IOWA STATE UNIVERSITY
Department of animal Science

Use of Hardware and Sensors Towards Phenomics to Deliver Complex Data and Advance Animal Breeding

Juan P. Steibel
Professor of Animal Science
J. Lush Endowed Chair of Animal Breeding and Genetics

Phenome, phenomics, phenotyping

Phenomics = the acquisition of high-dimensional phenotypic data on an organism-wide scale.

“Some of the most scientifically disrupting and industry-relevant challenges relate to ‘phenomics’ as much as to ‘genomics’”

Pérez-Enciso and Steibel *Genet Sel Evol* (2021) 53:22
https://doi.org/10.1186/s12711-021-00618-1

Genetics Selection Evolution

OPINION **Open Access**

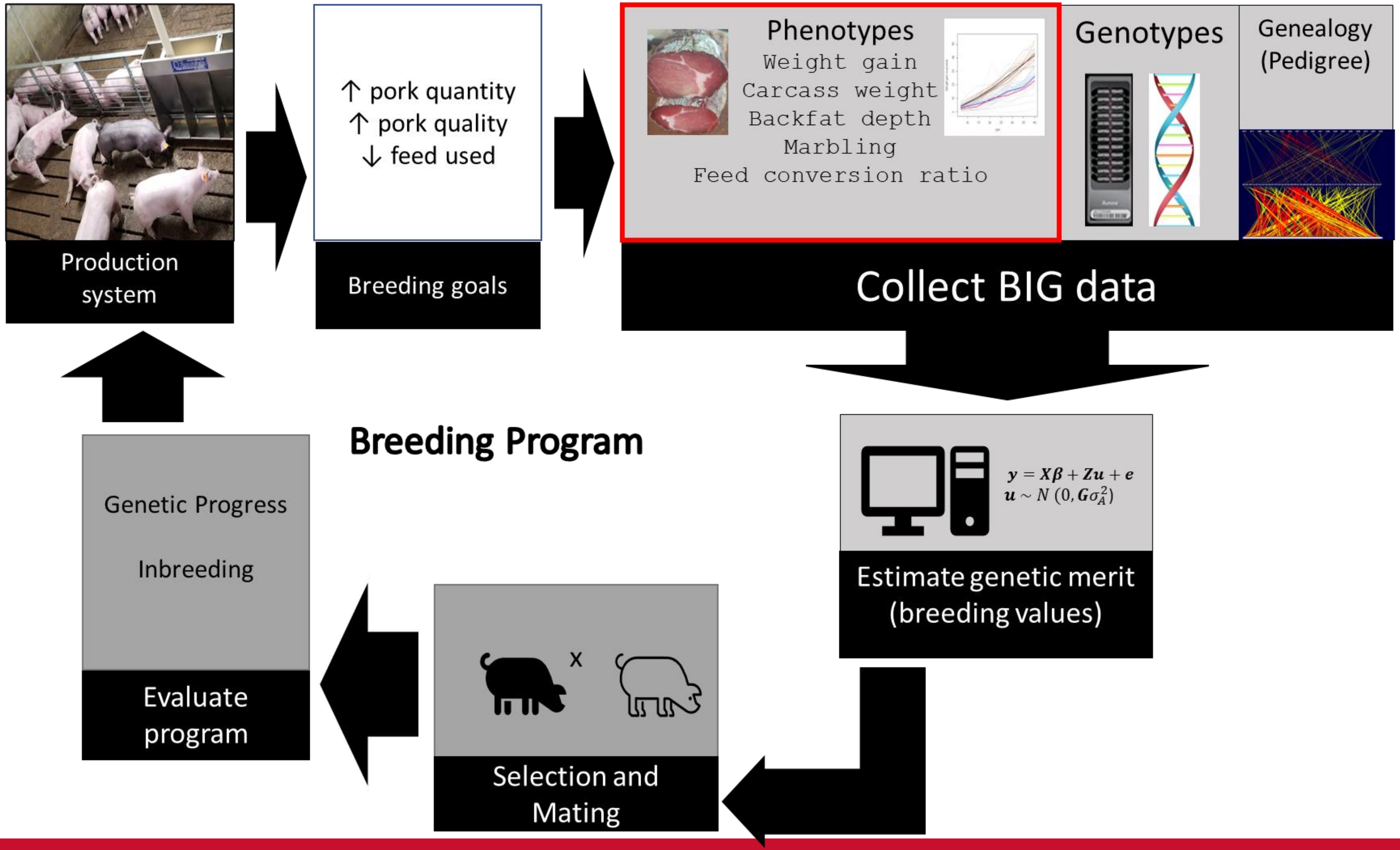
Phenomes: the current frontier in animal breeding

Miguel Pérez-Enciso[1,2*] and Juan P. Steibel[3,4]

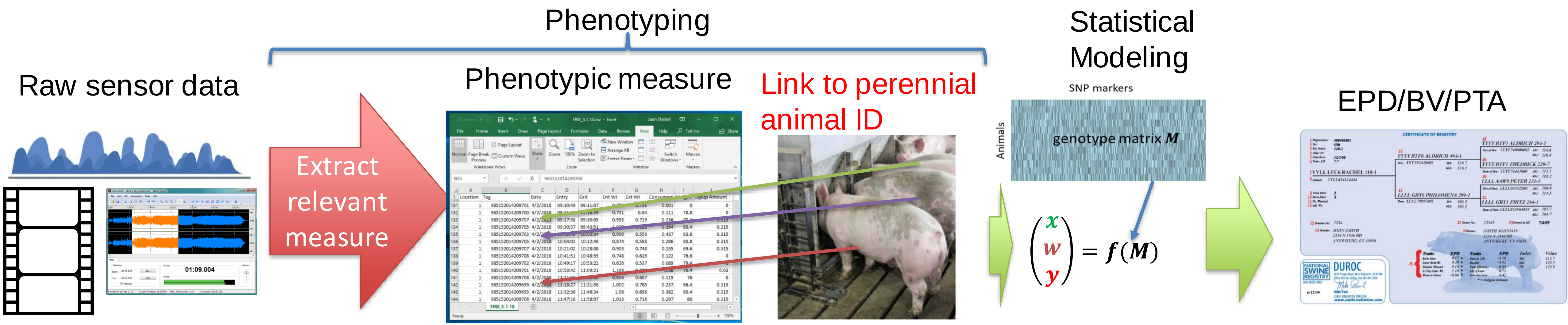
What is novel in novel phenotyping?

Novel / Hard to measure traits	Massive collection of common traits
Welfare/Health related	Real Time
Behavioral	"All" animals
Physiological	Across farms world-wide
Gas emissions	Under typical production conditions
Feed Conversion	

Breeding programs



Phenomics in animal breeding



The need for phenotyping

Phenotyping

Management
Group-level indicators
Individual indicators
Enable Intervention

Genetic improvement
Improve relevant traits
Evaluate in the relevant environment

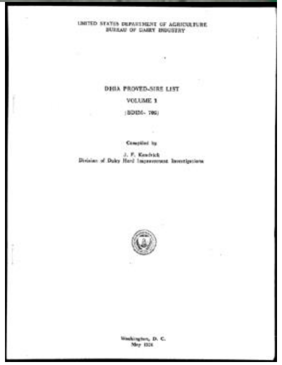
Defined by socio-economic conditions: The production system and the farmers/community.

It's hard to improve what we don't measure (attributed to P. Drucker)

An example from the USA: DHIA

1890s: Babcock's test: How to measure butterfat.

1905: Helmer Rabild starts DHIA in Michigan



UNITED STATES DEPARTMENT OF AGRICULTURE
BUREAU OF DAIRY INDUSTRY

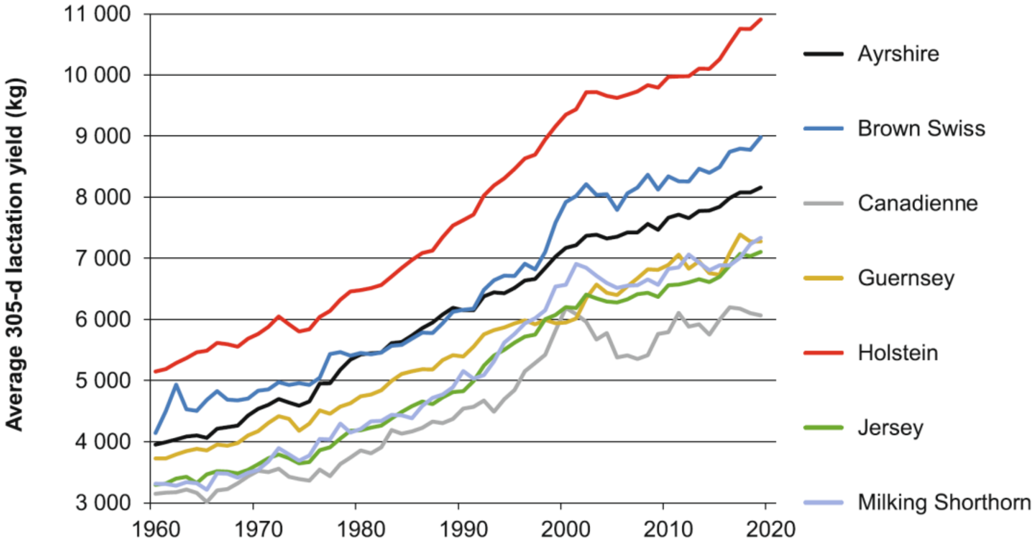
DHIA PROVED-SIRE LIST
VOLUME 1

Compiled by
J. F. Kendrick
Division of Dairy Herd Improvement Investigations

Washington, D. C.

