Generalized gametic relationships for flexible analyses of parent-of-origin effects

N. Reinsch, M. Mayer, I. Blunk

Institute of Genetics and Biometry, Leibniz-Institute for Farm Animal Biology, Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany
Abstract

Genomic imprinting causes alleles to influence the phenotype in a parent-of-origin-specific manner. In attempts to determine the effects of imprinted loci, gametic relationship matrices have widely been used in pedigree-based parent-of-origin analyses of population data. One drawback of this is the size of these matrices because they represent each individual by two gametic effects. Significantly fewer equations are needed if a previously published reduced imprinting model is used that relates observations from progeny without its own offspring to the transmitting abilities of their parents. This can be accomplished using a numerator relationship matrix, with only a single row and column per parent and ancestors. However, the reduced model is not applicable when the parents have records. To better handle the curse of dimensionality, we propose a combination of average gametic effects (transmitting abilities) for individuals without their own records and single gametic effects for others. The generalized gametic relationship matrix is the covariance of this mixture of genetic effects that allows for a significant reduction in the number of equations in gametic models depending on the trait, depth of pedigree, and population structure. It can also render the reduced model much more flexible by including observations from parents. Rules for setting-up its inverse from a pedigree are derived and implemented on an open-source program. The application of the same principles to phased marker data leads to a genomic version of the generalized gametic relationships. The implementation of generalized gametic models to the ASReml package is illustrated through worked examples.
Shortly after its discovery, it was recognized that the gametic relationship matrix (Smith and Allaire, 1985; Schaeffer et al., 1989) can help isolate fractions of the genetic variance in quantitative traits caused by genomically imprinted loci. Alleles of the latter are expressed in a parent-of-origin-specific manner. In the early stages of pedigree-based imprinting analysis, animal models were augmented by an additional vector of paternal (alternatively, maternal) gametic effects, usually modeled as uncorrelated with any other effect. Its variance was assumed to be the product of a gametic relationship matrix and a variance component that can be explained by polymorphisms at loci with only paternal (maternal) gene activity. Pioneered by DeVries et al. (1994), these models were in use for more than a decade. However, they can account only for a single kind of classical imprinting, where either maternal or paternal alleles are fully silenced through, e.g., the methylation of DNA. A proposal (Hill and Keithly, 1988) to consider both kinds of imprinting simultaneously did not materialize in any pedigree-based analysis of empirical data. Further, there was uncertainty regarding ways to account for the effects of partially imprinted loci, where both alleles are expressed but at different strengths depending on their parental origins.

A model for parent-of-origin analysis was subsequently developed (Neugebauer et al., 2010a, b) that is comprehensive in the sense that it accounts for all kinds of imprinting, be it full or partial, maternal or paternal (Blunk et al., 2014). This so-called reduced imprinting model relates observations from non-parents (final progeny, e.g., animals used for meat) to transmitting abilities (half of the breeding values) of their parents. There are two correlated genetic effects per parent, a transmitting ability as sire and a transmitting ability as dam, which reflect an animal’s genetic effect on its offspring under a paternal or maternal imprinting pattern. In the presence of genomically imprinted loci, these two genetic effects are different. The variance of these differences has been called the imprinting variance because it summarizes contributions from all kinds of possible imprinted loci. A numerator relationship matrix is needed for parents only, as the final progeny with observations but without offspring do not appear in the underlying pedigree and the resulting relationship matrix. The null hypothesis of the absence of polymorphic imprinted loci with an effect on the trait under investigation (i.e., a zero imprinting variance) can be tested by a restricted maximum likelihood (REML) ratio test.

Alternatively to the above, a comprehensive gametic model can be used to estimate the same set of genetic covariances, including the imprinting variance (Tier and Meyer, 2012; Meyer and Tier, 2012). This requires four gametic effects to be estimated per individual, two as sire and two as dam, where the relationships include the final progeny with observations. As an advantage over the reduced
model, the gametic model allows for records from parents. Moreover, it can be extended to account for maternal effects (see Appendix A5).

The use of measured genotypes in genomic best linear unbiased prediction models (gBLUP) that include imprinting effects has been outlined by Nishio and Satoh (2015). The first (GBLUP-I1) of the two variants of the proposed model contains an imprinting effect that is modeled as independent of the action of un-imprinted Mendelian locus, summarized as an additive genetic effect. The second model (GBLUP-I2) considers a paternal and a maternal gametic effect with zero mutual correlation. This clearly could be turned into a comprehensive model by abandoning the assumption of a zero correlation and replacing pedigree-derived gametic relationships by a genomic counterpart of equal size and structure. In cases where not all pedigreed individuals are genotyped, this enables a combined analysis of the genotyped and un-genotyped individuals in a single-step approach (Legarra et al., 2009; Aguilar et al., 2010; Christensen and Lund, 2010). The first model (GBLUP-I1), by contrast, cannot easily be extended to have such a pedigree-derived counterpart.

The downside of the gametic model is the large number of equations (Smith and Allaire, 1985) used to represent the random genetic effects, in particular when variance components are to be estimated. A pedigree with a size of approximately half a million is a technical barrier for REML estimation in animal models using currently available software packages (Shor et al., 2019). With a gametic parent-of-origin model, the same number of equations is reached with only a quarter of individuals. Therefore, the question arises if there is any option for models that retain the flexibility of the gametic model while allowing for a considerably smaller number of equations for random genetic effects, as close as possible to the reduced imprinting model.

As a solution, we propose a much smaller re-defined vector of genetic effects obtained by a proper linear transformation of the gametic effects. This is rendered applicable by introducing a version of a corresponding relationship matrix, called the generalized gametic relationship matrix, together with rules for its rapid inversion from the pedigree. As a result, the size of the gametic model can be reduced to a more manageable one while retaining all of its advantages. We also show how the same kind of transformation can be applied to measured genotypes to obtain conformable genomic and pedigree-derived versions of the new relationship matrix.

THEORY

Generalized gametic relationships

In gametic models, each individual \( i \) is represented by the additive genetic effects of its paternal gamete \( g_{i,1} \) and maternal gamete \( g_{i,2} \) (Schaeffer et al., 1989), which usually are arranged in a pair-
wise manner in a vector $g$ of length $2t$, which is twice the number $t$ of individuals in the pedigree.

The model equation for a phenotypic observation $y_i$ of individual $i$ then is

$$y_i = \mu_i + g_{i,1} + g_{i,2} + e_i ,$$

With $\mu_i = x'\beta$ as a place-holder for any combination of explanatory variables in vector $x'$ with fixed effects $\beta$, and the residual $e_i$. Thus, the gametic model splits the additive genetic value (breeding value) $b_i$ of individual $i$ into paternally derived and maternally derived parts, $b_i = g_{i,1} + g_{i,2}$.

The basic idea of reducing equations in gametic models by a considerable number is to replace the two gametic effects of a subset of $u$ individuals by their pair-wise average:

$$\frac{1}{2}(g_{i,1} + g_{i,2}) = a_i ,$$

which is known as the transmitting-ability (half the breeding value) of individual $i$.

The vector $g$ of gametic effects can be arranged such that the gametic effects of all $u$ individuals precede the gametic effects of the $v$ that are bound to retain their distinct gametic effects. The corresponding subdivision of $g$ is

$$g = \begin{bmatrix} g_u \\ g_v \end{bmatrix} .$$

The sub-vectors $g_u$ and $g_v$ have respective lengths of $2u$ and $2v$. The covariances of all gametic effects in $g$ are the elements of the $2t \times 2t$ gametic relationship matrix $G$ (Schaeffer et al., 1989). It can be partitioned into sections that correspond to the relationships between the gametic effects in $g_u$ and $g_v$.

$$\text{Var} \begin{bmatrix} g_u \\ g_v \end{bmatrix} = \begin{bmatrix} G_{uu} & G_{uv} \\ G_{vu} & G_{vv} \end{bmatrix} = G$$

The required average gametic effects can be obtained by a linear transformation that is defined by a matrix $K'$, such that

$$K'g = \begin{bmatrix} K'_u & 0_1 \\ 0_2 & I_v \end{bmatrix} \begin{bmatrix} g_u \\ g_v \end{bmatrix} = \begin{bmatrix} a_u \\ a_v \end{bmatrix} = a .$$
In effect, all gametic effects of individuals in $g_u$ are replaced by their transmitting abilities in $a_u$. The upper-left partition $K'_u$ of the transformation matrix $K'$ has dimensions $u \times 2u$, and is defined as the Kronecker product of a $u \times u$ identity matrix $I_u$ and a row vector with two elements equal to $\frac{1}{2}$:

$$K'_u = I_u \otimes \left[ \begin{array}{c} \frac{1}{2} \\ \frac{1}{2} \end{array} \right].$$

Further, $K'$ comprises a $2v \times 2v$ identity matrix $I_v$ and two null matrices, $0_1$ and $0_2$, with respective dimensions of $u \times 2v$ and $2v \times 2u$.

