

PRIMUS

There are currently two main functions of PRIMUS. The first is an algorithm to reconstruct pedigrees within a genetic dataset. PRIMUS can verify expected pedigree structures from genetic data, and it can identify and incorporate novel, cryptic relationships into pedigrees. The second function of PRIMUS is an algorithm adapted from graph theory that identifies the maximum set of unrelated individuals in any dataset, and allows weighting parameters to be utilized in unrelated sample selection.

International Requests:

University of Washington agreements require additional review if the requesting entity is located in, or affiliated with the government of, China (Including Hong Kong; not including Taiwan), Iran, North Korea, Russia, or Syria. For requests from these countries, please **allow for an additional month of processing time** for a response.

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