

# Package: ASmiR (via r-universe)

October 29, 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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**Config/pak/sysreqs** python3 zlib1g-dev

**Repository** <https://ukpradhan.r-universe.dev>

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**RemoteUrl** <https://github.com/cran/ASmiR>

**RemoteRef** HEAD

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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.

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|                |                                       |
|----------------|---------------------------------------|
| 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.

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|                   |                                 |
|-------------------|---------------------------------|
| 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. |
|--------|------------------------------------------------------------|

**Value**

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

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|               |                                                              |
|---------------|--------------------------------------------------------------|
| 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 <a href="#">asmir_read_fasta</a> .                                    |
| 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.

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|                  |                               |
|------------------|-------------------------------|
| 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. |
|---|------------------------------------------------------------------------------------------------------------------------------|

**Value**

A data frame with sequence\_id and sequence columns.

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`asmir_validate_sequences`*Validate ASmiR RNA Sequences*

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**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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