Integrating metabolomics and genomics

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Data

   681 D(YL) pigs

   Genotypes

   NMR – metabolomics on blood sample

   Total feed intake

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Models

GBLUP

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_{\mathrm{p}}\mathbf{p} + \mathbf{Z}_l\mathbf{l} + \mathbf{Z}_{\mathrm{g}}\mathbf{g} + \mathbf{e}$$

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

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

Cross validation design: Half sip family

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Models

GBLUP

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_p\mathbf{p} + \mathbf{Z}_l\mathbf{l} + \mathbf{Z}_g\mathbf{g} + \mathbf{e}$$
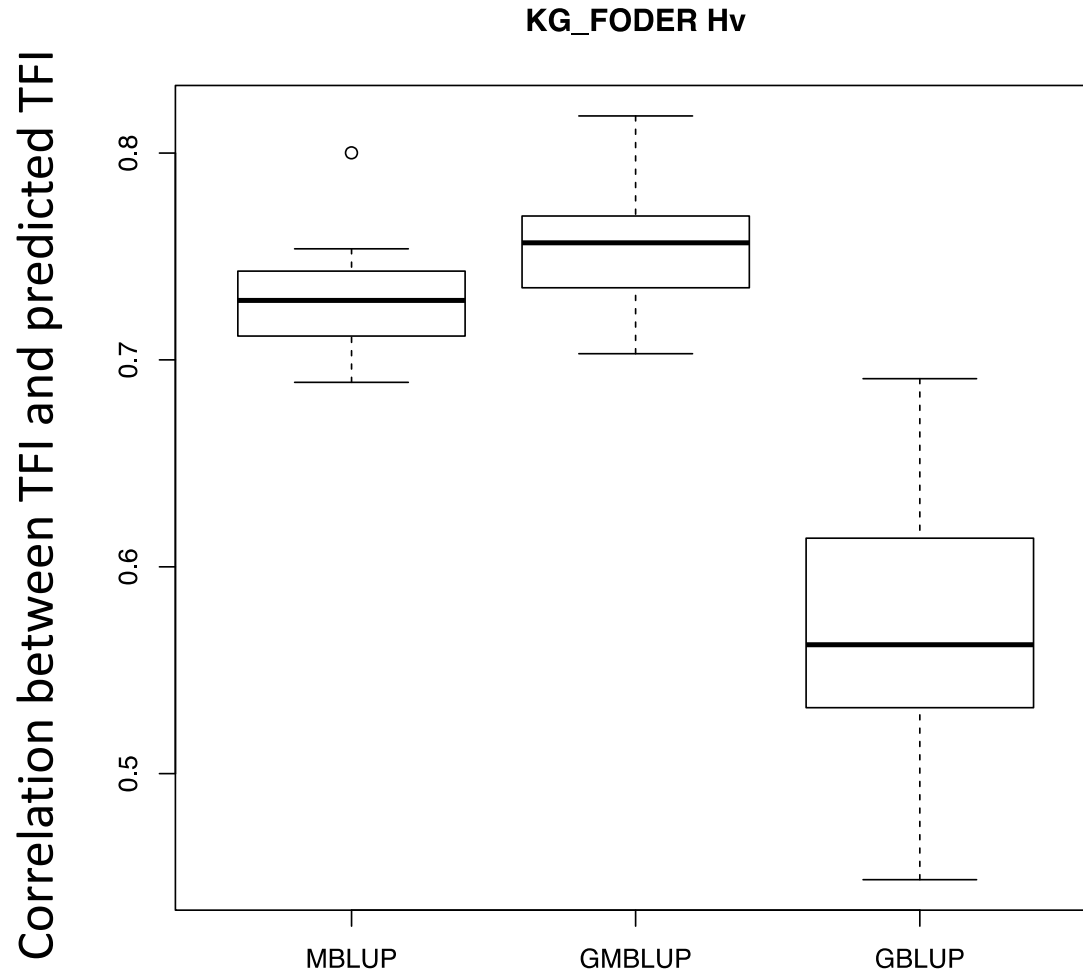
MBLUP

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_p\mathbf{p} + \mathbf{Z}_l\mathbf{l} + \mathbf{Z}_m\mathbf{m} + \mathbf{e}$$

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

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

Cross validation design: Half sip family

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Models

GBLUP

$$y = Xb + Z_p p + Z_l l + Z_g g + e$$

MBLUP

$$y = Xb + Z_p p + Z_l l + Z_m m + e$$

GMBLUP

$$y = Xb + Z_p p + Z_l l + Z_m m + Z_g g + e$$

Cross validation design: Half sip family

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KG_FODER Hv

Higher prediction ability of MBLUP and GMBLUP models!

2300 additional NMR samples being analysed
ETA end of 2017!