

Information of Packages adopted by iPDA

2007/4/13

BLAST	
Version	2.2.9-ia32-linux
Download	ftp://ftp.ncbi.nlm.nih.gov/blast/executables/
Input	seq.fa (Query sequence)
Output	seq.pssm (PSSM) ; seq.log (alignment)
Command	<code>./blastpgp -d db/nr -j 3 -i seq.fa -C seq.tmp -Q seq.pssm -m 9 > seq.log</code>
Comment	*Sequence alignment from nr.

ClustalW	
Version	1.8
Download	ftp://ftp.ebi.ac.uk/pub/software/unix/clustalw/clustalw1.8.UNIX.tar.gz
Input	seq.train (Query sequence and its homologous proteins)
Output	seq.aln (Multiple sequence alignment); seq.dnd (hierarchical tree)
Command	<code>./clustalw seq.train</code>
Comment	Use blast with E-value of 0.01 to find the homologous proteins of the query sequence. If there are less than four homologous proteins, blast will be executed with E-value of 10 to find more remote homologous ones of the query sequence.

WildSpan	
Version	0.1
Download	http://biominer.bime.ntu.edu.tw/wildspan/wildspan.tar.gz
Input	seq.train (Query sequence and its homologous proteins)
Output	seq.cons (Concurrent conserved residues)
Command	<code>./wildspan seq.train -d seq -b 3 -e 3 -k 1 -t 60 -T 600 -q -O -v</code>
Comment	The user-defined parameters for iterative-wildspan: -b : number of blocks -k : number of pattern *Find homology from SwissProt v50.

Jnet	
Version	0.1
Download	http://www.compbio.dundee.ac.uk/~www-jpred/jnet/download/jnet.linux.tar.gz
Input	seq.fa (Query sequence)
Output	seq.jnet
Command	./jnet -z seq.fa > seq.jnet
Comment	

PSIPred	
Version	2.5
Download	http://bioinf.cs.ucl.ac.uk/downloads/psipred/psipred25.tar.gz
Input	seq.fa (Query sequence)
Output	seq.ss2; seq.horiz
Command	./runpsipred seq.fa
Comment	*Generate PSSM from uniref90

CARD	
Version	1.0
Download	http://bioinfo.knu.ac.kr/research/CARD/
Input	seq.fa (Query sequence)
Output	seq.card
Command	./card seq.fa 30 15 30 > seq.card
Comment	

CD-HIT	
Version	2.0.4 beta
Download	http://bioinformatics.org/download.php/cd-hit/cd-hit-Mar-08-04.tar.gz
Input	seq.fa (Query sequence)
Output	seq.card
Command	./card seq.fa 30 15 30 > seq.card
Comment	