A diagonal preconditioner for solving single-step SNPBLUP efficiently

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PROGRESS IN PIGS

Single-step SNPBLUP

- Prediction of
  - genomic breeding values for genotyped and non-genotyped animals
  - SNP effects

- Two ssSNPBLUP variants explored
  - Mantysaari and Stranden (2016)
  - Liu et al. (2014)

Preconditioned conjugate gradient

- PCG = Iterative solver
    - Commonly used for breeding values estimation

- Preconditioning

    = Transforming a linear system into another system with more favourable properties for iterative solving

- "Usual" PCG + ssSNPBLUP

    ➔ Convergence issues

➔"Usual" preconditioner not well adapted for ssSNPBLUP

Aim

To develop

a preconditioner

that improves the PCG convergence applied to ssSNPBLUP

at low costs,

and

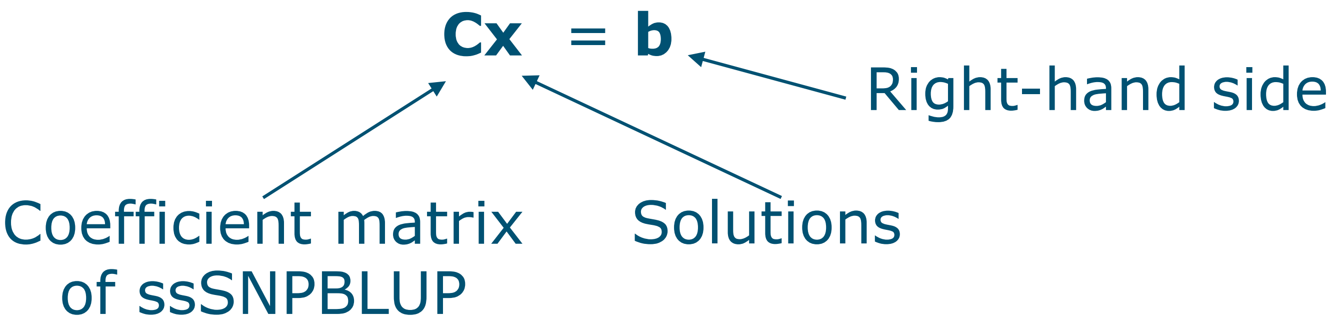
to compare

its performance against the usual PCG method

applied to two ssSNPBLUP models

How to solve **Cx=b** ?

- Linear system to be solved



$$\mathbf{Cx} = \mathbf{b}$$

Right-hand side

Coefficient matrix of ssSNPBLUP

Solutions

How to solve $\mathbf{Cx}=\mathbf{b}$?

- PCG

$$\mathbf{M}^{-1}\mathbf{Cx} = \mathbf{M}^{-1}\mathbf{b}$$

Diagonal preconditioner

- Easy to compute
- Poor (no) convergence of ssSNPBLUP

Usual: $\mathbf{M} = \mathrm{diag}(\mathbf{C})$

How to solve $\mathbf{Cx=b}$?

- PCG

$$\mathbf{M^{-1}Cx} = \mathbf{M^{-1}b}$$

- Deflated PCG

$$\mathbf{PM^{-1}Cx} = \mathbf{PM^{-1}b}$$

Deflation matrix

- Can be cumbersome (dense matrix)
- Good convergence of ssSNPBLUP

How to solve **Cx=b** ?

- PCG

$$\mathbf{M}^{-1}\mathbf{Cx} = \mathbf{M}^{-1}\mathbf{b}$$

- Deflated PCG

$$\mathbf{PM}^{-1}\mathbf{Cx} = \mathbf{PM}^{-1}\mathbf{b}$$

- PCG + second-level diagonal preconditioner

$$\mathbf{D}^{-1}\mathbf{M}^{-1}\mathbf{Cx} = \mathbf{D}^{-1}\mathbf{M}^{-1}\mathbf{b}$$

