Genetic evaluation for three way crossbreeding

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Motivation (pigs)

- Crossbreeding is predominant in the production. Commonly:
  - Crossbred sows from two dam lines
  - Crossbred production pigs from sire line and crossbred sows.
- Genomic selection implemented for purebreds, but also gives options for crossbreds
- Ideally:
  - Include records on crossbreds
  - Compute breeding values for crossbred performance.

Aim here: develop methods

- Three-breed terminal crossbreeding
- Additive relationships from pedigree and marker genotypes

Scenario

- Three breeds, $\mathcal{A}$, $\mathcal{B}$ and $\mathcal{C}$
- Breeds $\mathcal{A}$ and $\mathcal{B}$ are mated to produce $\mathcal{AB}$ sows
- Breed $\mathcal{C}$ boars are mated to $\mathcal{AB}$ sows to produce $\mathcal{C}(\mathcal{AB})$ crossbreds
- Phenotypes on purebreds $\mathcal{A}$, $\mathcal{B}$ and $\mathcal{C}$ and crossbreds $\mathcal{C}(\mathcal{AB})$.
- Pedigree information exist and some animals are genotyped.

Previous work (two way crossbreeding)

(Wei and van der Werf, 1994, Christensen et al., 2014)

$$\begin{aligned}\mathbf{y}_{\mathcal{A}} &= \mathbf{X}_{\mathcal{A}}\boldsymbol{\beta}_{\mathcal{A}} + \mathbf{Z}_{\mathcal{A}}\mathbf{a}_{\mathcal{A}} + \mathbf{e}_{\mathcal{A}},\\ \mathbf{y}_{\mathcal{B}} &= \mathbf{X}_{\mathcal{B}}\boldsymbol{\beta}_{\mathcal{B}} + \mathbf{Z}_{\mathcal{B}}\mathbf{a}_{\mathcal{B}} + \mathbf{e}_{\mathcal{B}},\\ \mathbf{y}_{\mathcal{AB}} &= \mathbf{X}_{\mathcal{AB}}\boldsymbol{\beta}_{\mathcal{AB}} + \mathbf{g}_{\mathcal{AB}} + \mathbf{e}_{\mathcal{AB}},\end{aligned}$$

where

- BVs for purebred performance: $\mathbf{a}_{\mathcal{A}}$, $\mathbf{a}_{\mathcal{B}}$.
- Relationships defined according to breed of origin.
- BVs for crossbred performance: $\mathbf{g}_{\mathcal{A}}$, $\mathbf{g}_{\mathcal{B}}$.
- Genetic correlation between purebred and crossbred performances.

Model for three way crossbreeding

- Model

$$
\begin{aligned}
\mathbf{y}_{\mathcal{A}} &= \mathbf{X}_{\mathcal{A}}\boldsymbol{\beta}_{\mathcal{A}} + \mathbf{Z}_{\mathcal{A}}\mathbf{a}_{\mathcal{A}} + \mathbf{e}_{\mathcal{A}},\\
\mathbf{y}_{\mathcal{B}} &= \mathbf{X}_{\mathcal{B}}\boldsymbol{\beta}_{\mathcal{B}} + \mathbf{Z}_{\mathcal{B}}\mathbf{a}_{\mathcal{B}} + \mathbf{e}_{\mathcal{B}},\\
\mathbf{y}_{\mathcal{C}} &= \mathbf{X}_{\mathcal{C}}\boldsymbol{\beta}_{\mathcal{C}} + \mathbf{Z}_{\mathcal{C}}\mathbf{a}_{\mathcal{C}} + \mathbf{e}_{\mathcal{C}},\\
\mathbf{y}_{\mathcal{C}(\mathcal{AB})} &= \mathbf{X}_{\mathcal{C}(\mathcal{AB})}\boldsymbol{\beta}_{\mathcal{C}(\mathcal{AB})} + \mathbf{g}_{\mathcal{C}(\mathcal{AB})} + \mathbf{e}_{\mathcal{C}(\mathcal{AB})},
\end{aligned}
$$

  where
  - BVs for purebred performance: $\mathbf{a}_{\mathcal{A}}$, $\mathbf{a}_{\mathcal{B}}$, $\mathbf{a}_{\mathcal{C}}$.
  - BVs for crossbred performance: $\mathbf{g}_{\mathcal{A}}$, $\mathbf{g}_{\mathcal{B}}$, $\mathbf{g}_{\mathcal{C}}$.
  - Relationships need to be defined !

Model for three way crossbreeding

- BVs for crossbred performance $\mathbf{g}_{\mathcal{A}}$ are correlated with with genetic effects $\mathbf{g}_{\mathcal{C}(\mathcal{AB})}$ (relationships) and BVs for purebred performance $\mathbf{a}_{\mathcal{A}}$ (genetic correlation).
- Supports a breeding goal with both purebred and crossbred performances.
- Allows different genetic variances in three breeds.
- Genetic correlation < 1: dominance effects and different genetic background, G × E
- Relationships defined such that the model can be fitted using standard animals breeding software.

