





### Strategies for inversion of the additive relationship matrix among genotyped animals

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✓ The inverse of A is computed as a sum of vector products (Henderson, 1976)

$$\mathbf{A}_{(i)}^{-1} = \begin{bmatrix} \mathbf{A}_{(i-1)}^{-1} & \mathbf{0} \\ \mathbf{0}' & \mathbf{0} \end{bmatrix} + \alpha_{(i)} \begin{bmatrix} -\mathbf{b}_{(i)} \\ 1 \end{bmatrix} \begin{bmatrix} -\mathbf{b}'_{(i)} & 1 \\ -\mathbf{b}'_{(i)} & 1 \end{bmatrix}$$



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$$\begin{bmatrix} \mathbf{A}_{(i)}^{-1} = \left(\mathbf{T}_{A(i)}^{-1}\right)' \mathbf{D}_{A(i)}^{-1} \mathbf{T}_{A(i)}^{-1} \\ -\mathbf{b}_{(i)}' \mathbf{1} \end{bmatrix} \begin{bmatrix} \mathbf{T}_{A(i-1)}^{-1} & \mathbf{0} \\ \mathbf{D}_{A(i)}^{-1} = \begin{bmatrix} \mathbf{D}_{A(i-1)}^{-1} & \mathbf{0} \\ \mathbf{0}' & \mathbf{\alpha}_{(i)} \end{bmatrix}$$







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✓ How sparse is the inverse of  $A_{22}$ ? ... How sparse is the inverse factor (**T**<sup>-1</sup>) of  $A_{22}$ ?

✓ How a putative sparsity could be used in computation of the inverse?

## → Main objective: To avoid useless computations



#### **Sparsity in the inverse factor of A**<sub>22</sub>

✓ How to deal with more complex cases?

✓ By a comprehensive search in the pedigree
 ✓ « SP Algorithm »
 ✓ Explores pedigree brances and apply simple rules
 ✓ Uses only pedigree and incidence vector
 ✓ Returns a symbolic inverse factorization



### **Sparsity in the inverse factor of A**<sub>22</sub>

#### $\checkmark$ Some **performances** on different sizes of $A_{22}$ :





#### 1. Successive construction of the inverse

$$\mathbf{A}_{22(i)}^{-1} = \begin{bmatrix} \mathbf{A}_{22(i-1)}^{-1} & \mathbf{0} \\ \mathbf{0}' & \mathbf{0} \end{bmatrix} + \alpha_{(i)} \begin{bmatrix} -\mathbf{b}_{(i)} \\ 1 \end{bmatrix} \begin{bmatrix} -\mathbf{b}'_{(i)} & 1 \end{bmatrix}$$

How to get **b**?

1. 
$$\mathbf{b}_{(i)} = \mathbf{A}_{22(i-1)}^{-1} \mathbf{A}_{22(i-1)}(:,1:i-1)$$
  
2.  $\mathbf{A}_{22(i-1)} \mathbf{b}_{(i)} = \mathbf{A}_{22(i-1)}(:,1:i-1)$ 



 Restricting the product only to elements of b different from 0

$$\mathbf{b}_{(i)} = \mathbf{A}_{22(i-1)}^{-1} \mathbf{A}_{22(i-1)}(:, 1:i-1) \rightarrow \mathbf{x} = \mathbf{Z}\mathbf{y}$$





#### 2. Solving a linear system of lower size









#### $\checkmark$ Order of $A_{22}$ = Number of genotyped animals $\checkmark$ Depends on the pedigree (depth, lines, ...) 90 Percentage of zeros [%] 80 70 60 50 40 16,000 32.000 48.000 64.000 80.000 96.000 112.000 128.000 Number of genotyped animals



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3. Storing the inverse of  $A_{22}$  from time to time and updating this inverse only for recent animals

$$\mathbf{A}_{22(t+1)}^{-1} = \begin{bmatrix} \mathbf{A}_{22(t)}^{-1} & \mathbf{0} \\ \mathbf{0}' & \mathbf{0} \end{bmatrix} + \boldsymbol{\alpha}_{(x)} \begin{bmatrix} -\mathbf{b}_{(x)} \\ 1 \end{bmatrix} \begin{bmatrix} -\mathbf{b}_{(x)}' & 1 \end{bmatrix}$$











#### **Take-home messages**

 Sparsity pattern of the inverse of A<sub>22</sub> can be set up without matrix computations, even for large matrices



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 As the order of A<sub>22</sub> increases, inversion shrinks to solve multiple small linear systems that are identified by SP algorithm



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