

Package: OryzaProbe (via r-universe)

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Type Package

Title Convert Rice Microarray Probe IDs to RAP-DB Gene IDs

Version 0.2.0

Description Converts probe identifiers from the rice microarray platforms GPL6864, GPL8852, and GPL2025 to targets from the Rice Annotation Project Database (RAP-DB). Conversion preserves input order, reports unmapped and non-RAP annotations, handles one-to-many mappings explicitly, and can combine multiple probes per target using the mean, maximum, or minimum.

License GPL-3

Encoding UTF-8

Depends R (>= 3.6)

RoxygenNote 7.3.2

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

URL <https://github.com/lym-bioinfo/OryzaProbe>,
<https://cran.r-project.org/package=OryzaProbe>

BugReports <https://github.com/lym-bioinfo/OryzaProbe/issues>

Repository <https://lym-bioinfo.r-universe.dev>

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probe_annotation	<i>Inspect the bundled probe annotation</i>
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Description

Returns an inspectable copy of the annotation used by OryzaProbe.

Usage

probe_annotation(platform)

Arguments

platform One supported GEO platform accession.

Value

A data frame with probe_id, target_id, and status. GPL8852 returns an empty table because its target is parsed from the composite row name rather than looked up in a bundled table.

probe_annotation_metadata	<i>Inspect annotation provenance</i>
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Description

The bundled GPL6864 and GPL2025 tables are preserved from OryzaProbe 0.1.0. This function makes that legacy provenance explicit so analyses can record the exact annotation snapshot they used.

Usage

probe_annotation_metadata()

Value

A data frame describing the mapping source and method for each supported platform.

`probe_conversion_report`*Inspect a probe conversion*

Description

Returns the row-level audit report attached to a converted expression matrix.

Usage

```
probe_conversion_report(x)
```

Arguments

`x` A matrix returned by `probe_convert()` or `probeConvert()`.

Value

A data frame with the source probe, original annotation, resolved target, status, inclusion flag, and output row ID.

`probe_conversion_summary`*Summarize a probe conversion*

Description

Returns summary metadata attached to a converted expression matrix.

Usage

```
probe_conversion_summary(x)
```

Arguments

`x` A matrix returned by `probe_convert()` or `probeConvert()`.

Value

A named list containing platform, input and output row counts, mapping-status counts, dropped rows, and aggregation method.

probe_convert	<i>Convert rice microarray probe IDs to annotated targets</i>
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Description

Converts probe IDs stored in expression-matrix row names to targets from the annotation bundled with OryzaProbe. Conversion preserves input order, records an auditable row-level report, and can merge probes that resolve to one target.

Usage

```
probe_convert(
  x,
  platform = "auto",
  merge_by = "none",
  unmapped = "keep",
  non_rap = "keep",
  multi_mapping = "keep",
  na_rm = FALSE,
  quiet = FALSE
)
```

Arguments

x	A numeric matrix or data frame. Row names must contain probe IDs.
platform	One of "auto", "GPL6864", "GPL2025", or "GPL8852". Automatic detection uses all row names. Supplying the platform explicitly is recommended for production analyses.
merge_by	One of "none", "mean", "max", or "min".
unmapped	How probes without a target should be handled: keep the original probe ID, drop the row, or raise an error.
non_rap	How annotations that are not canonical RAP-DB gene IDs should be handled: keep, drop, or raise an error.
multi_mapping	How targets containing multiple IDs separated by /// should be handled: keep the combined label, use the first target, expand the row once per target, drop it, or raise an error.
na_rm	Whether missing values should be removed during aggregation. If every value in a group is missing, the result remains NA.
quiet	If TRUE, suppress the conversion summary message.

Value

A numeric matrix with class `oryza_probe_matrix` and unique row names. Use `probe_conversion_report()` to inspect how each input row was handled.

Examples

```
expression <- matrix(
  c(2, 4, 6, 8),
  nrow = 2,
  dimnames = list(c("36144", "37310"), c("sample_1", "sample_2"))
)

converted <- probe_convert(
  expression,
  platform = "GPL6864",
  merge_by = "mean"
)
converted
probe_conversion_report(converted)
```

probeConvert

Backward-compatible probe conversion interface

Description

Preserves the original OryzaProbe function name and its first three arguments. New code should prefer `probe_convert()`, whose options make annotation edge cases explicit.

Usage

```
probeConvert(
  exprMatrix,
  probeMerge = FALSE,
  mergeBy = "mean",
  platform = "auto",
  unmapped = "keep",
  na.rm = FALSE,
  quiet = FALSE,
  ...
)
```

Arguments

<code>exprMatrix</code>	A numeric matrix or data frame with probe IDs as row names.
<code>probeMerge</code>	Whether probes resolving to the same target should be merged.
<code>mergeBy</code>	Aggregation method used when <code>probeMerge = TRUE</code> .
<code>platform</code>	Platform name or "auto".
<code>unmapped</code>	How unmapped probes should be handled.
<code>na.rm</code>	Whether missing values should be removed during aggregation.
<code>quiet</code>	Whether the conversion summary should be suppressed.
<code>...</code>	Additional arguments passed to <code>probe_convert()</code> , such as <code>non_rap</code> and <code>multi_mapping</code> .

Value

A numeric matrix; see `probe_convert()`.

Examples

```
expression <- matrix(
  1:4,
  nrow = 2,
  dimnames = list(c("13", "12"), c("sample_1", "sample_2"))
)
probeConvert(expression, platform = "GPL6864")
```

supported_platforms	<i>List supported rice microarray platforms</i>
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Description

Lists the platforms accepted by OryzaProbe's conversion functions.

Usage

```
supported_platforms()
```

Value

A character vector of supported GEO platform accessions.

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