



Re-Livestock

RESILIENT FARMING SYSTEMS

Practical: Estimation of genetic parameters for sniffer methane emissions

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Overview: First part

1. Starting with Jupyter Notebook in Annuna (WUR)
2. Opening Github to see the files
3. Cloning files from Github to Jupyter Notebook
4. Ready for practicals

How to connect to the WUR server

<https://notebook.anunna.wur.nl>



How to clone files/folders from Github to Jupyter

1. Open Jupyter Notebook online in your web browser.
2. Click on the “New” button in the top right corner of the screen.
3. Select “Terminal” from the dropdown menu.
4. In the terminal window, type the following command:

```
git clone https://github.com/ogrecio/RelivestockMethaneCourse
```

Files in RelivestockMethaneCourse/Day2 folder

GITHUB

1. Database to run in ASReml: `dat.dat`
2. Pedigree to run in ASReml: `ped.ped`
3. Scripts to run ASReml: `uni.as`, `biv.as`, `RR.as`
4. Bash file to run ASReml: `bash2.sh`

useful commands Linux

useful commands Linux

ls (to see files) ls -d */ (to see directories)

less (to see the files inside) less -S (useful for genotypes) q
(to quit from less)

head (head of the file)

wc -l file (number of rows)

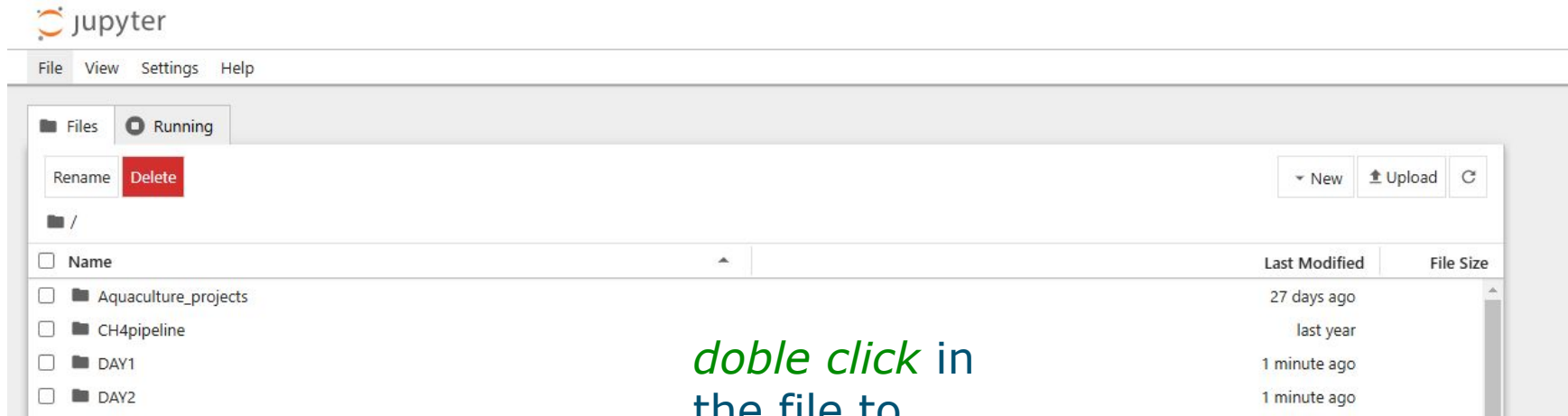
awk '{print NF; exit}' file (number of columns)

cd folder (change directory) cd .. (comeback to the previous level)

rm -rf directory or rm file

How it looks

RelivestockMetaneCourse/Day2



The screenshot shows the JupyterLab file browser interface. The top menu bar includes File, View, Settings, and Help. Below the menu bar, there are tabs for Files and Running. The Files tab is active, showing a directory structure. The directory structure includes a root folder (/) and several subfolders: Aquaculture_projects, CH4pipeline, DAY1, and DAY2. The interface also includes buttons for Rename, Delete, New, Upload, and Refresh. A table lists the files and folders with their last modified times and file sizes.

Name	Last Modified	File Size
Aquaculture_projects	27 days ago	
CH4pipeline	last year	
DAY1	1 minute ago	
DAY2	1 minute ago	

double click in
the file to
edit: .as, .sh

How Terminal look like

```
KLW          Scripts    VSNi         VSNi-2024-11-07 phen_compar    test2.ipynb
MiXBLUP      THI         VSNi-2024-10-08 VSNi-2025-01-07 plot_timeseries_cow59_event1.pdf

manza003@node251:~$ less output.txt
manza003@node251:~$ git clone https://github.com/cmanzanillap/DAY2
Cloning into 'DAY2'...
remote: Enumerating objects: 5, done.
remote: Counting objects: 100% (5/5), done.
remote: Compressing objects: 100% (5/5), done.
remote: Total 5 (delta 0), reused 0 (delta 0), pack-reused 0 (from 0)
Unpacking objects: 100% (5/5), 295.31 KiB | 4.10 MiB/s, done.
manza003@node251:~$ ls
Aquaculture_projects  MiXBLUP      THI         VSNi-2024-10-08 VSNi-2025-01-07    plot_timeseries_cow59_event1.pdf
CH4pipeline           R            Untitled.ipynb VSNi-2024-10-21 jupyterhub_slurmspawner_55605067.log reading_rawCH4data.ipynb
DAY2                  Relivestock  Untitled1.ipynb VSNi-2024-10-30 output.txt          script_slurm.sh
KLW                   Scripts      VSNi         VSNi-2024-11-07 phen_compar        test2.ipynb

manza003@node251:~$ git clone https://github.com/cmanzanillap/DAY1
Cloning into 'DAY1'...
remote: Enumerating objects: 5, done.
remote: Counting objects: 100% (5/5), done.
remote: Compressing objects: 100% (5/5), done.
remote: Total 5 (delta 0), reused 0 (delta 0), pack-reused 0 (from 0)
Unpacking objects: 100% (5/5), 3.04 MiB | 7.83 MiB/s, done.
manza003@node251:~$ cd DAY2
manza003@node251:~/DAY2$ ls
DB4co4.dat  ped4gen_ord2.ped  test.as
manza003@node251:~/DAY2$ head DB4co4.dat
98905,1,69,3,88,13, NA, NA, NA,6172.62, NA, NA, NA,98905
98905,1,71,3,102,53,365.00,1957.99,1.96,7370.22,0.03, NA, NA,98905
98905,1,69,3,88,8, NA, NA, NA,7053.29, NA, NA, NA,98905
98905,1,71,3,102,52,601.92,2360.75,1.96,7876.21,0.06, NA, NA,98905
98905,1,69,3,88,12, NA, NA, NA,6581.15, NA, NA, NA,98905
```