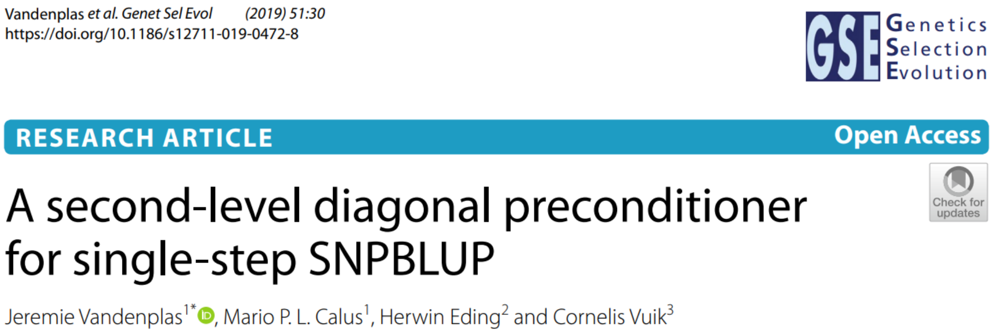
Second-level diagonal preconditioner

- Easy to compute
- Good convergence of ssSNPBLUP

Second-level diagonal preconditioner **D**

$$\mathbf{D}^{-1} = \begin{bmatrix} \mathbf{I} & \mathbf{0} \\ \mathbf{0} & \mathbf{I}k \end{bmatrix}$$

- *k*
  - Only applied to the SNP equations
  - Depends on the extremal eigenvalues of $\mathbf{M}^{-1}\mathbf{C}$
  - Ideal *k: 0.01-0.001*
- No additional costs
  - Combined with the preconditioner **M**



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A second-level diagonal preconditioner for single-step SNPBLUP

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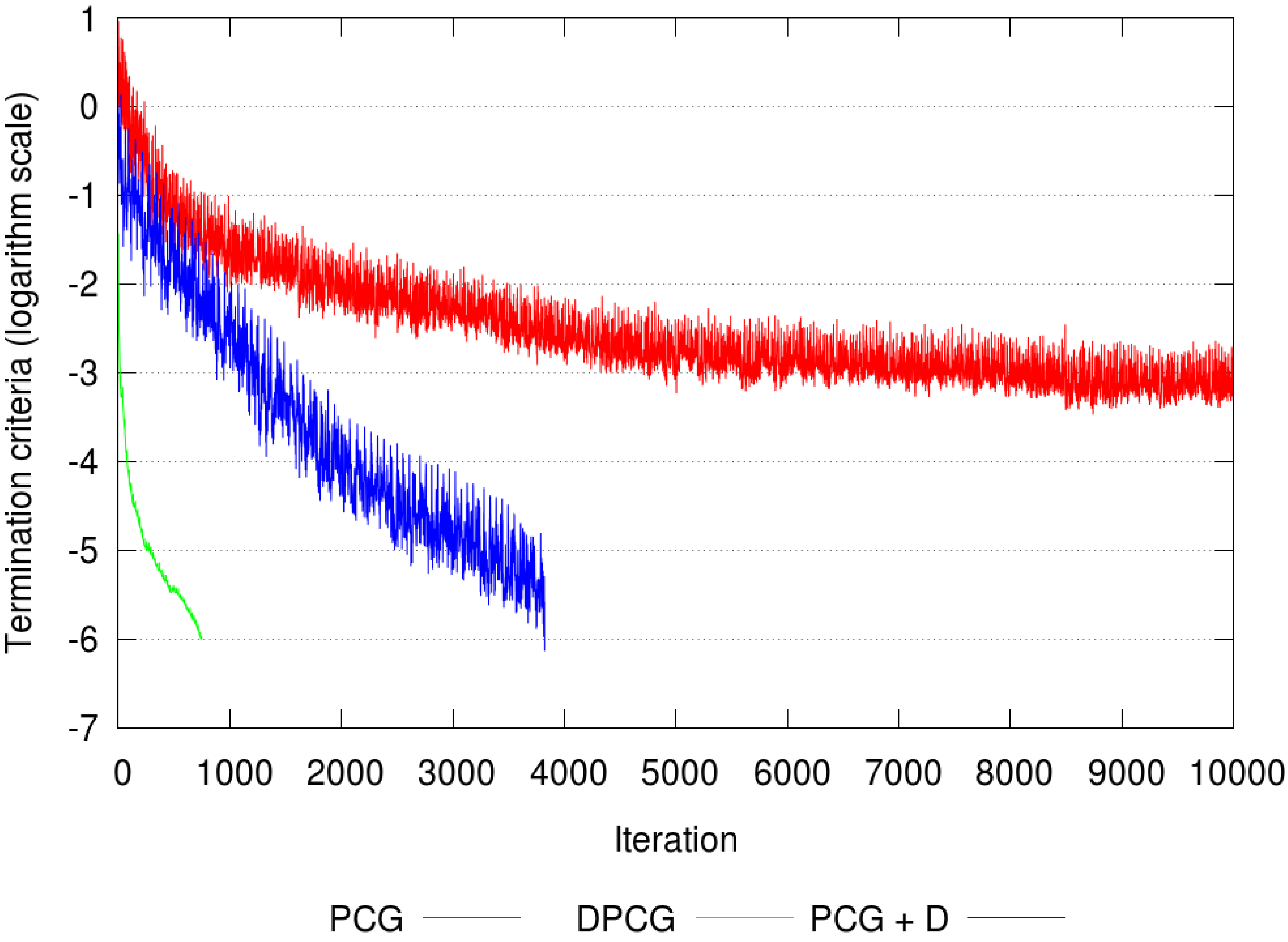
Data

