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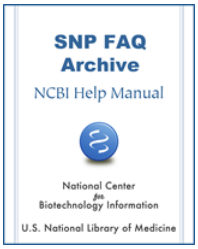
Bookshelf URL: https://www.ncbi.nlm.nih.gov/books/



Automated SNP Collection (Data Mining)

Created: July 23, 2005; Updated: February 18, 2014.

What parameters does dbSNP use to identify a SNP from a given nucleotide sequence?

Try looking in the SNP Handbook and the FAQ Archive for information on this subject. The FAQ archive contains a question that addresses automated SNP collection, and the handbook contains a table that lists all of methods of SNP discovery that our submitters use. (**3/14/06**).

Does dbSNP collect SNPs using automated SNP detection and external submissions, or do you also collect SNPs from peer-reviewed literature?

Currently, dbSNP does not have the staff to mine literature citations for new variation records, so we rely on the authors and editors involved in the publication process to submit their data to dbSNP.

Given the current levels of funding for dbSNP, I do not expect this policy to change in the near future. I would point out that other groups, such as the Cardiff Human Gene Mutation Database, have been actively compiling lists of variations from the literature for many years. The Cardiff dataset, however, is protected by copyright; therefore, Cardiff refuses permission to migrate the data to dbSNP.