Files inside Day2

<https://github.com/cmanzanillap/DAY2>

1. Input file ASReml: `uni.as`,
`biv.as`, `RR.as`
2. Data file for ASReml: `dat.dat`,
`datRR.dat`
3. Ped file for ASReml: `ped.ped`
4. Bash file: `bash2.sh`

Files needed to run ASReml

1. Input file (.as file)
2. database (.dat file)
3. pedigree (.ped file)

Lets run ASReml

1. Open settings ➡ New ➡ Terminal

2. Type `cd Day2`

3. Load modules

```
ml use /lustre/shared/Courses/RELIVESTOCK2025/modules
```

```
module load asreml/4.2.1
```

4. Run ASReml: `time asreml -n uni.as # biv.as, RR.as`

5. or Run Bash file: `bash2.sh`

6. EXERCISE: Complete the bivariates and try a trivariate (if you want)

7. Check the outputs `.asr`, `.pvc`, `.sln`

Example of .as file

```
!W 10000 !CYCLE !RENAME !ARG 1 2 3 4 5 6 7 8 // !DOPART $1
Title: test_course
ID !P
herd !A
HYS !I 41
parity !I 3
ACC
lact_week
avgCH4
speaks
npeaks
avgCO2
ratio
CH4gr
MeI
npeaks100 != upeaks !*100
peID !A 1173

ped.ped !MAKE !CSV !SORT
dat.dat !SKIP !MAXIT 2000 !AISING !continue !TOLERANCE !MVINCLUDE

### UNIVARIATE N ###

!PART 1

avgCH4 ~ mu HYS lact_week ACC.parity !r nrm(ID) peID

VPREDICT !DEFINE
P Var_P 1 2 3 # 4
H h2 2 4
H c2 1 4
```

First line

```
!W 10000 !CYCLE !RENAME !ARG 1 2 3 4 5 6 7 8 // !DOPART $1  
Title: test course
```

workspace

Making sure it run in cycle for all the arguments

Effects and Traits

```
!W 10000 !CYCLE !RENAME !ARG 1 2 3 4 5 6 7 8 // !DOPART $1
```

Title: test_course

```
ID !P
herd !A
HYS !I 41
parity !I 3
ACC
lact_week
```

```
avgCH4
speaks
npeaks
avgCO2
ratio
CH4gr
MeI
npeaks100 != _npeaks !*100
peID !A 1173
```

ID linked to the pedigree

Effects

Methane traits

npeaks multiplied by 100

ID for the permanent env

Reading pedigree and dataset

```
ped.ped    !MAKE !CSV !SORT  
dat.dat    !SKIP !MAXIT 2000 !AISING !continue !TOLERANCE !MVINCLUDE
```

!MAKE make pedigree

!CSV read csv

!SORT sort pedigree

!SKIP n if needed

!MAXIT sets the maximum number of iterations

!AISING singularities in AI

!TOLERANCE modifies the ability of ASReml to detect singularities in the mixed model

equations. This is intended for use on the occasions when ASReml detects singularities after the 1st iteration

!MVINCLUDE missing values are treated as zeros

!DV transformation to drop the records with the missing values

Univariate model and VPREDICT statements

!PART 1

```
avgCH4 ~ mu HYS lact_week ACC.parity !r nrm(ID) peID
```

$$y = \mu + \text{herd-year-season} + \text{lact week} + \text{ACC.parity} + a + pe + e$$

```
VPREDICT !DEFINE
```

```
P Var_P      1 2 3
```

```
H h2         2 4
```

```
H c2         1 4
```

4 F forms linear combinations of variance components

VPREDICT !DEFINE in the .as file creates a .pin file to compute h2, c2, rg, rp

H is for forming heritabilities, the ratio of two components

R is for forming the correlation from a covariance component

Main output files of ASReml

1. Main output file
(.asr)
2. Heritabilities
and correlations
(.pvc)
3. Solutions for
EBV (.sln)
4. Residuals (.res)

Table 14.1: Summary of ASReml output files

file	Description
Key output files	
<code>.asr</code>	contains a summary of the data and analysis results.
<code>.msv</code>	contains final variance parameter values in a form that is easy to edit for resetting the initial values if <code>!MSV</code> or <code>!CONTINUE 3</code> is used, see Table 5.4 .
<code>.pvc</code>	contains the report produced with the <code>P</code> option.
<code>.pvs</code>	contains predictions formed by the <code>predict</code> directive.
<code>.res</code>	contains information from using the <code>pol()</code> , <code>spl()</code> and <code>fac()</code> functions, the iteration sequence for the variance components and some statistics derived from the residuals.
<code>.rsv</code>	contains the final parameter values for reading back if the <code>!CONTINUE</code> qualifier is invoked, see Table 5.4 .
<code>.sln</code>	contains the estimates of the fixed and random effects and their corresponding standard errors.
<code>.tab</code>	contains tables formed by the <code>tabulate</code> directive.
<code>.tsv</code>	contains variance parameter values in a form that is easy to edit for resetting the initial values if <code>!TSV</code> or <code>!CONTINUE 2</code> is used, see Table 5.4 .
<code>.yht</code>	contains the predicted values, residuals and diagonal elements of the hat matrix for each data point.

Lets run ASReml

1. Open settings ➡ New ➡ Terminal

2. Type `cd Day2`

3. Load modules

```
ml use /lustre/shared/Courses/RELIVESTOCK2025/modules
```

```
module load asreml/4.2.1
```

4. Run ASReml: `time asreml -n uni.as # biv.as, RR.as`

5. or Run Bash file: `bash2.sh`

6. EXERCISE: Complete the bivariates and try a trivariate (if you want)

7. Check the outputs `.asr`, `.pvc`, `.sln`

Explaining .asr file

- The 1st line gives the version of ASReml used (in square brackets) and the title of the job.
- The 2nd line gives the build date for the program and indicates whether it is a 32bit or 64bit version.
- The 3rd line gives the date and time that the job was run and reports the size of the workspace.
- The general announcements box (outlined in asterisks) at the top of the file notifies the user of current release features.
- The remaining lines report a data summary, the iteration sequence, the estimated variance parameters and a table of Wald F statistics. The final line gives the date and time that the job was completed and a statement about convergence.