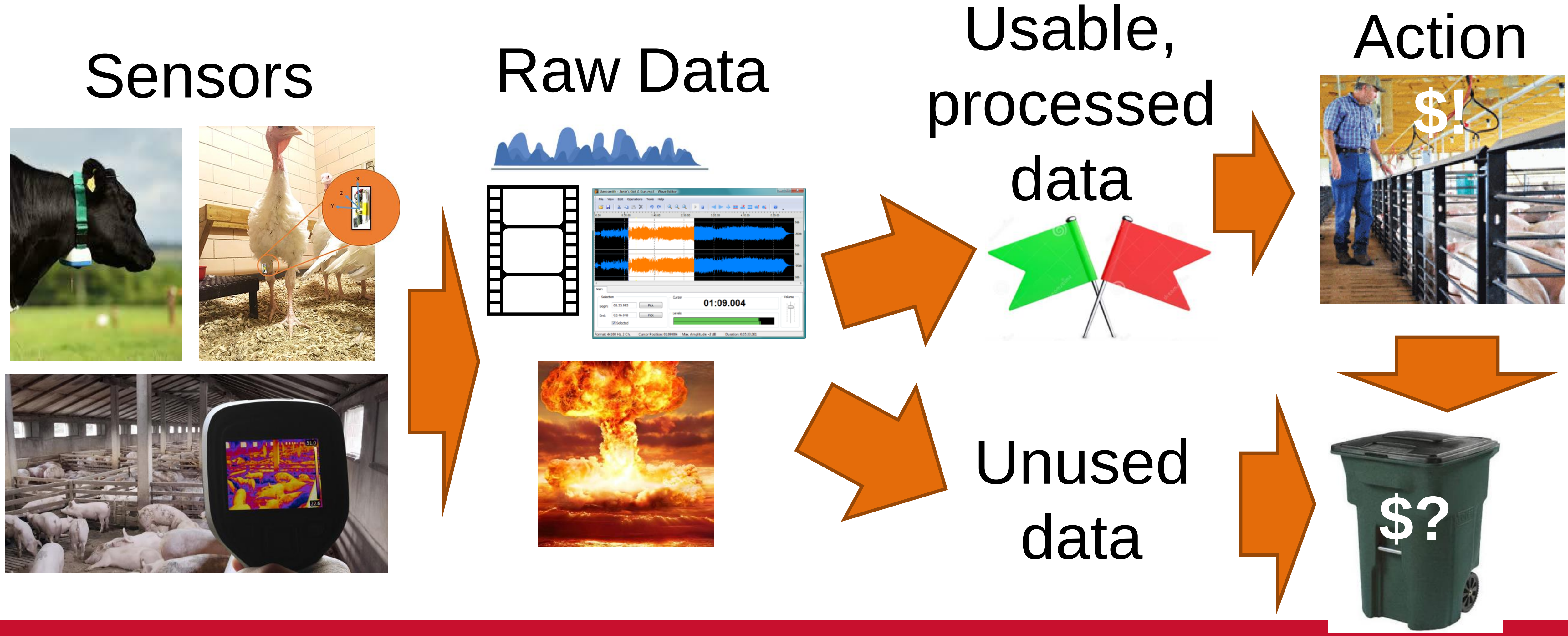
1936 1st proven sire list

- Provided useful data for management
- Built on existing infrastructure
- Fed sire comparisons (genetic evaluation)



Source: Brito et al 2021.

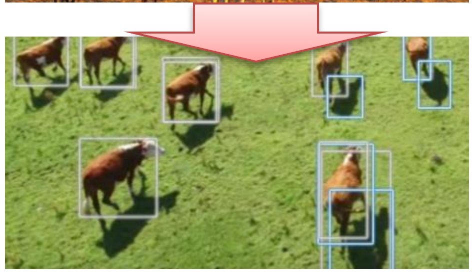
(re) using data collected through precision livestock farming systems

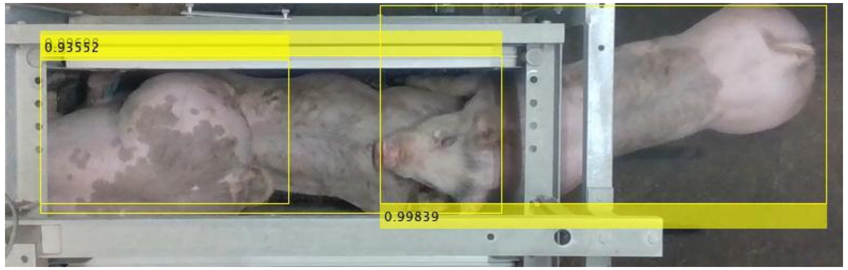


Types of sensors

Remote

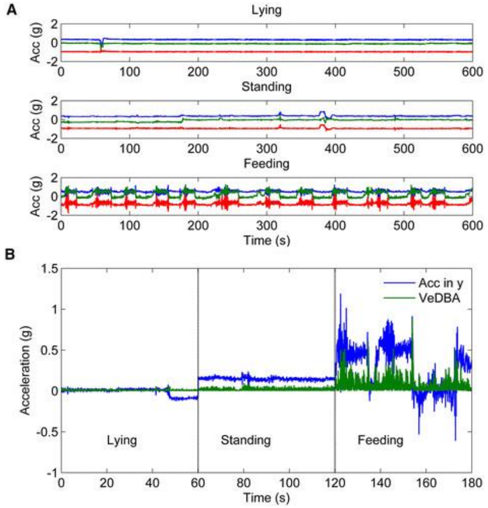






Wearable





Diosdado et al 2015.

Proximal


Combination (most phenotyping technologies)

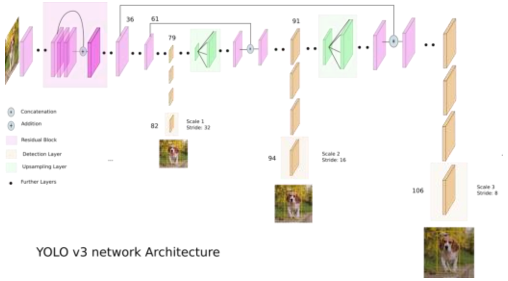
One sensors measures the phenotype, the other sensor IDs the animal

Challenges in using sensors for phenomics

Challenge 1: Extracting (valid) phenotypes from sensor signal

Training data:
Images + Annotation

Model

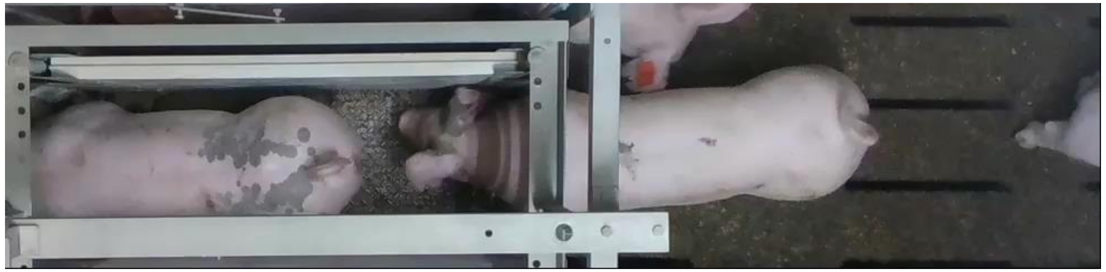


Test data (images):

Performance under cross validation		
True Positives	False Positives	False Negatives
Mask accuracy		

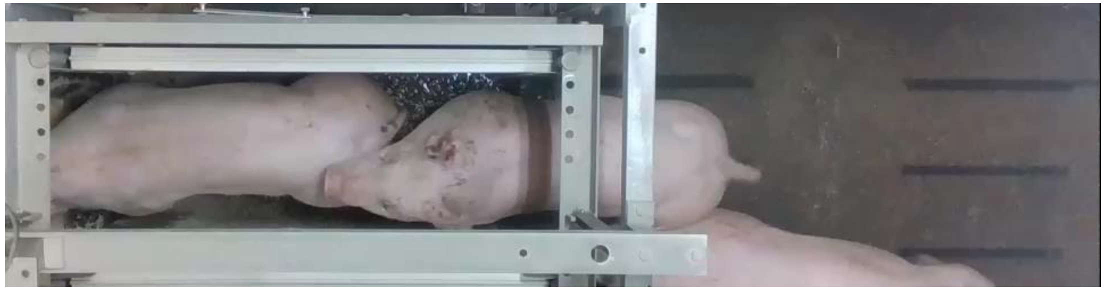
Classifying interactions at the feeder

No Contact

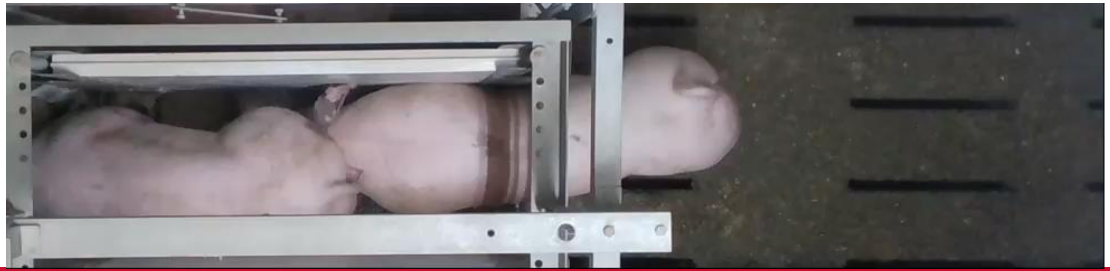


Head to Body (direct)

