

Package: ASmiR (via r-universe)

October 28, 2026

Type Package

Title Prediction of Abiotic Stress-Specific miRNAs in Plants

Version 0.1.1

Description Provides functions for predicting plant microRNAs (miRNAs) associated with cold, drought, heat, and salt stress using the ASmiR machine learning framework. Implements PseKNC feature generation and stress-specific support vector machine models described by Pradhan et al. (2023), ``ASmiR: a machine learning framework for prediction of abiotic stress-specific miRNAs in plants'', Functional & Integrative Genomics, 23(2), article 92, <[doi:10.1007/s10142-023-01014-2](https://doi.org/10.1007/s10142-023-01014-2)>.

License GPL-3

Encoding UTF-8

Depends R (>= 4.1.0)

Imports Biostrings, e1071, stats

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Config/roxygen2/version 8.1.0

SystemRequirements Python (>= 3.7)

NeedsCompilation no

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asmir_check_python	<i>Check Python Runtime</i>
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Description

Checks whether a Python executable is available for the ASmiR PseKNC feature-generation workflow. The executable can be configured with the ASMiR_PYTHON environment variable.

Usage

```
asmir_check_python()
```

Value

Returns TRUE invisibly when Python can be invoked; otherwise raises an error.

asmir_features	<i>Generate ASmiR PseKNC Features</i>
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Description

Generates the PseKNC feature representation used by ASmiR for validated plant miRNA sequences. This function invokes the bundled Python feature-generation script and requires Python 3.

Usage

```
asmir_features(x)
```

Arguments

x Input supported by [asmir_read_fasta](#).

Value

A numeric matrix with 1,379 feature columns and one row per input sequence.

asmir_model_files	<i>Locate ASmiR Model Files</i>
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Description

Returns paths to the bundled stress-specific support vector machine models and feature-ranking files used by ASmiR.

Usage

```
asmir_model_files(stress = c("cold", "drought", "heat", "salt", "all"))
```

Arguments

stress	Stress model to locate: cold, drought, heat, salt, or all.
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Value

A named character vector containing paths to the model and feature-ranking files for the requested stress model or models.

asmir_predict	<i>Predict Abiotic Stress Association of miRNA Sequences</i>
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Description

Predicts whether input plant miRNA sequences are associated with cold, drought, heat, or salt stress using the bundled ASmiR models. The function generates PseKNC features and applies the relevant stress-specific model.

Usage

```
asmir_predict(  
  x,  
  stress = c("cold", "drought", "heat", "salt", "all"),  
  threshold = 0.5,  
  model_file = NULL,  
  feature_file = NULL  
)
```

Arguments

x	Input supported by asmir_read_fasta .
stress	Stress model to use: cold, drought, heat, salt, or all.
threshold	Numeric probability threshold between 0 and 1 for assigning the stress-associated class.
model_file	Optional path to an RDS model file, used when predicting a single stress.
feature_file	Optional path to a feature-ranking file, used when predicting a single stress.

Value

A data frame containing sequence names, stress labels, predicted stress probabilities, confidence-like probabilities, and predicted class labels.

asmir_read_fasta	<i>Read ASmiR FASTA Input</i>
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Description

Converts a FASTA file, compatible data frame, or character vector of sequences into the standardized sequence data frame used by ASmiR.

Usage

asmir_read_fasta(x)

Arguments

x	A FASTA file path, a data frame containing sequence identifier and sequence columns, or a character vector of RNA sequences.
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Value

A data frame with sequence_id and sequence columns.

`asmir_validate_sequences`*Validate ASmiR RNA Sequences*

Description

Checks whether input sequences are non-empty and contain only the RNA nucleotide symbols A, U, G, and C.

Usage

```
asmir_validate_sequences(x)
```

Arguments

`x` Input supported by [asmir_read_fasta](#).

Value

A data frame containing sequence identifiers, sequence lengths, validity flags, and validation messages.

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