

Package ‘r4subpharma’

September 11, 2026

Title 'pharmaverse' Adapters for R4SUB Submission Readiness Evidence

Version 0.1.0

Description Bridges the 'pharmaverse' clinical reporting stack and the R4SUB (Ready for Submission) ecosystem. Converts 'metacore' metadata objects and ADaM (Analysis Data Model) datasets - such as those built with 'admiral' - into standardized R4SUB evidence table rows via 'r4subcore', so that submission readiness can be scored with 'r4subscore' without changing an existing pharmaverse pipeline.

License MIT + file LICENSE

URL <https://r4sub.github.io/r4subpharma/>,
<https://github.com/R4SUB/r4subpharma>

BugReports <https://github.com/R4SUB/r4subpharma/issues>

Depends R (>= 4.2)

Imports cli, r4subcore, tibble

Suggests knitr, metacore, pharmaverseadam, r4subdata, r4subprofile,
r4subscore, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.3.3

NeedsCompilation no

Author Pawan Rama Mali [aut, cre, cph] (ORCID:
<<https://orcid.org/0000-0001-7864-5819>>)

Maintainer Pawan Rama Mali <prm@outlook.in>

Repository CRAN

Date/Publication 2026-09-11 13:00:02 UTC

Contents

adam_to_evidence	2
as_variable_metadata	3
metacore_to_evidence	4
submission_readiness	5
Index	6

adam_to_evidence	<i>Convert an ADaM Dataset to Submission Readiness Evidence</i>
------------------	---

Description

Compares a built ADaM dataset - such as one produced by an 'admiral' pipeline

- against its metadata and emits R4SUB evidence rows about conformance. The checks are computed directly from the dataset and metadata, so they work whether or not the dataset was passed through 'xport' or 'metatools'.

Usage

```
adam_to_evidence(
  data,
  metadata,
  ctx,
  dataset_name = NULL,
  source_name = "adam",
  source_version = NULL
)
```

Arguments

data	A data.frame: one ADaM dataset.
metadata	A Metacore object or a data.frame accepted by as_variable_metadata() .
ctx	An r4subcore::r4sub_run_context providing run and study identifiers.
dataset_name	Character or NULL. Which dataset in metadata to check data against. May be omitted when the metadata covers a single dataset.
source_name	Character. Label recorded as the evidence source. Default "adam".
source_version	Character or NULL. Optional version label.

Details

Four indicators are evaluated:

T-ADAM-001 Each variable described in the metadata is present in the dataset (traceability).

T-ADAM-002 Each dataset column is described in the metadata; columns that are not are flagged (traceability).

Q-ADAM-001 Present variables have the data type family the metadata specifies (quality).

Q-ADAM-002 Present variables carry a non-empty label attribute (usability).

Value

A data.frame conforming to the R4SUB evidence schema.

See Also

`metacore_to_evidence()`, `submission_readiness()`

Examples

```
# Check the CDISC pilot ADSL from pharmaverseadam against the ADaM metadata
# shipped in r4subdata.
ctx <- suppressMessages(r4subcore::r4sub_run_context("CDISCPIL0T01", "DEV"))
ev <- suppressMessages(adam_to_evidence(
  pharmaverseadam::adsl,
  r4subdata::adam_metadata,
  ctx,
  dataset_name = "ADSL"
))
table(ev$indicator_id, ev$result)
```

as_variable_metadata *Coerce Metadata to the Variable-Metadata Contract*

Description

Normalizes the accepted metadata inputs into a single tidy table with one row per dataset variable. A metacore object is unpacked into its dataset, variable, and derivation components; a data.frame is checked for the required dataset and variable columns and completed with any missing optional columns.

Usage

```
as_variable_metadata(metadata)
```

Arguments

metadata	Either a Metacore object or a data.frame with at least the columns dataset and variable. Optional columns label, type, origin, derivation, and is_derived are used when present.
----------	--

Value

A [tibble](#) with columns dataset, variable, label, type, origin, derivation, and is_derived.

Examples

```
# The example ADaM metadata shipped in r4subdata.
meta <- as_variable_metadata(r4subdata::adam_metadata)
head(meta)
```

metacore_to_evidence *Convert Metadata to Submission Readiness Evidence*

Description

Turns dataset metadata - either a metacore object or a plain data.frame - into standardized R4SUB evidence rows describing how completely each variable is documented. This lets metadata assembled for a 'pharmaverse' pipeline feed the same evidence table and Submission Confidence Index as any other source.

Usage

```
metacore_to_evidence(
  metadata,
  ctx,
  source_name = "metacore",
  source_version = NULL
)
```

Arguments

metadata	A Metacore object or a data.frame accepted by as_variable_metadata() .
ctx	An r4subcore::r4sub_run_context providing run and study identifiers.
source_name	Character. Label recorded as the evidence source. Default "metacore".
source_version	Character or NULL. Optional version label for the metadata source.

Details

Two indicators are evaluated, reusing the identifiers emitted by [r4subcore::define_xml_to_evidence\(\)](#) so that metadata- and Define-XML-sourced evidence group together in scoring and explainability:

Q-DEFINE-002 Variable is documented (has a label and a data type).

Q-DEFINE-003 Derivation text is present for derived variables.

Value

A data.frame conforming to the R4SUB evidence schema.

See Also

[adam_to_evidence\(\)](#), [submission_readiness\(\)](#)

Examples

```
# The example ADaM metadata shipped in r4subdata.
ctx <- suppressMessages(r4subcore::r4sub_run_context("STUDY01", "DEV"))
ev <- suppressMessages(metacore_to_evidence(r4subdata::adam_metadata, ctx))
table(ev$indicator_id, ev$result)
```

submission_readiness *Score Submission Readiness for a 'pharmaverse' Deliverable*

Description

A single entry point that harvests evidence from metadata and one or more ADaM datasets and, when 'r4subscore' is available, computes the Submission Confidence Index (SCI) in one call. It is the fastest way to go from a 'pharmaverse' pipeline to a readiness score.

Usage

```
submission_readiness(data, metadata, ctx, config = NULL)
```

Arguments

data	A named list of ADaM data.frames (names are dataset identifiers, e.g. "ADSL"), or a single data.frame when the metadata covers one dataset.
metadata	A Metacore object or a data.frame accepted by as_variable_metadata() .
ctx	An r4subcore::r4sub_run_context providing run and study identifiers.
config	An optional sci_config (see r4subscore::sci_config_default()). When NULL, the r4subscore default is used.

Value

An object of class "submission_readiness": a list with evidence (the combined evidence data.frame), pillar_scores, and sci (an sci_result, or NULL if 'r4subscore' is not installed).

See Also

[metacore_to_evidence\(\)](#), [adam_to_evidence\(\)](#)

Examples

```
# Score the CDISC pilot ADSL against the ADaM metadata in r4subdata.
ctx <- suppressMessages(r4subcore::r4sub_run_context("CDISCPIL0T01", "DEV"))
res <- suppressMessages(submission_readiness(
  list(ADSL = pharmaverseadam::adsl),
  r4subdata::adam_metadata,
  ctx
))
nrow(res$evidence)
```

Index

adam_to_evidence, [2](#)
adam_to_evidence(), [4](#), [5](#)
as_variable_metadata, [3](#)
as_variable_metadata(), [2](#), [4](#), [5](#)

metacore_to_evidence, [4](#)
metacore_to_evidence(), [3](#), [5](#)

r4subcore::r4sub_run_context, [2](#), [4](#), [5](#)
r4subcore::sci_config_default(), [5](#)

submission_readiness, [5](#)
submission_readiness(), [3](#), [4](#)

tibble, [3](#)