Number of	
Traits	4
Records	3.8 million
Pedigree animals	6.1 million
Genotypes	90,963
SNPs	37,994

- Heritabilities: 0.11 – 0.22
- Residual polygenic variance = 5%

Mantysaari and Stranden (2016)



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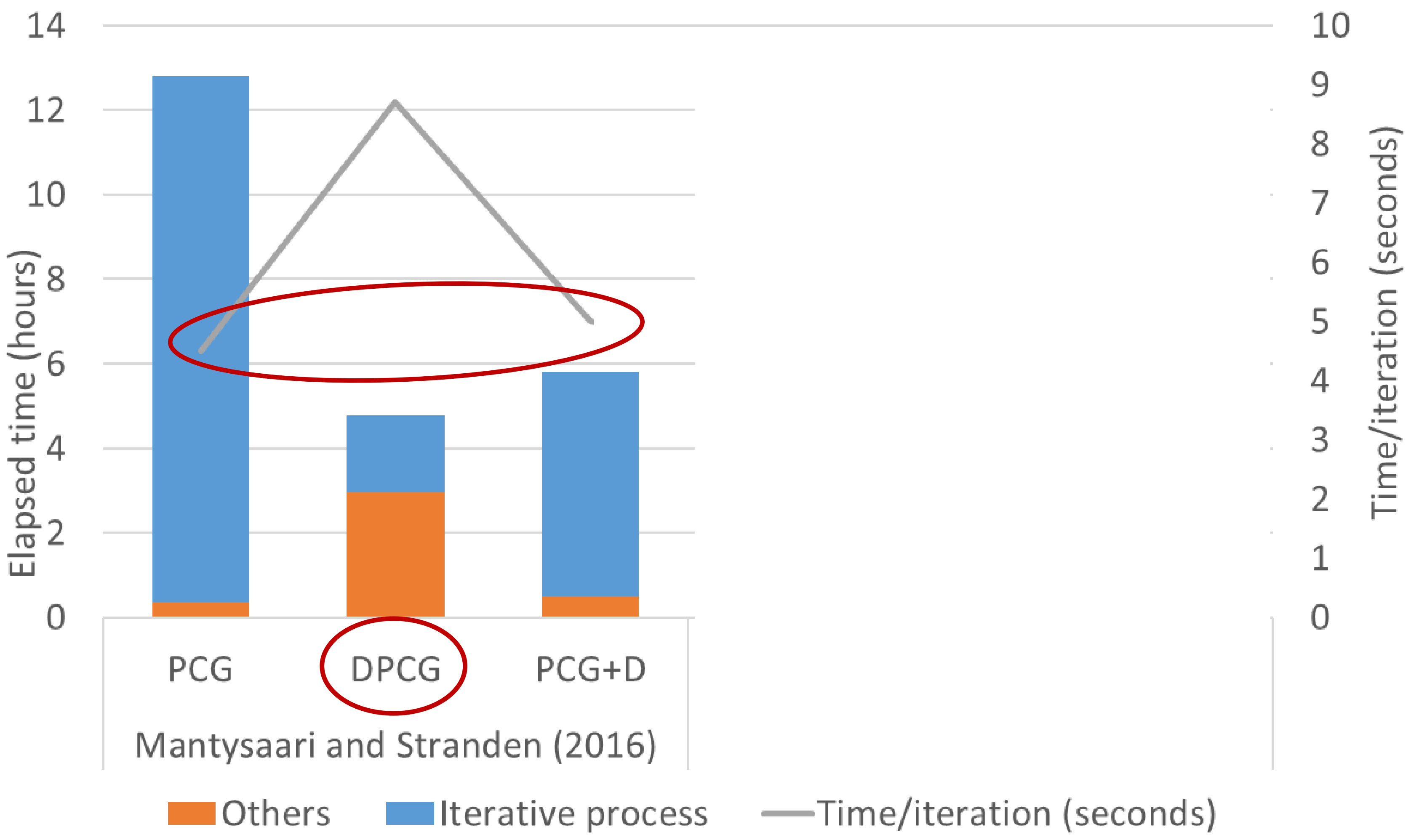

