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Searching for genes targeted by selection in humans.

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Until very recently, the only practical approach to identify genes under recent positive selection has been to examine candidate genes. While candidate gene studies have had some successes, with the massive amounts of data becoming available, we can now take a much more powerful genomic approach to search for regions in the genome that have been under recent positive selection.

Maynard Smith & Haigh (1974) introduced the idea of the “selective sweep” – that regions surrounding a selectively favored gene show a decrease of genetic variation due to linkage along a chromosome. This basic principle has been utilized in numerous approaches to find genes targeted by selection, such as searching for reduction in genetic diversity, high-frequency derived alleles, frequency differences among populations, and extended haplotypes.

This project aims at testing new methods for finding genes targeted by selection in addition to some of the known methods. The new approaches include haplotype based statistics using sliding windows and statistics that capture high-frequency haplotypes that are unique to a population.

This search will utilize a dense genome-wide, world-wide, population-genetic data set consisting of >1000 individuals sampled from >50 population across the globe and each typed for >550,000 SNPs (Jakobsson et al. 2008, *Nature* 451: 998-1003; Li et al. 2008, *Science* 319:1100-1104). In total, the data consists of >600 million genotypes.

I am looking for a highly motivated individual who is interested in population genetics and computational biology. Quantitative skills are required and proficiency in some programming language (C, perl, matlab, R) would be very useful. The results are expected to be published in a scientific journal. The research environment is international, and the working language is English.

If you are interested in this project or have any other questions, please contact me at:
mattias.jakobsson@ebc.uu.se

Sincerely,

Mattias Jakobsson