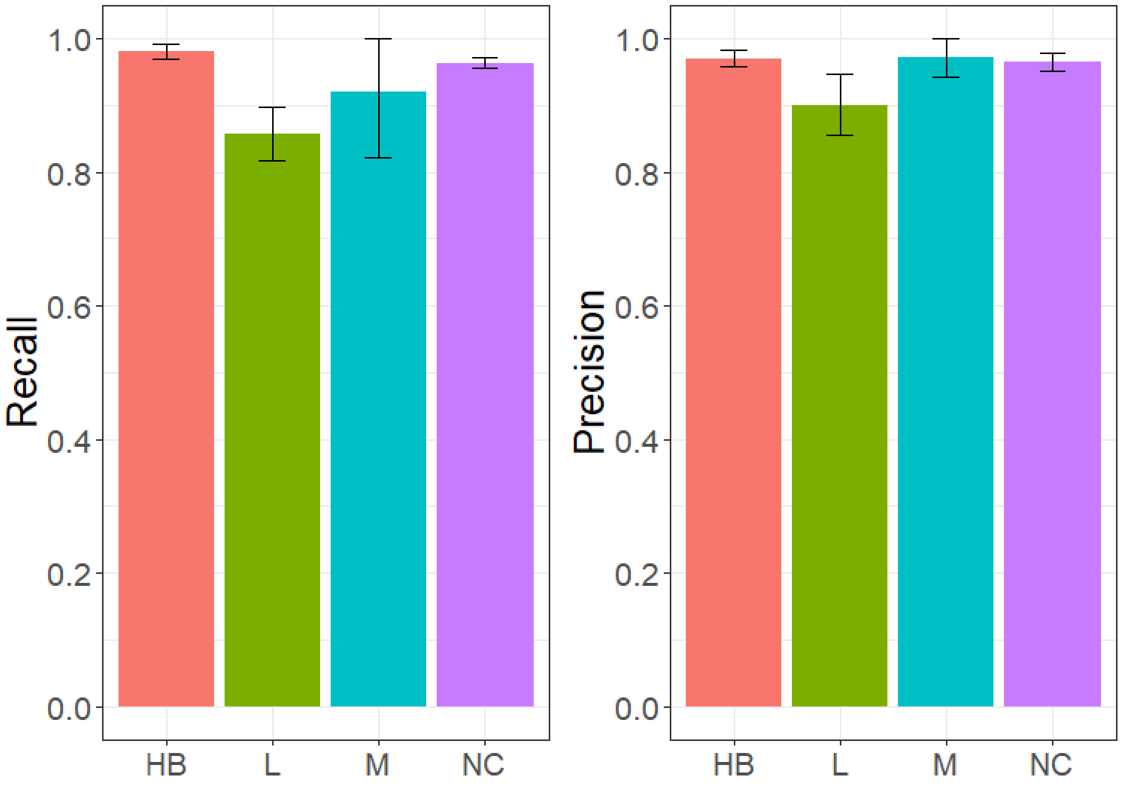
Mounting



Levering



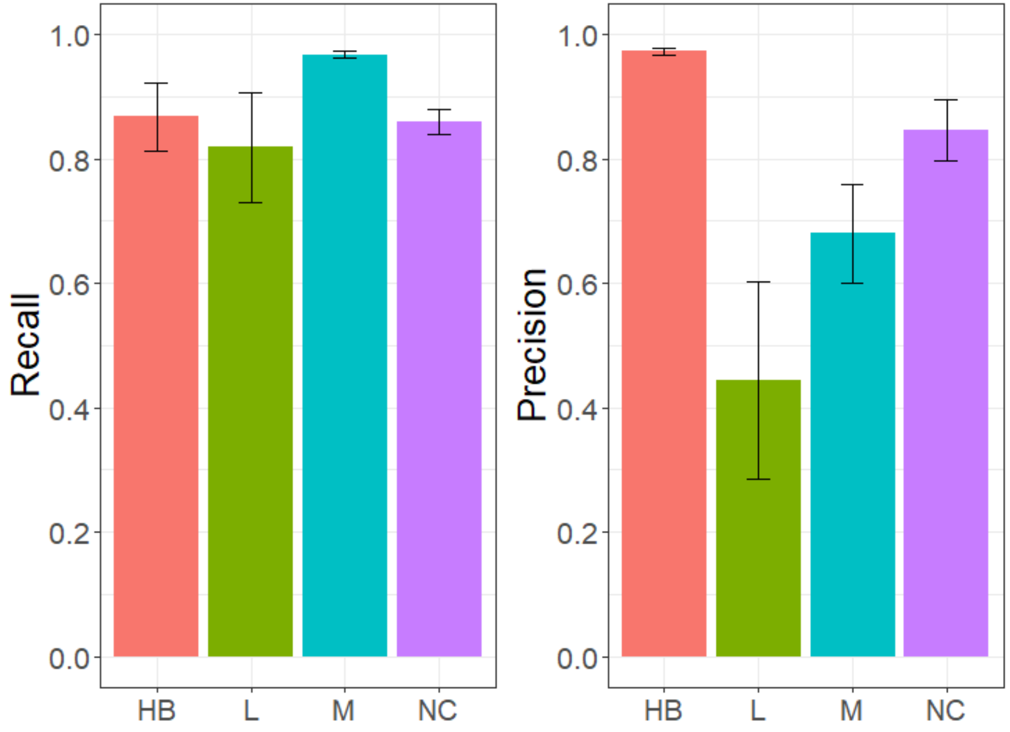
Overall accuracy under random cross validation

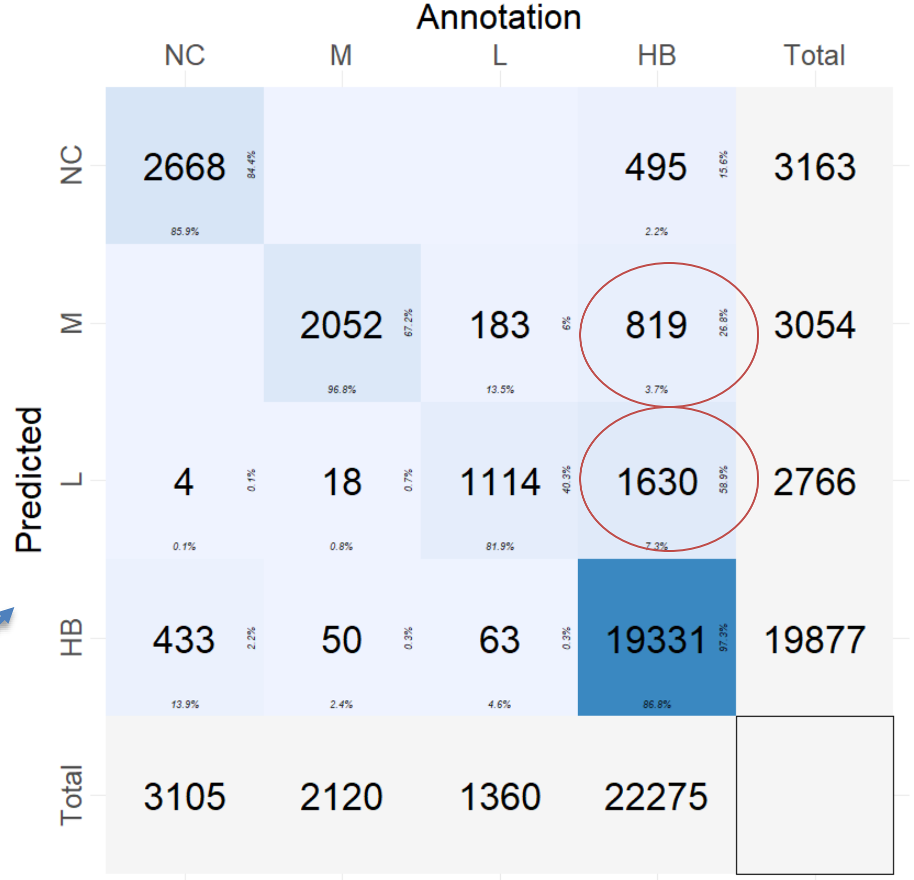


Recall: proportion of videos labeled (ground truth) as <**X**> that are correctly classified.

Precision: proportion of videos classified as <**X**> that are actually labeled (ground truth) as such.

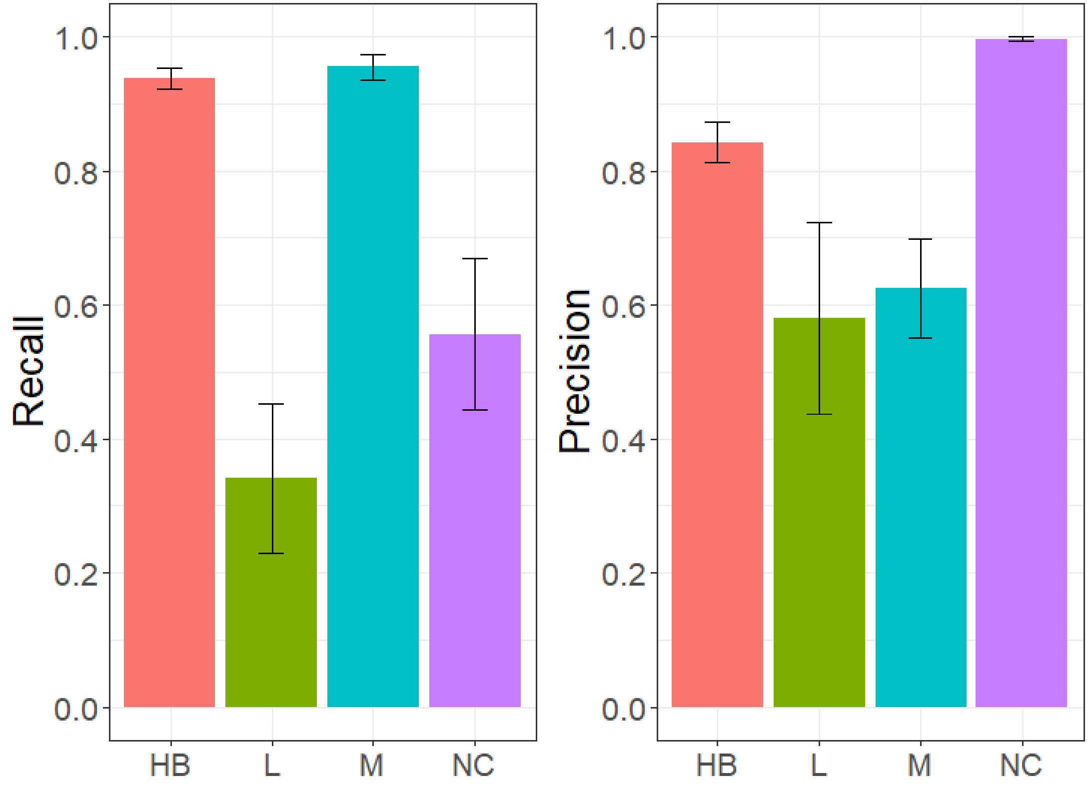
Performance under across time validation