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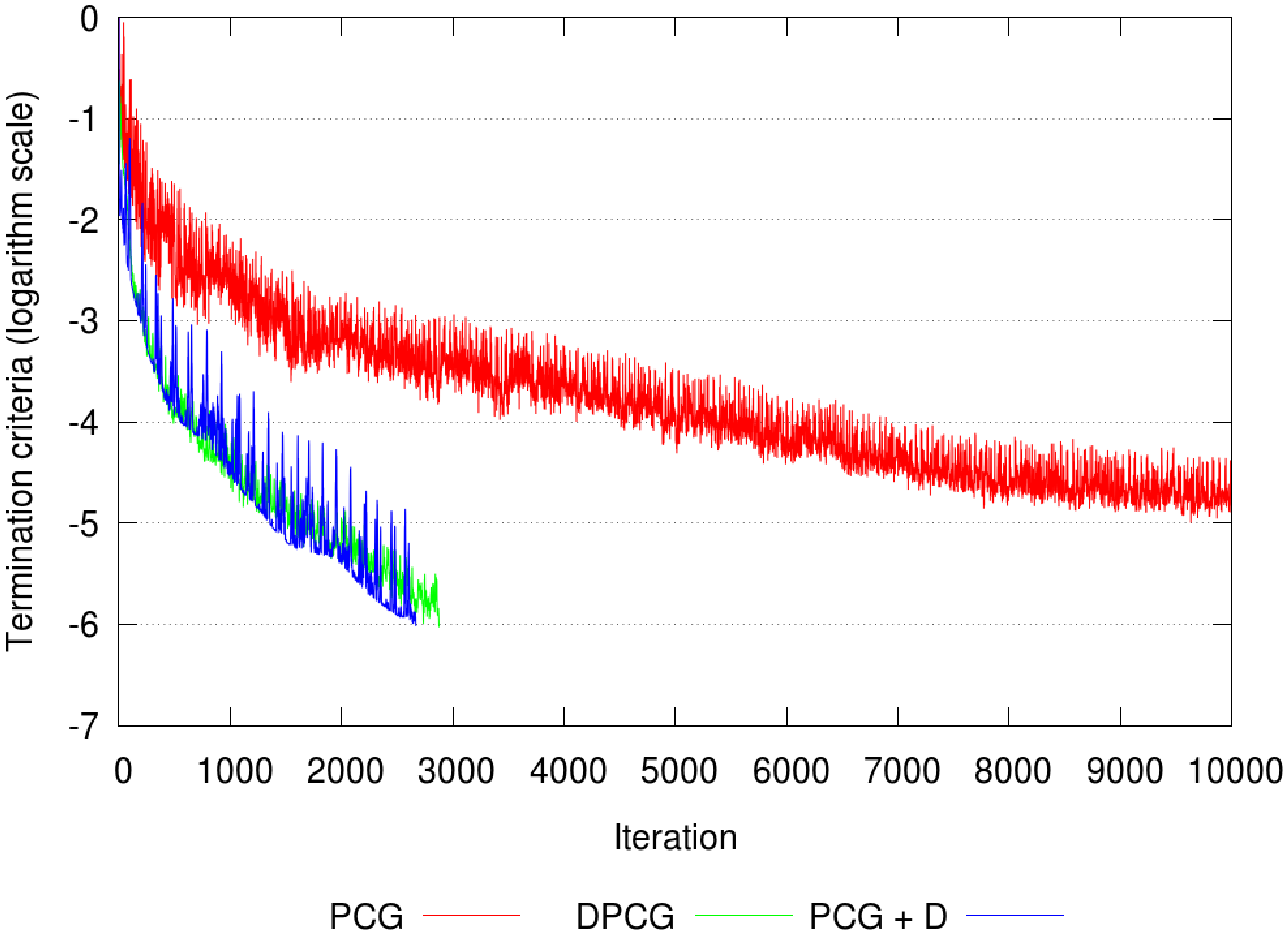

