Pfeature Library

Pfeature is a comprehensive package which will allow users to compute most of the protein features that have been discovered over the past decades. Using different functional modules of this package, users will be able to access six major categories of protein features:

- i) Composition-based features
- ii) Binary profile of sequences
- iii) Evolutionary information based features
- iv) Structural descriptors
- v) Pattern based descriptors
- vi) Model building

Additionally, users will also be able to generate these features for sub-parts of protein/peptide sequences. This will be helpful to annotate structure, function and therapeutic properties of proteins.

Users can access the webserver for Pfeature at: https://webs.iiitd.edu.in/raghava/pfeature/

Usage of functions as follows:

Name of the Function	Function call	
Composition	Composition Based Features	
Amino-acid Composition	aac_wp(inputfile,outputfile)	
Amino-acid Composition of N-Terminal	aac_nt(inputfile,outputfile,number)	
Amino-acid Composition of C-Terminal	aac_ct(inputfile,outputfile,number)	
Amino-acid Composition of Rest	aac_rt(inputfile,outputfile,number1,number2)	
Amino-acid Composition of N- and C-Terminal	aac_nct(inputfile,outputfile,number)	
Amino-acid Composition of split	aac_st(inputfile,outputfile,number)	
Dipeptide Composition	dpc_wp(inputfile,outputfile,order)	
Dipeptide Composition of N-Terminal	dpc_nt(inputfile,outputfile,number,order)	
Dipeptide Composition of C-Terminal	dpc_ct(inputfile,outputfile,number,order)	
Dipeptide Composition of Rest	dpc_rt(inputfile,outputfile,number1,number2,order)	
Dipeptide Composition of N- and C-Terminal	dpc_nct(inputfile,outputfile,number,order)	
Dipeptide Composition of split	dpc_st(inputfile,outputfile,lambda,number_of_splits)	
Tripeptide Composition	tpc_wp(inputfile,outputfile)	
Tripeptide Composition of N-Terminal	tpc_nt(inputfile,outputfile,number)	
Tripeptide Composition of C-Terminal	tpc_ct(inputfile,outputfile,number)	
Tripeptide Composition of Rest	tpc_rt(inputfile,outputfile,number1,number2)	
Tripeptide Composition of N- and C-Terminal	tpc_nct(inputfile,outputfile,number)	
Tripeptide Composition of split	tpc_st(inputfile,outputfile,number)	
Atom Composition	atc_wp(inputfile,outputfile)	
Atom Composition of N-Terminal	atc_nt(inputfile,outputfile,number)	
Atom Composition of C-Terminal	atc_ct(inputfile,outputfile,number)	
Atom Composition of Rest	atc_rt(inputfile,outputfile,number1,number2)	

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atc_nct(inputfile,outputfile,number)
atc_st(inputfile,outputfile ,number)
btc_wp(inputfile,outputfile)
btc_nt(inputfile,outputfile,number)
btc_ct(inputfile,outputfile,number)
btc_rt(inputfile,outputfile,number1,number2)
btc_nct(inputfile,outputfile,number)
btc_st(inputfile,outputfile ,number)
pcp_wp(inputfile,outputfile)
non nt/inputfile outputfile number)
pcp_nt(inputfile,outputfile,number)
pcp_ct(inputfile,outputfile,number)
pcp_rt(inputfile,outputfile,number1,number2)
pcp_nct(inputfile,outputfile,number)
pcp_st(inputfile,outputfile ,number)
aai_wp(inputfile,outputfile)
aai_nt(inputfile,outputfile,number)
aai_ct(inputfile,outputfile,number)
aai_rt(inputfile,outputfile,number1,number2)
aai_nct(inputfile,outputfile,number)
aai_st(inputfile,outputfile ,number)
rri_wp(inputfile,outputfile)
rri_nt(inputfile,outputfile,number)
rri_ct(inputfile,outputfile,number)
rri_rt(inputfile,outputfile,number1,number2)
rri_nct(inputfile,outputfile,number)
rri_st(inputfile,outputfile ,number)
ddr_wp(inputfile,outputfile)
ddr_nt(inputfile,outputfile)
ddr_ct(inputfile,outputfile)
ddr_rt(inputfile,outputfile)
ddr_nct(inputfile,outputfile)
ddr_st(inputfile,outputfile, number of splits)
pri_wp(inputfile,outputfile)
pri_nt(inputfile,outputfile,number)
pri_ct(inputfile,outputfile,number)
pri_rt(inputfile,outputfile,number1,number2)

