PEA-m6A User Manual (version 1.0)

- PEA-m6A is an ensemble learning framework for predicting m6A modifications at regional-scale.
- PEA-m6A consists of four modules:**Sample Preparation, Feature Encoding, Model Development and Model Assessment**, each of which contains a comprehensive collection of functions with pre-specified parameters available.
- PEA-m6A was powered with an advanced packaging technology, which enables compatibility and portability.
- PEA-m6A project is hosted on http://github.com/cma2015/PEA-m6A
- PEA-m6A docker image is available at http://hub.docker.com/r/malab/peam6a
- PEA-m6A server can be accessed via http://peam6a.omstudio.cloud

PEA-m6A Model Development

This module contains the **Prediction System Constrction** used to construct an RNA modification predictor at region-scale and provides predictive function among 12 plant species.

Functions	Description	Input	Output	Reference
Prediction System Constrction	construct an RNA modification predictor at region-scale and provides predictive function among 12 plant species.	Positive feature matrix and negative feature matrix	A predictor and model evaluation results	In-house scripts

Prediction System Constrction

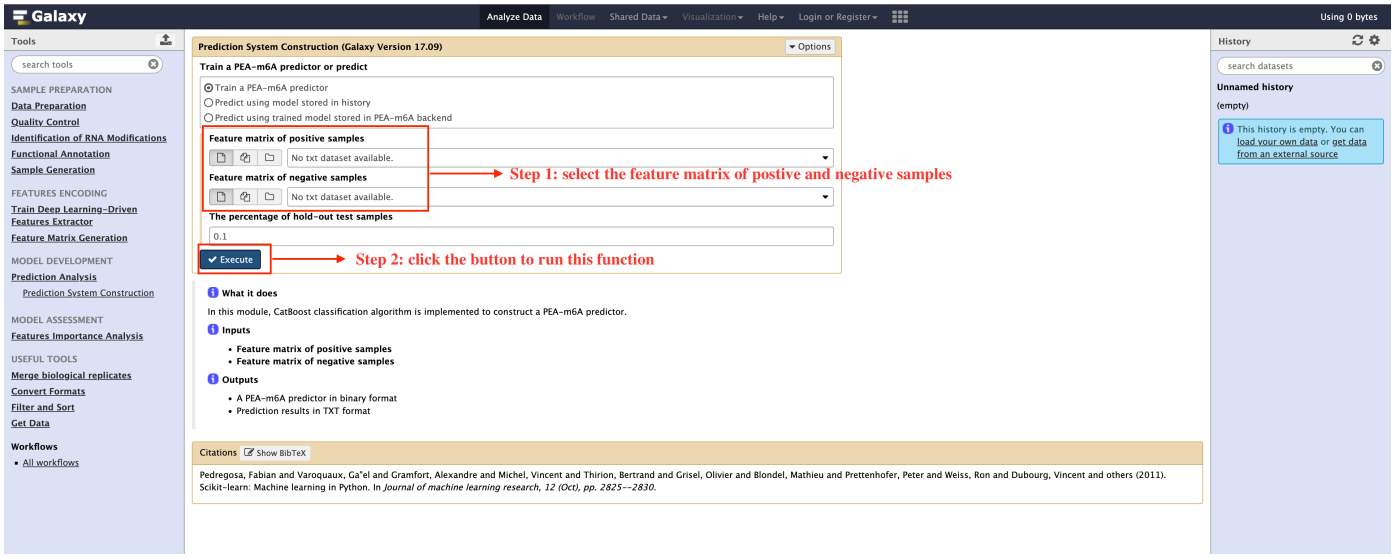
This function contains the **Prediction System Constrction** used to construct an RNA modification predictor at region-scale and provides predictive function among 12 plant species.

Input

- **Feature matrix of positive samples**
- **Feature matrix of negative samples**

Output

- An RNA modification predictor in binary format


Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Help
Login or Register
Using 0 bytes
Tools
search tools
SAMPLE PREPARATION
Data Preparation
Quality Control
Identification of RNA Modifications
Functional Annotation
Sample Generation
FEATURES ENCODING
Train Deep Learning-Driven Features Extractor
Feature Matrix Generation
MODEL DEVELOPMENT
Prediction Analysis
Prediction System Construction
MODEL ASSESSMENT
Features Importance Analysis
USEFUL TOOLS
Merge biological replicates
Convert Formats
Filter and Sort
Get Data
Workflows
All workflows
Prediction System Construction (Galaxy Version 17.09)
Options
Train a PEA-m6A predictor or predict
Train a PEA-m6A predictor
Predict using model stored in history
Predict using trained model stored in PEA-m6A backend
Feature matrix of positive samples
No txt dataset available.
Feature matrix of negative samples
No txt dataset available.
Step 1: select the feature matrix of postive and negative samples
The percentage of hold-out test samples
0.1
Execute
Step 2: click the button to run this function
What it does
In this module, CatBoost classification algorithm is implemented to construct a PEA-m6A predictor.
Inputs
Feature matrix of positive samples
Feature matrix of negative samples
Outputs
A PEA-m6A predictor in binary format
Prediction results in TXT format
Citations
Show BibTeX
Pedregosa, Fabian and Varoquaux, Ga"el and Gramfort, Alexandre and Michel, Vincent and Thirion, Bertrand and Grisel, Olivier and Blondel, Mathieu and Prettenhofer, Peter and Weiss, Ron and Dubourg, Vincent and others (2011). Scikit-learn: Machine learning in Python. In Journal of machine learning research, 12 (Oct), pp. 2825--2830.
History
search datasets
Unnamed history
(empty)
This history is empty. You can load your own data or get data from an external source