SEQLinco: A Novel Approach to Use Sequence Data for Linkage Analysis

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**Methods**

***Combined Haplotype Pattern coding***

We propose a *Combined Haplotype Pattern* (CHP)method to …

***Haplotype reconstruction***

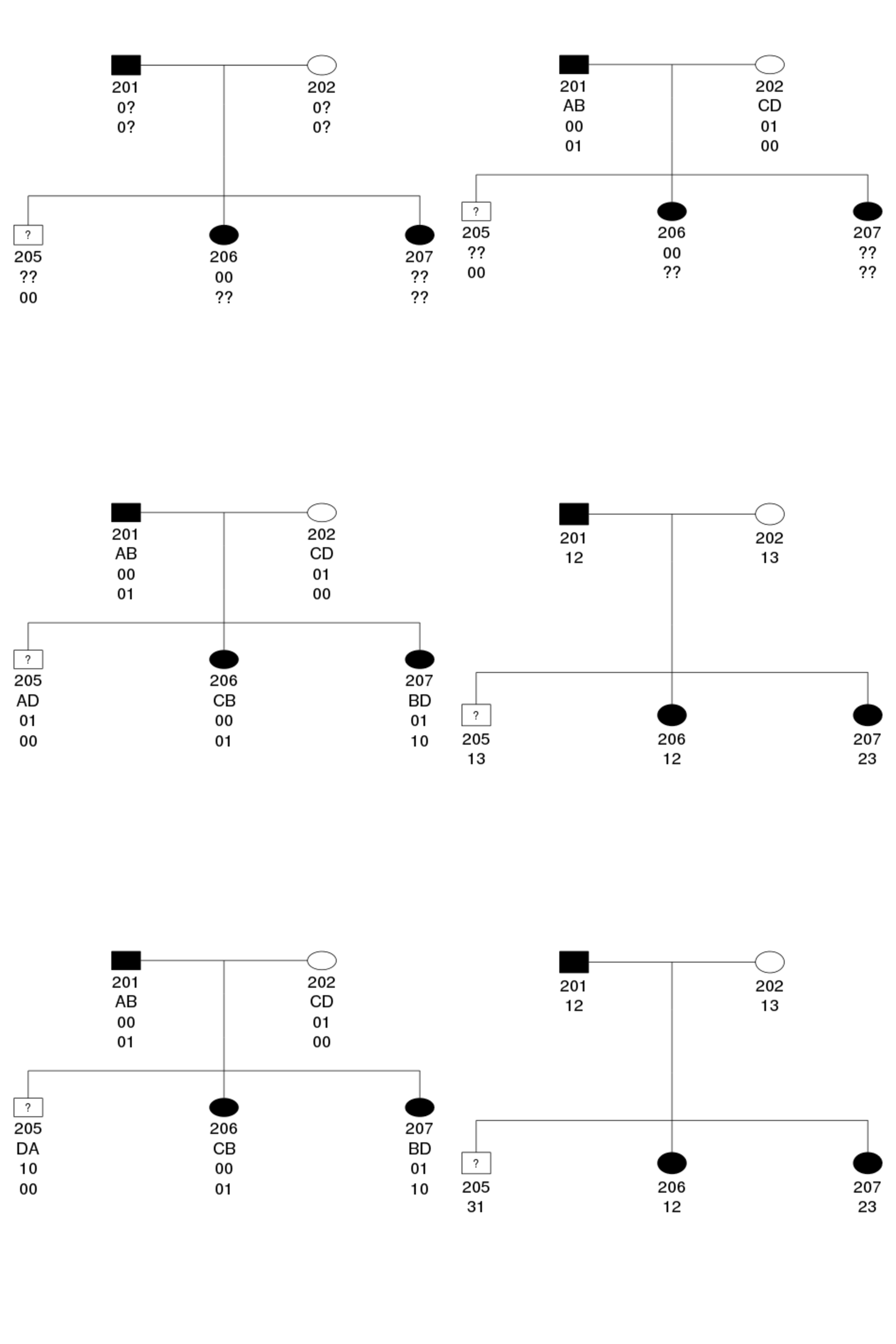
Rule 1: For heterozygous sites, always place 1 to the right side if it is the first 1 being placed to the haplotype. Check for Mendelian conflict before placing in new 1s and if there are still multiple choices, still place 1 to the right side.

First we work on sites where any offspring is 00 or 11:

1. *Resolve parental sites using 00&11 sites in offspring*: For sites where any offspring is 00, configuration of that site on both parents should be 00, 01 or 10. Given knowledge of parental genotype we apply Rule 1 to determine the parental haplotypes for that site. The same applies for 11 sites in offspring.
   1. Figure 1.1: From site 2 in #205 and site 1 in #206 we can determine the left side of all sites in #201 and #202.
   2. Figure 1.2: Determination of the right side of all sites in #201 and #202 are straightforward given knowledge of parental genotype.
2. *Determine more sites on offspring using parents*: For sites where parental haplotypes are all available due to previous step, we use Rule 1 to determine offspring haplotypes on those sites based on parental haplotypes and offspring genotypes.
   1. Figure 1.3 and 1.4: For site 1 in #205 and site 2 in #206 by Rule 1 we determine the haplotypes as 01. For site 1 in #207 by Rule 1 we place 01, and also by Rule 1 we check for Mendelian conflict and determine the haplotype as 10. We then apply CHP*.*
   2. Figure 1.5 and 1.6: What if we do not apply Rule 1 and use a different arbitrarily picked configuration for an offspring? For example for site 1 in #205 we use another configuration. The resulting CHP result is not effected.

We then move on to sites where no offspring is 00 or 11:

1. *Resolve sites with parental 00 or 11*: For sites where one parent is 00, we place the site on the other parent as 01 or 11 (smaller coding goes on the left). The corresponding sites for offspring are determined by any arbitrarily picked configuration that does not result in Mendelian conflict.
   1. Figure 2.1: We consider two more sites in addition to the sites already determined in Figure 1 (called site 3 and site 4). From site 3 in #201 we write site 3 in #202 as 01
   2. Figure 2.2: We determine offspring haplotypes on site 3



***Recombination events***

***Missing data***

**Figure legends**

**Figure 1.**

**Appendix**