

# Package ‘snpAIMeR’

July 23, 2025

**Type** Package

**Title** Assess the Diagnostic Power of Genomic Marker Combinations

**Version** 2.1.1

**Description** Population genetics package for designing diagnostic panels.

Candidate markers, marker combinations, and different panel sizes are assessed for how well they can predict the source population of known samples. Requires a genotype file of candidate markers in STRUCTURE format. Methods for population cross-validation are described in Jombart (2008)  [<doi:10.1093/bioinformatics/btn129>](https://doi.org/10.1093/bioinformatics/btn129).

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**URL** <https://github.com/OksanaVe/snpAIMeR>

**Depends** R (>= 2.10)

**Imports** adegenet, doParallel, dplyr, forcats, foreach, ggplot2, graphics, magrittr, parallel, readr, tidyr, utils, withr, yaml

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Encoding** UTF-8

**RoxygenNote** 7.3.1

**NeedsCompilation** no

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### Description

Population genetics package for optimizing diagnostic panels. User-selected candidate markers are assessed individually and in combination for how well they can predict the source population of known samples. Requires a genotype file in STRUCTURE format.

### Usage

```
snpAIMeR(run_mode, config_file = NULL, verbose = TRUE)
```

### Arguments

|             |                                                                                   |
|-------------|-----------------------------------------------------------------------------------|
| run_mode    | Modes are "interactive", "non-interactive", or "example"; mode must be in quotes. |
| config_file | Yaml file required for "non-interactive" mode; filename/path must be in quotes.   |
| verbose     | Default is TRUE.                                                                  |

### Details

Yaml file format for "non-interactive" mode (do not include bullet points):

- min\_range: <minimum panel size>
- max\_range: <maximum panel size; we recommend no more than 15 markers>
- assignment\_rate\_threshold: <value from 0 to 1>
- cross\_validation\_replicates: <we recommend 100 minimum>
- working\_directory: <path name in quotes>
- structure\_file: <path name in quotes>
- number\_of\_individuals: <same as adegenet's "n.ind">
- number\_of\_loci: <same as adegenet's "n.loc">
- one\_data\_row\_per\_individual: <TRUE or FALSE>
- column\_sample\_IDs: <column number>
- column\_population\_assignments: <column number>
- column\_other\_info: <column number>
- row\_markernames: <row number>
- no\_genotype\_character: <default is "-9">
- optional\_population\_info: <optional>

- `genotype_character_separator`: <optional>

Minimizing run time: Because of the number of possible combinations, we recommend testing no more than 15 markers. For example, testing 15 markers in panel sizes of 1 to 15 (32,767 total combinations) with 1,000 cross-validation replicates on a system with 48 processor cores took about 5 hours and 20 GB RAM. Reducing the number of cross-validation replicates will reduce run time, however, we recommend no less than 100 replicates.

**Value**

Cross-validation assignment rates for individual markers, marker combinations, and panel sizes. Outputs three .csv and two .pdf files to a user-specified directory.

**See Also**

<https://github.com/OksanaVe/snpAIMeR>

**Examples**

```
if (requireNamespace("adeigenet", quietly = TRUE)) {  
  data(nancycats, package = "adeigenet")  
  snpAIMeR("example", verbose = TRUE)  
}
```

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