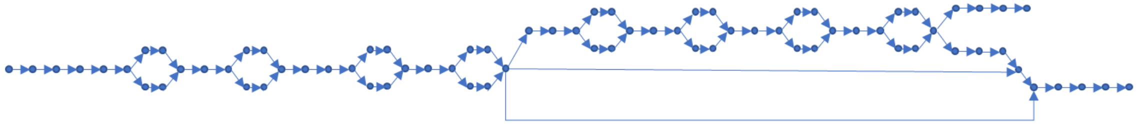


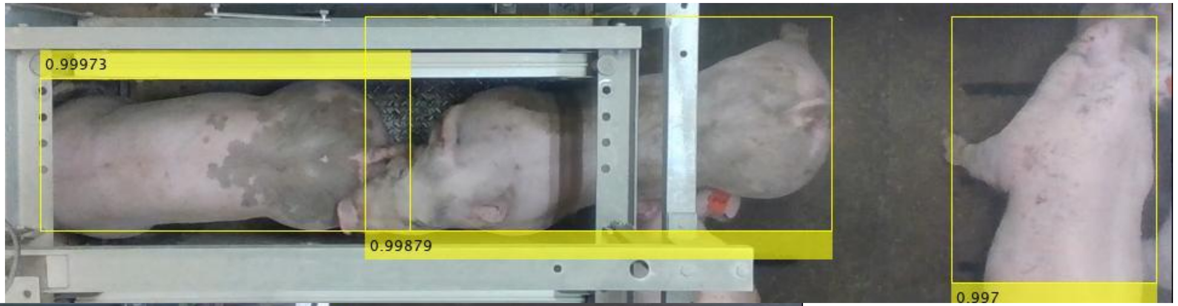
Drop in precision for most labels

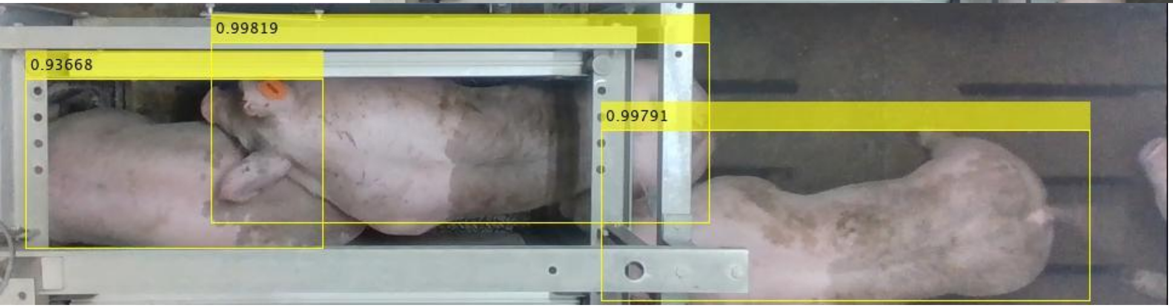
Performance of validation across feeders

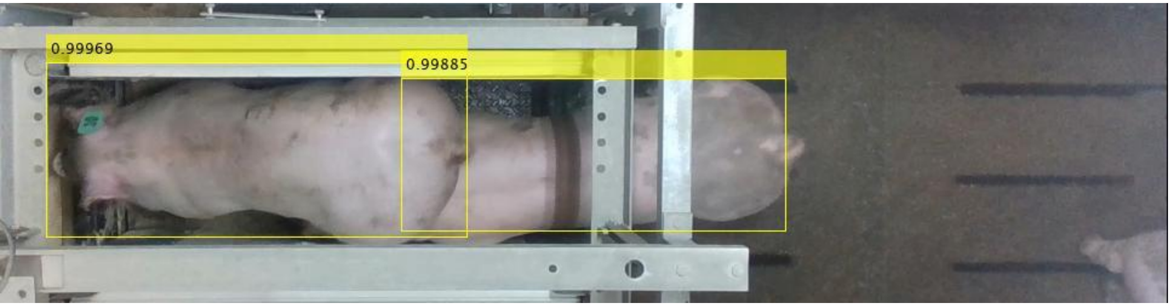


Another example: Animal detection









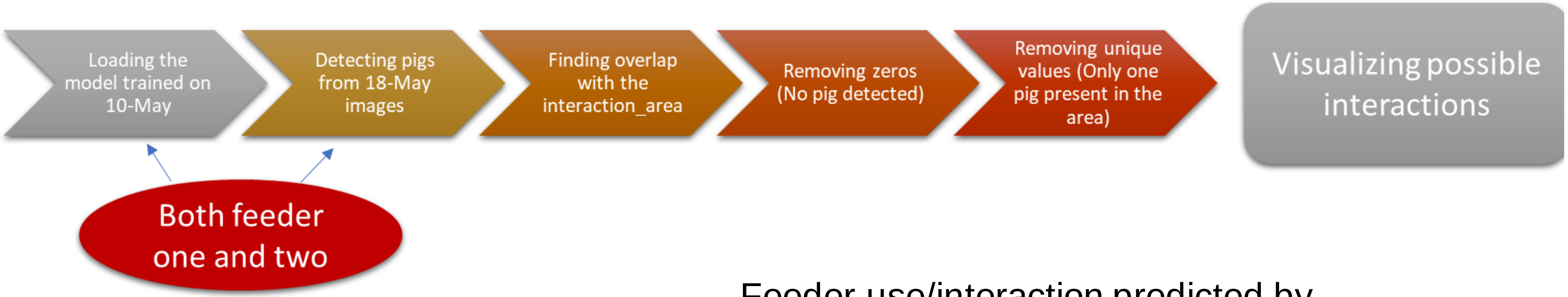
Goal: draw a box around each animal, evaluate its performance.

Then use the box to extract relevant phenotypes

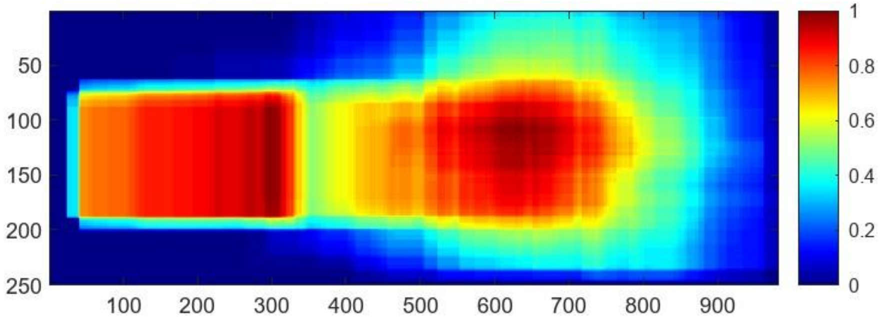
Performance of pig detection over time

Training set	Test set	Precision	IOU
10-May	11-May	0.9302	0.71
10-May	17-May	0.8733	0.725
10-May	18-May	0.7988	0.687
10-May	24-May	0.843	0.705
10-May	25-May	0.8718	0.688

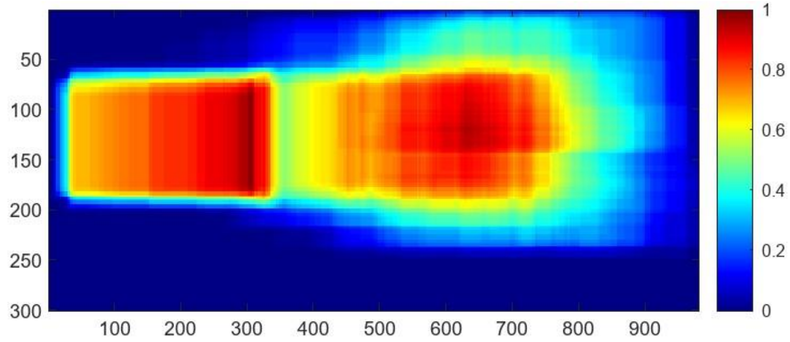
Another example: Animal detection



Observed Feeder use/interaction



Feeder use/interaction predicted by model

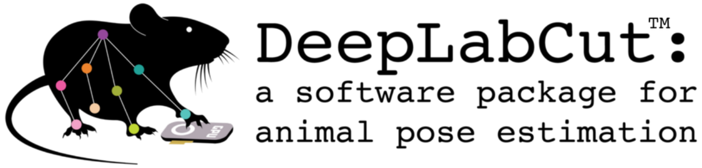


This model may be useful for predicting feeder use, but not so much for interactions at the feeder

And another one: Key point detection

Here the goal is to detect previously selected key points in unmarked images of animals

Use “canned” software:



Trained on labeled videos of unknown (to us horses).

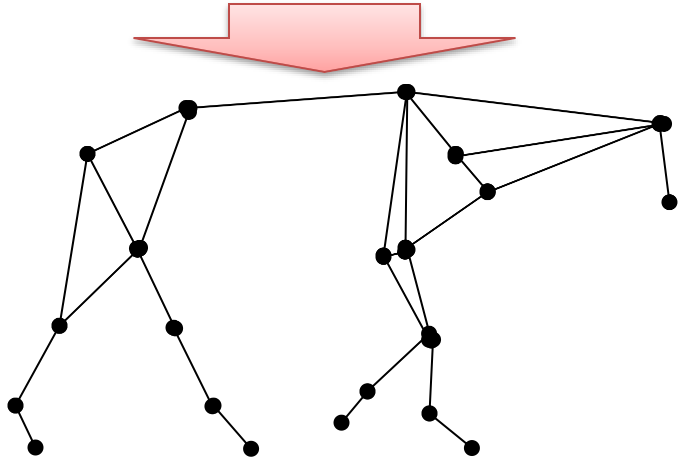
Validated on horses recorded at MSU. It works!!!

…Until it doesn’t

And another one: Key point detection

If the key points are well placed, what phenotypes can we extract from them?

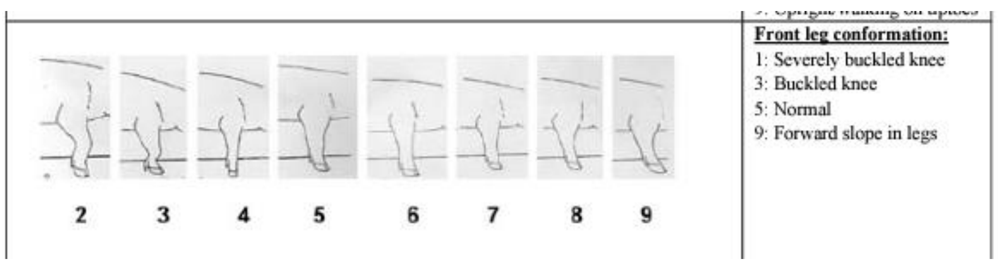
	bodyparts								
	Nose	Nose	Nose	Eye	Eye	Eye	Nearknee	Nearknee	Nearknee
Frame	x	y	likelihood	x	y	likelihood	x	y	likelihood
0	232.87	74.34	1.00	231.50	49.55	1.00	158.60	118.27	0.46
1	232.90	74.53	1.00	231.51	49.61	1.00	158.49	118.33	0.49
2	236.78	73.94	1.00	235.15	49.65	1.00	159.46	118.85	1.00
3	241.27	74.52	0.99	238.44	49.59	1.00	159.35	118.95	1.00
4	242.60	73.11	1.00	241.56	47.23	1.00	158.83	118.55	1.00
5	243.56	72.66	0.99	242.64	45.72	1.00	158.11	119.03	1.00
6	244.86	70.36	0.99	242.40	42.86	1.00	157.53	118.61	1.00
7	248.45	68.27	0.99	242.95	42.35	1.00	156.34	118.92	1.00
8	248.28	66.83	0.99	242.89	41.68	1.00	155.15	118.48	1.00
9	248.75	65.12	0.98	242.10	37.25	1.00	154.70	117.83	1.00
10	248.96	64.10	0.99	241.65	36.06	1.00	155.12	119.07	1.00
11	253.06	62.78	1.00	242.50	36.40	1.00	156.83	118.53	0.99
12	253.92	61.01	1.00	242.20	35.23	1.00	156.62	118.01	0.98
13	252.46	59.61	1.00	242.01	34.86	1.00	157.04	117.64	0.99
14	253.91	58.41	1.00	243.56	34.56	1.00	160.37	118.94	0.99
15	254.22	57.68	1.00	244.50	33.71	1.00	163.35	120.60	0.99