The covariance matrix of the transformed vector of gametic effects $a$ then becomes

$$Var \begin{bmatrix} a_u \\ g_u \end{bmatrix} = K'GK = \bar{G},$$

which in the following is called a generalized gametic relationship matrix. A natural choice is to retain the gametic effects of all individuals with their own phenotypes in vector $g_u$ and let all their ancestors without records be represented by their transmitting abilities, constituting $a_u$. The subdivisions of $\bar{G}$ then are

$$\bar{G} = \begin{bmatrix} K'_u G_{uu} K'_u & K'_u G_{uv} I_v \\ I_u G'_u K'_u & I_u G'_{uv} I_v \end{bmatrix} = \begin{bmatrix} \frac{1}{2} A_u & S_{uv} \\ S_{uv} & G_{vv} \end{bmatrix}.$$

The upper-left part $\frac{1}{2} A_u$ is equal to the co-ancestry matrix (half the numerator-relationship matrix) of all ancestors without own records, while $G_{vv}$ reflects relationships between the gametic effects of all individuals with their own observations. Finally, $S_{uv}$ contains the covariances between transmitting abilities and gametic effects. See the small example involving four individuals (IDs).

There are three transmitting abilities for individuals 1, 2, and 3, with corresponding pair-wise elements of $\frac{1}{2}$ in the transformation matrix $K'$ and two gametic effects, for which the elements in $K'$ are one. The resulting generalized gametic relationship matrix $\bar{G}$ has dimensions $5 \times 5$.

| ID | sire | dam |
|----|------|-----|
| 1  | 0    | 0   |
| 2  | 0    | 0   |
| 3  | 1    | 2   |
| 4  | 1    | 3   |

$$K' = \begin{bmatrix} \frac{1}{2} & \frac{1}{2} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{2} & \frac{1}{2} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{2} & \frac{1}{2} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \quad G = \begin{bmatrix} \frac{1}{2} & 0 & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} \\ 0 & \frac{1}{2} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} \\ \frac{1}{2} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} \\ \frac{1}{2} & 0 & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} \\ \frac{1}{4} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} & \frac{1}{4} & 1 \end{bmatrix}$$

Generalized gametic relationships in a gametic model

In light of the above, the model equation for an observation $y_i$ can be retained as in the gametic model, and a mixed model that considers parent-of-origin effects (POEs) and uses the generalized relationship matrix becomes
\[ Y = X\beta + Z_s a_s + Z_d a_d + e \, , \]

where \( Y \) is a vector of observations, \( \beta \) comprises the fixed effects, and \( X \) is the corresponding incidence matrix. The covariance of random effects is assumed to be

\[
\text{Var} \begin{bmatrix} a_s \\ a_d \\ e \end{bmatrix} = \begin{bmatrix} \mathbf{G} \sigma_s^2 & \mathbf{G} \sigma_{sd} & 0 \\ \mathbf{G} \sigma_{sd} & \mathbf{G} \sigma_d^2 & 0 \\ 0 & 0 & \mathbf{I} \sigma_r^2 \end{bmatrix}.
\]

This generalized gametic model contains the gametic effect vectors \( \mathbf{g}_s \) and \( \mathbf{g}_d \) replaced by their transformed counterparts \( \mathbf{a}_s \) and \( \mathbf{a}_d \), respectively, and, consequently, uses the corresponding relationship matrix \( \mathbf{G} \) instead of the classical gametic relationships of \( \mathbf{G} \). Further, incidence matrices \( Z_s \) and \( Z_d \) link observations to the random gametic effects in \( \mathbf{a}_s \) and \( \mathbf{a}_d \), respectively, while no observation is linked to any of the transmitting abilities in the latter vectors. As a result, any incidence matrix \( Z^r = \begin{bmatrix} 0^r & Z^r \end{bmatrix} \) that links observations to gametic effects in the generalized vector \( \mathbf{a}' = \begin{bmatrix} \mathbf{a}_u' & \mathbf{g}_u' \end{bmatrix} \) can be considered a converted incidence matrix

\[
Z^r = Z^g K'.
\]

This transformation retains all columns in the partition \( Z^g \), i.e., one per gametic effect of individuals with records, while the number of null columns in \( 0^r \) of \( Z^u \) collapses to half of that of \( 0^{2u} \) in \( Z^g \). In the same manner, both incidence matrices \( Z_s \) and \( Z_d \) from the previous model equation are converted versions of their counterparts in the classical gametic imprinting model, which forms the basis for the proof of equivalence of the classical and the generalized gametic models involving \( \mathbf{G} \) (see Appendix A1).

Reduced gametic model

The reduced imprinting model as initially described by Neugebauer et al. (2010a, b) relates each observation from the final progeny \( i \) to the transmitting abilities as sire \( a_s' \) and as dam \( a_d' \) of the parents \( si \) (sire of \( i \)) and \( di \) (dam of \( i \)), respectively. For a single observation \( y_i \), we have the observation equation

\[ y_i = \mu_i + a_s' + a_d' + r_i. \quad (1) \]

Here, the residual \( r_i \) is a sum of the Mendelian sampling effects of both parents (\( m_s \) and \( m_d \)) and the measurement noise (\( e_i \)). The latter is identical to the residual of the gametic model. Thus,

\[ r_i = m_s + m_d + e_i. \]
Its variance is a function of the inbreeding coefficients $F_{si}$ and $F_{di}$ of the parents of $i$:

$$\text{var}(r_i) = \frac{1}{2}(1-F_{si})\sigma_s^2 + \frac{1}{2}(1-F_{di})\sigma_d^2 + \sigma_e^2.$$ 

By rewriting the transmitting abilities of the parents as the averages of the respective gametic effects, i.e., $a_{si} = \frac{1}{2}(g_{1,si} + g_{2,si})$ and $a_{di} = \frac{1}{2}(g_{1,di} + g_{2,di})$, we get an observation equation in terms of gametic effects:

$$y_i = \mu + \frac{1}{2}(g_{1,si} + g_{2,si}) + \frac{1}{2}(g_{1,di} + g_{2,di}) + r_i.$$  \hspace{1cm} (2)

The covariance of the gametic effects then is

$$\text{Var} \left[ \begin{array}{c} g_s \\ g_d \end{array} \right] = \begin{bmatrix} \sigma_s^2 & \sigma_{sd} \\ \sigma_{sd} & \sigma_d^2 \end{bmatrix} \otimes G = \begin{bmatrix} G\sigma_s^2 & G\sigma_{sd} \\ G\sigma_{sd} & G\sigma_d^2 \end{bmatrix}.$$ 

Here, the relationship matrix $G$ of the gametic effects that define the involved transmitting abilities includes only the parents and their ancestors. The advantage of this gametic version of the reduced imprinting model over the previously published version that uses only transmitting abilities and their relationship matrix $\frac{1}{2}A$ is that it enables us to easily integrate observations from parents by linking them to the respective gametic effects. Hence, for observations of any parent $i$, the observation equation becomes

$$y_i = \mu_i + g_{1,i} + g_{2,i} + e_i.$$  \hspace{1cm} (3)

**Generalized reduced gametic model**

The drawback of the reduced gametic model is that it has twice the number of equations compared to a version that uses $\frac{1}{2}A$. For all individuals without own records, it is however possible to reduce the number of equations for random genetic effects by representing the individuals through their transmitting abilities (average gametic effects) while retaining separate gametic effects for all parents with records, i.e., vectors of gametic effects $g_s$ and $g_d$ are replaced by appropriately transformed counterparts $a_s$ and $a_d$, respectively. Consequently the covariances of random genetic effects in a parsimonious generalized reduced gametic model that allows for parents with records is

$$\text{Var} \left[ \begin{array}{c} a_s \\ a_d \end{array} \right] = \begin{bmatrix} G\sigma_s^2 & G\sigma_{sd} \\ G\sigma_{sd} & G\sigma_d^2 \end{bmatrix}.$$ 

Further, we need a diagonal matrix $W$ of weights equal to $w_i = 1$ for observations from parents, for which model Equation (3) applies and
for the final progeny, where parents without their own records are represented by transmitting
abilities or both parents have a record and are represented by gametic effects (the respective
observation equations are (1) and (2)). The same weight applies to mixed kinds of representation
that arise from cases where one parent of a final progeny has a record while the other does not. The
corresponding observation equations for observations $y_i$ of such final progeny are

$$y_i = \mu_i + a_{di} + \frac{1}{2} \left( g_{1,di} + g_{2,di} \right) + r_i$$  \hspace{1cm} (4)

and

$$y_i = \mu_i + \frac{1}{2} \left( g_{1,di} + g_{2,di} \right) + a_{di} + r_i$$  \hspace{1cm} (5)

A general model for parent-of-origin analyses

A general comprehensive model for parent-of-origin analyses banks on the generalized gametic
relationship matrix. Special cases of the generalized gametic relationship matrix $\mathbf{G}$ are the classical
gametic relationship matrix $\mathbf{G} = \mathbf{G}$ in the gametic model and $\mathbf{G} = \frac{1}{2} \mathbf{A}$ as in the reduced imprinting
model. Correspondingly, the matrix $\mathbf{W}$ of weights can be an identity matrix that fits the classical
gametic model, or a matrix all the weights of which are different from one as those in the reduced
model for records of the final progeny. A general model can be specified for parent-of-origin analyses
containing these two basic kinds of comprehensive imprinting models as well as models with any
combination of gametic effects and transmitting abilities that can be obtained using our
transformation matrix $\mathbf{K}'$. In matrix notation, the general model is

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_d\mathbf{a}_d + \mathbf{Z}_s\mathbf{a}_s + \mathbf{\epsilon},$$

where $\mathbf{\epsilon}$ is a vector of residuals. That is, $\epsilon_i = e_i$ for records from individuals represented by two
gametic effects, or $\epsilon_i = r_i$ for observations from final progeny linked to the genetic effects of their
parents. The respective weights are