.asr file Univariate

```
ASReml 4.2ni [14 Feb 2024] Title: uni_rep
Linux (x64)      9.8 Gbyte  uni1  14 Feb 2025 13:56:01.078
* Licensed to: Wageningen University and Research Ce... - VS3AM1:[VOF16129]    30-apr-2025
*****
* Contact support@asrem1.co.uk for licensing and support      *
***** ARG *
Folder: /lustre/backup/WUR/ABGC/shared/ABGC_Projects/Relivestock/CH4_course/gen_ana/tests
ID          !P
herd        !A
HYS         !I 41
parity      !I 3
peID        !A 1173
npeaks100   !=npeaks !*100
ped.ped     !MAKE !CSV !SORT
Notice: Sorted pedigree written to: ped.ped.SRT
       First 5763 rows include all parents and base individuals.
Reading pedigree file ped.ped.SRT: skipping      0 lines
  6700 identities in the pedigree,
    generations on Sire side range 1 to 12
    generations on Dam side range 1 to 10
  Sire  Sire_of_Sire  Dam_of_Sire      Dam  Sire_of_Dam  Dam_of_Dam
1347      431      966      4416      995      2803
Using an adapted version of Meuwissen & Luo GSE 1992 305-313:
PEDIGREE [ped.ped.SRT ] has      6700 identities,  21792 Non zero elements
  0 NRM      6700      7      -3544.08      0
QUALIFIERS: !SKIP !MAXIT 2000 !AISING !CONTINUE !TOLERANCE !MVINCLUDE
QUALIFIER: !DOPART 1 is active
Reading dat.dat  FREE FORMAT skipping      0 lines
```

.asr file Univariate

Univariate analysis of avgCH4

Summary of 12318 records retained of 13366 read

Model term		Size	#miss	#zero	MinNon0	Mean	MaxNon0	StndDevn
1 ID	!P	6700	0	0	80	5889	6700	
2 herd		5	0	0	1	3.6124	5	
3 HYS		41	0	0	2	20.8019	41	
4 parity		3	0	0	1	2.1133	3	
5 ACC			0	0	17.00	41.24	120.0	21.59
Warning: Fewer levels found in lact_week than specified								
6 lact_week		60	0	53	1	22.3246	59	
7 avgCH4	Variate		0	0	1.340	535.2	1080.	210.7
8 speaks			919	0	0.2700	816.6	2685.	528.6
9 npeaks			227	0	0.2500	1.053	2.850	0.5503
10 avgCO2			2660	0	1547.	7170.	0.1231E+05	1804.
11 ratio			2805	198	0.2000E-01	0.7046E-01	0.1300	0.2110E-01
12 CH4gr			3405	0	61.02	343.5	615.0	81.91
13 MeI			3274	1	0.6000E-01	9.673	19.65	3.135
14 peID		1173	0	0	1	705.6551	1173	
15 npeaks100			227	0	25.00	105.3	285.0	55.03
16 mu				1				
17 ACC.parity				3	5 ACC	1	4 parity	:
18 nrm(ID)	!P	6700	0	0	80	5889	6700	:

Forming 7978 equations: 105 dense.
Initial updates will be shrunk by factor 0.316

Warning: Failed to find file unil.rsv

.asr file Univariate

```
Notice: Failed to read .rsv file          90
* This job uses all of the 1 processor threads. *
Notice: LogL values are reported relative to a base of -60000.000
Notice: 118 singularities detected in design matrix.
  1 LogL= -5485.72      S2= 14102.      12286 df
  2 LogL= -5291.67      S2= 13402.      12286 df
  3 LogL= -5088.65      S2= 12591.      12286 df
  4 LogL= -4967.13      S2= 11969.      12286 df
  5 LogL= -4918.32      S2= 11553.      12286 df
  6 LogL= -4910.29      S2= 11391.      12286 df
  7 LogL= -4909.52      S2= 11343.      12286 df
  8 LogL= -4909.49      S2= 11331.      12286 df
  9 LogL= -4909.48      S2= 11329.      12286 df
```

.asr file Univariate

```
    - - - Results from analysis of      avgCH4 - - -  
Akaike Information Criterion  129824.97 (assuming 3 parameters).  
Bayesian Information Criterion 129847.22
```

Model_Term		Gamma	Sigma	Sigma/SE	% C
peID	IDV_V 1200	0.438510	4967.66	3.98	0 P
nrm(ID)	NRM_V 140515	0.992763	11246.5	6.30	0 P
Residual	SCA_V 12328	1.00000	11328.5	74.31	0 P

Source of Variation		Wald F statistics
	NumDF	F-inc
15 mu	1	711.64
3 HYS	37	108.60
6 lact_week	1	22.85
16 ACC.parity	3	94.95
14 peID	1200 effects fitted (91 are zero)	
17 nrm(ID)	140515 effects fitted (13652 are zero)	

```
* This job used at least 2.1 of the 9.8 Gbyte of primary workspace. *
```

```
95 possible outliers in Section 11: see .res file
```

```
Finished: 24 Jan 2025 12:19:11.471 LogL Converged
```


.pvc output file Univariate

```
ASReml 4.2ni [14 Feb 2024] Title: test_course  
new_test1.pvc created 24 Jan 2025 12:19:11.471
```

```
- - - Results from analysis of std_avgCH4 - - -
```

```
1 peID          V 1200  
2 nrm(ID)       V 140515  
3 Residual      V 12328
```

```
P Var_P        1 2 3
```

```
4 Var_P
```

```
H h2           2 4
```

```
h2             = nrm(ID)      2/Var_P      4=
```

```
H c2           1 4
```

```
c2             = peID        1/Var_P      4=
```

```
Notice: The parameter estimates are followed by  
their approximate standard errors.
```

σ^2_a σ^2_{pe} σ^2_e and SE

4967.66	1248.16
11246.5	1785.16
11328.5	152.449

27543.	968.56
--------	--------

σ^2_p and SE

0.4083	0.0551
--------	--------

0.1804	0.0475
--------	--------

h^2 and c^2 and
SE

.sln file Univariate

Model_Term	Level	Effect	seEffect
ACC.parity	1.003	-4.093	0.3026
ACC.parity	1.002	-3.866	0.4823
ACC.parity	1.001	-6.999	0.7724
lact week	1	0.3202	0.1265
HYS	72	-40.00	6.168
HYS	73	-124.7	8.548
nrm(ID)	136626	0.5438E-01	106.0
nrm(ID)	1073	0.000	106.0
nrm(ID)	137387	0.1372	106.0
nrm(ID)	5927	0.6331E-01	112.4
nrm(ID)	136357	0.2965	106.8
mu	1	864.6	37.09
peID	14125	37.84	59.24
peID	14126	0.000	70.49
peID	25056	-55.23	56.24
peID	25280	69.74	57.00
peID	31791	91.95	57.85
peID	31792	-47.85	57.91
peID	33562	-36.37	58.66
peID	37287	0.000	70.49
peID	37288	-71.37	57.86

The .sln file is containing the **estimated effects**, intercept and random effects in this order (column 3) with standard errors (column 4).

