

Use of metabolomics in pigs, barley and cattle





Nordic Seed



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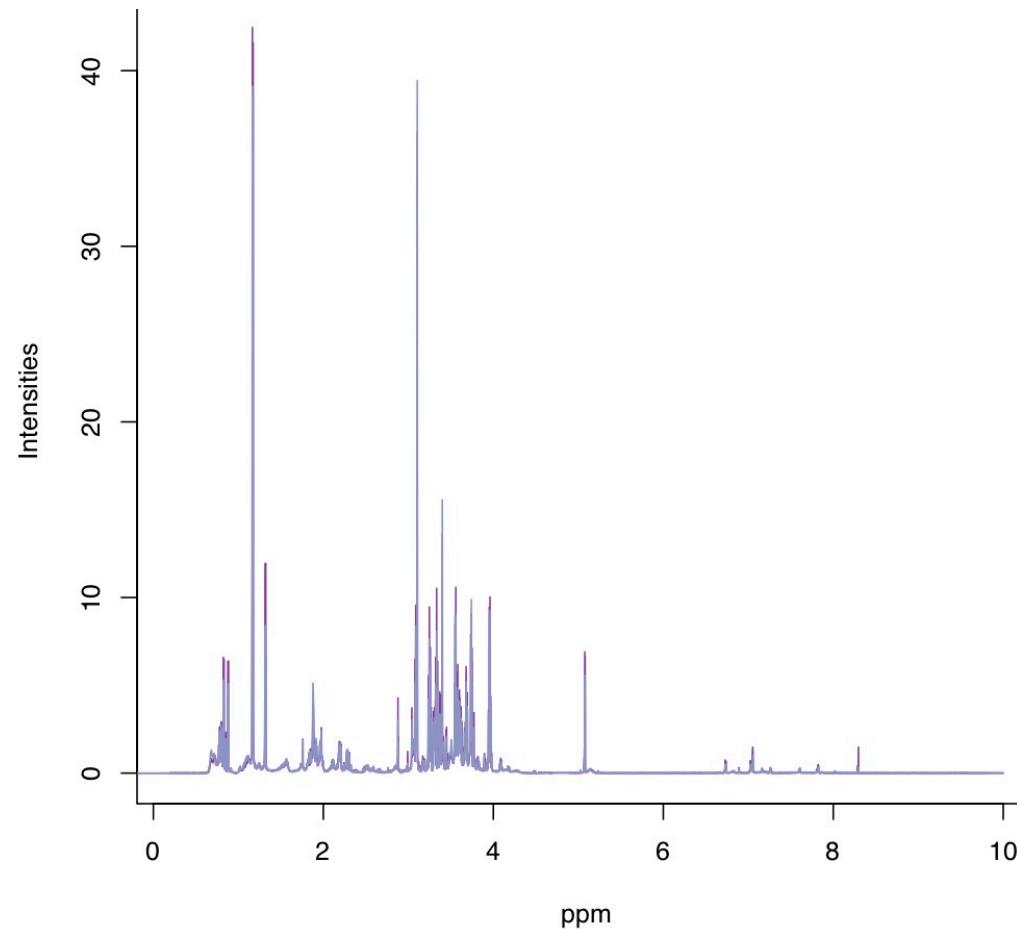
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Background

NMR metabolomics:
Measuring of all
small metabolites
(e.g. sugars, amino acids)
in a biological sample
(e.g. blood sample,
plant extract).