$w_i = 1$
and

\[ w_i = \left[ \frac{1}{v} (1 - F_s) \sigma_s^2 + \frac{1}{v} (1 - F_d) \sigma_d^2 + \sigma_e^2 \right]^{-1} \]

Random genetic effects and residuals are assumed to have covariance:

\[
\begin{bmatrix}
\mathbf{a}_s \\
\mathbf{a}_d \\
\mathbf{e}
\end{bmatrix}
\begin{bmatrix}
\mathbf{G} \sigma_s^2 & \mathbf{G} \sigma_{sd} & 0 \\
\mathbf{G} \sigma_{sd} & \mathbf{G} \sigma_d^2 & 0 \\
0 & 0 & \mathbf{W} \sigma_e^2
\end{bmatrix}
\]

The resulting mixed model equations are

\[
\begin{bmatrix}
\mathbf{X}' \mathbf{W}^{-1} \mathbf{X} & \mathbf{X}' \mathbf{W}^{-1} \mathbf{Z}_s & \mathbf{X}' \mathbf{W}^{-1} \mathbf{Z}_d \\
\mathbf{Z}_s' \mathbf{W}^{-1} \mathbf{X} & \mathbf{Z}_s' \mathbf{W}^{-1} \mathbf{Z}_s + \mathbf{G}^{-1} \mathbf{\alpha}_1 & \mathbf{Z}_s' \mathbf{W}^{-1} \mathbf{Z}_d + \mathbf{G}^{-1} \mathbf{\alpha}_2 \\
\mathbf{Z}_d' \mathbf{W}^{-1} \mathbf{X} & \mathbf{Z}_d' \mathbf{W}^{-1} \mathbf{Z}_s + \mathbf{G}^{-1} \mathbf{\alpha}_2 & \mathbf{Z}_d' \mathbf{W}^{-1} \mathbf{Z}_d + \mathbf{G}^{-1} \mathbf{\alpha}_3
\end{bmatrix}
\begin{bmatrix}
\mathbf{\beta} \\
\mathbf{a}_s \\
\mathbf{a}_d
\end{bmatrix}
= \begin{bmatrix}
\mathbf{X}' \mathbf{W}^{-1} \mathbf{y} \\
\mathbf{Z}_s' \mathbf{W}^{-1} \mathbf{y} \\
\mathbf{Z}_d' \mathbf{W}^{-1} \mathbf{y}
\end{bmatrix}
\]

with

\[
\begin{bmatrix}
\mathbf{\alpha}_1 & \mathbf{\alpha}_2 \\
\mathbf{\alpha}_2 & \mathbf{\alpha}_3
\end{bmatrix}
= \sigma_e^2 \begin{bmatrix}
\sigma_s^2 & \sigma_{sd} \\
\sigma_{sd} & \sigma_d^2
\end{bmatrix}^{-1}
\]

The general model comprehends any combination of observation Equations (1) to (5) to provide a large degree of flexibility in parent-of-origin analyses. Model variants may be chosen to minimize the number of equations for random genetic effect by using as many reduced observation equations as possible, which comes at the expense of the need for the recomputation of weights when estimating the components of variance. Alternatively, the repeated recomputation of weights may be avoided by representing all individuals with an observation using gametic effects. The underlying reason for this flexibility is that for the given data (observations, fixed effects, and pedigree), each possible general imprinting model has as an equivalent the same classical gametic model (that follows from Appendices A2 and A3). Consequently, any two general models that share the same equivalent classical model are also equivalent, and can replace each other, especially for the sake of estimating the components of variance.
Setting-up the inverse generalized gametic relationship matrix is key to any large-scale application. Rules for direct inversion can be derived by factoring the inverse $\mathbf{G}^{-1}$ into inverses of a matrix $\mathbf{T}'$ and a diagonal matrix $\mathbf{D}$ of inverse Mendelian sampling variances

$$
\mathbf{G}^{-1} = (\mathbf{T}')^{-1} \mathbf{D}^{-1} \mathbf{T}^{-1}.
$$

The above is known from the direct inversion of the numerator relationship matrix (Henderson, 1976; Quaas, 1976) and the classical gametic relationship matrix (Schaeffer et al., 1989). The matrix $(\mathbf{T}')^{-1}$ is lower triangular, as shown in Figure 1. The underlying pedigree of this example (Supplement) comprises 12 individuals. Nine of them are represented by a single transmitting ability while the remaining three by two gametic effects. The kind of representation is indicated by the respective values of one and two in the last column of the pedigree file. Consequently, the dimensions of the inverse of the example are $15 \times 15$. Each of the 15 rows of $(\mathbf{T}')^{-1}$ pertain to a single genetic effect, which itself may be derived from different kinds of genetic parental predecessor effects: An individual’s transmitting ability may be derived from two unknown parents (a-00) or a single unknown parent, where the known parent may be represented by a transmitting ability (a-0a, a-a0) or two gametic effects (a-0gg, a-gg0). Two known parents may show up as any combination of transmitting abilities or gametic effects (a-aa, a-agg, a-gga, a-gggg). Likewise, a gametic effect may be derived from an unknown parent (g-0), or a known parent enrolled by either a transmitting ability or two gametic effects (g-a, g-gg). These 12 cases need to be distinguished for directly inverting the generalized gametic relationship matrix. The example pedigree was constructed such that each case appeared at least once. For each effect related to a particular row of the lower-triangular matrix in Figure 1, the case is indicated in the last column. Note that the six cases a-0gg, a-gg0, a-agg, a-gga, a-gggg, and g-a are specific to the generalized gametic relationship matrix as they appear neither in the direct inversion of the numerator relationship matrix—involving only a-00, a-0a, a-a0, and a-aa—nor the classical gametic relationship matrix, for which only g-0 and g-gg need to be distinguished.

Mendelian sampling variances that define the diagonal elements of $\mathbf{D}$ are different for transmitting abilities and gametic effects. Further, they depend on the occurrence of unknown parents and the inbreeding coefficients of the known ones. In particular, this is $F_{\text{known parent}}$ when an individual with a transmitting ability in the matrix has only one known parent, or $F_{\text{sire}}$ and $F_{\text{dam}}$ in case of full parentage information. For gametes, we need to account for the inbreeding coefficient $F_{\text{parent}}$ of the known parent from which a gamete is derived. Accordingly, the 12 cases (a-00, a-0a, ... , g-00) are grouped into five classes with distinct formulae for the inverse Mendelian sampling variance $\delta$: 

---

The copyright holder for this preprint made available under a CC-BY 4.0 International license (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under a CC-BY 4.0 International license.
For any arbitrary order of genetic effects, the inverse generalized gametic relationship matrix can be constructed step by step from the pedigree. In each step, a matrix contribution $U_i$ is added for genetic effect $i$ to a matrix composed of an inverse $G^{-1}_{i-1}$ that already covers the preceding $i-1$ effects and zeroes:

$$
G^{-1}_i = \begin{bmatrix}
G^{-1}_{i-1} & 0 \\
0' & 0
\end{bmatrix} + U_i,
$$

where $0$ is a column vector of $i-1$ zeroes and

$$
U_i = u_i' u_i \delta_i
$$

is the contribution made for each genetic effect $i$. The row-vector $u_i'$ consists of all zeros, except for those elements with indices indicating the genetic effects of the respective parent(s). At minimum, the i-th element is always equal to unity as a non-zero element in this vector. All other non-zero elements are negative, with values of either $-\frac{1}{2}$ or $-\frac{1}{4}$. Thus, the number of non-zero entries varies from one to five, as can be derived from the rows of the example triangular matrix $(T')^{-1}$ in Figure 1. For all 12 possible cases, the non-zero coefficients in $u_i'$ and their indices are summarized in Table 1.

The non-zero elements of the resulting matrix $U_i = u_i' u_i \delta_i$ correspond to the (scaled) cross-products of the elements of the non-zero vector, and their coordinates in the matrix are the respective combinations of indices.

**Table 1:** about here

Transforming measured genotypes in a generalized genomic gametic relationship matrix

Parent-of-origin analyses may also use genomic relationships, or combined genomic and pedigree relationships. A specific feature of this is that ordinary marker genotypes (AA, AB, BB) are not sufficient for this purpose, and the parental origin of the marker alleles at each locus has to be...
inferred instead (Lawson et al., 2013, and references therein) and summarized as ordered genotypes
AA, AB, BA, and BB, where the first allele is paternally derived. This is, however, not always possible
for all members of a genealogy. In such a case, the principles above are beneficial for integrating
ordered and unordered genomic information into a single genomic version of the generalized
gametic relationship matrix.

Let us assume that all $t$ individuals are genotyped with $p$ markers and all genotypes are phased into
$2t$ haplotypes. Information on the number (zero or one at each locus before centering) of minor
alleles for all marker loci on each haplotype can be summarized in a column-wise mean-centered
$2t \times p$ matrix $\mathbf{C}$. To this matrix, each individual $i$ contributes two $p$-row-vectors $\mathbf{c}_i^1$ and $\mathbf{c}_i^2$, where
the centered allele accounts for its first and second haplotype. Matrix $\mathbf{C}$ can then be split into two
submatrices $\mathbf{C}_v$ and $\mathbf{C}_u$:

$$
\mathbf{C} = \begin{bmatrix} \mathbf{C}_v \\ \mathbf{C}_u \end{bmatrix}.
$$

For imprinting analyses, at least all $u$ individuals with records need to have their paternal and
maternal haplotypes identified in $\mathbf{C}_u$. This can be achieved by adding at least one preceding
generation without records but with genotypes. In case of only a single generation, all their $2v$
haplotypes in partition $\mathbf{C}_v$ would be left unordered. If the additional $v$ genotyped individuals contain
more than a single successive generation, only a part of their genotypes may qualify as ordered, with
the exceptions coming from the founders.

