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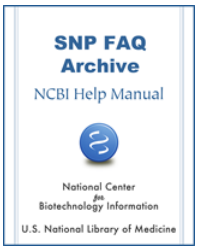

Links from Other Online Data Resources to dbSNP Reports

Created: July 7, 2005; Updated: February 18, 2014.

Can you explain the different types of Linkouts available in dbSNP?

Currently, there are two kinds of LinkOuts available on the dbSNP site:

- **NCBI LinkOut**: is established when a submitter contacts the NCBI LinkOut group and provides them with links back to the submitter. For example, Applied Biosystems has provided many links between dbSNP refSNPs and Applied Biosystems probes using NCBI LINKOUTs. This particular example shows a single linkout, but one SNP can have multiple linkouts.
- **dbSNP Linkout**: is established when a submitter provides a contact URL in their submission that provides additional information about the submitted SNP. A submitter may only submit a single linkout_url per submission. This url goes to the submitter's primary website, and if the submitter has additional links for the ss, they can be accessed there.

(**11/30/07**)

When I look at NM_205850 in Entrez Nucleotide, I'm unable to add "SNP" to the selected display features, but can add "SNP" to the selected display features for NM_005007.

We use a direct BLAST method to find reliable SNP hits, which entails building a BLAST database out of sequences of interest and conducting a BLAST search for all SNPs against this database.

Most of the SNPs we look for in this search were originally isolated in genomic rather than in mRNA sequence, so a BLAST search for genomic-based SNPs on mRNA sequences is problematic as it returns large gapped alignments between the SNP and the mRNA sequence. In the vast majority of cases, these large gaps occur where the query (SNP flanking) sequence aligns to the mRNA sequence (as in the case of NM_205850). Each gap reduces the quality alignment score for that alignment, and as a result, prevents the hit from being recorded in dbSNP, therefore causing the SNP annotation to the mRNA to fail.

We have tried a variety of approaches to improve this situation, and have settled upon using a projection method to annotate sequences that cannot be annotated using a direct BLAST alignment. This method "projects" hits between mRNAs and genomic sequences by using alignments of previously annotated contigs to the problematic sequences. This method, however, has its own pros and cons. It is much faster than direct BLAST and allows for the annotation of problem sequences, but it is not very accurate as it is based on several different alignments. Also, alignment quality scores are not available for this method and can only be estimated.

We are currently checking the software which implements projection method on various pairs of SNP and sequences and in next two weeks (if we see no critical errors) it will be moved into production as a part of annotation pipeline. (**8/7/07**)