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## Linkage disequilibrium

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Linkage disequilibrium (LD) refers to the correlation among neighboring alleles, reflecting common haplotype ancestry. In the May 10 *Nature*, Reich *et al.* describe a systematic, genome-wide analysis of LD within human populations (*Nature* 2001, **411**:199-204). They analyzed 19 random chromosomal regions, each of which centers around a core SNP (single length polymorphism) in the coding region of a gene. Extensive sequencing of 44 individuals from Utah identified 272 'high frequency' SNPs at 0-160 kilobases (kb) from the core SNP. The authors measured LD between two SNPs using the classical statistic  $D'$ . They found that the LD 'half length' (the distance at which the average  $D'$  value drops below 0.5) was about 60 kb, significantly longer than previous predictions. Similar LD estimates were found for US and north-European populations, but were markedly shorter (half-length of less than 5 kb) in a Nigerian population. The authors propose that large-scale LD analysis may be applied to disease gene mapping and the study of population history.

## References

1. Prospects for whole-genome linkage disequilibrium mapping of common disease genes.
2. *Nature*, [<http://www.nature.com>]
3. A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms.
4. On measures of gametic disequilibrium.