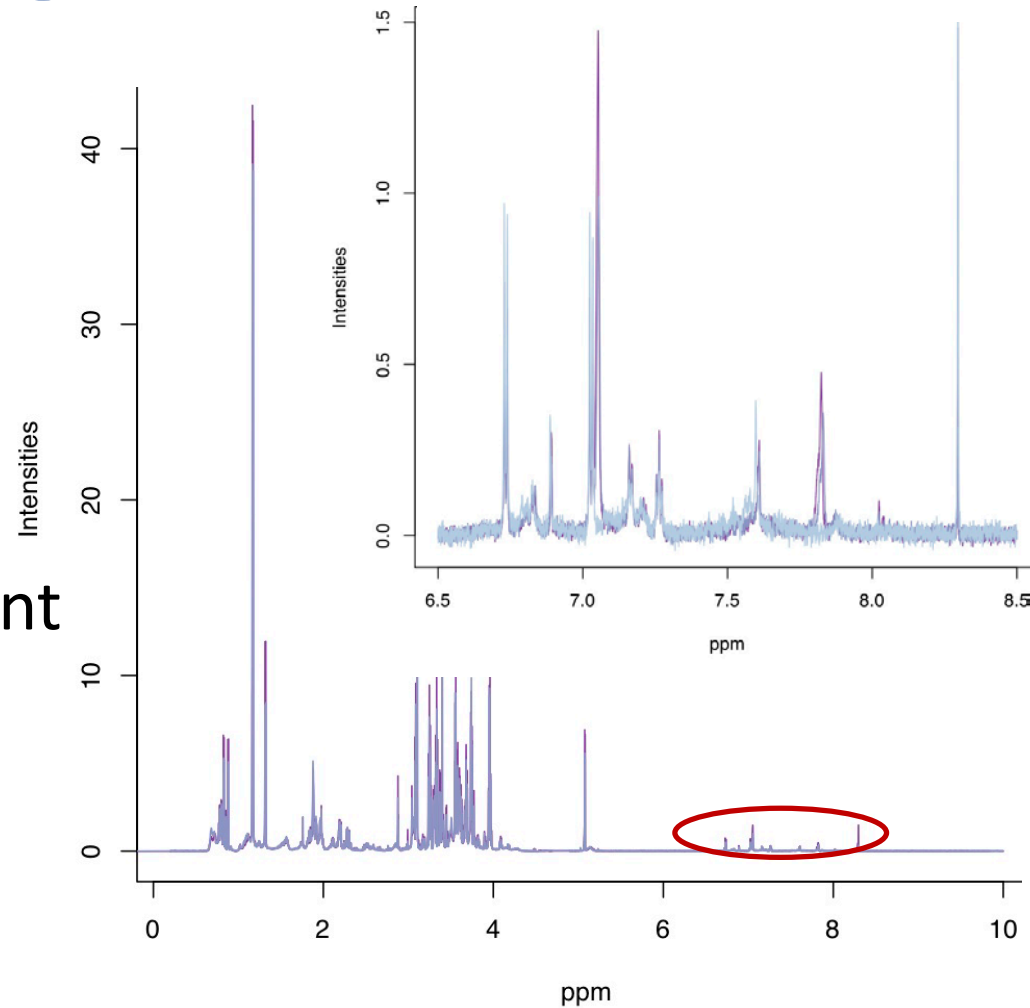
~5 Euro per sample



Background

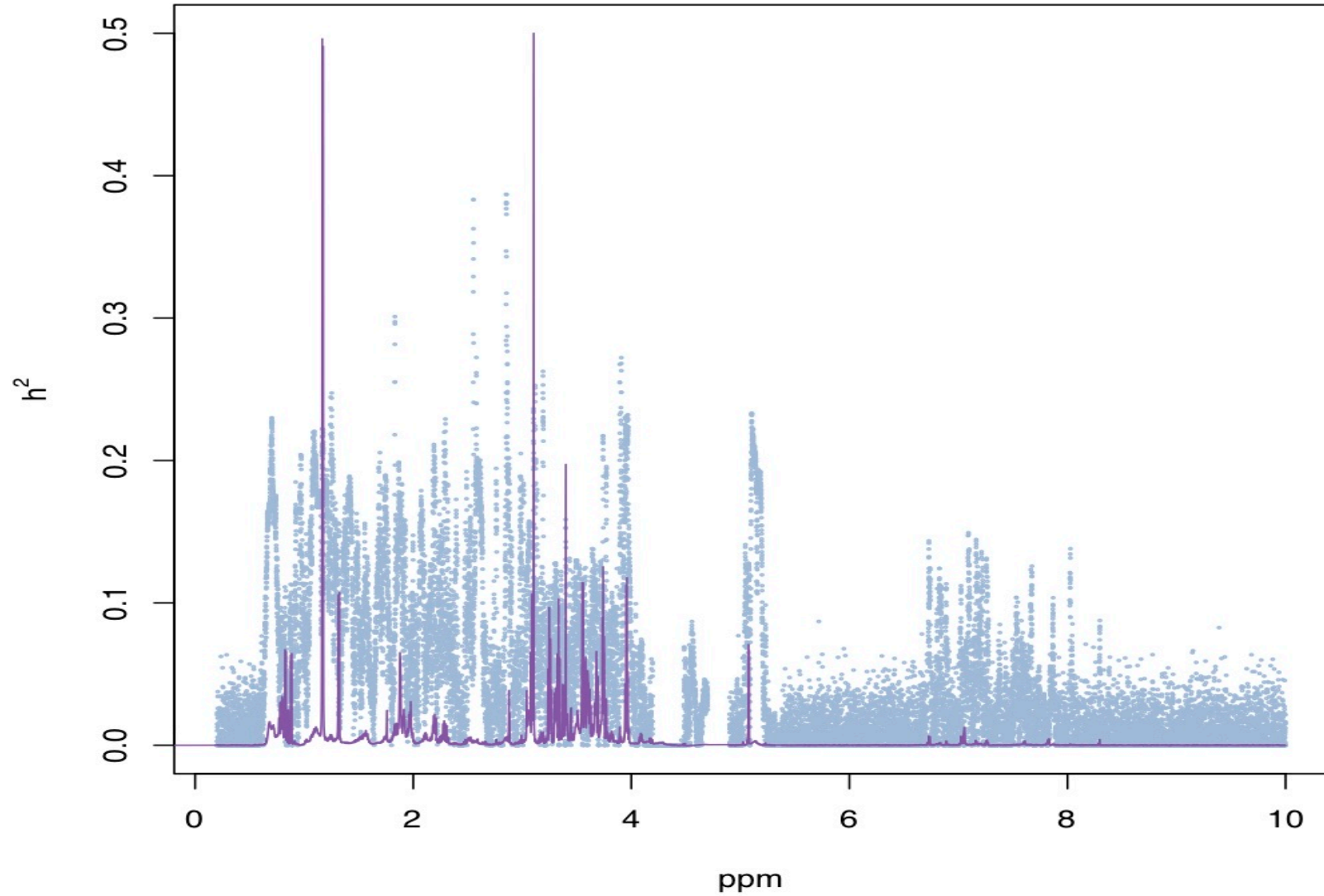
NMR metabolomics:
Spectra data – not a
1 to 1 metabolite-peak
relationship

We treat each data point
In the spectra as a
Metabolomic feature
(~31K features)