Physico-chemical properties repeat Composition of	pri_nct(inputfile,outputfile,number)
N- and C-Terminal	pri_neninpatrie,outputrie,numoer)
Physico-chemical properties repeat Composition of Split	pri_st(inputfile,outputfile ,number)
Shannon Entropy	sep_wp(inputfile,outputfile)
Shannon Entropy of N-Terminal	sep_nt(inputfile,outputfile,number)
Shannon Entropy of C-Terminal	sep_ct(inputfile,outputfile,number)
Shannon Entropy of Rest	sep_rt(inputfile,outputfile,number1,number2)
Shannon Entropy of N- and C-Terminal	sep_nct(inputfile,outputfile,number)
Shannon Entropy of Split	sep_st(inputfile,outputfile ,number)
Shannon Entropy of Residue Level	ser_wp(inputfile,outputfile)
Shannon Entropy of Residue Level for N-Terminal	ser_nt(inputfile,outputfile,number)
Shannon Entropy of Residue Level for C-Terminal	ser_ct(inputfile,outputfile,number)
Shannon Entropy of Residue Level for Rest	ser_rt(inputfile,outputfile,number1,number2)
Shannon Entropy of Residue Level for N-Terminal	ser_nct(inputfile,outputfile,number)
Shannon Entropy of Residue Level for Split	ser_st(inputfile,outputfile,number)
Shannon Entropy of Physicochemical Property	spc_wp(inputfile,outputfile)
Shannon Entropy of Physicochemical Property for	spc_nt(inputfile,outputfile,number)
N- Terminal	spc_nt(inputme,outputme,number)
Shannon Entropy of Physicochemical Property for	spc_ct(inputfile,outputfile,number)
C- Terminal Shannon Entropy of Physicochemical Property for	
Rest	spc_rt(inputfile,outputfile,number1,number2)
Shannon Entropy of Physicochemical Property for	spc_nct(inputfile,outputfile,number)
N- and C-Terminal	
Shannon Entropy of Physicochemical Property for Split	spc_st(inputfile,outputfile,number)
Autocorrelation	acr_wp(inputfile,outputfile,lag)
Autocorrelation of N-Terminal	acr_nt(inputfile,outputfile,number,lag)
Autocorrelation of C-Terminal	acr_ct(inputfile,outputfile,number,lag)
Autocorrelation of Rest	acr_rt(inputfile,outputfile,number1,number2,lag)
Autocorrelation of N- and C-Terminal	acr_nct(inputfile,outputfile,number,lag)
Autocorrelation of Split	acr_st(inputfile,outputfile,number,lag)
Conjoint Triad Calculation	ctc_wp(inputfile,outputfile)
Conjoint Triad Calculation for N-Terminal	ctc_nt(inputfile,outputfile,number)
Conjoint Triad Calculation for C-Terminal	ctc_ct(inputfile,outputfile,number)
Conjoint Triad Calculation for Rest	ctc_rt(inputfile,outputfile,number1,number2)
Conjoint Triad Calculation for N- and C-Terminal	ctc_nct(inputfile,outputfile,number)
Conjoint Triad Calculation for Split	ctc_st(inputfile,outputfile,number)
Composition enhanced Transition Distribution	ctd_wp(inputfile,outputfile)
Composition enhanced Transition Distribution of	
N-Terminal	ctd_nt(inputfile,outputfile,number)
Composition enhanced Transition Distribution of	ctc_ct(inputfile,outputfile,number)
C-Terminal	