From $\mathbf{C}$, a genomic gametic relationship matrix can be derived:

$$
\mathbf{G}_g = \frac{\mathbf{C} \mathbf{C}'}{s} = \begin{bmatrix} \mathbf{C}_u \mathbf{C}_u' & \mathbf{C}_u \mathbf{C}_v' \\ \mathbf{C}_v \mathbf{C}_u' & \mathbf{C}_v \mathbf{C}_v' \end{bmatrix}^{-1} = \begin{bmatrix} \mathbf{G}_{guu} & \mathbf{G}_{guv} \\ \mathbf{G}_{gvu} & \mathbf{G}_{gvv} \end{bmatrix},
$$

where $s$ is a scaling factor, $s = \sum p_j(1 - p_j)$, and $p_j$ is the frequency of the allele at marker $j$.

In all cases where the parental origin of the two haplotypes can be traced back, the first haplotype of
each individual is assumed to be paternal and the second maternal ($\mathbf{c}_{i1}' = \mathbf{c}_{ip}'$ and $\mathbf{c}_{i2}' = \mathbf{c}_{im}'$);
otherwise, the ordering of haplotypes is arbitrary. This is where the concept of generalization from
above is used. A transformation matrix $\mathbf{K}'$ can be defined such that for all individuals $i$ with
unordered genomic information, the two row vectors $\mathbf{c}_{i1}'$ and $\mathbf{c}_{i2}'$ are replaced by their averages:
\[ \bar{c}_i = \frac{1}{2} (c_{i1} + c_{i2}) . \]

\( \bar{c}_i \) does not depend on the order or the parental origin of the haplotypes of an individual:

\[ \bar{c}_i = \frac{1}{2} (c_{i1} + c_{i2}) = \frac{1}{2} (c_{ip} + c_{im}) . \]

That is, \( \bar{c}_i \) is also the vector of average paternal- and maternal-centered number of gene counts. Consequently, a generalized genomic gametic relationship matrix can be defined as

\[ \bar{G}_g = K'CC'K_{\bar{G}}^{-1} = K'G_gK' , \]

with \( K' \) defined as before. The partition \( C_sC_s' \) of \( G_g \) can be used to determine only the ordered genomic information of all individuals with records and, as such, is sufficient to estimate the components of genetic variance in a parent-of-origin analysis. All respective gametic effects of these individuals can also be estimated. The entire matrix \( G_g \) delivers gametic effects (as sire and dam) for all individuals, including those with no phenotypes. The generalized variant \( G_g \) by design is also appropriate for parent-of-origin analyses, with no other requirements for \( K' \) as for the pedigree-derived counterpart. Thus, the general model for parent-of-origin analyses is also applicable to genomic relationships, provided the marker haplotypes of individuals with observations can be ordered.

### Software and data availability

A detailed guide to practical implementation is available on the RADAR repository (https://www.radarservice.eu/radar/dataset/get/IGjshdpCzWftGAQ?lang=en&token=DpsQIXcXJRuDklmbwzB – this is a temporary link for the purpose of review only and will later be replaced by a permanent DOI). It includes the source code of a program to directly set-up the inverse of the generalized gametic relationship matrix from a pedigree file, a detailed program description and example input and output files. There we also provide a collection of six worked toy examples demonstrating in very detail how various mixed models with generalized gametic relationships can be implemented using the ASReml package. Each example is also accompanied with R-code to check details and the correctness of the ASReml results.
DISCUSSION

The outlined generalization introduces elements of the reduced imprinting model to the gametic model and vice versa, accompanied by gains in flexibility and substantial savings in terms of the number of equations used. The latter is important especially for estimating the components of variance (Shor et al., 2019). The matrix $G$ contains two limiting cases that set the boundaries for the ratio of equations that can be eliminated. The first is the classical gametic relationship matrix itself (dimensions $2t \times 2t$), when $K'$ is an identity matrix. The other limiting case is $K'=I \otimes \left[ \frac{1}{2} \ 1 \right]$, such that $G = \frac{1}{2}A$ with dimensions $t \times t$. Therefore, the reduction in the number of equations for genetic effects can take a range of 0%–50%, compared with a classical gametic model. However, the actual savings depend on the specifics of each dataset. As examples, two animal datasets were considered: the first was from an analysis of daily net gain in Brown Swiss fattening bulls (Blunk et al., 2018; Blunk et al., 2019), with a pedigree of 663,515 individuals (173,051 non-parents with records), whereas the second dealt with litter size in an experimental line of mice (2,137 females with an observation for first-parity litter size; necessary pedigree size for variance component estimation: 4544; total pedigree size 15222; unpublished data). In the Brown Swiss, the number of gametic effects for all animals was 1,327,030, compared with 836,566 with gametic effects for animals with observations only. The relative saving was 37% in terms of the number of equations and 32% in terms of the number of non-zero elements of the half-stored inverse. The respective numbers of equations in the mice example were 9088 versus 6681, with relative savings of 26% and 25%. In particular, small proportions of individuals that have records cause large reductions as all ancestors without a record are assigned only one equation. This applied to the mice example, as only females that had reproduced had records of litter size. If all available animals from the same number of generations were included (no “pruning” performed; 15222 animals), as one would prefer e.g. for the estimation of the genetic trend, there were 30,444 gametic effects versus 17,359 effects with the generalized relationships, with relative savings of 42% of equations and 56% of non-zero elements. The vast majority of this pedigree included males, females from older generations with no data, and non-reproducing females of younger generations.

Sex-specific traits such as litter size, number of eggs, or milk yield provide the opportunity to represent all males by their transmitting abilities. Thus, the resulting number of equations is considerably smaller in comparison with a trait recorded in both sexes. The family structure also has an effect: More equations are saved in the presence of typically small paternal groups of offspring, given that sires without own phenotypes are represented by their transmitting abilities. Further, it makes sense in imprinting analyses to add a high ratio of ancestors without phenotypes to better reflect inbreeding, and the relationships between genetic effects as sire and dam. Including their
transmitting abilities rather than gametic effects in the model therefore also leads to a large number of saved equations.

A certain fraction of individuals with records might have either not reproduced at all or not yet reproduced at the time of data recall (i.e. they appear as final progeny), which provides the opportunity for representing them by reduced observational equations rather than having their own gametic effects in the model. In the Brown Swiss example, where all observations were from final progeny, this leads to a fully reduced model with relationships of 490,464 ancestors, a reduction of 63%. In the small mouse example more equations for 634 final progeny can be saved (3910 animals and 5413 equations left), forcing the relative savings up to 40% of equations.

In certain cases, one could, however, abstain from reduced observational equations, which has the advantage that no weights are required that depend on as-yet undetermined components of variance. That has not proven to be a particular problem in the REML estimation of the components of variance (Neugebauer et al., 2010a, b; Blunk et al., 2017a,b), but may be beneficial to avoid in Bayesian approaches that employ Markov chain Monte Carlo methods, where the values of the components of variance change from iteration to iteration. By capitalizing on the flexibility of the generalized approach, weights become obsolete by representing all individuals with records—be they final progeny or not—by two gametic effects, which helps offset the computational burden resulting from repeated reweighting. At the same time, individuals without observations can be integrated by single equations.

For reasons of principle, a maternal genetic component of variance provides a special challenge as it is difficult to separate from the imprinting variance. Okamoto et al. (2019) showed that when estimated with a model variant that uses information only on the sire and maternal grandsire (Blunk et al., 2017; Okamoto et al., 2019), the imprinting variance may also be interpreted as maternal genetic. Similarly, for the reduced imprinting model, it can be shown that the imprinting variance and maternal genetic variance cannot be disentangled when both are present, and instead only a composite component of variance can be inferred (Appendix A4). A way out of this is to avoid reduced model equations and, instead, to represent individuals with records explicitly by their gametic effects in a model that includes maternal genetic effects. Then, gametic variances as sire and dam can, at least in principle, be separated from the maternal genetic variance (Appendix A5). In practice, however, this may be hampered by limitations in the amount and structure of the data, as has been reported for Mendelian models (Heydarpour et al., 2008). Like maternal effects models, other kinds of imprinting models may also comprise more than a single genetic effect as sire and dam per individual—e.g., random regression models or multitrait models. As they all suffer from a large number of gametic equations, they benefit even more from generalized relationships.
In applications where all \( v \) individuals with records plus at least one preceding generation have measured genotypes and variance components are to be estimated, it is sufficient to include only the subset of these \( v \) individuals with their genomic covariance \( G_{vv} \). If there is interest in the genetic effects of the \( n \) founders as sire and dam, either \( G_g \) or \( G_g \) is the choice. An example is an \( F_2 \) line-cross experiment with phenotypes recorded only in the \( F_2 \) generation, and the genotypes of \( F_1 \) and \( P_0 \) generations needed only for phasing and determining line origins of the markers.