Additive genetic relationships

Relationships can be defined either "within" or "across" breeds.

- Within breed:
  - Partial relationship matrices (Garcia-Cortes and Toro, 2006): 3 breed specific matrices, 1 breed segregation matrix.
  - Having marker genotypes on crossbreds: split according to breed of origin, construct marker-based partial relationship matrices.
- Across breeds:
  - Pedigree relationships on founders within breeds and across breeds (Legarra et al. 2015).
  - Estimate founder relationships from marker genotypes.
  - presented here!

Genetic relationships across breeds

- Relationships between base individuals:

$$\boldsymbol{\Gamma} = \left[\begin{array}{ccc} \gamma_{\mathcal{A}} & \gamma_{\mathcal{A},\mathcal{B}} & \gamma_{\mathcal{A},\mathcal{C}} \\ \gamma_{\mathcal{A},\mathcal{B}} & \gamma_{\mathcal{B}} & \gamma_{\mathcal{B},\mathcal{C}} \\ \gamma_{\mathcal{A},\mathcal{C}} & \gamma_{\mathcal{B},\mathcal{C}} & \gamma_{\mathcal{C}} \end{array} \right].$$

- Pedigree relationships defined recursively: $\mathbf{A}(\boldsymbol{\Gamma})$

- Genomic relationships: $\mathbf{G} = \mathbf{m}\mathbf{m}^{\mathrm{T}}$. Estimate $\boldsymbol{\Gamma}$ by matching $\mathbf{G}$ and $\mathbf{A}(\boldsymbol{\Gamma})_{22}$.

- Combined relationships: $\mathbf{H}(\boldsymbol{\Gamma})$ where

$$(\mathbf{H}(\boldsymbol{\Gamma}))^{-1} = \left[\begin{array}{cc} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - (\mathbf{A}(\boldsymbol{\Gamma})_{22})^{-1} \end{array} \right] + (\mathbf{A}(\boldsymbol{\Gamma}))^{-1},$$

- Usual procedure for computing $(\mathbf{A}(\boldsymbol{\Gamma}))^{-1}$ and $\mathbf{A}_{22}(\boldsymbol{\Gamma})$.

Variance-covariance of genetic effects

$$\mathrm{Var}\left[\begin{array}{c} \mathbf{a}_{\mathcal{A}} \\ \star \\ \star \\ \star \\ \star \\ \hdashline \star \\ \mathbf{a}_{\mathcal{B}} \\ \star \\ \star \\ \star \\ \hdashline \star \\ \star \\ \mathbf{a}_{\mathcal{C}} \\ \star \\ \star \\ \hdashline \mathbf{g}_{\mathcal{A}} \\ \mathbf{g}_{\mathcal{B}} \\ \mathbf{g}_{\mathcal{C}} \\ \mathbf{g}_{\mathcal{AB}} \\ \mathbf{g}_{\mathcal{C}(\mathcal{AB})} \end{array}\right] = \boldsymbol{\Sigma} \bigotimes \mathbf{H}(\boldsymbol{\Gamma}),$$

Variance-covariance of genetic effects

- Variance-covariance of genetic effects equals $\mathbf{\Sigma} \bigotimes \mathbf{H}(\mathbf{\Gamma})$ where

$$\mathbf{\Sigma} = \begin{bmatrix} \sigma^2_{a,\mathcal{A}} & \sigma_{a,\mathcal{A},\mathcal{B}} & \sigma_{a,\mathcal{A},\mathcal{C}} & \sigma_{ag,\mathcal{A}} \\ \sigma_{a,\mathcal{A},\mathcal{B}} & \sigma^2_{a,\mathcal{B}} & \sigma_{a,\mathcal{B},\mathcal{C}} & \sigma_{ag,\mathcal{B}} \\ \sigma_{a,\mathcal{A},\mathcal{C}} & \sigma_{a,\mathcal{B},\mathcal{C}} & \sigma^2_{a,\mathcal{C}} & \sigma_{ag,\mathcal{C}} \\ \sigma_{ag,\mathcal{A}} & \sigma_{ag,\mathcal{B}} & \sigma_{ag,\mathcal{C}} & \sigma^2_{g} \end{bmatrix}.$$

- 10 genetic parameters.
- BLUP, REML available using standard animal breeding software (input: inverse relationship matrix).

Conclusions

- Methods for genetic evaluation for three-way crossbreeding are available.
- Relationships either "within" or "across" breed
- Implemented in standard animal breeding software

First step !!

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Future work

- Analyse data from Danish Duroc× (Landrace× Large White).
- Can the 10 genetic genetic parameters be estimated accurately?