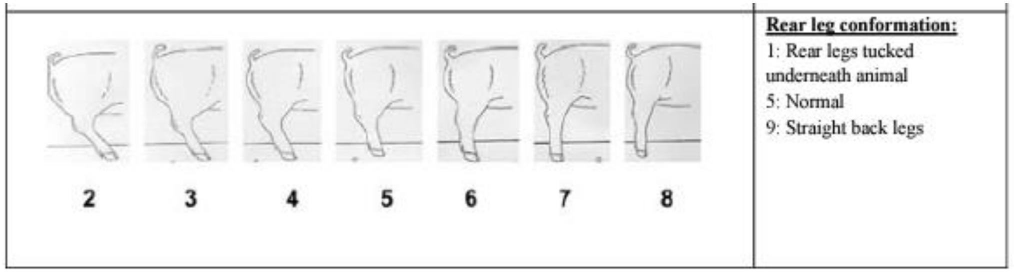


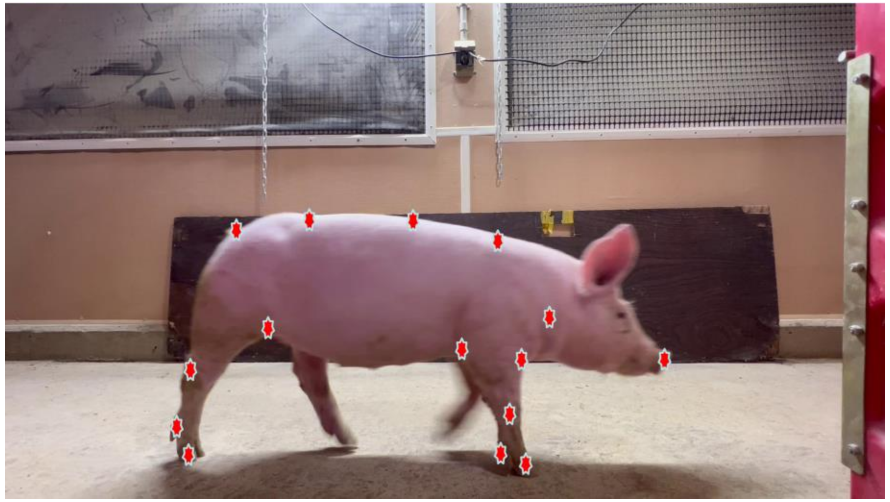
Form follows function?

And another one: Key point detection

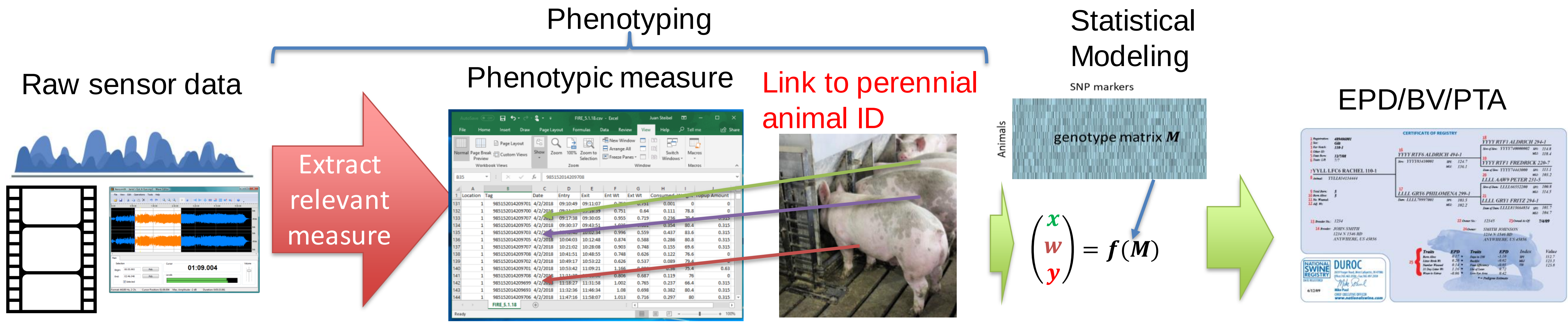
Pure transfer learning
using horse model





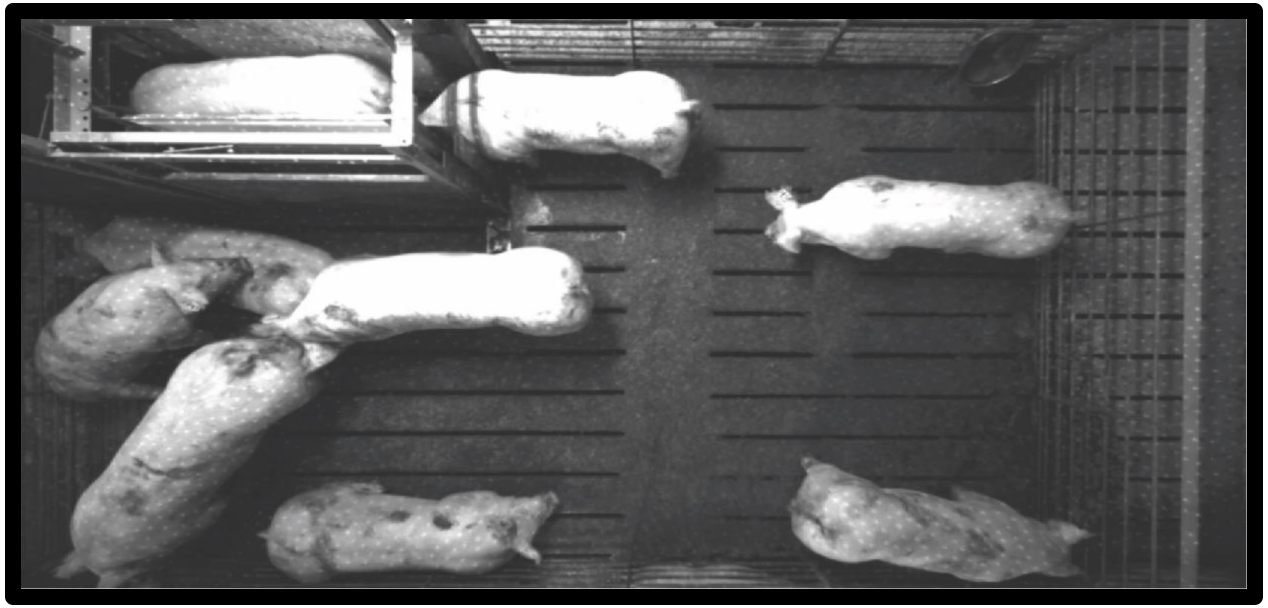


Challenge 2: Animal identification



Key step in phenotyping is to link measurement to a perennial animal ID that can connect to genotypic and pedigree records

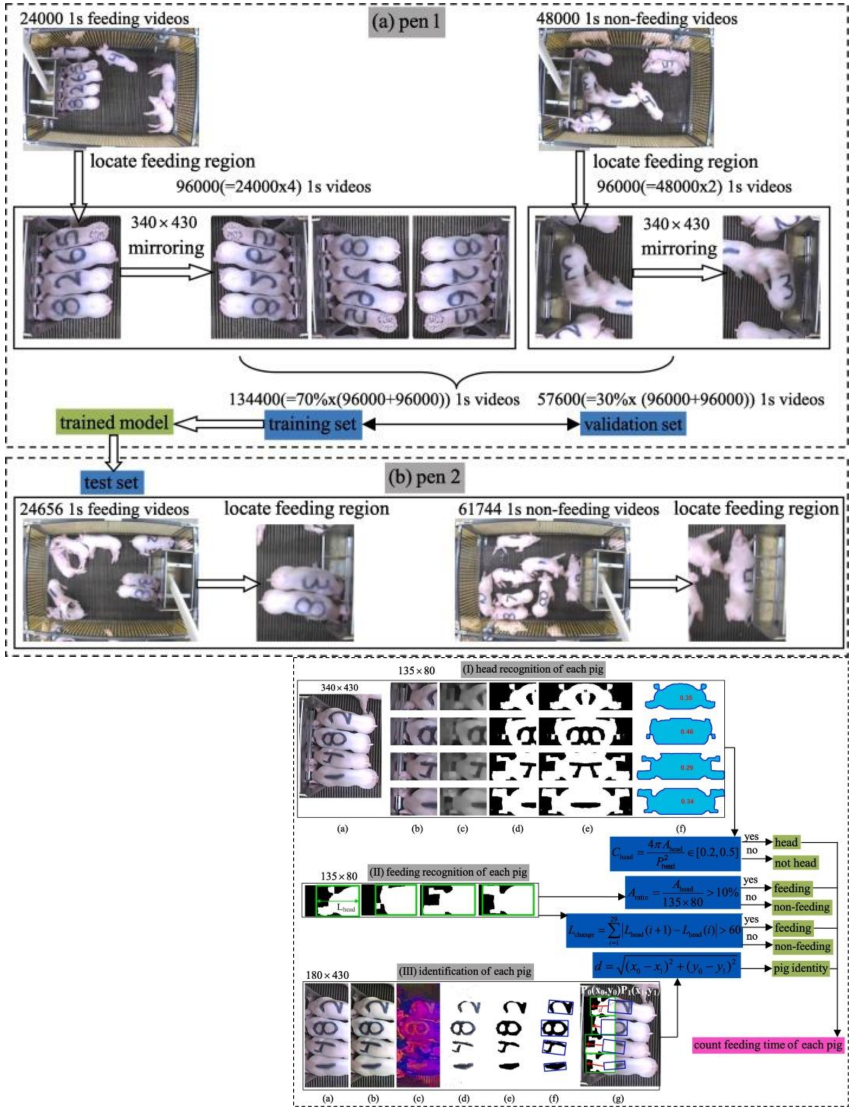
Challenge 2: Animal identification



(in most cases)

