Supplementary S7 – Web Server Description

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Caution

This online service is developed on Python, Django, Celery and Redis. Three message queues with different priorities are used to handle three different time-consuming tasks.

For security reasons, no part of the site's functionality will be open sourced. If you encounter any problems or are interested in the development of this online service, please contact me¹.

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1. Introduction

The web server consists of three functions:

- Classification function, calculating whether the two ncRNAs are in the same family. When the sequences in the FASTA format of the two RNAs are input by a user, the server obtains similarities between two ncRNAs and evaluate whether they are in the same family.
- 2) Clustering function, clustering of multiple sequences based on a classification matrix and affinity propagation algorithm. The clustering function implements the derivation of bulk ncRNA family attribution and makes the classification matrix available for download, allowing users to further build phylogenetic trees based on the classification matrix, etc.
- 3) Batch feature extraction function. For the batch sequence input by users, features can be extracted automatically. For those who just want to use multi-view features, we provide unmatched feature extraction, where the extracted features can be applied to the study of multi-categorization of ncRNA and the study of interactions with ncRNA and protein.

The web server is available at <u>http://bmbl.sdstate.edu/gcfm/</u>. The web server has been tested on several different browsers, including Microsoft Internet Explorer, Mozilla Firefox, Google Chrome and MacOS safari and also on Android OS.

This supplementary file provides a brief instruction to display the usage of the web server of GCFM.

GCF14	
Bioinformatics Function 2	
Intro Classification Clustering Extraction Download About&Help	
Function 1 Function 3	
Abstract	
Motivation	
Non-coding RNAs (ncRNAs) play crucial roles in multiple biological processes. However, only a few ncRNAs' functions have been well stud Given the significance of ncRNAs classification for understanding ncRNAs' functions, more and more computational methods have be introduced to improve the classification automatically and accurately. Result	.ed. een
In this paper, based on a convolutional neural network and a deep forest algorithm, multi-grained cascade forest (GcForest), we propose a n deep fusion learning framework, GcForest fusion method (GCFM), to classify alignments of ncRNA sequences for accurate clustering of ncRNA Gregates a multi-view structure faeture representation including sequence-structure alignment encoding, structure image representation and shape alignment encoding of structural subunits, enabling us to capture the potential specificity between ncRNAs. For the classificatio pairwise alignment of two ncRNA sequences, the F-value of GCFM improves 6% than an existing alignment-based method. Furthermore, clustering of ncRNA families is cared on the classification matrix generated from GCFM. Results suggest better performance (with 2 Accuracy improved) than existing ncRNA clustering methods (RNAclust, Ensembleclust, and CNNclust). Additionally, we apply GCFM to const a phylogenetic ree of ncRNA and predict the probability of interactions between RNAs. Most ncRNAs are located correctly in the phylogenetic ree, and the prediction Accuracy of RNA interaction is 90.63%.	ovel As. ion, the 0% ruct etic





2. Classification function

Predict if the two sequences belong to the same ncRNA family. First, click on the "**Classification**" button to go to the classification function page. Next, enter the sequence in the two text boxes in step two. Click on the "**Run**" button. The results will be displayed in the "**Result**" area.

GC	GCFM Bioinformatics					
Intro	Classification	Clustering	Extraction	Download	About&Help	
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Seque	ence2		Step T	wo		
GTG1 ATGC	TCGCTTTGGC/	AGCATGTGT AGGATGAC	ATTAAGATT	GCACCAATA TGTGAAGTC	CAGAGAAGA GTTTAATTTAA	TTAGG AA
S	Step Three (Run		Clear]	
They	belong to the sa	ame family				
Exam	Result	t				
>RNU6_8 GCACTCA TCCCTAT	96P_ENST00000362376.1 ACTTCAGCAGCACATATAC TTTT	TAAAATTGGAAGGAT/	ACAGACAAGATTAGC	ATGTTCCCTGTGCAA	GCATGACATGTAAATTT	GTGAAGCAT
>RNU6_1 GTGTTCC GTTTAAT	197P_ENST00000391183.1 SCTTTGGCAGCATGTGTAT TTAAAA	TAAGATTGCACCAAT/	ACAGAGAAGATTAGG	ATGGCCCCAGTGCC	AGGATGACACACAAATT	TGTGAAGT
>SNORD1 GCCAAA1	17_ENST00000584949.1 GATGTTTATTTGAAACAGG	AGCACCTCAGTGCA	AGGACGACTCTTATC	TATCACCCATGACT	GATGGCT	
>SNORD1 GGATGG/	16_28_ENST00000516123. ATGACGACTTAAAAATGAA	1 CTCGTTGGAATCTG	AGCAAAACGAGTGA	GCAAACCACTTCTGT	GCAGTTCTGTGAACTG	AGGTCA

3. Clustering function

First, click on the "**Clustering**" button to go to the clustering function page. Next enter multiple sequences in the text box in step two or click the "**Browse**" button to upload a file containing the sequences in fasta format. Then click on the "**Run**" button to create the task and get the Job ID, which is displayed in the "**Job ID**" area. Click "**Copy**" to copy the Job ID, check the status and get the results in the Download page.

