

# NCBI2R: An R package to navigate and annotate genes and SNPs

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NCBI2R is a new R package that annotates lists of SNPs and/or genes, with current information from NCBI. Functions are provided that with one command will annotate the results from genome wide association studies to provide a broader context of their meaning. Other functions enable comparisons between a user's GWA results, and candidate snp/gene lists that are created from keywords, such as specific diseases, phenotypes or gene ontology terms. Commands are simple to follow and designed to work with R objects to integrate into existing workflows. The output produces text fields and weblinks to more information for items such as: gene descriptions, OMIM, pathways, phenotypes, and lists of interacting and neighboring genes. Annotation can then be used in R for further analysis, or the objects can be customized for use in spreadsheet programs or web browsers. The NCBI2R package was designed to allow those performing genome analysis to produce output that could easily be understood by a person not familiar with R.