Uniform coat colors makes ID without markings difficult…

Challenge 2: Animal identification

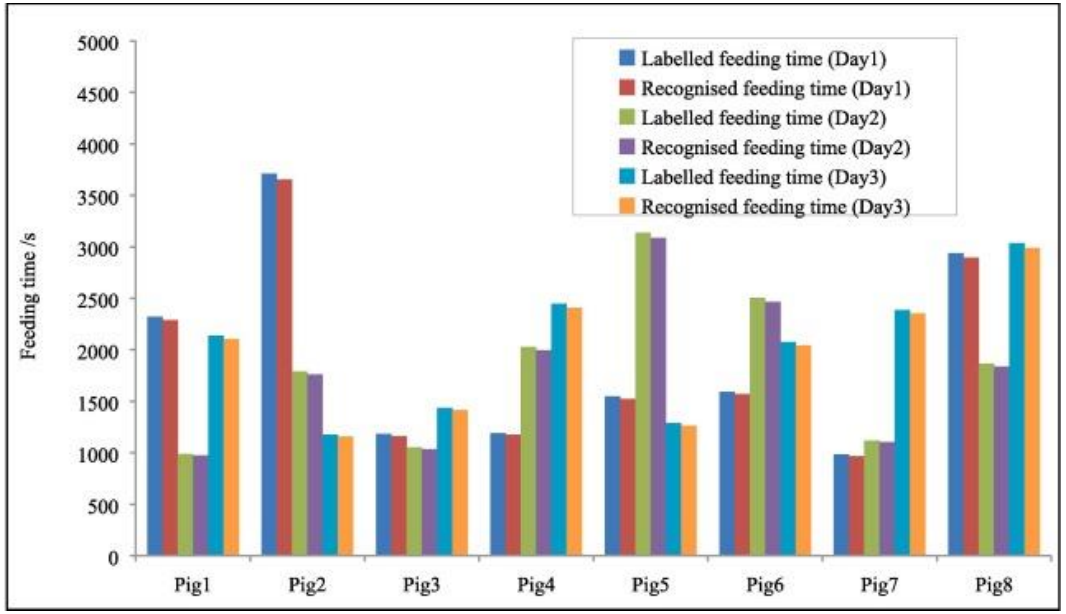


Computers and Electronics in Agriculture

Volume 176, September 2020, 105642

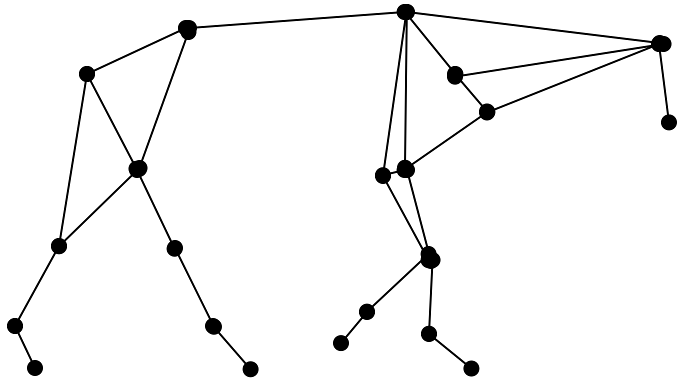
Recognition of feeding behaviour of pigs and determination of feeding time of each pig by a video-based deep learning method

Chen Chen [a, b], Weixing Zhu [a], Juan Steibel [c], Janice Siegford [c], Junjie Han [c], Tomas Norton [b]



Challenge 2: Animal identification

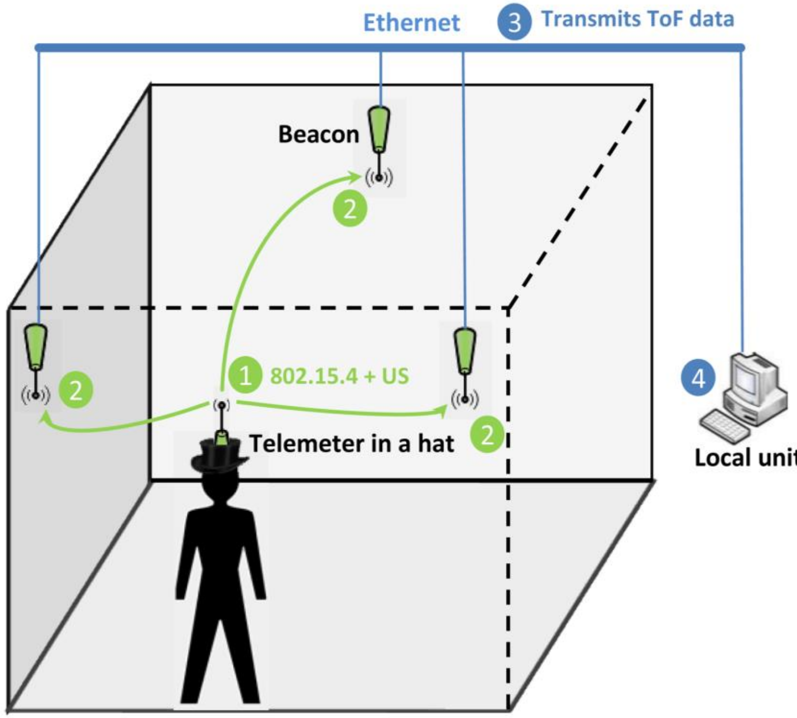
Morphometrics?



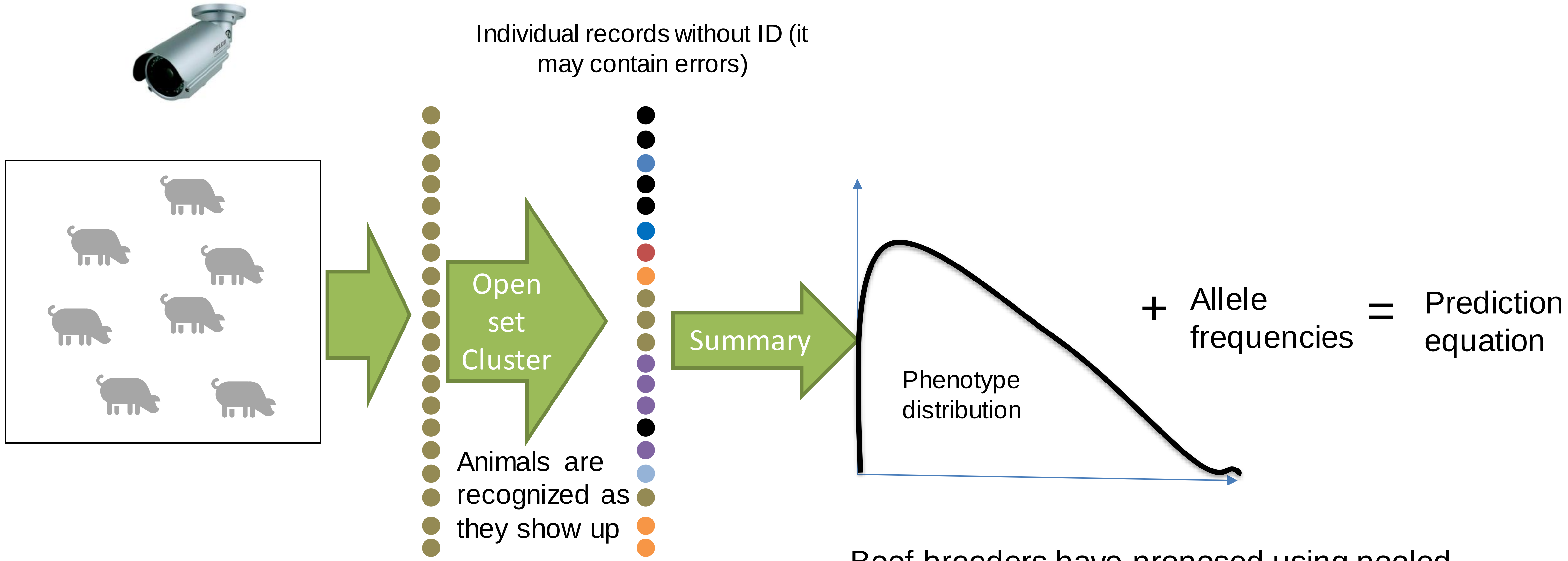
https://www.innovationnewsnetwork.com/

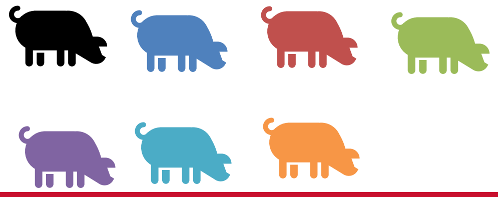
Read ear tags?

Combine it with other wearables



Open set problem: individual records without ID?

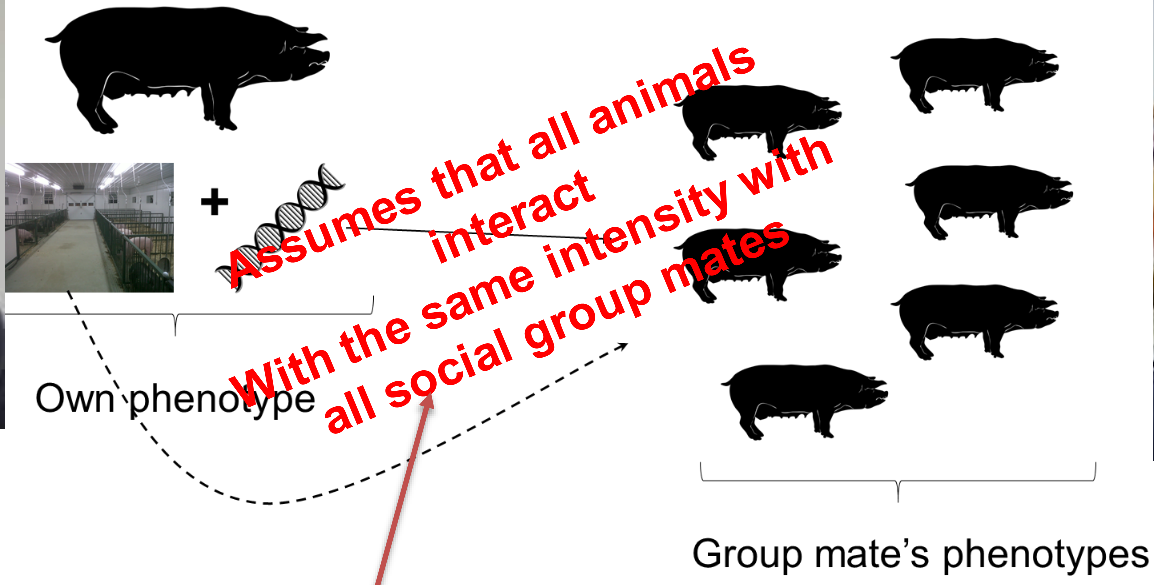




Beef breeders have proposed using pooled genotyping. Those ideas can be combined with individual phenotypes without IDs

