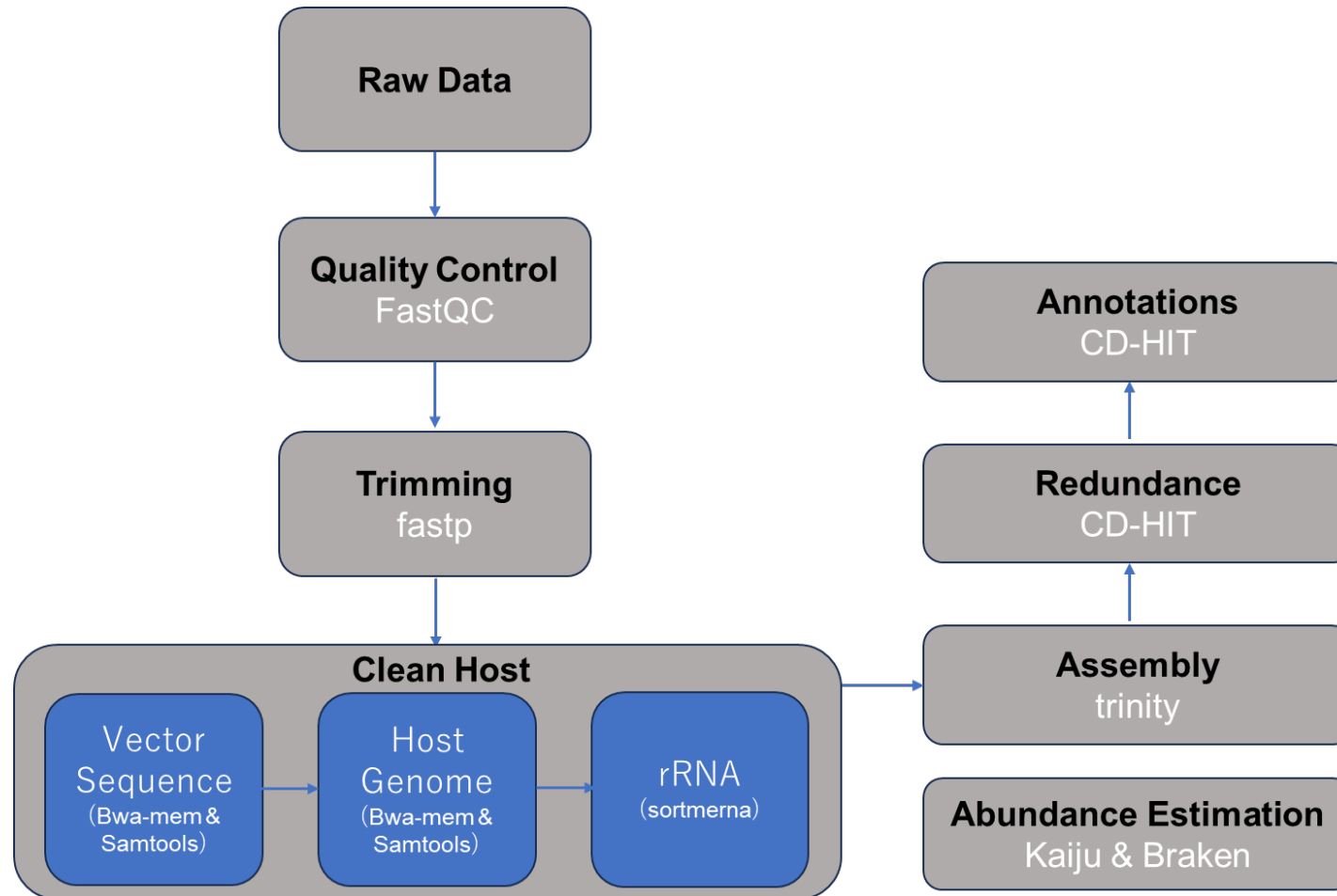
Data-4: Long read sequencing for annotation