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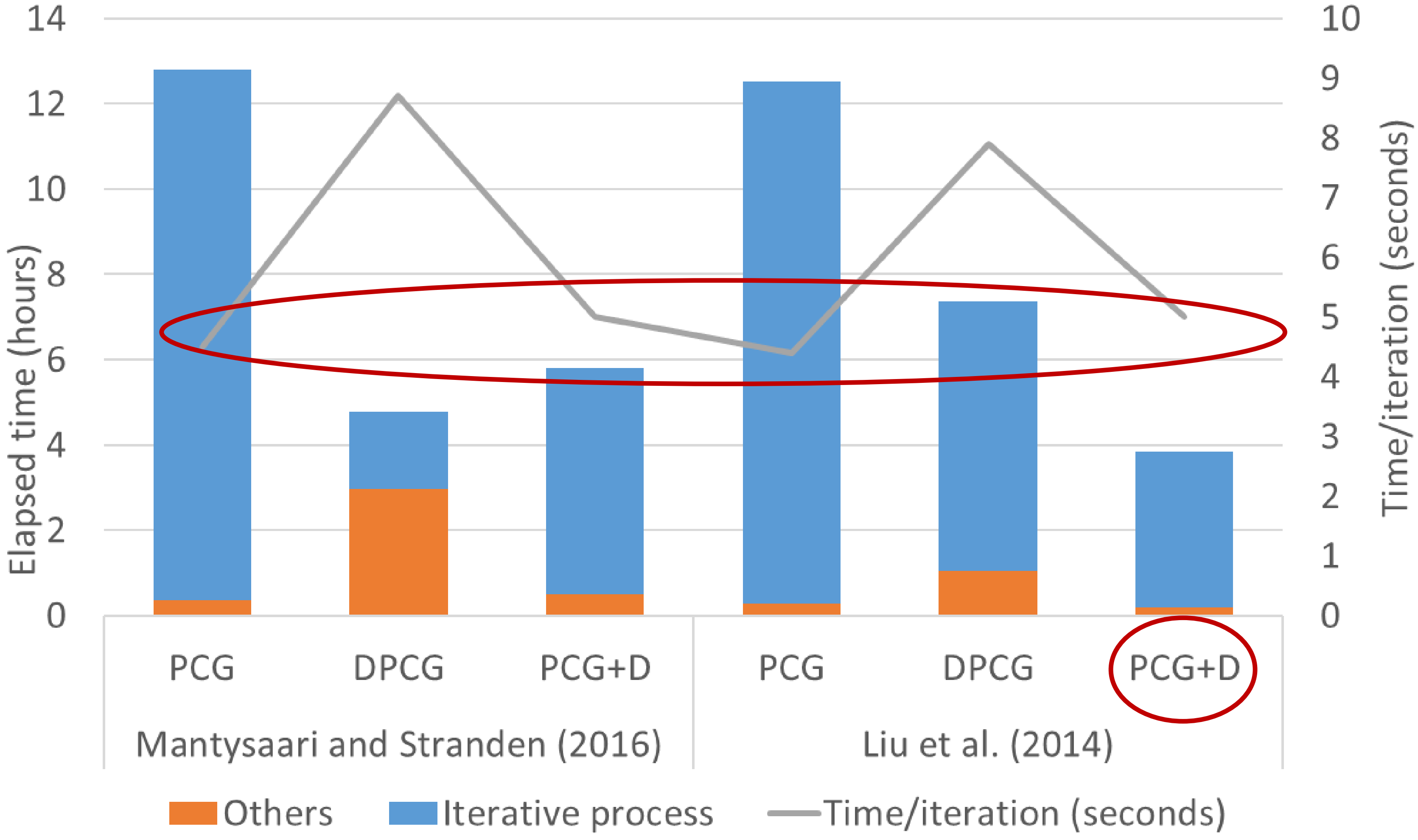

→**Efficient and simple** second-level preconditioner **D**

Conclusions

- Second-level preconditioner **D**
  - Efficient and simple
    - ➔Allows routine ssSNPBLUP
  - Also with more complex models and large datasets
    - Vandenplas et al. (2019), Abstract p. 211, EAAP

- Liu et al. (2014)
  - Better properties for PCG than MS model
  - Best approach when solved with **PCG + D**

Thank you!

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