Often in animal breeding, large pedigrees are combined with smaller cohorts of genotyped individuals. Then, certain individuals are the first in their genealogy to be genotyped while the pedigree can be traced further back. In contrast to their own descendants, haplotypes of such a candidate cannot be ordered, which renders uncertain whether the first of two unordered marker haplotypes matches the paternal gametic effect in a pedigree-derived gametic relationship matrix or the maternal one. Consequently, a combined relationship matrix that is suitable for parent-of-origin analyses cannot be constructed. This problem can be solved by collapsing gametic effects into transmitting abilities both in the genomic relationships and the pedigree-derived ones. Then, generalized pedigree relationships for all animals can be combined with their matching generalized genomic counterparts \( G_g \) for the genotyped cohort in a way that allows for the easy integration of unordered genomic information. To this end, the available theory (Legarra et al. 2009; Christensen and Lund 2010; Aguilar et al. 2010) can be used to combine pedigree-derived relationships (here, \( G \)) and genomic relationships (\( G_g \)) into a joint matrix, at least in the many cases where candidates with unordered genotypes have no record, such as dairy bulls.

In conclusion the generalized gametic relationship matrix provides the necessary flexibility to adapt imprinting analyses to specific computational and analytical needs in a large variety of situations through tailored versions of the general imprinting model. The most important aspects are the effective estimation of the imprinting variance in REML and Bayesian approaches in case the parents have records and the inclusion of maternal genetic effects and genomic relationships that integrate ordered and unordered genomic information. All things considered, these new possibilities are expected to stimulate systematic research on the importance of parent-of-origin effects for the genetic variation of quantitative traits in farm animals and other species.
Acknowledgements

Inga Blunk was funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) project 418890112 “Making unused data resources available for imprinting analyses by using new methods to uncover parent-of-origin effects in human and livestock”.

References

Aguilar, I., I. Misztal, D. L. Johnson, A. Legarra, S. Tsuruta et al., 2010: Hot topic: A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. J. Dairy Sci. 93: 743–752.

Blunk, I., und N. Reinsch, 2014: Genetic variance components when fluctuating imprinting patterns are present. Proceedings of the 10th World Congress Applied to Livestock Genetics, 17-22. August 2014, Vancouver, BC, Canada, pp. 17-22

Blunk, I., M. Mayer, H. Hamann, and N. Reinsch, 2017 a: Parsimonious model for analyzing parent-of-origin effects related to beef traits in dual-purpose Simmental. J. Anim. Sci. 95, 559-571

Blunk, I., Mayer, M., Hamann, H. and Reinsch, N., 2017 b: A new model for parent-of-origin effect analyses applied to Brown Swiss cattle slaughterhouse data. Animal 11, 1096-1106.

Blunk, I., M. Mayer, H. Hamann, and N. Reinsch, 2019: Scanning the genomes of parents for imprinted loci acting in their un-genotyped progeny. Sci. Rep. 9, 654

Christensen, O. F., and M. S. Lund, 2010: Genomic prediction when some animals are not genotyped.

Genet. Sel. Evol. 42: 2.

De Vries, A. G., R. Kerr, B. Tier, T. Long, and T. H. E. Meuwissen, 1994: Gametic imprinting effects on rate and composition of pig growth. Theor. Appl. Genet. 88:1037–1042.

Gibson, J.P., B.W. Kennedy, L.R.  Schaeffer, and O.I. Southwood, 1998: Gametic models for estimation of autosomal and genetic effects that are expressed only when received from either a male or female parent. J. Dairy Sci. 71, 143 (Abstr.)

Henderson, C.R. 1985: Equivalent Linear Models to Reduce Computations. J. Dairy Sci. 68(9): 2267–2277

Henderson, C.R, 1976: A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. Biometrics 32, 69-83

Heydarpour, M., L.R. Schaeffer, and M.H. Yazdi, 2008: Influence of population structure on estimates of direct and maternal parameters. J. Anim. Breed. Genet. 125: 89–99

Hill, W.G., and P.D. Keightly, 1988: Interaction between molecular and quantitative genetics. In Proceedings of the World Symposium in Honour of Professor R.D. Politiek, Wageningen (eds Korver, S. et al.) 45-55 (Advances in Animal Breeding, Wageningen, The Netherlands, 1988).
Lawson, H. A., J. M. Cheverud, and J. B. Wolf, 2013: Genomic imprinting and parent-of-origin effects on complex traits. *Nat. Rev. Genet.* 14: 609-617.

Legarra, A., I. Aguilar, and I. Misztal, 2009: A relationship matrix including full pedigree and genomic information. *J. Dairy Sci.* 92: 4656–4663.

Meyer, K., and B. Tier (2012): Estimates of variances due to parent of origin effects for weights of Australian beef cattle. *Animal Production Science* 52(4) 215-224.

Neugebauer, N., I. Räder, H.J. Schild, D. Zimmer, and N. Reinsch, 2010 a: Evidence for parent-of-origin effects on genetic variability of beef traits. *J. Anim. Sci.* 88, 523-532.

Neugebauer, N., Luther, H. & Reinsch, N., 2010 b: Parent-of-origin effects cause genetic variation in pig performance traits. *Animal* 4, 672-681.

Nishio, M., and M. Satoh, 2015: Genomic linear best unbiased prediction method including imprinting effects for genomic evaluation. *Genet. Sel. Evol.* 47:32.

Okamoto, K., Oishi, K., Nakamura, L., Abe, A., Inoue, K., Kumagi, H., and H. Hirooka, 2019: Parent-of-origin effects on carcass traits in Japanese Black cattle. *J. Anim. Breed. Genet.* 136(3): 190-198.

Quaas, R.L., 1976: Computing the diagonal elements and inverse of a large numerator relationship matrix. *Biometrics* 32, 949-953.

Schaeffer, L.R., B.W. Kennedy, and J.P.Gibson, 1989: The inverse of the gametic relationship matrix. *J. Dairy Sci.* 72, 1266-1272.

Shor, T., Kalka, I., Geiger, D., Erlich, Y., and O. Weissbrod, 2019: Estimating variance components in population scale family trees. *PloS Genet* 15(5): e1008124.

Smith S-P. and F.R. Allaire, 1985: Efficient selection rules to increase non-linear merit: application to mate selection. *Genet. Sel. Evol.* 17(3): 387-406.

Tier, B., and K.Meyer, 2012: Analysing quantitative parent-of-origin effects with examples from ultrasonic measures of body composition In Australian beef cattle. *J. Anim. Breed. Genet.* 129, 359-368.
Appendix A1: Equivalence of the classical gametic model and the generalized gametic model in which all individuals with records have two gametic effects.

Both models have the same expectation $E(y) = X\beta$ of the vector of observations $y$.

The variance of observations in the classical gametic model is

$Var(y) = Q_e + I\sigma^2_e$,

where

$$Q_e = [Z_s \quad Z_d]\begin{bmatrix} G\sigma^2_s & G\sigma_{sd} \\ G\sigma_{sd} & G\sigma^2_d \end{bmatrix}[Z'_s \quad Z'_d] = Z_sGZ'_s\sigma^2_s + Z_sGZ'_d\sigma_{sd} + Z_dGZ'_s\sigma_{sd} + Z_dGZ'_d\sigma^2_d.$$  

The first term can be rewritten as

$$Z_sGZ'_s = [0^{2u} \quad Z'_s]\begin{bmatrix} G_{uv} & G_{vv} \\ G_{uv} & G_{vv} \end{bmatrix}\begin{bmatrix} 0^{2u} \\ (Z'_s)' \end{bmatrix} = Z'_sG_{vv}Z'_s.'$$

Likewise,

$$Z_sGZ'_d = Z'_sG_{vv}Z'_d, \quad Z_dGZ'_s = Z'_dG_{vv}Z'_s' \quad \text{and} \quad Z_dGZ'_d = Z'_dG_{vv}Z'_d'.$$

Finally,

$$Q_e = Z'_sG_{vv}Z'_s\sigma^2_s + Z'_sG_{vv}Z'_d\sigma_{sd} + Z'_dG_{vv}Z'_s\sigma_{sd} + Z'_dG_{vv}Z'_d\sigma^2_d.$$  

In the generalized case, the variance of observations is

$$Var(y) = Q_g + I\sigma^2_e$$

with

$$Q_g = [Z_sK \quad Z_dK]\begin{bmatrix} \tilde{G}\sigma^2_s & \tilde{G}\sigma_{sd} \\ \tilde{G}\sigma_{sd} & \tilde{G}\sigma^2_d \end{bmatrix}[K'Z'_s \quad K'Z'_d].$$

We make use of $Z_sK = \begin{bmatrix} 0^v \quad Z'_s \end{bmatrix}$ and $Z_dK = \begin{bmatrix} 0^v \quad Z'_d \end{bmatrix}$, and rewrite

$$Z_sK\tilde{G}K'Z'_s = \begin{bmatrix} 0^v \quad Z'_s \end{bmatrix}\begin{bmatrix} \frac{1}{2} A_u & S_{av} \\ S_{av}' & G_{vv} \end{bmatrix}\begin{bmatrix} 0^v \\ (Z'_s)' \end{bmatrix} = Z'_sG_{vv}Z'_s.'$$
In the same manner,

\[ Z_sK\tilde{G}K'Z_d' = Z_s'G_vZ_d' \], \[ Z_sK\tilde{G}K'Z_j' = Z_s'G_vZ_j' \] and \[ Z_sK\tilde{G}K'Z_d' = Z_s'G_vZ_d' \].

From this, we get

\[ Q_{ij} = Z_s'G_vZ_j' \sigma_{ij}^2 + Z_s'G_vZ_d' \sigma_{jd} + Z_s'G_vZ_j' \sigma_{sd} + Z_s'G_vZ_d' \sigma_{sd} \] and \[ Q_{ij} = Q_{ij} \].