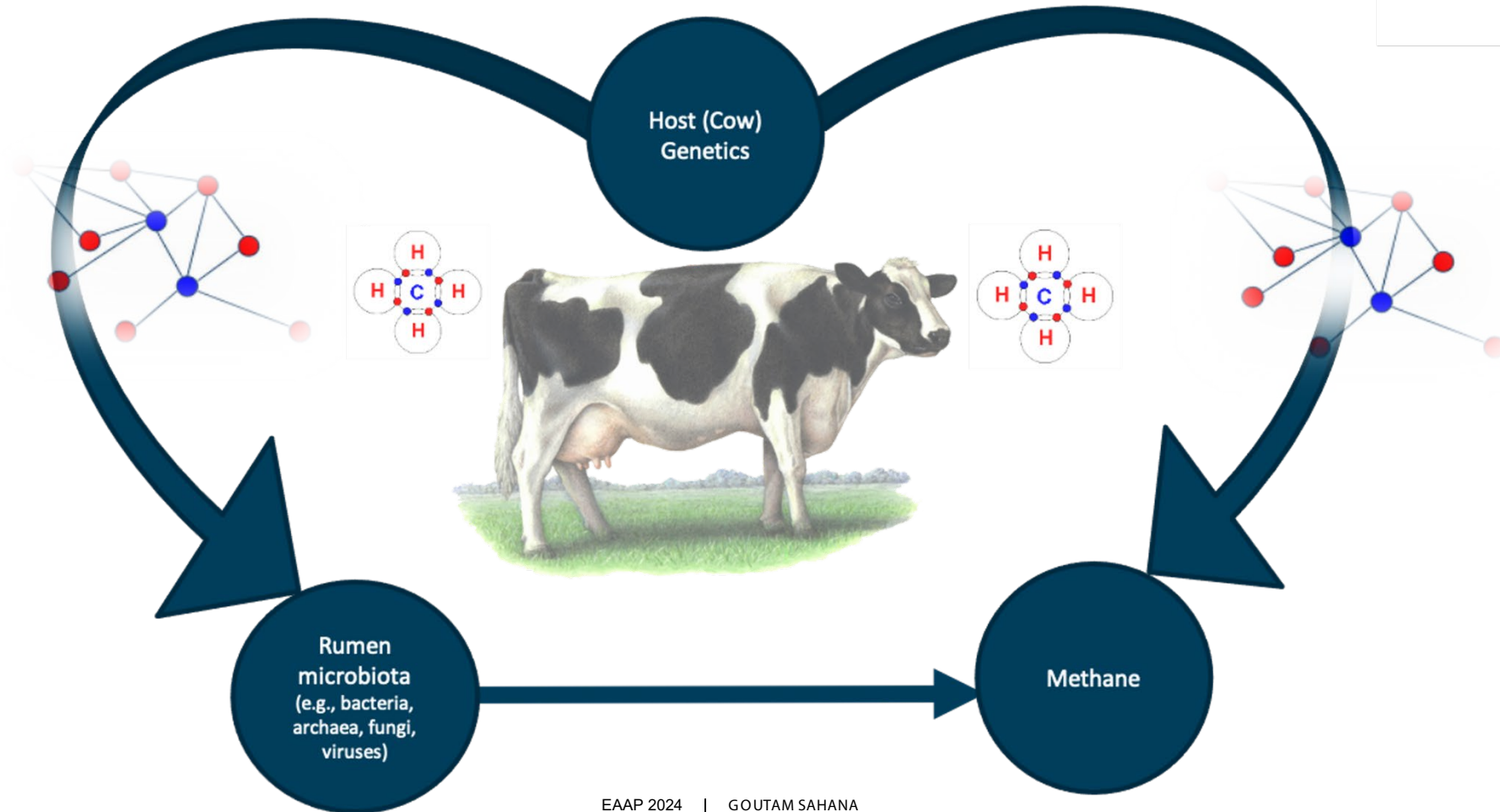
Computational workflow - MetaG



Computational workflow - MetaT

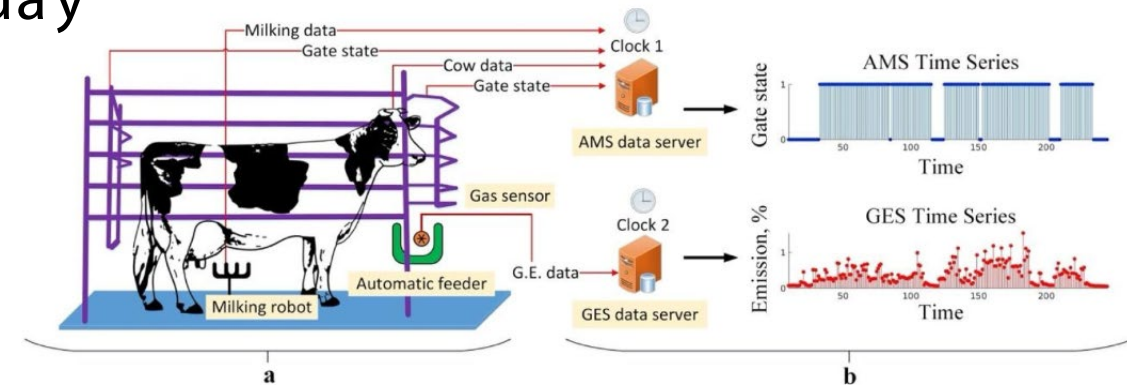
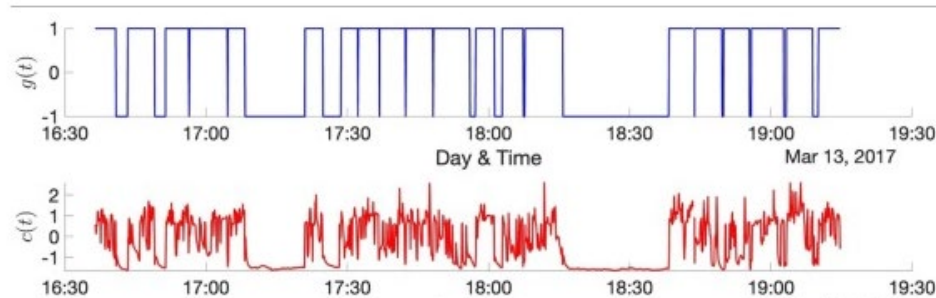


Model development



Methane phenotyping

- 16000 dairy cows recorded
- Daily measurements from 14 farms (5 CFIT)
- Methane registrations from ~3300 cows / day
- 38 sniffers



58.14 Genetic parameters of Methane emission in Danish Jersey dairy cows
Rikke Krogh Nielsen

Statistical model development



GENETICS, 2021, 219(2), iyab130
DOI: 10.1093/genetics/iyab130
Advance Access Publication Date: 7 August 2021
Genomic Prediction

Genetic evaluation including intermediate omics features

Ole F. Christensen ^{1,*} Vinzent Bömer,¹ Luis Varona,² and Andres Legarra ³


NextGP.jl

Search docs

Home

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- Unstable

Modules

Examples

- Example
- PBLUP
- BWGR
- Multiple marker sets
- BayesLV

Citation

Version v0.2.0

Home

[Edit on GitHub](#)