Bivariate model and VPREDICT statements

```
!PART 1
avgCH4 speaks Trait Trait.HYS Trait.lact_week Trait.parity.ACC !r us(Trait !GP).nrm(ID) us(Trait !GP).peID
residual units.us(Trait !GP)
```

$$y = \mu + \text{herd-year-season} + \text{lact week} + \text{ACC.parity} + a + pe + e$$

```
VPREDICT !DEFINE
P Var_P1      1 4 7      # 10
P Cov_P      2 5 8      #11
P Var_P2      3 6 9      # 12
H h2_1        7 10
H h2_2        9 12
H c2_1        1 10
H c2_2        3 12
R cor_G       7 8 9
R cor_P       10 11 12
```

VPREDICT !DEFINE in the .as file creates a .pin file to compute h2, c2, rg, rp

F forms linear combinations of variance components

H is for forming heritabilities, the ratio of two components

R is for forming the correlation from a covariance component

.asr file Bivariate

```

- - - Results from analysis of avgCH4 speaks - - -
Akaike Information Criterion 258910.76 (assuming 9 parameters)
Bayesian Information Criterion 258983.37

Model_Term                                Sigma      Sigma      Sigma/SE      % C
units.us(Trait)                          24730 effects
Trait      US_V 1 1 11196.4              11196.4      74.18      0 P
Trait      US_C 2 1 15944.8              15944.8      57.35      0 P
Trait      US_V 2 2 49498.5              49498.5      71.15      0 P
us(Trait).peID                            2346 effects
Trait      US_V 1 1 4822.60              4822.60      4.01      0 P
Trait      US_C 2 1 1092.30              1092.30      0.50      0 P
Trait      US_V 2 2 6813.96              6813.96      1.30      0 P
us(Trait).nrm(ID)                        13400 effects
Trait      US_V 1 1 10773.1              10773.1      6.57      0 P
Trait      US_C 2 1 24419.6              24419.6      7.49      0 P
Trait      US_V 2 2 60468.9              60468.9      7.71      0 P
ID      NRM 6700

Covariance/Variance/Correlation Matrix US Residual
0.1120E+05  0.6773
0.1594E+05  0.4950E+05

Covariance/Variance/Correlation Matrix US us(Trait).peID
4824.      0.1911
1097.      6826.

Covariance/Variance/Correlation Matrix US us(Trait).nrm(ID)
0.1076E+05  0.9567
0.2440E+05  0.6042E+05

Source of Variation      Wald F statistics
                          NumDF      F-inc
17 Trait                2          1004.27
18 Trait.HYS            74          116.09
19 Trait.lact_week      118          3.65
21 Trait.parity.ACC     6          57.33
25 us(Trait).peID       2346 effects fitted ( 128 are zero)
24 us(Trait).nrm(ID)    13400 effects fitted ( 108 are zero)

* This job used at least .8 of the 8.8 Gbyte of primary workspace. *
413 possible outliers in Section 11: see .res file
Finished: 14 Feb 2025 13:54:05.582 LogL Converged

```

.pvc output file Bivariate

```
ASReml 4.2ni [14 Feb 2024] Title: biv_rep
biv1.pvc created 14 Feb 2025 13:54:05.582
```

-- Results from analysis of avgCH4 speaks -- σ^2a σ^2pe σ^2e and SE

```
units.us(Trait)          24730 effects
 1 units.us(Trait);us(Trait)      V  1  1
 2 units.us(Trait);us(Trait)      C  2  1
 3 units.us(Trait);us(Trait)      V  2  2
us(Trait).peID           2346 effects
 4 us(Trait).peID;us(Trait)        V  1  1
 5 us(Trait).peID;us(Trait)        C  2  1
 6 us(Trait).peID;us(Trait)        V  2  2
us(Trait).nrm(ID)        13400 effects
 7 us(Trait).nrm(ID);us(Trait)     V  1  1
 8 us(Trait).nrm(ID);us(Trait)     C  2  1
 9 us(Trait).nrm(ID);us(Trait)     V  2  2
ID                          NRM      6700
```

```
P Var_P1      1 4 7
10 Var_P1
P Cov_P        2 5 8
11 Cov_P
P Var_P2      3 6 9
12 Var_P2
H h2_1         7 10
  h2_1         = us(Trait  7/Var_P1  10=
H h2_2         9 12
  h2_2         = us(Trait  9/Var_P2  12=
H c2_1         1 10
  c2_1         = units.us  1/Var_P1  10=
H c2_2         3 12
  c2_2         = units.us  3/Var_P2  12=
R cor_G        7 8 9
  cor_G        = us(Trait/SQR[us(Trait*us(Trait)=
R cor_P        10 11 12
  cor_P        = Cov_P /SQR[Var_P1 *Var_P2 ]=
```

Notice: The parameter estimates are followed by their approximate standard errors.

11196.4	150.936
15944.8	278.026
49498.5	695.692
4822.60	1202.64
1092.30	2184.60
6813.96	5241.51
10773.1	1639.74
24419.6	3260.29
60468.9	7842.92

26792.	896.87
41457.	1756.8
0.11678E+06	4194.9

0.4021	0.0528
0.5178	0.0540
0.4179	0.0146
0.4239	0.0159

SE

σ^2p and SE

Univariate model Random Regression

```
!PART 7
avgCH4 ~ mu HYS lact_week parity.leg(lact_week,1) parity.leg(ACC,2) !r us(leg(lact_week,1)).nrm(ID) us(leg(lact_week,1)).id(peID)

!VPREDICT !DEFINE
F Perm peID * 1
F AddVar nrm(ID) * 1
K Leg1_0 0.70711 -1.22474
K Leg1_10 0.70711 -0.61237
K Leg1_20 0.70711 0.00000
K Leg1_30 0.70711 0.61237
K Leg1_40 0.70711 1.22474
M Genmat Leg AddVar
M Pemat Leg Perm
F Phenvar AddVar Perm Residual
F Phenvar0 14 29 Residual
F Phenvar10 16 31 Residual
F Phenvar20 19 34 Residual
F Phenvar30 23 38 Residual
F Phenvar40 28 43 Residual
H H2_0 14 47
H H2_10 16 48
H H2_20 19 49
H H2_30 23 50
H H2_40 28 51
H C2_0 29 47
H C2_10 31 48
H C2_20 34 49
H C2_30 38 50
H C2_40 43 51
R Gencorr Genmat
R Pecorr Pemat
```

.as Random Regression

!PART 7

```
avgCH4 ~ mu HYS lact_week parity.leg(lact_week,1) parity.leg(ACC,2) !r us(leg(lact_week,1)).nrm(ID) us(leg(lact_week,1)).id(peID)
```

$$y = \mu + \text{herd-year-season} + \text{lact week} + \text{leg1,lw.parity} + \text{leg2,ACC.parity} + \text{leg1,lw.a} + \text{leg1,lw.pe} + e$$