From \[ Q_{ij} = Q_{ij} \], it follows that \[ \text{Var}(y) \] is the same in both models and that they are equivalent.

Appendix A2: Equivalence of classical and generalized gametic relationships in reduced models.

We consider a reduced model with classical gametic relationships. With classical gametic relationships all parents of final progeny and their ancestors have two gametic effects in the model with covariance \( G \). In the generalized case the gametic effects of \( u \) of them are collapsed into transmitting abilities, while the remaining \( v \) individuals retain their gametic effects. For the sake of generality the latter group, among an arbitrary choice of others, includes all parents who may have records. Parents with records need to have gametic effects, while all other individuals may be modelled by gametic effects or by transmitting abilities. As final progeny have no genetic effects of their own in the reduced model the variance of residuals \( W \sigma_{ij}^2 \) is not affected by relationships. With classical gametic relationships the variance of observations is

\[ \text{Var}(y) = Q_e + W \sigma_{ij}^2, \]

where

\[ Q_e = \begin{bmatrix} Z_s' & Z_d' \end{bmatrix} \begin{bmatrix} G \sigma_{ij}^2 & G \sigma_{jd} & G \sigma_{sd} & G \sigma_{sd} \end{bmatrix} \begin{bmatrix} Z_s' \\ Z_d' \end{bmatrix} \].

The incidence matrix \( Z_s \) for genetic effects can be partitioned as \( Z_s = \begin{bmatrix} Z_s^{2u} & Z_s' \end{bmatrix} \). In the first partition are two adjacent columns per individual, i.e. \( Z_s^{2u} = Z_i' \otimes \begin{pmatrix} 1 \\ 2 \end{pmatrix} = Z_i' \begin{pmatrix} I_u \otimes \begin{pmatrix} 1 \\ 2 \end{pmatrix} \end{pmatrix} \),

where \( Z_i' \) is the corresponding partition from the same kind of incidence matrix in the model with generalized gametic relationships and \( I_u \) is a \( u \times u \) identity matrix. Note that a multiplication with \( K \) cannot apply here for the conversion of the matrix \( [Z_s^{2u} \ Z_s'] \) into \( [Z_i^u \ Z_i'] \), because \( Z_i' \) may both have entries of single ones for records of parents and of pairs of one half for records from final progeny. All of that also applies in an analogous manner to \( Z_d^{2u} \) and \( Z_d' \).
The first component of $Q$ is

$$Z_i GZ_i' = \left[ Z_{is} \right]^{2u} \left[ Z_{is} \right] \begin{bmatrix} G_{wu} \sigma_s^2 & G_{uv} \sigma_s^2 \\ G_{wu} \sigma_s^2 & G_{vv} \sigma_s^2 \end{bmatrix} \begin{bmatrix} (Z_i s) \end{bmatrix} =$$

$$Z_{is}^2 G_{wu} (Z_i s) \sigma_i^2 + Z_{is}^2 G_{uv} (Z_i s) \sigma_i^2 + Z_{is} G_{uv} (Z_i s) \sigma_i^2 + Z_{s} G_{vv} (Z_i s) \sigma_i^2 =$$

$$Z_i \left[ I \bigotimes \left( \frac{1}{2} \frac{1}{2} \right) \right] G_{wu} \left[ I \bigotimes \left( \frac{1}{2} \frac{1}{2} \right) \right] (Z_i s)^2 + Z_i G_{uv} (Z_i s)^2 +$$

$$Z_i G_{uv} \left[ I \bigotimes \left( \frac{1}{2} \frac{1}{2} \right) \right] (Z_i s)^2 + Z_i G_{vv} (Z_i s)^2 =$$

$$= Z_{is}^2 A(Z_i s) \sigma_i^2 + Z_{is} S_{uv} (Z_i s) \sigma_i^2 + Z_{is} S_{uv} (Z_i s) \sigma_i^2 + Z_i G_{vv} (Z_i s) \sigma_i^2 .$$

Similarly,

$$Z_i GZ_i' = \left[ Z_{is} \right]^{2u} \left[ Z_{is} \right] \begin{bmatrix} G_{wu} \sigma_d s & G_{uv} \sigma_d s \\ G_{wu} \sigma_d s & G_{vv} \sigma_d s \end{bmatrix} \begin{bmatrix} (Z_i d) \end{bmatrix} =$$

$$Z_i \left[ I \bigotimes \left( \frac{1}{2} \frac{1}{2} \right) \right] G_{wu} \left[ I \bigotimes \left( \frac{1}{2} \frac{1}{2} \right) \right] (Z_i d)^2 + Z_i G_{uv} (Z_i d)^2 +$$

$$Z_i G_{uv} \left[ I \bigotimes \left( \frac{1}{2} \frac{1}{2} \right) \right] (Z_i d)^2 + Z_i G_{vv} (Z_i d)^2 =$$

$$= Z_{is}^2 A(Z_i s) \sigma_d s + Z_{is} S_{uv} (Z_i s) \sigma_d s + Z_{is} S_{uv} (Z_i s) \sigma_d s + Z_i G_{vv} (Z_i s) \sigma_d s ,$$

and

finally

$$Z_i GZ_i' = \left[ Z_{is} \right]^{2u} \left[ Z_{is} \right] \begin{bmatrix} G_{wu} \sigma_d^2 & G_{uv} \sigma_d^2 \\ G_{wu} \sigma_d^2 & G_{vv} \sigma_d^2 \end{bmatrix} \begin{bmatrix} (Z_i d) \end{bmatrix} =$$

$$Z_i \left[ I \bigotimes \left( \frac{1}{2} \frac{1}{2} \right) \right] G_{wu} \left[ I \bigotimes \left( \frac{1}{2} \frac{1}{2} \right) \right] (Z_i d)^2 + Z_i G_{uv} (Z_i d)^2 +$$

$$Z_i G_{uv} \left[ I \bigotimes \left( \frac{1}{2} \frac{1}{2} \right) \right] (Z_i d)^2 + Z_i G_{vv} (Z_i d)^2 =$$

$$= Z_{is}^2 A(Z_i s) \sigma_d^2 + Z_{is} S_{uv} (Z_i s) \sigma_d^2 + Z_{is} S_{uv} (Z_i s) \sigma_d^2 + Z_i G_{vv} (Z_i s) \sigma_d^2 .$$
From this, $Q_c$ can be summarized as

$$Q_c = \left( \begin{array}{cc} Z_i^c & Z_j^c \end{array} \right) \left( \begin{array}{cc} Z_i^c & Z_j^c \end{array} \right)^\prime \left( \begin{array}{cc} \sigma_s^2 & \sigma_{sd}^2 \\ \sigma_{sd}^2 & \sigma_d^2 \end{array} \right) \otimes \left[ \frac{1}{2} A_{uv} \ S_{uv} \ G_{vu} \right] \left( \begin{array}{cc} Z_i^c & Z_j^c \end{array} \right)^\prime,$$

which is equal to the equivalent quantity $Q_r$ using generalized gametic relationships

$$Q_r = \left( \begin{array}{cc} Z_i^r & Z_j^r \end{array} \right) \left( \begin{array}{cc} Z_i^r & Z_j^r \end{array} \right)^\prime \left[ \begin{array}{cc} \bar{G} \sigma_s^2 & \bar{G} \sigma_{sd}^2 \\ \bar{G} \sigma_{sd}^2 & \bar{G} \sigma_d^2 \end{array} \right] \left( \begin{array}{cc} Z_i^r & Z_j^r \end{array} \right)^\prime.$$ 

Thus

$$Var(y) = Q_c + W \sigma_{e, c}^2 = Q_r + W \sigma_{e, r}^2, \text{ q.e.d..}$$

**Appendix A3: Equivalence between the model with gametic effects for all individuals and and the reduced model with gametic effects for parents**

We consider a classical gametic model that includes a number $f$ of final progeny. The vector $g'$ is partitioned into two components; in $g'_f$ are the $2f$ gametic effects of the final $f$ progeny, and other gametic effects are in $g'_g$. The covariance of $g'$ then is

$$Var(g) = Var \begin{bmatrix} g_g \\ g_f \end{bmatrix} = \begin{bmatrix} G_{gg} & G_{gf} \\ G_{fg} & G_{ff} \end{bmatrix} = G.$$

The incidence matrices for gametic effects are

$$Z_{all}^s = \begin{bmatrix} Z_{s1}^s & 0 \\ 0 & Z_{s2}^s \end{bmatrix} \text{ and } Z_{all}^d = \begin{bmatrix} Z_{d1}^d & 0 \\ 0 & Z_{d2}^d \end{bmatrix},$$

where $Z_{s1}^s$ ($Z_{d1}^d$) relates the observations to the gametic effects as sire (as dam) of individuals that are not in the set of the $f$ final progeny. Accordingly $Z_{f}^s$ ($Z_{f}^d$) relates observations of the $f$ final progeny to their respective gametic effects as sire (as dam).