Opportunity: better results from “old” models with new data

Social genetic effects



Assumes that all animals interact
With the same intensity with all social group mates

$$\begin{bmatrix} & f_{12} & f_{13} & f_{14} & & & & \\ f_{21} & & f_{23} & f_{24} & & & & \\ f_{31} & f_{32} & & f_{34} & & & & \\ f_{41} & f_{42} & f_{43} & & & & & \\ & & & & & f_{56} & f_{57} & f_{58} \\ & & & & f_{65} & & f_{67} & f_{68} \\ & & & & f_{75} & f_{76} & & f_{78} \\ & & & & f_{85} & f_{86} & f_{87} & \end{bmatrix} \Longleftrightarrow \begin{bmatrix} & 1 & 1 & 1 & & & & \\ 1 & & 1 & 1 & & & & \\ 1 & 1 & & 1 & & & & \\ 1 & 1 & 1 & & & & & \\ & & & & & 1 & 1 & 1 \\ & & & & 1 & & 1 & 1 \\ & & & & 1 & 1 & & 1 \\ & & & & 1 & 1 & 1 & \end{bmatrix}$$

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Z}_d\boldsymbol{u}_d + \boldsymbol{Z}_c\boldsymbol{u}_c + \boldsymbol{e} \qquad \boldsymbol{e} \sim \boldsymbol{N}(0, \boldsymbol{I}\sigma_e^2)$$

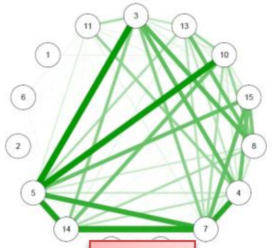
Estimation of indirect social genetic effects for skin lesion count in group-housed pigs by quantifying behavioral interactions[1] FREE

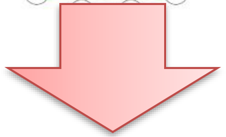
Belcy K Angarita, Rodolfo J C Cantet, Kaitlin E Wurtz, Carly I O'Malley, Janice M Siegford, Catherine W Ernst, Simon P Turner, Juan P Steibel

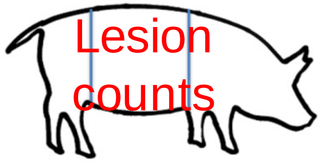
Journal of Animal Science, Volume 97, Issue 9, September 2019, Pages 3658–3668,
https://doi.org/10.1093/jas/skz244
Published: 03 September 2019 **Article history**




Intensity of interaction



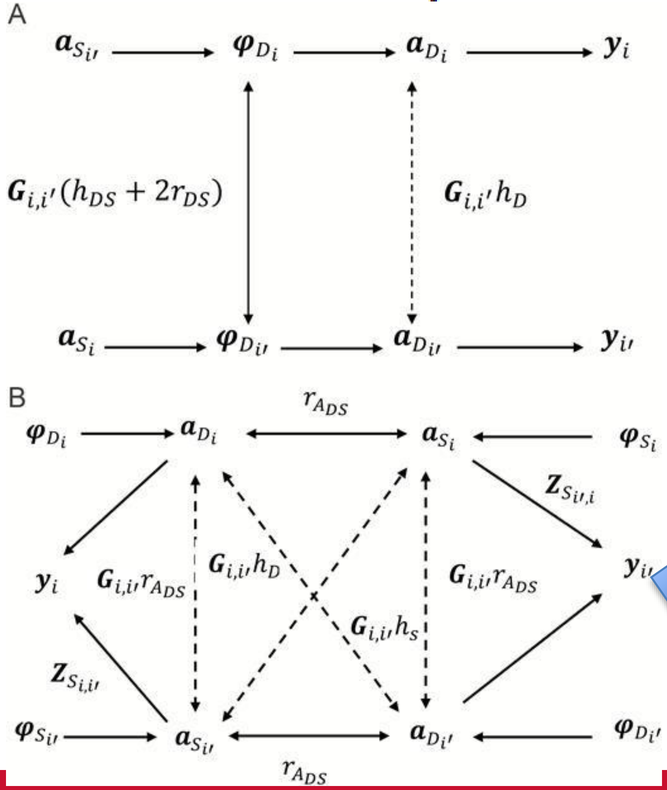




Response phenotype

Ignoring behavioral interactions and social effects

Modeling social effects accounting for behavior



~50% > direct h^2

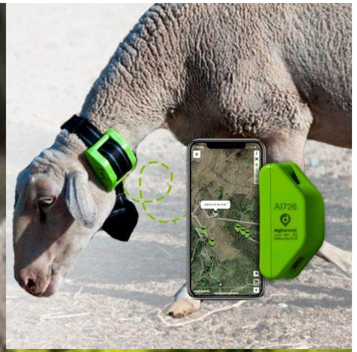
$1.2\sigma_d^2 < \sigma_c^2 < 2.0\sigma_d^2$

Behavioral phenotyping?

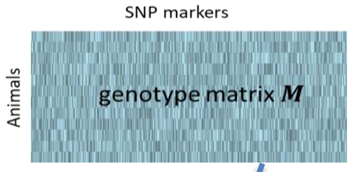
More opportunities for improving classic models

GxE using reaction norm models is nothing new, except that… We could have an air temperature sensor mounted on the back of a cow: Measure the environment CHOSEN by the animal ☺.

Maternal effects models are not new, but now we can model the maternal effect as a function of mother-progeny distance: Separate effect of milk production from maternal attention.



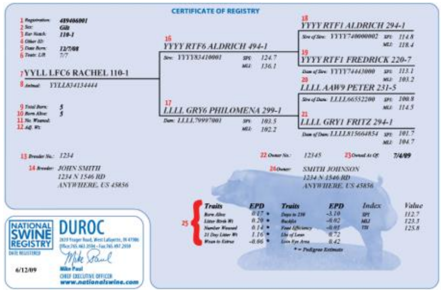
Opportunity: New models for new data: Dyadic data



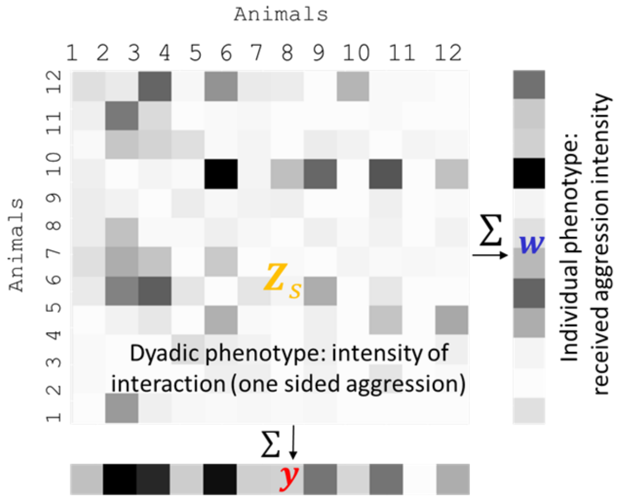
$$\begin{pmatrix} x \\ w \\ y \end{pmatrix} = f(M)$$

MT-GLMM

EPD/BV/PTA

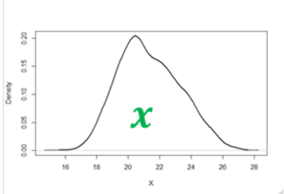


a) Behavioral phenotyping



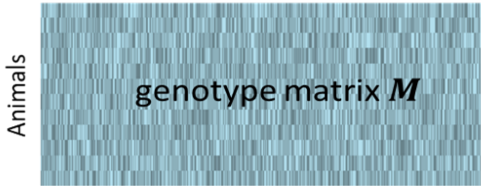
Individual phenotype: intensity of delivered aggression

b) Genomics and other phenotypes



Commercial trait phenotypes

SNP markers



c) Classic modeling

Multi-trait model with individual behavior and production trait

$$\begin{pmatrix} x \\ w \\ y \end{pmatrix} = f(M)$$

MT-GLMM

Social effect model: production trait and social interaction matrix

$$x = f(M, Z_s)$$

SGE

d) Novel models

Predict dyadic interactions from genomic information

$$Z_s = f(M)$$

Dyadic or social relation model (SRM)

Joint prediction of interactions and production trait

$$\begin{pmatrix} x \\ Z_s \end{pmatrix} = f(M)$$

MT-SRM

Challenge: genomic prediction for traits expressed in pairs of individuals

Modeling **directional** dyadic data (probit binary model)

$$P(y_{ijk}=1)=\Phi(\mu_{ijk})$$

Expected interaction

Giver effect

r?

receiver effect

dyad effect

Social group

$$\mu_{ijk} = b_0 + FE_{ijk} + \underbrace{g_i + r_j + d_{ijk} + sg_k}_{\text{Random effects}}$$

$\boldsymbol{g}\sim N(0,\boldsymbol{G}\sigma_g^2)$

$\boldsymbol{r}\sim N(0,\boldsymbol{G}\sigma_r^2)$

$\boldsymbol{d}\sim N(0,\boldsymbol{I}\sigma_d^2)$

$\boldsymbol{sg}\sim N(0,\boldsymbol{I}\sigma_{sg}^2)$

Measure (genetic) of similarity

$$FE_{ijk} = \overbrace{sex_k + \alpha w_{jk} + \beta w_{ik}}^{\text{Animal-level effects}} + \overbrace{\delta_1 z'_{ijk} + \delta_2 z''_{ijk} + \delta_3 s'_{ijk}}^{\text{Dyad-level effects}}$$

Weight of giver and receiver

$$z''_{ijk}\begin{cases}1\ if\ i,j\ shared\ same\ litter\\ 0, otherwise\end{cases}$$

$$z'_{ijk}\begin{cases}1\ if\ i,j\ shared\ same\ nursery\ pen\\ 0, otherwise\end{cases}$$

