

Package: wickragenome (via r-universe)

October 7, 2026

Type Package

Title A Vector Database of the Market over the Streaming Indicators

Version 0.2.0

Description R bindings for wickra-genome over its C ABI hub: every asset a live vector over the streaming indicators, with similarity search, clustering and anomaly detection - byte-identical to the CLI and every other binding.

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URL <https://github.com/wickra-lib/wickra-genome>

BugReports <https://github.com/wickra-lib/wickra-genome/issues>

Depends R (>= 4.1)

Encoding UTF-8

NeedsCompilation yes

SystemRequirements the wickra-genome C ABI shared library (WKGENOME_LIB) and its header (WKGENOME_INC).

Config/roxygen2/version 8.0.0

Repository <https://wickra-lib.r-universe.dev>

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RemoteUrl <https://github.com/wickra-lib/wickra-genome>

RemoteRef v0.2.0

RemoteSha 672042ce26d4808cf749979fd5d31a7a4bfa0f3c

RemoteSubdir bindings/r

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wkgenome_command	<i>Apply a command JSON and return the resulting response JSON.</i>
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Description

Apply a command JSON and return the resulting response JSON.

Usage

```
wkgenome_command(genome, cmd_json)
```

Arguments

genome	A genome handle from [wkgenome_new()].
cmd_json	A command JSON string ('build', 'feed', 'vector', 'similar', 'cluster', 'anomaly', 'version').

Value

The response as a JSON string.

wkgenome_new	<i>Build a genome handle from a spec JSON.</i>
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Description

Build a genome handle from a spec JSON.

Usage

```
wkgenome_new(spec_json)
```

Arguments

spec_json	A 'GenomeSpec' JSON string (a non-empty 'features' and 'symbols').
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Value

A 'wickra_genome' handle (an external pointer).

wkgenome_version	<i>The wickra-genome library version.</i>
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Description

The wickra-genome library version.

Usage

```
wkgenome_version()
```

Value

A version string.

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