About

What is available

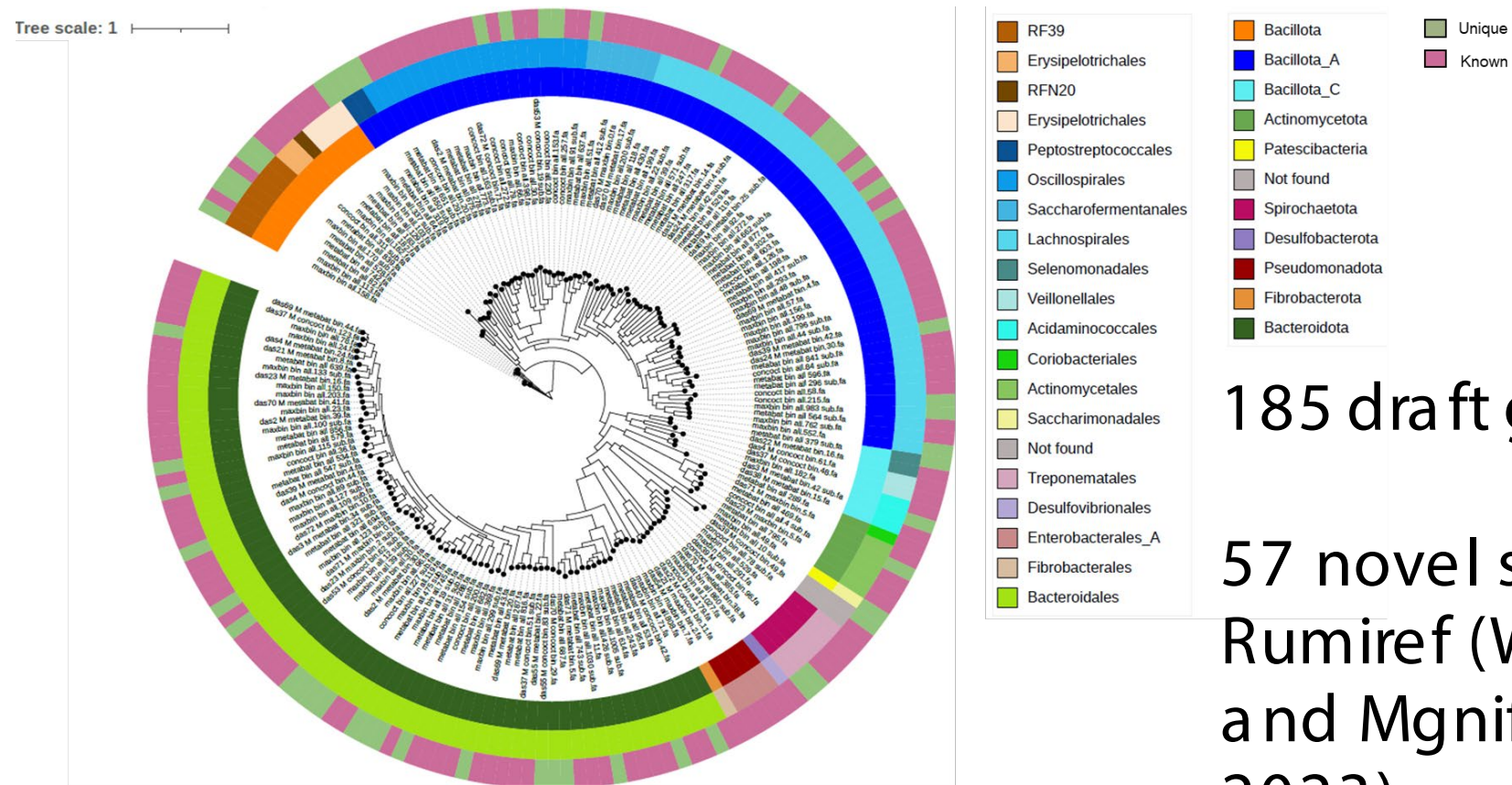
- Currently, only univariate analysis are implemented
- Rely on [StatsModels.jl](#) package for model formulation and fixed effects definitions
- Any kind of random effects including random marker effects
 - Additive genetic effects
 - Maternal effects
 - Permanent environmental effects
- Bayesian whole-genome regression methods
 - BayesPR (BayesA<->BRR)
 - BayesB
 - BayesC