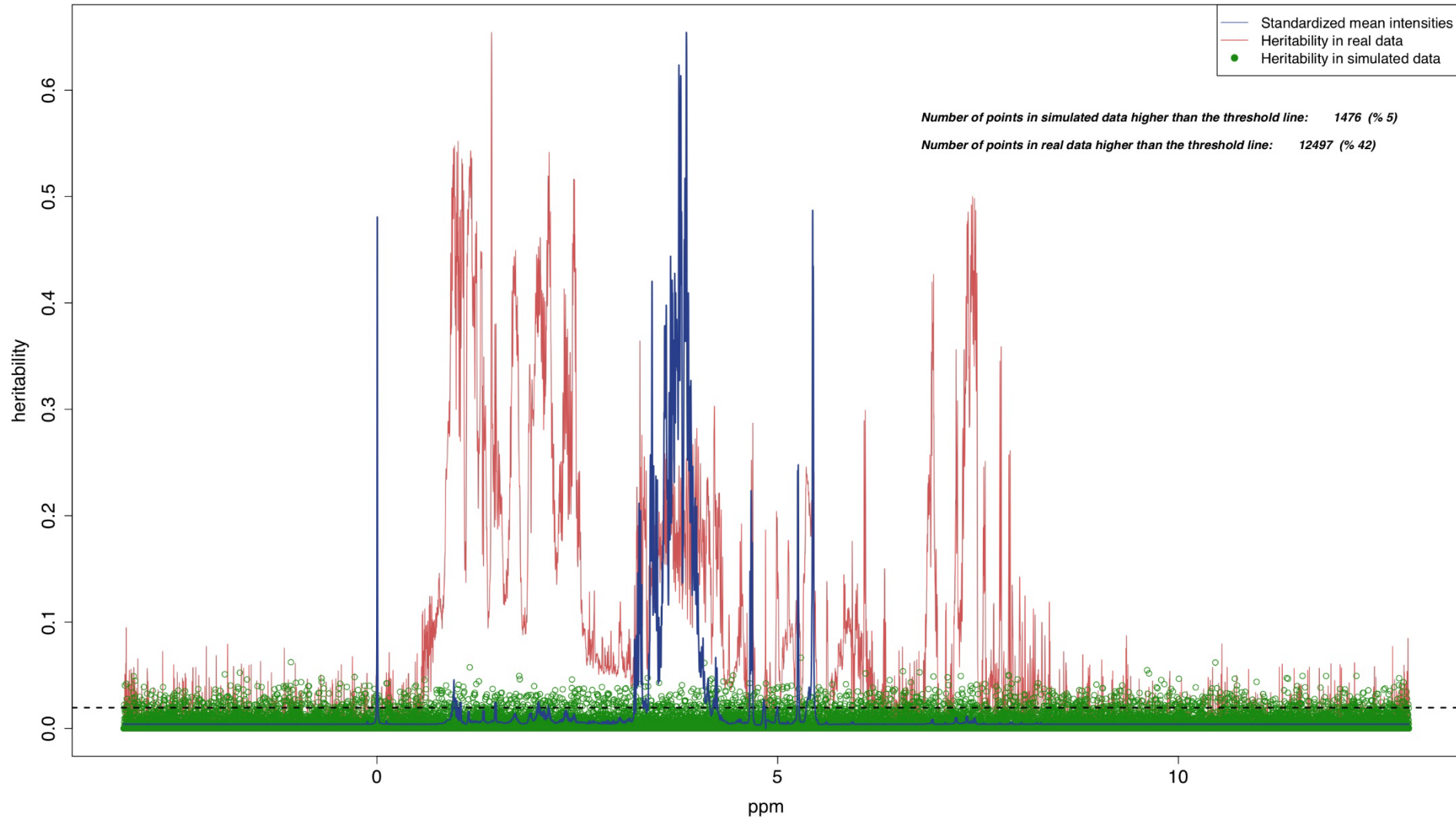


Are the metabolomic features heritable?