By contrast, in a reduced model, all observations of the $f$ final progeny are to be related to the gametic effects as sire (as dam) of their parents. The respective incidence matrices are

$$Z_{s}^{red} = \begin{bmatrix} Z_{s1}^g & 0 \\ Z_{s2}^g & 0 \end{bmatrix} \text{ and } Z_{d}^{red} = \begin{bmatrix} Z_{d1}^g & 0 \\ Z_{d2}^g & 0 \end{bmatrix},$$

where $Z_{s}^{red}$ and $Z_{d}^{red}$ have only zero entries in columns for gametic effects of final progeny.
The relationships between the incidence matrices of the two types of models are

\[
Z_{s}^{\text{red}} = \begin{bmatrix} Z_{s1}^{g} & 0 \\ 0 & Z_{s2}^{g} \end{bmatrix} - \begin{bmatrix} 0 & 0 \\ -Z_{s1}^{g} & Z_{s2}^{g} \end{bmatrix} = Z_{s}^{\text{all}} - Z_{s}^{g},
\]

The matrix \( Z_{s}^{g} \) is the difference between \( Z_{s}^{\text{all}} \) and \( Z_{s}^{\text{red}} \):

\[
Z_{s}^{g} = \begin{bmatrix} 0 & 0 \\ -Z_{s1}^{g} & Z_{s2}^{g} \end{bmatrix}, \text{ and analogously } Z_{d}^{g} = \begin{bmatrix} 0 & 0 \\ -Z_{d1}^{g} & Z_{d2}^{g} \end{bmatrix},
\]

\[
Z_{s}^{\text{all}} = Z_{s}^{\text{red}} + Z_{s}^{g}, \text{ and } Z_{d}^{\text{all}} = Z_{d}^{\text{red}} + Z_{d}^{g}.
\]

For the proof of equivalence of the two models, we express the variance of observations \( \text{Var}(y) \) in terms of model-specific incidence matrices and show their equality by making use of the last two identities.

For any reduced observation equation the variances of the relevant Mendelian sampling effects are part of the residual. For each paternal gamete as sire of a final progeny, the Mendelian sampling effect is the difference between the effect of the paternal gamete and the transmitting ability of the individual’s sire as sire. The respective vector is

\[
m_{s} = Z_{s}^{g} g_{f},
\]

and the maternal counterpart as dam is

\[
m_{d} = Z_{d}^{g} g_{f}.
\]

The common covariance matrix is

\[
\text{Var} \begin{bmatrix} m_{s} \\ m_{d} \end{bmatrix} = \begin{bmatrix} Z_{s}^{g} G \left( Z_{s}^{g} \right)^{\prime} \sigma_{s}^{2} & Z_{s}^{g} G \left( Z_{d}^{g} \right)^{\prime} \sigma_{sd} \\ Z_{d}^{g} G \left( Z_{d}^{g} \right)^{\prime} \sigma_{sd} & Z_{d}^{g} G \left( Z_{d}^{g} \right)^{\prime} \sigma_{d}^{2} \end{bmatrix} = \begin{bmatrix} Z_{s}^{g} G \left( Z_{s}^{g} \right)^{\prime} \sigma_{s}^{2} & 0 \\ 0 & Z_{d}^{g} G \left( Z_{d}^{g} \right)^{\prime} \sigma_{d}^{2} \end{bmatrix}.
\]

The covariance between \( m_{s} \) and \( m_{d} \) is zero as all rows of \( Z_{s}^{g} \) have their non-zero entries at places other than the rows of \( Z_{d}^{g} \), causing \( Z_{s}^{g} G \left( Z_{d}^{g} \right)^{\prime} \) to be a matrix of zeroes.

In detail the product is

\[
Z_{s}^{g} G \left( Z_{d}^{g} \right)^{\prime} = \left\{ \sum_{i,j} \left( z_{s,i}^{g} \right)^{\prime} G \right\}_{ij} = \{0\}_{ij},
\]
where \( \cdot \) denotes element-wise multiplication, sum (\( \cdot \)) is the sum of all matrix elements in (\( \cdot \)), and (\( \mathbf{z}_{i,j}^\delta \))\(^\prime\) and (\( \mathbf{z}_{i,j}^\delta \))\(^\prime\) are the \( i \)th and \( j \)th rows of the two involved incidence matrices.

The total \( \text{Var}(\mathbf{y}) \) in the reduced model is

\[
\text{Var}(\mathbf{y}) = \mathbf{Q}_{\text{red}} + \text{Var}(\mathbf{m}_s) + \text{Var}(\mathbf{m}_d) + \mathbf{I}\sigma^2_v.
\]

with

\[
\mathbf{Q}_{\text{red}} = \begin{bmatrix}
\mathbf{Z}_s^\text{red} & \mathbf{Z}_d^\text{red}
\end{bmatrix}
\begin{bmatrix}
\sigma^2_s & \sigma_{sd} \\
\sigma_{sd} & \sigma^2_d
\end{bmatrix}
\otimes
\begin{bmatrix}
\mathbf{G}(\mathbf{Z}_s^\text{red}) \\
\mathbf{G}(\mathbf{Z}_d^\text{red})
\end{bmatrix}
\]

\[
= \mathbf{Z}_s^\text{red} \mathbf{G}(\mathbf{Z}_s^\text{red})' \sigma^2_s + \mathbf{Z}_s^\text{red} \mathbf{G}(\mathbf{Z}_d^\text{red})' \sigma_{sd} + \mathbf{Z}_d^\text{red} \mathbf{G}(\mathbf{Z}_s^\text{red})' \sigma_{sd} + \mathbf{Z}_d^\text{red} \mathbf{G}(\mathbf{Z}_d^\text{red})' \sigma^2_d.
\]

In the classical gametic model the variance of observations \( \text{Var}(\mathbf{y}) \) is

\[
\mathbf{Q}_{\text{all}} + \mathbf{I}\sigma^2_v.
\]

The first component is

\[
\mathbf{Q}_{\text{all}} = \begin{bmatrix}
\mathbf{Z}_s^\text{all} & \mathbf{Z}_d^\text{all}
\end{bmatrix}
\begin{bmatrix}
\sigma^2_s & \sigma_{sd} \\
\sigma_{sd} & \sigma^2_d
\end{bmatrix}
\otimes
\begin{bmatrix}
\mathbf{G}(\mathbf{Z}_s^\text{all}) \\
\mathbf{G}(\mathbf{Z}_d^\text{all})
\end{bmatrix}
\]

\[
= \begin{bmatrix}
\mathbf{Z}_s^\text{red} + \mathbf{Z}_s^\delta & \mathbf{Z}_d^\text{red} + \mathbf{Z}_d^\delta
\end{bmatrix}
\begin{bmatrix}
\sigma^2_s & \sigma_{sd} \\
\sigma_{sd} & \sigma^2_d
\end{bmatrix}
\otimes
\begin{bmatrix}
\mathbf{G}(\mathbf{Z}_s^\text{red} + \mathbf{Z}_s^\delta) \\
\mathbf{G}(\mathbf{Z}_d^\text{red} + \mathbf{Z}_d^\delta)
\end{bmatrix}
\]

This results in a sum of 16 terms, of which the first four are

\[
= \mathbf{Z}_s^\text{red} \mathbf{G}(\mathbf{Z}_s^\text{red})' \sigma^2_s + \mathbf{Z}_s^\text{red} \mathbf{G}(\mathbf{Z}_d^\text{red})' \sigma_{sd} + \mathbf{Z}_d^\text{red} \mathbf{G}(\mathbf{Z}_s^\text{red})' \sigma_{sd} + \mathbf{Z}_d^\text{red} \mathbf{G}(\mathbf{Z}_d^\text{red})' \sigma^2_d.
\]

This is equal to \( \mathbf{Q}_{\text{red}} \) in the reduced model. Further, we have two more terms

\[
\mathbf{Z}_s^\delta \mathbf{G}(\mathbf{Z}_s^\delta)' \sigma^2_s + \mathbf{Z}_d^\delta \mathbf{G}(\mathbf{Z}_d^\delta)' \sigma^2_d,
\]

equivalent to \( \text{Var}(\mathbf{m}_s) + \text{Var}(\mathbf{m}_d) \). The remaining 10 terms in
all are zero matrices. Thus, \( Q \text{all} = Q \text{red} + \text{Var}(m_d) + \text{Var}(m_s) \) and, therefore, the variance \( \text{Var}(y) \) in the classical gametic model and the reduced model with gametic relationships are identical. As both models also have identical expectations of \( y \), they are equivalent; \textit{q.e.d.}.

### Appendix A4: Maternal genetic variance in a reduced model.

We consider a reduced model equation for a single observation:

\[
y_i = \mu + m_d + a_d^s + a_s^d + r_i.
\]

This equation comprises the maternal breeding value \( m_d \) of the dam \( d \) of individual \( i \), together with the transmitting ability as dam \( a_d^s \) of the dam \( d \) of \( i \), the transmitting ability as sire \( a_s^d \) of the sire \( s \) of \( i \), and the residual \( r_i \).

Then, the covariance of the respective vectors of random genetic effects is

\[
\text{Var} \begin{bmatrix} m \\ a^s \\ a^d \end{bmatrix} = \begin{bmatrix} \sigma_m^2 & \sigma_{ms} & \sigma_{md} \\ \sigma_{ms} & \sigma_s^2 & \sigma_{sd} \\ \sigma_{md} & \sigma_{sd} & \sigma_d^2 \end{bmatrix} \otimes \frac{1}{2} A,
\]

where \( \sigma_m^2 \) is the maternal gametic variance. As we use \( \frac{1}{2} A \) as relationship matrix (assuming all records are from final progeny) the incidence matrix for maternal breeding values needs to have non-zero entries of two to match this set of covariances.