Composition enhanced Transition Distribution of Rest	ctd_rt(inputfile,outputfile,number1,number2)
Composition enhanced Transition Distribution of N- and C-Terminal	ctd_nct(inputfile,outputfile,number)
Composition enhanced Transition Distribution	ctd_st(inputfile,outputfile ,number)
Pseudo Amino-acid Composition	paac_wp(inputfile,outputfile,lamda,weight)
Pseudo Amino-acid Composition of N-Terminal	paac_nt(inputfile,outputfile,number,lamda,weight)
Pseudo Amino-acid Composition of C-Terminal	paac_ct(inputfile,outputfile,number,lamda,weight)
Pseudo Amino-acid Composition of Rest	paac_rt(inputfile,outputfile,number1,number2,lamda,weight)
Pseudo Amino-acid Composition of N- and C- Terminal	paac_nct(inputfile,outputfile,number,lamda,weight)
Pseudo Amino-acid Composition of split	paac_st(inputfile,outputfile,lambda,number)
Amphiphilic Pseudo Amino-acid Composition	apaac_wp(inputfile,outputfile,lamda,weight)
Amphiphilic Pseudo Amino-acid Composition of N- Terminal	apaac_nt(inputfile,outputfile,number,lamda,weight)
Amphiphilic Pseudo Amino-acid Composition of C- Terminal	apaac_ct(inputfile,outputfile,number,lamda,weight)
Amphiphilic Pseudo Amino-acid Composition of Rest	apaac_rt(inputfile,outputfile,number1,number2,lamda, weight)
Amphiphilic Pseudo Amino-acid Composition of N- and C-Terminal	apaac_nct(inputfile,outputfile,number,lamda,weight)
Amphiphilic Pseudo Amino-acid Composition of split	<pre>apaac_st(inputfile,outputfile,number1,number2,lamda, weight)</pre>
Quasi-Sequence Order	qos_wp(inputfile,outputfile,gap,weight)
Quasi-Sequence Order of N-Terminal	qos_nt(inputfile,outputfile,number,gap,weight)
Quasi-Sequence Order of C-Terminal	qos_ct(inputfile,outputfile,number,gap,weight)
Quasi-Sequence Order of Rest	qos_rt(inputfile,outputfile,number1,number2,gap,weight)
Quasi-Sequence Order of N- and C-Terminal	qos_nct(inputfile,outputfile,number,gap,weight)
Quasi-Sequence Order of split	qos_st(inputfile,outputfile,Number_of_splits,gap,weight)
Sequence Order Coupling	soc_wp(inputfile,outputfile,gap)
Sequence Order Coupling for N-Terminal	soc_nt(inputfile,outputfile,number,gap)
Sequence Order Coupling for C-Terminal	soc_ct(inputfile,outputfile,number,gap)
Sequence Order Coupling for Rest	<pre>soc_rt(inputfile,outputfile,number1,number2,gap)</pre>
Sequence Order Coupling for N- and C-Terminal	<pre>soc_nct(inputfile,outputfile,number,gap)</pre>
Sequence Order Coupling of split	soc_split(inputfile,outputfile,Number_of_splits,gap)
Binary Profi	le Based Features
Binary Profile of amino acid	aab_wp(inputfile,outputfile)
Binary Profile of N-Terminal amino acid	aab_nt(inputfile,outputfile,number)
Binary Profile of C-Terminal of amino acid	aab_ct(inputfile,outputfile,number)
Binary Profile of rest of amino acid	<pre>aab_rt(inputfile,outputfile,number1,number2)</pre>
Binary Profile of N- and C-Terminal amino acid	aab_nct(inputfile,outputfile,number)
Binary Profile of split of amino acid	aab_st(inputfile,outputfile,number)