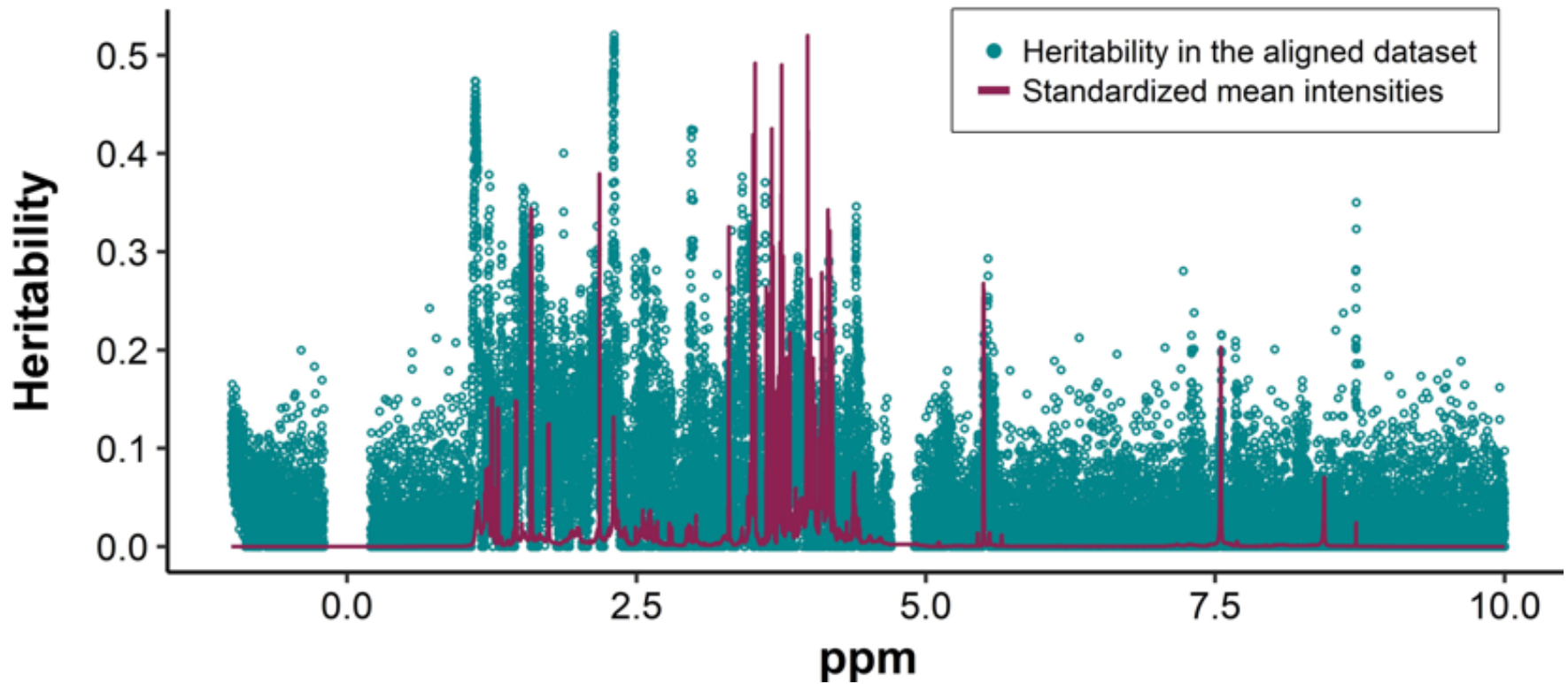
Pig



Barley malt extract



Holstein bull calves



Can we use NMR data to predict breeding relevant phenotypes?

Models

GBLUP

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{Z}_g\mathbf{g} + \mathbf{e}$$

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

$$\mathbf{G} = (\mathbf{W}\mathbf{W}'/n)$$

Models

MBLUP

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{Z}_m\mathbf{m} + \mathbf{e}$$