Intro	Classification	Clustering	Extraction	Download	About&Help	
Cluste	ering based on c	lassification m	atrix			
GGG GGAU	A_AIA_AGC_II_ GAAUUAGCUC JCGAUGCCCG A_AIa_AGC_13 GAAUUAGCUC	_ I AAAUGGUAG CAUUCUCCA _1		GCUUAGCAL	JGCGAGAGG	UAGCG
GGG GGAU >tRN/ GGG <u>GGA</u> U	JCGAUGCCCA A_Ala_AGC_13 GAAUUAGCUC JCGAUGCCCA	CAUUCUCCA _2 AAGCGGUAG CAUUCUCCA	GAGCGCUU	GCUUAGCAU	JGCAAGAGG	UAGUG
GGGI GGAI >tRN/ GGGI GGAI	JCGAUGCCCA A_Ala_AGC_13 GAAUUAGCUC JCGAUGCCCA	AAGCGGUAG _2 AAGCGGUAG CAUUCUCCA	GAGCGCUU	GCUUAGCA	JGCAAGAGG	UAGUG UAGUG tep Tr
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4. Batch feature extraction function

First, click on the "**Extraction**" button to go to the extraction function page. Next enter multiple sequences in the text box in step two or click the "**Browse**" button to upload a file containing the sequences in fasta format. Then click on the "**Run**" button to create the task and get the Job ID, which is displayed in the "**Job ID**" area. Click "**Copy**" to copy the Job ID, check the status and get the results in the Download page.

	GCFM Bioinformatics		Step One		
Intro	Classification	Clustering	Extraction	Download	About&Help
Multi-	view feature extr	action			
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GGG	GAAUUAGCUC/	-' AAAUGGUA(GAGCGCUCG	GCUUAGCAL	JGCGAGAGGUAGC
GGAI	JCGAUGCCCG	CAUUCUCC	A		
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>tRN, GGG GGAI Or uploa	A_Ala_AGC_13_ GAAUUAGCUC/ JCGAUGCCCA(ad fasta file here:	2 AAGCGGUAG CAUUCUCCA Step Thr Run 5bd4de8f-0	GAGCGCUUC A 'ee 	Clear 0617467549	JGCAAGAGGUAGU Step 1 Brows

5. Download

The download page provides four main functions.

 Query the status of the job created by the clustering and feature extraction functions.

Operation:

Firstly, click on the "**Download**" button to go to the Download function page. Next, enter the Job ID number in the Job ID box in Step two. Then click on the "**Query**" button to view the status in the "Job Status" area. If the task status is successful, you can download the relevant data by clicking on the blue link.

- Clustering and feature extraction results can be downloaded when the task is completed.
- 3) View clustering results online.

Note:

When the query is for a clustering job, the corresponding content is displayed in the "Classification Matrix" and "Clustering Results" areas.

4) Download source code and related data.

Note:

The download link can be found at the bottom of the Download page.

Job query and result download Input your job ID: Step Two Job Status Step Three Your job is successful Download by elick this line (but/rest-leads-tredstor/200) Step Four Classification matrix: 	Classification C	lustering	Extractio	on Do	ownload	Abou	it&Help
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Name Class tRNA_Ala_AGC_11_1 0 tRNA_Ala_AGC_13_1 0 tRNA_Ala_AGC_13_2 0 tRNA_Ala_AGC_8_1 0 tRNA_Ala_TGC_3_1 0 RF00019_ENST0000365176.1 1 RF00019_ENST0000365512.1 1 RF00019_ENST0000365512.1 1		[0, 0, 1, 0	, 0, 0, 0, 0, 0, 0,	0, 1, 1, 1,	, , ,]		
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Image: transformed state transformed state <thtradit at="" state<="" th="" the=""> transform state</thtradit>			Ala_AGC_13	_2		0	
RF00019_ENST00000365176.1 1 RF00019_ENST00000363041.1 1 RF00019_ENST00000365512.1 1 RF00019_ENST00000365512.1 1 RF00019_ENST000003652554.1 1		tRNA	Ala TGC 3	<u>-'</u> 1		0	Clustering
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RF00019_ENST00000411339.1 1 Results RF00019_ENST00000365512.1 1 RF00019_ENST00000362554.1 1		RF00019_E	NST000036	3041.1		1	
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SNORA80D ENST0000384488.1 2		SNORA80D	ENST000003	384488.1		2	
SNORA70H_ENST00000383910.1 2		SNORA70H_	ENST000003	383910.1		2	
SNORA16A_ENST00000628458.1 2		SNORA16A	ENST00000	628458.1		2	
SNORA21_ENST00000362423.1 2		SNORA21_E	ENST000003	62423.1		2	
		SINOKADUB_	ENS100005	11198.2		2)