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Title: Enhancing the Scalability of Selected Inversion Factorization Algorithms in Genomic Prediction

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- A parallel approach for selected inversion in genomic prediction is presented.
- The technique is used in maximizing the likelihood function of the AI-REML method.
- Strong and weak scaling tests on Cray XC40 supercomputers are performed.
- The approach is validated on real, large-scale genomic data.

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