.asr Random Regression

```

-- Results from analysis of avgCH4 --
Notice: US structures were modified 2 times to make them positive definite.
If ASReml has fixed the structure [flagged by B], it may not have
converged to a maximum likelihood solution.
Used !EMFLAG 5 Single standard EM update when AI update unacceptable
You could try !GU (negative definite US) or use XFA instead.

Akaike Information Criterion 116966.34 (assuming 7 parameters).
Bayesian Information Criterion 117017.54

Model_Term          SCA_V 11184    1.00000    10142.6    68.59    0 P
Residual
us(leg(lact_week,1)).id(peID) 2346 effects
leg(lact_week,1)    US_V 1 1 0.632288    6413.06    2.31    0 ?
leg(lact_week,1)    US_C 2 1 -0.990536E-01 -1004.66    -0.69    0 ?
leg(lact_week,1)    US_V 2 2 0.278145E-01  282.112    0.19    0 ?
us(leg(lact_week,1)).nrm(ID) 13400 effects
leg(lact_week,1)    US_V 1 1 2.04697    20761.7    5.72    0 P
leg(lact_week,1)    US_C 2 1 0.161127    1634.25    0.87    0 P
leg(lact_week,1)    US_V 2 2 0.760484    7713.30    4.20    0 P
rm
nrm 6700

Warning: Code B - fixed at a boundary (!GP) F - fixed by user
? - liable to change from P to B P - positive definite
C - Constrained by user (!VCC) U - unbounded
S - Singular Information matrix
S means there is no information in the data for this parameter.
Very small components with Comp/SE ratios of zero sometimes indicate poor
scaling. Consider rescaling the design matrix in such cases.
Covariance/Variance/Correlation Matrix US us(leg(lact_week,1))
6413. -0.7469
-1005. 282.1
Covariance/Variance/Correlation Matrix US us(leg(lact_week,1))
0.2076E+05 0.1291
1634. 7713.

Wald F statistics
Source of Variation NumDF F-inc
16 mu 1 1525.66
3 HYS 37 96.83
6 lact_week 40 3.91
18 parity.leg(lact_week,1) 4 21.35
20 parity.leg(ACC,2) 6 23.58
25 us(leg(lact_week,1)).id(peID) 2346 effects fitted ( 266 are zero)
23 us(leg(lact_week,1)).nrm(ID) 13400 effects fitted ( 166 are zero)
* This job used at least .7 of the 9.8 Gbyte of primary workspace. *
79 possible outliers in Section 11: see .res file
Finished: 14 Feb 2025 11:59:02.968 LogL Converged

```


LEG coefficients in .res file

```
==== Residual statistics for RR1.asr ====
Notice: ASReml will have merged any design points closer than 0.004000
Use !POLPOINTS 100000 on the data file line to increase the resolution.
leg(lact_week,1) has 2 levels
0.00000 0.70711 -1.22474
1.00000 0.70711 -1.16351
2.00000 0.70711 -1.10227
3.00000 0.70711 -1.04103
4.00000 0.70711 -0.97980
5.00000 0.70711 -0.91856
6.00000 0.70711 -0.85732
7.00000 0.70711 -0.79608
8.00000 0.70711 -0.73485
9.00000 0.70711 -0.67361
10.00000 0.70711 -0.61237
11.00000 0.70711 -0.55114
12.00000 0.70711 -0.48990
13.00000 0.70711 -0.42866
14.00000 0.70711 -0.36742
15.00000 0.70711 -0.30619
16.00000 0.70711 -0.24495
17.00000 0.70711 -0.18371
18.00000 0.70711 -0.12247
19.00000 0.70711 -0.06124
20.00000 0.70711 0.00000
21.00000 0.70711 0.06124
22.00000 0.70711 0.12247
23.00000 0.70711 0.18371
24.00000 0.70711 0.24495
25.00000 0.70711 0.30619
26.00000 0.70711 0.36742
27.00000 0.70711 0.42866
28.00000 0.70711 0.48990
29.00000 0.70711 0.55114
30.00000 0.70711 0.61237
31.00000 0.70711 0.67361
32.00000 0.70711 0.73485
33.00000 0.70711 0.79608
34.00000 0.70711 0.85732
35.00000 0.70711 0.91856
36.00000 0.70711 0.97980
37.00000 0.70711 1.04103
38.00000 0.70711 1.10227
39.00000 0.70711 1.16351
40.00000 0.70711 1.22474
```

use them to create the
VPREDICT file


```
!VPREDICT !DEFINE
F Perm    peID    * 1
F AddVar  nrm(ID) * 1
K Leg1_0   0.70711 -1.22474
K Leg1_10  0.70711 -0.61237
K Leg1_20  0.70711  0.00000
K Leg1_30  0.70711  0.61237
K Leg1_40  0.70711  1.22474
M Genmat  Leg AddVar
M Pemat   Leg Perm
```

- F forms linear combinations of variance components,
- H is for forming heritabilities, the ratio of two components,
- K sets a vector (or matrix) of coefficients for use by M,
- M pre/post multiplies a US matrix by the K matrix,
- R is for forming the correlation from a covariance component,

```
!VPREDICT !DEFINE
F Perm    peID    * 1
F AddVar  nrm(ID)  * 1
K Leg1_0   0.70711 -1.22474
K Leg1_10  0.70711 -0.61237
K Leg1_20  0.70711  0.00000
K Leg1_30  0.70711  0.61237
K Leg1_40  0.70711  1.22474
M Genmat  Leg AddVar
M Pemat   Leg Perm
F Phenvar AddVar Perm Residual
F Phenvar0 14 29 Residual
F Phenvar10 16 31 Residual
F Phenvar20 19 34 Residual
F Phenvar30 23 38 Residual
F Phenvar40 28 43 Residual
H H2_0 14 47
H H2_10 16 48
H H2_20 19 49
H H2_30 23 50
H H2_40 28 51
H C2_0 29 47
H C2_10 31 48
H C2_20 34 49
H C2_30 38 50
H C2_40 43 51
R Gencorr Genmat
R Pecorr Pemat
```

- F forms linear combinations of variance components,
- H is for forming heritabilities, the ratio of two components,
- K sets a vector (or matrix) of coefficients for use by M,
- M pre/post multiplies a US matrix by the K matrix,
- R is for forming the correlation from a covariance component,