Binary Profile of Dipeptide	dpb_wp(inputfile,outputfile,order)	
Dipeptide Binary Profile of N-Terminal	dbp_nt(inputfile,outputfile,number,order)	
Dipeptide Binary Profile of C-Terminal	dpb_ct(inputfile,outputfile,number,order)	
Dipeptide Binary Profile of Rest	dpb_rt(inputfile,outputfile,number1,number2,order)	
Dipeptide Binary Profile of N- and C-Terminal	dbp_nct(inputfile,outputfile,number,order)	
Dipeptide Binary Profile of Split	dpb_st(inputfile,outputfile,lag,Number_of_splits)	
Atomic Binary Profile	atb_wp(inputfile,outputfile)	
Atomic Binary Profile of N-Terminal	atb_nt(inputfile,outputfile,number)	
Atomic Binary Profile of C-Terminal	atb_ct(inputfile,outputfile,number)	
Atomic Binary Profile of rest	atb_rt(inputfile,outputfile,number1,number2)	
Atomic Binary Profile of N- and C-Terminal	atb_nct(inputfile,outputfile,number)	
Atomic Binary Profile of split	atb_st(inputfile,outputfile ,Number_of_splits)	
Binary Profile of bond	btb_wp(inputfile,outputfile)	
Bonds Binary Profile of N-Terminal	btb_nt(inputfile,outputfile,number)	
Bonds Binary Profile of C-Terminal	btb_ct(inputfile,outputfile,number)	
Bonds Binary Profile of N. and C. Tarminal	btc_rt(inputfile,outputfile,number1,number2)	
Bonds Binary Profile of N- and C-Terminal	btb_nct(inputfile,outputfile,number)	
Bonds Binary Profile of split	btb_st(inputfile,outputfile ,number_of_splits)	
Binary Profile of Physicochemical Property	pcb_wp(inputfile,outputfile)	
Binary Profile of Physicochemical Property of N-Terminal	pcb_nt(inputfile,outputfile,number)	
Binary Profile of Physicochemical Property of C-	pcb_ct(inputfile,outputfile,number)	
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Binary Profile of Physicochemical Property of Rest	pcb_rt(inputfile,outputfile,number1,number2)	
Binary Profile of Physicochemical Property of N-and C-Terminal	pcb_nct(inputfile,outputfile,number)	
Binary Profile of Physicochemical Property of Split	pcb_st(inputfile,outputfile,number_of_splits)	
Binary Profile of AAIndex	aib_wp(inputfile,outputfile)	
Binary Profile of AAIndex of N-Terminal	aib_nt(inputfile,outputfile,number)	
Binary Profile of AAIndex of C-Terminal	aib_ct(inputfile,outputfile,number)	
Binary Profile of AAIndex of Rest	aib_rt(inputfile,outputfile,number1,number2)	
Binary Profile of AAIndex of N- and C-Terminal	aib_nct(inputfile,outputfile,number)	
Binary Profile of AAIndex of split	aib_st(inputfile,outputfile,number_of_splits)	
PSSM Ba	sed Features	
PSSM composition	pssm_comp(inputfile,outputfile)	
Normalization of PSSM profile using method 1	pssm_n1(inputfile,outputfile)	
Normalization of PSSM profile using method 2	pssm_n2(inputfile,outputfile)	
Normalization of PSSM profile using method 3	pssm_n3(inputfile,outputfile)	
Normalization of PSSM profile using method 4	pssm_n4(inputfile,outputfile)	
Pattern Based Features		
Binary Profile of generated pattern	pat_bin(inputfile,outputfile,window_length)	
Physico-chemical properties composition of generated pattern	pat_pcp(inputfile,outputfile,window_length)	
Pattern generated from sequences	pat_str(inputfile,outputfile,window_length)	
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Pattern generated from CSV file	pat_csv(inputfile,outputfile,window_length)
Amino acid index composition of generated pattern	pat_aai(inputfile,outputfile,window_length)