The variance of observations has the non-residual component

\[
Q_{\text{rm}} = \begin{bmatrix} Z_m & Z_s & Z_d \end{bmatrix} \begin{bmatrix} \sigma_m^2 & \sigma_{ms} & \sigma_{md} \\ \sigma_{ms} & \sigma_s^2 & \sigma_{sd} \\ \sigma_{md} & \sigma_{sd} & \sigma_d^2 \end{bmatrix} \otimes \frac{1}{2} A \begin{bmatrix} Z_m^t \\ Z_s^t \\ Z_d^t \end{bmatrix},
\]

involving the incidence matrices \( Z_m, Z_s, \) and \( Z_d \) that link observations to maternal genetic effects, transmitting abilities as sire, and transmitting abilities as dam, respectively. \( Q_{\text{rm}} \) is a sum of nine
matrices; of them, the following matrix equalities can be found by dropping the respective components of variance:

\[
\begin{align*}
Z_m A Z_m' &= Z_d A Z_d' = Z_m A Z_d' = Z_d A Z_m' \\
Z_m A Z_m' &= Z_d A Z_s' \\
Z_s A Z_m' &= Z_s A Z_d'.
\end{align*}
\]

The underlying fact is that the incidence matrices \(Z_m\) and \(Z_d\) link all observations to genetic effects of the same animals, i.e., of the dam of each final progeny. Thus, the incidence matrices \(Z_m = Z_d\) are equal, and constitute equalities from above. Consequently, \(Q_{rm}\) can be rewritten as

\[
Q_{rm} = \frac{1}{2} \left[ Z_m A Z_m' \sigma_m^2 + Z_d A Z_d' \sigma_d^2 + Z_m A Z_d' \sigma_{md} + Z_d A Z_m' \sigma_{md} + Z_m A Z_s' \sigma_{ms} + Z_d A Z_s' \sigma_{sd} \right] Z_s A Z_d',
\]

which, in terms of the incidence matrices of the reduced model without maternal genetic effects, is

\[
Q_{rm} = \frac{1}{2} \left[ Z_d A Z_d' \left( \sigma_d^2 + \sigma_m^2 + 2 \sigma_{md} \right) + Z_m A Z_s' \left( \sigma_{ms} + \sigma_{ms} \right) \right] Z_s A Z_d'.
\]

The variance in the transmitting ability as dam and the covariance with the transmitting ability as sire are therefore contaminated by components of the maternal genetic (co-)variances. This shows that in the presence of maternal genetic effects, \(\sigma_d^2\) and \(\sigma_s^2\) cannot be inferred from the reduced model. Moreover, we cannot correctly calculate the weights of the observations as this would require that we know these two components of variance.

Interestingly, we can assume the absence of genomic imprinting and make use of \(\sigma_e^2 = \sigma_s^2 = \sigma_d^2 = \sigma_{ad}\), from which the residual variance of observation \(i\) becomes

\[
\frac{1}{2} \left( 1 - F_{e,i} \right) \sigma_e^2 + \frac{1}{2} \left( 1 - F_{d,i} \right) \sigma_d^2 + \sigma_e^2.
\]

Consequently, the imprinting variance becomes

\[
\sigma_i^2 = \left( \sigma_d^2 + \sigma_m^2 + 2 \sigma_{md} + \sigma_s^2 \right) - 2 \left( \sigma_{ad} + \sigma_{ms} \right) = \sigma_m^2.
\]

**Appendix A5: Maternal variance in a classical gametic model.**

The model equation for a single observation \(y_i\) in a gametic model with maternal effects is
\[ y_i = \mu + g^m_{d,1} + g^m_{d,2} + g^s_{i,1} + g^d_{i,2} + e_i. \]

In this, we have the maternal effect \( g^m_{d,1} \) of the paternal \( g^m_{d,2} \) gamete \( g^m_{d,1} \) and the maternal \( g^m_{d,2} \) gamete \( g^m_{d,2} \) of the dam \( d \) of individual. \( g^s_{i,1} \) is the effect of the paternal gamete of individual \( i \) as sire, \( g^d_{i,2} \) is the effect of the maternal allele of individual \( i \) as dam, and \( e_i \) is the residual. The covariance of random gametic effects is

\[
\text{Var} \begin{bmatrix} g^m_m \n g^s \n g^d d \end{bmatrix} = \begin{bmatrix} \sigma^2_m & \sigma_{ms} & \sigma_{md} \\
\sigma_{ms} & \sigma^2_s & \sigma_{sd} \\
\sigma_{md} & \sigma_{sd} & \sigma^2_d \end{bmatrix} \otimes G.
\]

The vector of observations \( y \) has covariance \( V = Q_{mm} + 1\sigma^2_r \), with

\[
Q_{mm} = [Z^\prime_m \ Z^\prime_s \ Z^\prime_d] \begin{bmatrix} \sigma^2_m & \sigma_{ms} & \sigma_{md} \\
\sigma_{ms} & \sigma^2_s & \sigma_{sd} \\
\sigma_{md} & \sigma_{sd} & \sigma^2_d \end{bmatrix} \otimes G \begin{bmatrix} Z^\prime_m \\
Z^\prime_s \\
Z^\prime_d \end{bmatrix}
\]

All other components of covariance are defined as before in appendix A4.

\( Q_{mm} \) has three components—\( Z^\prime_m GZ\sigma^2_m \), \( Z^\prime_d GZ\sigma^2_d \), and —related to components of variance, and another three—\( Z^\prime_m GZ\sigma_{ms} + Z^\prime_d GZ\sigma_{sd} \), \( Z^\prime_m GZ\sigma_{md} + Z^\prime_d GZ\sigma_{md} \), and—that are connected to the covariances. In contrast to the reduced model, the incidence matrices \( Z^\prime_m \) and \( Z^\prime_d \) relating the records to different gametic effects and, therefore, are not equal. As a result, all six addends of \( Q_{mm} \) are linearly independent and all components of variance can be separated.
Figure 1: Example of a lower triangular matrix \((T')^{-1}\) from a decomposed inverse of a generalized gametic relationship matrix. Each row of the matrix pertains to a particular genetic effect. The last column indicates the respective combination of each kind of genetic effect (a: transmitting ability; g: gametic effect) with the genetic effects of the parents (a: transmitting ability; gg: pair of gametic effects; 0: unknown parent, and combinations thereof).

\[
\begin{array}{cccccccccccccccc}
1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & a - 00 \\
0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & g - 0 \\
0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & g - 0 \\
-0.5 & -0.25 & -0.25 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & a - agg \\
0 & 0 & 0 & -0.5 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & a - 0a \\
-0.5 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & a - a0 \\
0 & 0 & 0 & 0 & -1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & g - a \\
0 & -0.5 & -0.5 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & g - gg \\
0 & 0 & 0 & 0 & 0 & -0.5 & -0.5 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & g - gg \\
0 & -0.5 & -0.5 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & g - gg \\
0 & -0.25 & -0.25 & 0 & 0 & 0 & -0.25 & -0.25 & 0 & 0 & 1 & 0 & 0 & 0 & a - gggg \\
-0.5 & 0 & 0 & -0.5 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & a - aa \\
0 & 0 & 0 & -0.5 & 0 & 0 & 0 & 0 & -0.25 & -0.25 & 0 & 0 & 0 & 0 & a - gga \\
0 & 0 & 0 & 0 & 0 & -0.25 & -0.25 & 0 & 0 & 0 & 0 & 1 & 0 & a - gg0 \\
0 & -0.25 & -0.25 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & a - 0gg
\end{array}
\]
Table 1: Size and indices of non-zero elements of vectors \( \mathbf{u}' \), by kind of genetic effect (a: transmitting ability; g: gametic effect). The cases indicate unique combinations of kind of genetic effect and kind of indices. The latter consist of \( i \): number of genetic effects; \( d \): transmission ability of dam; \( s \): transmission ability of sire; \( u \): paternal gamete of dam; \( v \): maternal gamete of dam; \( p \): paternal gamete of sire; \( q \): maternal gamete of sire. For gametic effects (cases g-a and g-gg), the respective effects of the known parent are indexed as for a sire.

| Kind of effect | Case  | Non-zero elements in \( \mathbf{u}' \) | Indices of non-zero elements |
|----------------|-------|-------------------------------------|-----------------------------|
| a              | a-00  | 1                                   | i                           |
| a              | a-0a  | \(-\frac{1}{2}\) 1                  | d, i                        |
| a              | a-0gg | \(-\frac{1}{4} -\frac{1}{4} 1\)     | u, v, i                     |
| a              | a-a0  | \(-\frac{1}{2} 1\)                  | s, i                        |
| a              | a-gg0 | \(-\frac{1}{4} -\frac{1}{4} 1\)     | p, q, i                     |
| a              | a-aa  | \(-\frac{1}{2} -\frac{1}{2} 1\)     | s, d, i                     |
| a              | a-agg | \(-\frac{1}{4} -\frac{1}{4} -\frac{1}{4} 1\) | s, u, v, i |
| a              | a-gga | \(-\frac{1}{4} -\frac{1}{4} -\frac{1}{2} 1\) | p, q, d, i |
| a              | a-gggg| \(-\frac{1}{4} -\frac{1}{4} -\frac{1}{4} -\frac{1}{4} 1\) | p, q, u, v, i |
| g              | g-a   | \(-1 1\)                            | s, i                        |
| g              | g-gg  | \(-\frac{1}{2} -\frac{1}{2} 1\)     | p, q, i                     |
| g              | g-0   | 1                                   | i                           |