NED, a script-based tool for annotating ChIP-seq peaks.

The script-based tool, NED (New gEne neighbourhooD), locates ChIP-seq peaks on a specific annotation. Since NED is a gene-oriented annotation system, it can identify simultaneous genes for each specific peak.
NED allows choosing the size of the regions before and after the Transcription Start Site (TSS) the genes, and identifies all the peaks that fall in the specified regions (see the figure). By using one or more annotations, the user can also detect all the peaks that fall in a particular genomic regions such as transcription factor sites, or other peaks derived by ChIP-seq experiments.
NED uses as input the peak location data generated by peak-calling tools (e.g. MACS, Zhang, et al., 2008) or any file in BED format, a specific annotation (e.g., RefSeq) and the ranges to be considered (e.g. 10000 bp before and 1000 bp after the TSS of the gene). A suffix for the output file (fileSuffix) is also required.
The output is a tab-delimited file with peak details, close genes and the distance between peak and gene.

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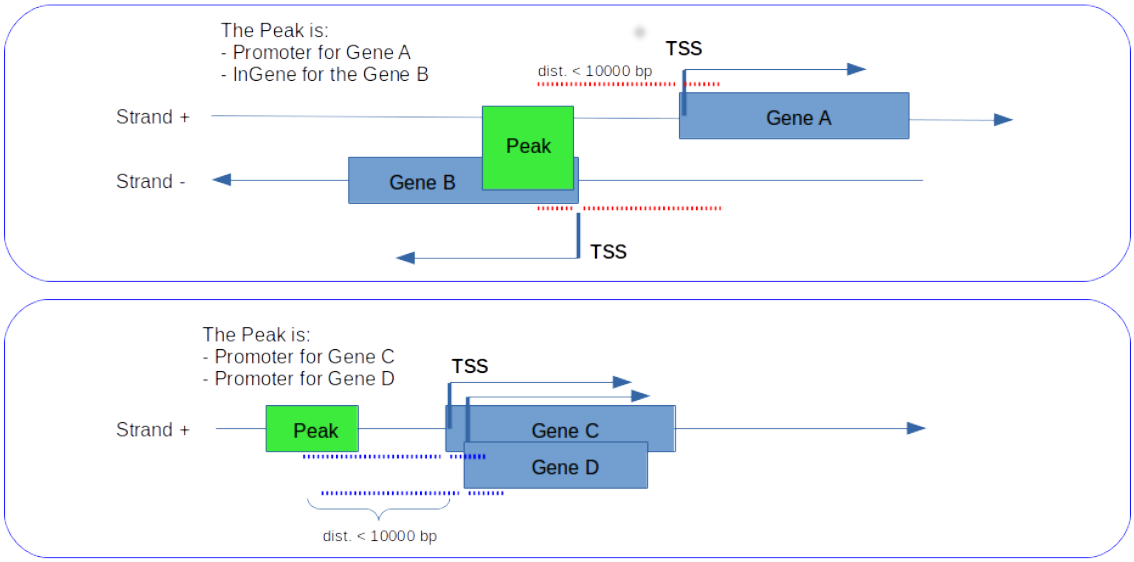
###Usage examples
# In this example NED defines “Promoters” the peaks that fall 10000 bp before
and 1000 bp after the TSS, and “inGene” the peaks that falls within the gene.
# perl Ned_0.13.pl peakFile.bed refSeq_hg19.csv fileSuffix 10000 1000
```



If you want to run an analysis by only considering the overlaps between the peaks and the annotated regions insert “overlap” as in the example:#perl Ned_0.13.pl peakFile.bed TFannotation.csv fileSuffix overlap