.pvc Random Regression

```
ASReml 4.2ni [14 Feb 2024] Title: uni_RR
      RR6.pvc created 13 Feb 2025 16:39:43.136

      - - - Results from analysis of avgCH4 - - -

      1 Residual                                V 11184      10172.5      148.201
us(leg(lact_week,1)).id(peID) 2346 effects
      2 us(leg(lact_week,1)).id(peID);us(leg(lact_week,1)      6746.36      2810.98
      3 us(leg(lact_week,1)).id(peID);us(leg(lact_week,1)    -849.853      1465.26
      4 us(leg(lact_week,1)).id(peID);us(leg(lact_week,1)     109.956      1570.80
us(leg(lact_week,1)).nrm(ID)      13400 effects
      5 us(leg(lact_week,1)).nrm(ID);us(leg(lact_week,1)      20715.1      3659.91
      6 us(leg(lact_week,1)).nrm(ID);us(leg(lact_week,1)      1638.77      1905.55
      7 us(leg(lact_week,1)).nrm(ID);us(leg(lact_week,1)      8183.02      1881.15
ID                                NRM      6700
F Perm   peID   * 1
      8 Perm                                6746.4      2811.5
      9 Perm                               -849.85      1473.2
     10 Perm                                109.96      1512.0
F AddVar nrm(ID)   * 1
     11 AddVar                             20715.      3659.8
     12 AddVar                             1638.8      1904.3
     13 AddVar                             8183.0      1882.4
K Leg1_0    0.70711  -1.22474
K Leg1_10   0.70711  -0.61237
K Leg1_20   0.70711   0.00000
K Leg1_30   0.70711   0.61237
K Leg1_40   0.70711   1.22474
M Genmat Leg AddVar
Calculating k m S k n' for 5 row vectors (k, Leg1 0...)
```

.pvc Random Regression

		m	n		
14	Genmat	1	1	19120.	4037.5
15	Genmat	2	1	14043.	2902.9
16	Genmat	2	2	11858.	2233.8
17	Genmat	3	1	8965.6	2211.0
18	Genmat	3	2	9673.3	1852.3
19	Genmat	3	3	10381.	1814.1
20	Genmat	4	1	3888.4	2384.7
21	Genmat	4	2	7488.5	1936.5
22	Genmat	4	3	11089.	2113.8
23	Genmat	4	4	14689.	2800.0
24	Genmat	5	1	-1188.9	3289.6
25	Genmat	5	2	5303.7	2438.7
26	Genmat	5	3	11796.	2638.7
27	Genmat	5	4	18289.	3723.8
28	Genmat	5	5	24781.	5163.3

σ^2_a

σ^2_p

M Pemat Leg Perm
Calculating k_m S k_n' for 5 row vectors (k, Leg1_0...) and matrix S (Perm)

		m	n		
29	Pemat	1	1	5369.8	3180.3
30	Pemat	2	1	4723.2	2260.5
31	Pemat	2	2	4182.4	1726.0
32	Pemat	3	1	4076.6	1724.2
33	Pemat	3	2	3641.6	1433.7
34	Pemat	3	3	3206.6	1389.6
35	Pemat	4	1	3430.0	1924.3
36	Pemat	4	2	3100.8	1529.6
37	Pemat	4	3	2771.5	1612.2
38	Pemat	4	4	2442.3	2117.1
39	Pemat	5	1	2783.4	2701.9
40	Pemat	5	2	2559.9	1957.3
41	Pemat	5	3	2336.5	2015.0
42	Pemat	5	4	2113.0	2826.2
43	Pemat	5	5	1889.6	3951.4

σ^2_{pe}

F Phenvar0 14 29 Residual
47 Phenvar0
F Phenvar10 16 31 Residual
48 Phenvar10
F Phenvar20 19 34 Residual
49 Phenvar20
F Phenvar30 23 38 Residual
50 Phenvar30
F Phenvar40 28 43 Residual
51 Phenvar40

34633.	1905.1
26183.	1077.5
23730.	884.73
27274.	1269.9
36814.	2239.0

.pvc Random Regression

					SE	
H H2_0 14 47						
H2_0	= Genmat	14/Phenvar0	47=	h^2	0.5659	0.1013
H H2_10 16 48					0.4560	0.0751
H2_10	= Genmat	16/Phenvar1	48=		0.4333	0.0670
H H2_20 19 49					0.5360	0.0867
H2_20	= Genmat	23/Phenvar3	50=		0.6754	0.1138
H H2_30 23 50						
H2_30	= Genmat	28/Phenvar4	51=			
H H2_40 28 51						
H2_40	= Genmat					
H C2_0 29 47						
C2_0	= Pemat	29/Phenvar0	47=	c^2	0.1432	0.0950
H C2_10 31 48					0.1576	0.0683
C2_10	= Pemat	31/Phenvar1	48=		0.1411	0.0603
H C2_20 34 49					0.0967	0.0788
C2_20	= Pemat	38/Phenvar3	50=		0.0548	0.1068
H C2_30 38 50						
C2_30	= Pemat					
H C2_40 43 51						
C2_40	= Pemat	43/Phenvar4	51=			

.pvc Random Regression

R Gencorr Genmat

```
Gencor 2 1 = Genma 15/SQR[Genma 14*Genma 16]=
Gencor 3 1 = Genma 17/SQR[Genma 14*Genma 19]=
Gencor 3 2 = Genma 18/SQR[Genma 16*Genma 19]=
Gencor 4 1 = Genma 20/SQR[Genma 14*Genma 23]=
Gencor 4 2 = Genma 21/SQR[Genma 16*Genma 23]=
Gencor 4 3 = Genma 22/SQR[Genma 19*Genma 23]=
Gencor 5 1 = Genma 24/SQR[Genma 14*Genma 28]=
Gencor 5 2 = Genma 25/SQR[Genma 16*Genma 28]=
Gencor 5 3 = Genma 26/SQR[Genma 19*Genma 28]=
Gencor 5 4 = Genma 27/SQR[Genma 23*Genma 28]=
```

R Pecorr Pemat

```
Pecorr 2 1 = Pemat 30/SQR[Pemat 29*Pemat 31]=
Pecorr 3 1 = Pemat 32/SQR[Pemat 29*Pemat 34]=
Pecorr 3 2 = Pemat 33/SQR[Pemat 31*Pemat 34]=
Pecorr 4 1 = Pemat 35/SQR[Pemat 29*Pemat 38]=
Pecorr 4 2 = Pemat 36/SQR[Pemat 31*Pemat 38]=
Pecorr 4 3 = Pemat 37/SQR[Pemat 34*Pemat 38]=
Pecorr 5 1 = Pemat 39/SQR[Pemat 29*Pemat 43]=
Pecorr 5 2 = Pemat 40/SQR[Pemat 31*Pemat 43]=
Pecorr 5 3 = Pemat 41/SQR[Pemat 34*Pemat 43]=
Pecorr 5 4 = Pemat 42/SQR[Pemat 38*Pemat 43]=
```

rg

0.9319
0.6243
0.8651
0.2048
0.5460
0.8925
-0.0854
0.2819
0.7251
0.9577

SE

0.0190
0.0879
0.0364
0.1389
0.1027
0.0300
0.1450
0.1355
0.0700
0.0121

0.9999
0.9996
0.9999
0.9988
0.9993
0.9998
0.9972
0.9981
0.9989
0.9997

0.0488
0.2401
0.0725
0.6803
0.3649
0.1122
1.5672
1.0636
0.5812
0.1827

rp

Notice: The parameter estimates are followed by
their approximate standard errors.