Estimation of genetic parameters

Only binary data: modeling probability of attacks

giver_id	8	18	22	42	48	50	70	86	90	96	110	114	120
8		0	1	1	0	1	1	1	1	1	0	1	0
18	1		0	0	0	0	1	1	1	1	1	0	1
22	0	0		0	0	1	1	1	0	0	0	0	0
42	1	1	1		1	1	1	1	1	1	1	0	1
48	1	1	1	1		1	1	1	1	0	1	1	1
50	1	1	0	0	0		1	0	0	1	1	0	1
70	0	1	0	0	0	0		0	0	0	0	0	1
86	0	0	0	0	0	1	1		1	0	0	0	0
90	0	0	1	1	0	1	1	1		0	0	1	0
96	0	0	1	0	0	0	0	0	0		0	1	0
110	0	0	1	1	1	1	1	1	0	1		1	1
114	1	1	0	0	0	1	1	1	1	0	0		0
120	1	1	0	1	0	0	0	0	0	1	0	0	

Quantiles of the posterior distribution of fixed effects

	2.5%	50%	97.5%
Sex	-0.193	-0.015	0.170
Common Nursery	-0.391	-0.310	-0.237
Common Litter	-0.199	0.001	0.212
Weight receiver	-0.007	0.000	0.007
Weight giver	0.002	0.013	0.023
Similarity	-0.167	0.198	0.582

Quantiles of the posterior distribution of variance components

	2.5%	50%	97.5%
Group	0.108	0.168	0.269
Receiver	0.030	0.047	0.072
Giver	0.543	0.670	0.823
Dyad	0.097	0.165	0.242
% giver	0.281	0.327	0.372
% receiver	0.015	0.023	0.035
% dyad	0.049	0.08	0.111

Posterior correlation between giver and receiver was not significant

Another example of dyadic data: Co-occurrence at the feeder

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Recognition of feeding behaviour of pigs and determination of feeding time of each pig by a video-based deep learning method

Chen Chen[a,b], Weixing Zhu[a,*], Juan Steibel[c], Janice Siegford[c], Junjie Han[c], Tomas Norton[b,*]

Estimation of direct and social effects of feeding duration in growing pigs using records from automatic feeding stations

Belcy K Angarita, Junjie Han, Rodolfo J C Cantet, Sarah K Chewning, Kaitlin E Wurtz, Janice M Siegford, Catherine W Ernst, Juan Pedro Steibel

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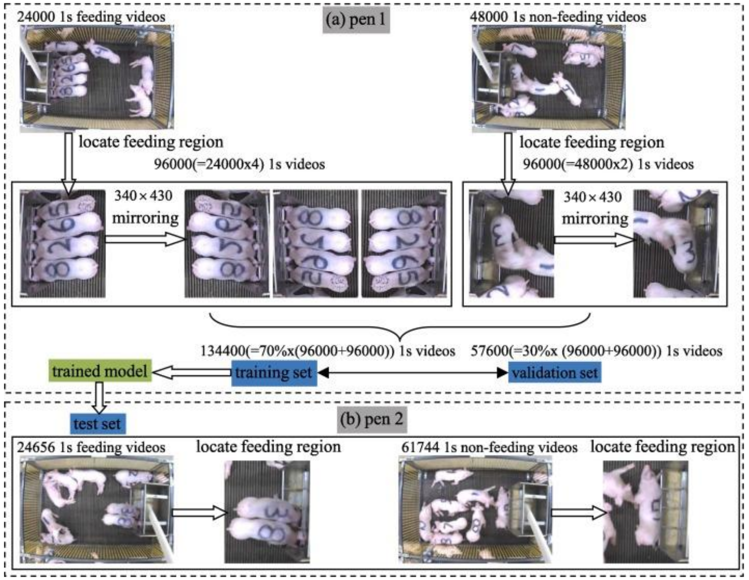
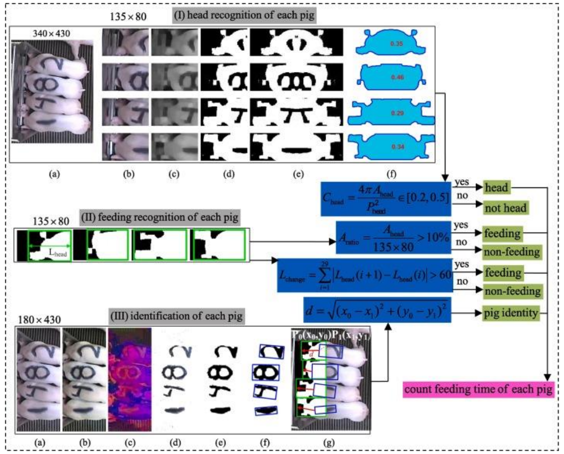
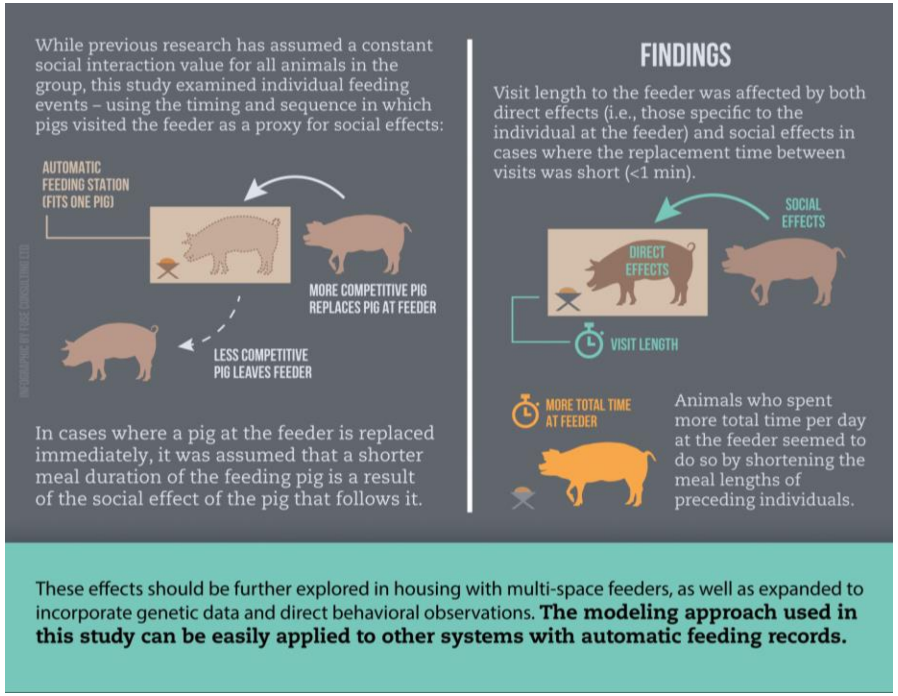
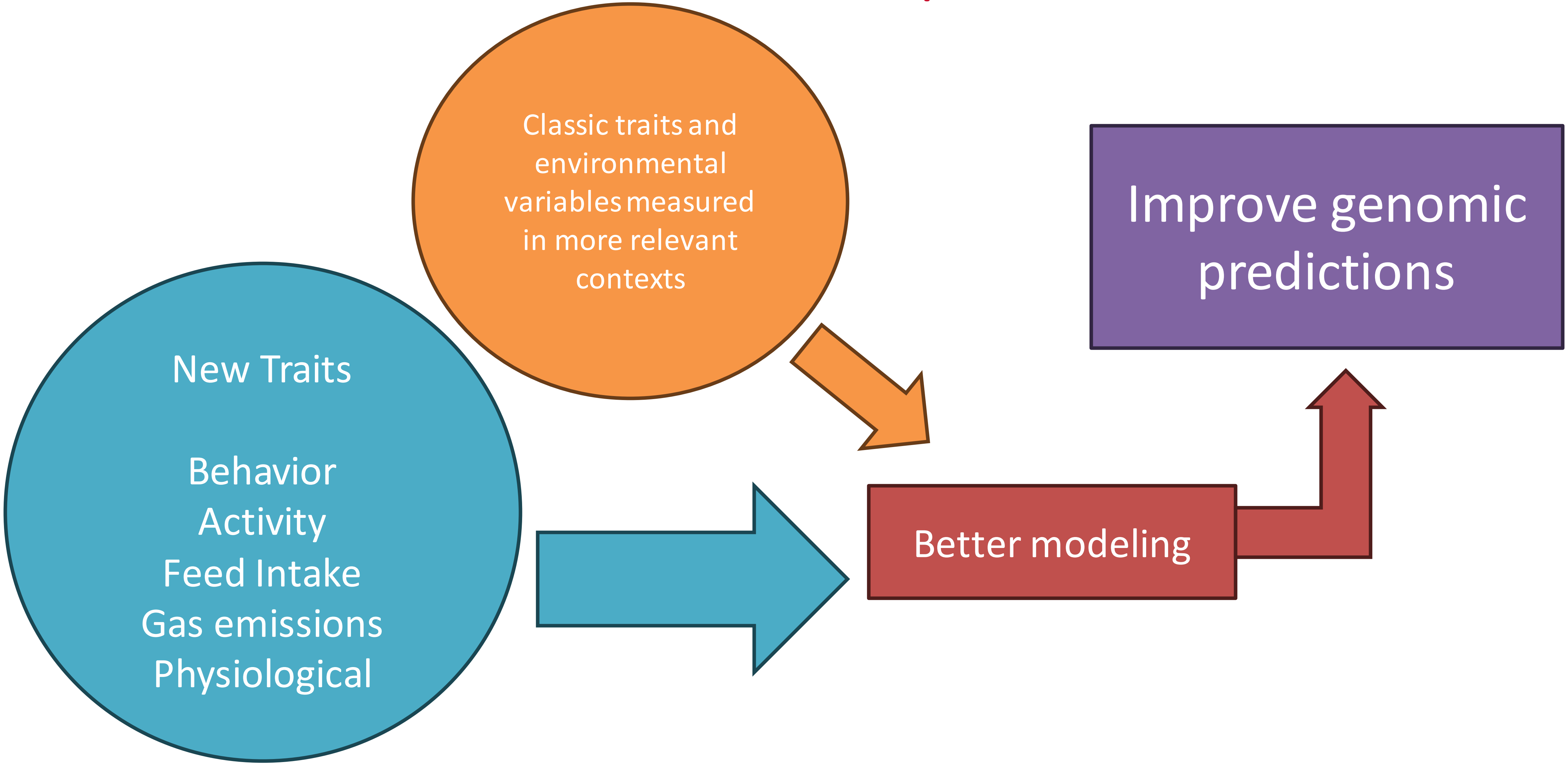






Conclusions: benefits of sensor-based phenomics for breeders



Conclusions: Challenges in livestock phenomics

Validate phenotyping algorithms in broad contexts

link phenotypes trough interoperable ID

Validate genomic predictions of novel traits

Work across disciplines, but remember we (breeders, animal scientists) understand better the sources of phenotypic variation.

Integrate data streams from multiple sensors, keep working across disciplines.

This is where our realm, let's shine ☺