 - BayesR
 - BayesLV
- Correlated marker effects (only for BayesPR)
- Unknown (co)variance components (e.g., marker, additive genetic, residual...)
- It is users responsibility to make sure that the order of the individuals in the data sets aligns

Pkg Registry

To install the latest official version, please use the following standard Julia command.

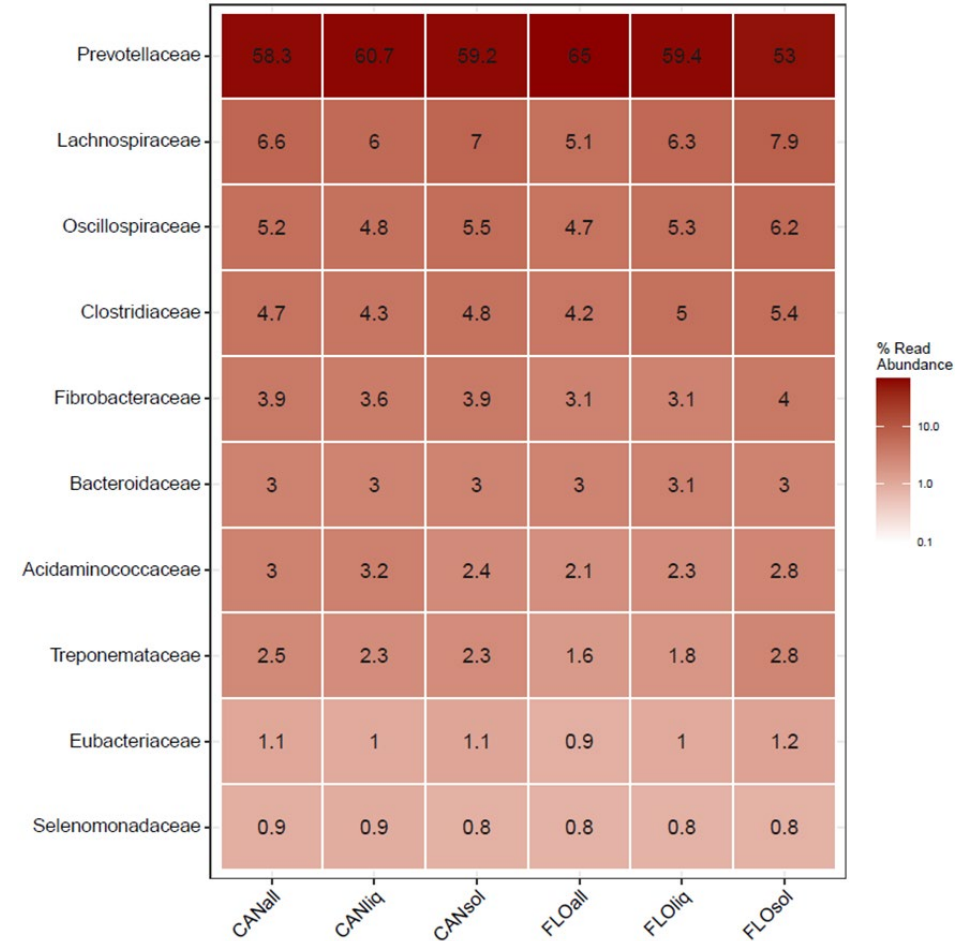
```
using Pkg
pkg> Pkg.add("NextGP")
```