$$\mathbf{m} \sim N(0, \mathbf{M}\sigma_m^2)$$

$$\mathbf{M} = (\mathbf{X}\mathbf{X}'/n)$$

**X = scaled and centered
metabolomic features**

Cross validation

y_{adj}



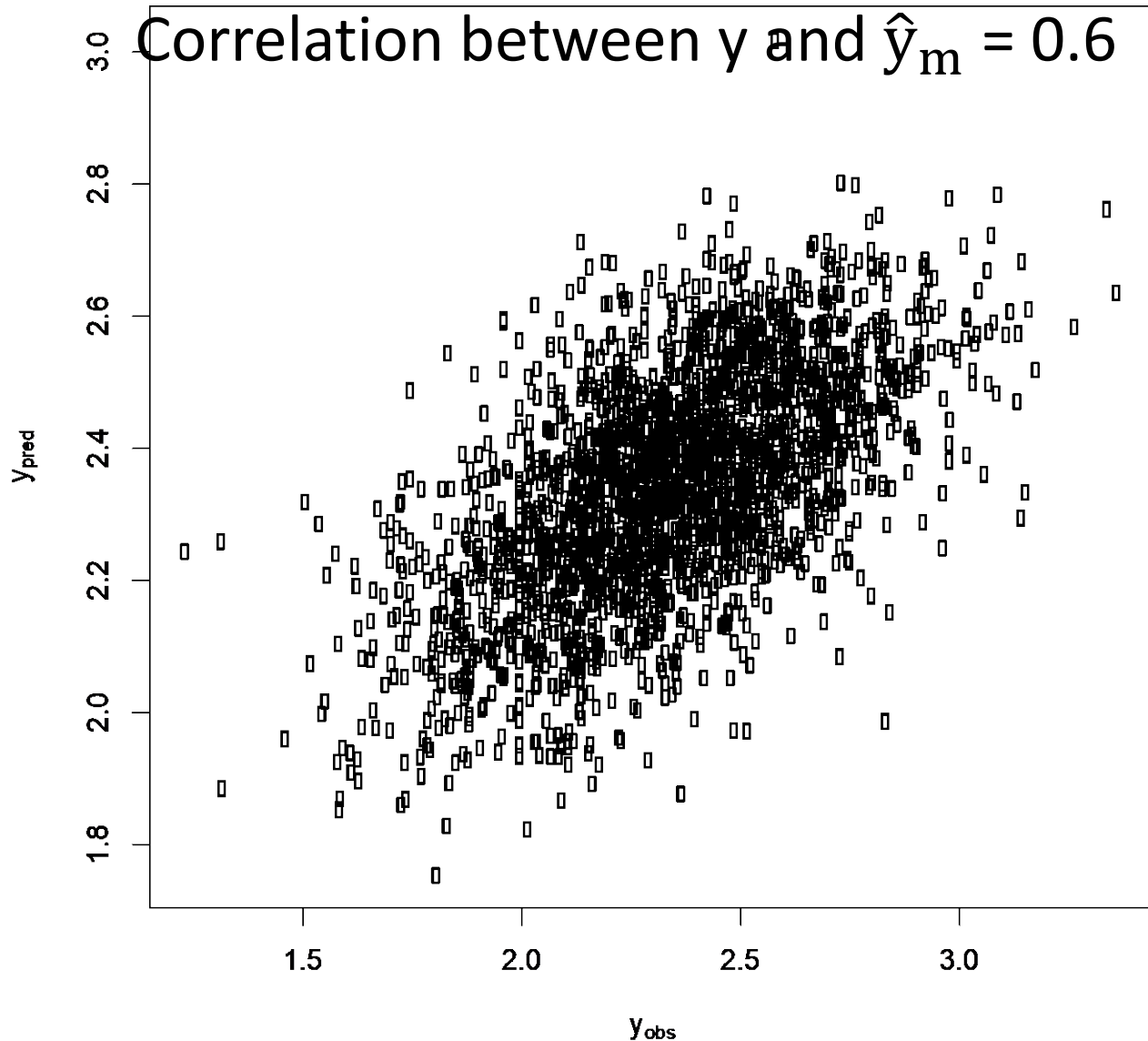
MBLUP

$$y = \mathbf{1}\mu + \mathbf{Z}_m \mathbf{m} + \mathbf{e}$$

$$\hat{y}_m = \hat{\mathbf{m}}$$

Prediction within environments and family, but across litter and sections.

Average daily feed intake



Can we use NMR data to predict genetic components of breeding relevant phenotypes?

Models

Bivariate GBLUP

$$\mathbf{y} = \mathbf{X}_{sec}\mathbf{sec} + \mathbf{X}_{sex}\mathbf{sex} + \mathbf{X}_{sw}\mathbf{SW} + \mathbf{Z}_1\mathbf{l} + \mathbf{Z}_g\mathbf{g} + \mathbf{e}$$
$$\hat{\mathbf{y}}_m = \mathbf{X}_{sec}\mathbf{sec} + \mathbf{X}_{sex}\mathbf{sex} + \mathbf{X}_{sw}\mathbf{SW} + \mathbf{Z}_1\mathbf{l} + \mathbf{Z}_g\mathbf{g} + \mathbf{e}$$

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

$$\mathbf{G} = (\mathbf{W}\mathbf{W}'/n)$$

Estimated variance

ADFI	\hat{y}_m		y	correlation	SE correlation
litter	0.0029	0.0018	0.0063	0.4149	0.1251
animal	0.0076	0.0099	0.0222	0.7649	0.0518
e	0.0149	0.0135	0.0452	0.5186	0.0222
h2	0.2979	0.2290	0.3008		

Conclusions

A high proportion of the metabolic profile is heritable in barley, pig and cattle

The metabolic profile can predict complex phenotypes

Predicted phenotypes have high genetic correlations with observed phenotypes and can be used for selective breeding

Questions?