.sln Random Regression

us(leg(lact_week,1))	1.020799	23.62	149.3
us(leg(lact_week,1))	1.014898	99.27	143.3
us(leg(lact_week,1))	1.112873	37.46	148.3
us(leg(lact_week,1))	1.010607	35.57	146.8
us(leg(lact_week,1))	1.040968	14.82	150.4
us(leg(lact_week,1))	1.014813	73.97	135.2
us(leg(lact_week,1))	1.044213	59.22	142.1
us(leg(lact_week,1))	2.067684	64.07	105.4
us(leg(lact_week,1))	2.091981	58.62	102.6
us(leg(lact_week,1))	2.014764	31.48	96.60
us(leg(lact_week,1))	2.098870	36.56	99.02
us(leg(lact_week,1))	2.025901	-1.902	108.4
us(leg(lact_week,1))	2.130188	-13.91	103.9

Solutions, need to be multiplied by ϕ



Re-Livestock

RESILIENT FARMING SYSTEMS

Examples of variance components for methane traits



Birgit Gredler-Grandl, Coralía Manzanilla-Pech, Ester Teran and Oscar González-Recio



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Zaragoza, February 25th, 2025

Genetic correlations among traits: International

Trait ¹	MeP	GSMet	MeY	MeI	RMet1	RMet2	RMet3
MeP		1.00 (0.01)	0.60 (0.01)	0.36 (0.01)	0.86 (0.00)	0.86 (0.01)	0.82 (0.01)
GSMet	0.99 (0.00)		0.57 (0.01)	0.34 (0.01)	0.89 (0.01)	0.83 (0.01)	0.80 (0.01)
MeY	0.46 (0.12)	0.37 (0.13)		0.49 (0.02)	0.90 (0.01)	0.69 (0.01)	0.86 (0.01)
MeI	0.41 (0.10)	0.43 (0.13)	0.70 (0.10)		0.46 (0.02)	0.63 (0.01)	0.62 (0.01)
RMet1	0.70 (0.08)	0.60 (0.11)	0.84 (0.06)	0.51 (0.14)		0.89 (0.00)	0.96 (0.00)
RMet2	0.74 (0.07)	0.68 (0.10)	0.35 (0.15)	0.70 (0.08)	0.82 (0.08)		0.97 (0.00)
RMet3	0.75 (0.08)	0.68 (0.11)	0.73 (0.10)	0.63 (0.11)	0.91 (0.04)	0.97 (0.02)	



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Research

Breeding for reduced methane emission and feed-efficient Holstein cows: An international response

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C.M. Richardson ^{2,3}, P. Stothard ⁸, J. Lassen ⁹



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Genetic correlations among traits: Denmark

ORIGINAL RESEARCH article

Front. Genet. , 26 May 2022

Sec. Livestock Genomics

Volume 13 - 2022 | <https://doi.org/10.3389/fgene.2022.885932>

This article is part of the Research Topic

Reducing the Environmental Footprint of Livestock Through Genomic Selection

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Selecting for Feed Efficient Cows Will Help to Reduce Methane Gas Emissions



Coralía Ines Valentina Manzanilla-Pech^{1*}



Rasmus Bak Stephansen¹



Gareth Frank Difford²



Peter Lovendahl¹



Jan Lassen^{1,3}

Trait	MeP	MeC	Mel	MeY	RMeP	RMeC
MeP	—	0.63 (0.02)	0.51 (0.02)	0.84 (0.01)	0.81 (0.01)	0.52 (0.02)
MeC	0.71 (0.12)	—	0.48 (0.02)	0.59 (0.02)	0.63 (0.01)	0.98 (0.00)
Mel	0.48 (0.16)	0.48 (0.16)	—	0.59 (0.02)	0.85 (0.01)	0.56 (0.02)
MeY	0.77 (0.07)	0.58 (0.14)	0.58 (0.14)	—	0.84 (0.01)	0.55 (0.02)
RMeP	0.82 (0.07)	0.70 (0.11)	0.85 (0.07)	0.88 (0.05)	—	0.65 (0.01)
RMeC	0.77 (0.08)	0.69 (0.12)	0.84 (0.08)	0.95 (0.02)	0.98 (0.01)	—

MeP = methane production, MeC = methane concentration, Mel = methane intensity, MeY = methane yield, RMeP = residual methane production on ECM and MBW, RMeC = residual methane concentration on ECM and MBW, RMeP = residual methane production on ECM, MBW, and DMI..



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Genetic correlations among traits: Netherlands

Table 3. Phenotypic (above the diagonal) and genetic correlations (below the diagonal) between methane (CH₄) and carbon dioxide (CO₂) recorded by GreenFeed (GF, production: CH₄p in grams/day) units or sniffers (concentration: CH₄c in ppm) and averaged per day or per week (±SE)¹

Item	GF CH ₄ p day	GF CO ₂ p day	GF CH ₄ p week	GF CO ₂ p week	Sniffer CH ₄ c day	Sniffer CO ₂ c day	Sniffer CH ₄ c week	Sniffer CO ₂ c week
GF CH ₄ p day	*0.19 ± 0.02	0.72 ± 0.01	0.70 ± 0.01 ²	0.53 ± 0.01	0.39 ± 0.03	0.20 ± 0.04	0.37 ± 0.04	0.18 ± 0.04
GF CO ₂ p day	0.68 ± 0.04	*0.24 ± 0.03	0.58 ± 0.01	0.77 ± 0.01 ²	0.32 ± 0.04	0.25 ± 0.04	0.35 ± 0.04	0.27 ± 0.04
GF CH ₄ p week	0.99 ± 0.01 ²	0.66 ± 0.05	*0.33 ± 0.04	0.75 ± 0.01	0.27 ± 0.04	0.15 ± 0.05	0.37 ± 0.05	0.19 ± 0.06
GF CO ₂ p week	0.64 ± 0.05	1.00 ± 0.01 ²	0.65 ± 0.05	*0.34 ± 0.05	0.22 ± 0.04	0.18 ± 0.04	0.31 ± 0.05	0.24 ± 0.06
Sniffer CH ₄ c day	0.71 ± 0.13	0.54 ± 0.15	0.74 ± 0.15	0.69 ± 0.16	*0.18 ± 0.01	0.78 ± >0.01	0.73 ± <0.01 ²	0.62 ± 0.01
Sniffer CO ₂ c day	0.39 ± 0.16	0.51 ± 0.15	0.47 ± 0.17	0.63 ± 0.16	0.93 ± 0.01	*0.20 ± 0.01	0.65 ± 0.01	0.76 ± <0.01 ²
Sniffer CH ₄ c week	0.71 ± 0.14	0.60 ± 0.15	0.76 ± 0.15	0.72 ± 0.16	1.00 ± <0.01 ²	0.92 ± 0.01	*0.32 ± 0.02	0.84 ± <0.01
Sniffer CO ₂ c week	0.35 ± 0.17	0.51 ± 0.15	0.41 ± 0.18	0.60 ± 0.17	0.91 ± 0.01	1.00 ± <0.01 ²	0.93 ± 0.01	*0.32 ± 0.02