Novel species from intensive study



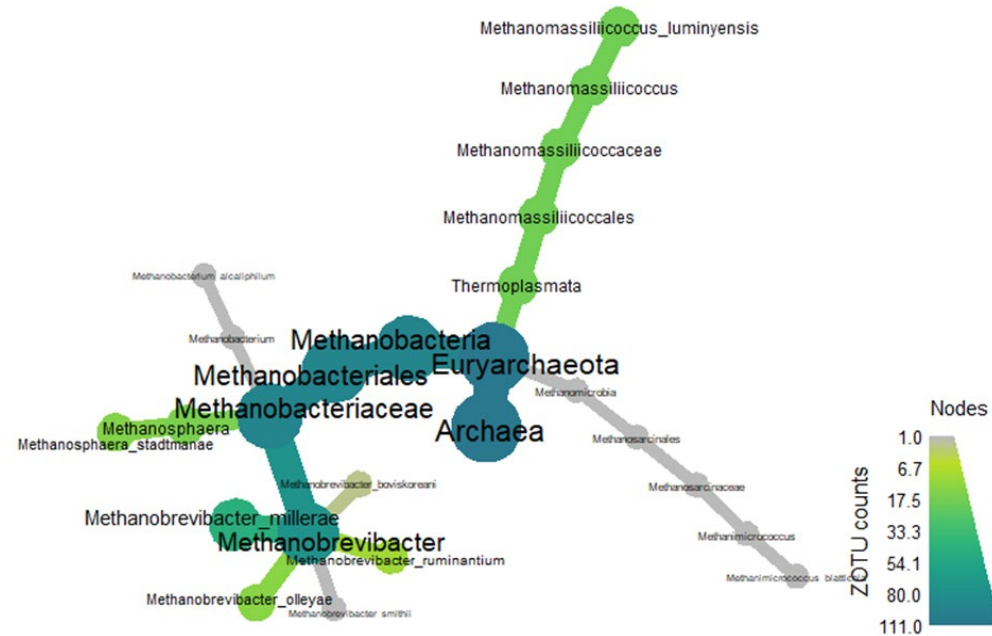
Sampling method –intensive study

- Sampling comparison
 - Flora scoop vs. Canula
 - Liquid fraction vs. Solid fraction vs. Mix



A portrait of a young man with dark hair, wearing glasses and a grey button-down shirt. He is looking directly at the camera against a blue background.

16S rRNA
Archaea



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Work is in progress

1. Pipelines for bioinformatics analysis ready
2. Long read sequencing for annotation
3. Understanding pathways for H₂ utilization
4. 16S rRNA vs. metagenomics
5. Comparison of metabolites from blood and rumen
 1. Indicator traits?
6. Prediction of methane and feed intake using
 1. Genome + metagenome
 2. Genome + metagenome + omics (metabolites, transcriptom)

Mælkeafgiftsfonden

/nnovation Fund Denmark



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Thank you for your attention