1046-Z1-1415   **Daisy L Phillips*** (`philli5@cc.wwu.edu`), 1446 Franklin St. Apt. A, Bellingham, WA 98225, and **Nathan W Hall**, **Laina Mercer** and **Amy D Anderson**. *Methods of estimating inbreeding coefficients by jointly estimating allele frequencies and accounting for the presence of null alleles.*

An organism receives two alleles at each locus: one from its mother and one from its father. If these two alleles are identical copies of the same allele from an ancestor that both parents share, we say that they are "identical by descent", or IBD. The inbreeding coefficient for an individual is the probability that these two alleles are IBD. Various methods exist to calculate inbreeding coefficients using already known or previously estimated allele frequencies. In practice, these frequencies are calculated without allowing for the presence of null alleles or the possibility that individuals in the sample may be inbred. We developed two iterative algorithms that use the method of maximum likelihood to estimate inbreeding coefficients. One jointly estimates population allele frequencies and inbreeding coefficients and the other additionally accounts for the possible presence of null alleles. We ran a simulation study using these algorithms, and concluded that jointly estimating allele frequencies does not significantly affect the estimation of individual inbreeding coefficients. However, by accounting for the presence of null alleles greater accuracy in the estimation of inbreeding coefficients may be achieved. (Received September 15, 2008)