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Research

Heritability and genetic correlations between enteric methane production and concentration recorded by GreenFeed and sniffers on dairy cows

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Re-Livestock

RESILIENT FARMING SYSTEMS

Examples of variance components for methane traits along the lactation



Birgit Gredler-Grandl, Coralía Manzanilla-Pech, Ester Teran and Oscar González-Recio



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Zaragoza, February 25th, 2025

Genetic correlations along lactation: Poland

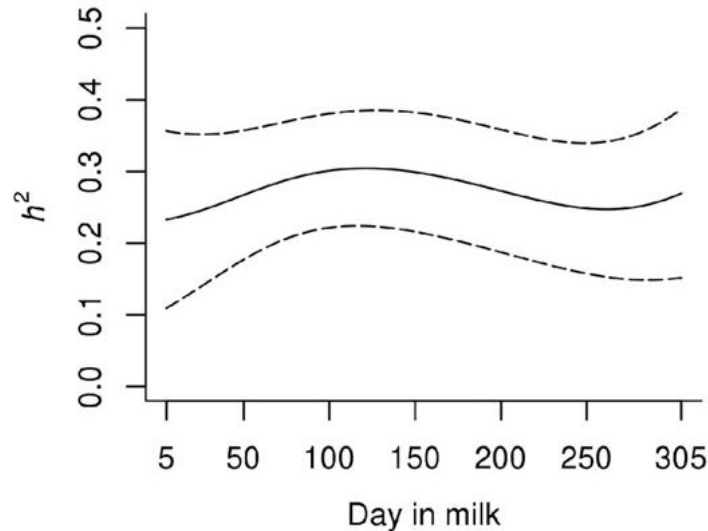


Figure 5. Heritability of estimated CH_4 emission over the course of lactation (solid line) with SE (dashed lines).

JOURNAL ARTICLE

Heritability of methane emissions from dairy cows over a lactation measured on commercial farms¹

M. Pszczola, K. Rzewuska, S. Mucha, T. Strabel ✉ [Author Notes](#)

Journal of Animal Science, Volume 95, Issue 11, November 2017, Pages 4813–4819,
<https://doi.org/10.2527/jas2017.1842>

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Genetic correlations along lactation: Denmark



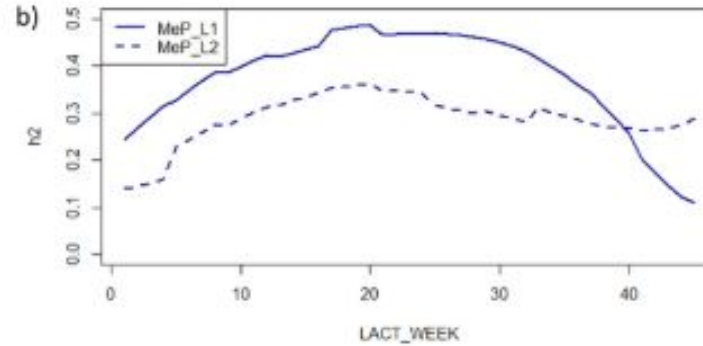
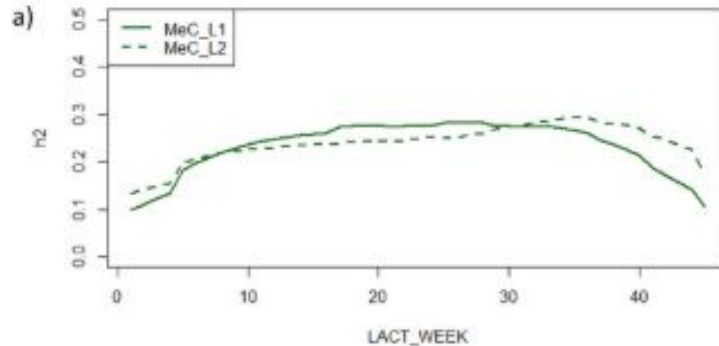
Journal of Dairy Science
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Research

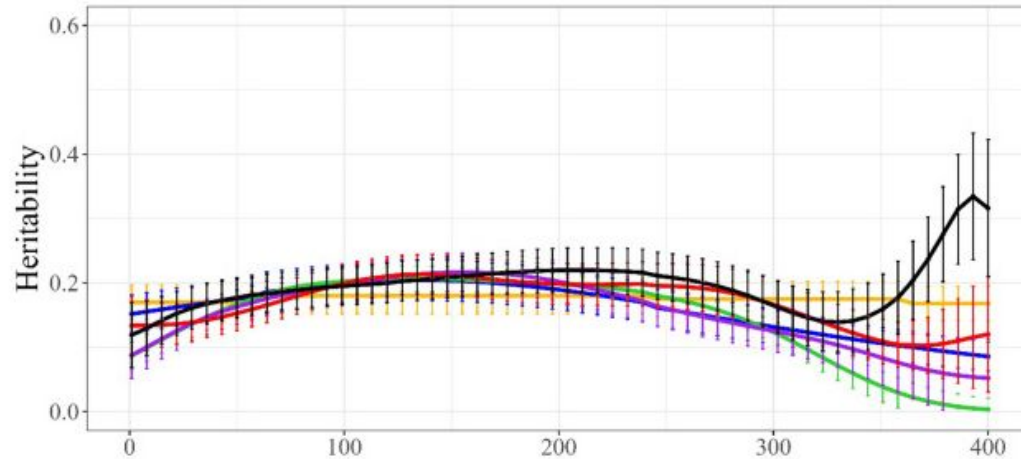
Genetic (co-)variation of methane emissions, efficiency, and production traits in Danish Holstein cattle along and across lactations

C.I.V. Manzanilla-Pech¹, G.F. Difford², P. Lovendahl¹, R.B. Stephansen¹, J. Lassen^{1,3}



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Genetic correlations along lactation: Netherlands



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Genetic parameter estimates for methane emission from breath during lactation and potential inaccuracies in reliabilities assuming a repeatability versus random regression model

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Re-Livestock

RESILIENT FARMING SYSTEMS



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