

Package: rwevalidate (via r-universe)

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Title Validate Patient Cohorts for Real-World Evidence Studies on the OMOP Common Data Model

Version 0.1.2

Description Validates instantiated patient cohorts on an Observational Medical Outcomes Partnership (OMOP) Common Data Model (CDM) database for real-world-evidence (RWE) studies. From a single function call it produces a structured validation report in Hypertext Markup Language (HTML) and JavaScript Object Notation (JSON) covering concept coverage, cohort attrition, temporal data density, and covariate feasibility against a comparator. The checks are aligned with the United States Food and Drug Administration (FDA) guidance on real-world data and evidence, FDA (2023) <<https://www.fda.gov/media/171667/download>>, the Harmonized Protocol Template to Enhance Reproducibility (HARPER), Wang and others (2022) <[doi:10.1002/pds.5507](https://doi.org/10.1002/pds.5507)>, and the Reporting of Studies Conducted Using Observational Routinely-Collected Data for Pharmacoepidemiology (RECORD-PE) statement, Langan and others (2018) <[doi:10.1136/bmj.k3532](https://doi.org/10.1136/bmj.k3532)>. A self-contained example database is bundled so the checks can be run without a live database connection.

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URL <https://github.com/tavakohr/rwevalidate>

BugReports <https://github.com/tavakohr/rwevalidate/issues>

Encoding UTF-8

Language en-US

Depends R (>= 4.1)

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build_check_summary	<i>Build the traffic-light validation summary table</i>
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Description

Collects each module’s flags into one row per validation section, mapping to the regulatory framework the section addresses.

Usage

build_check_summary(results)

Arguments

results The combined results list (named module outputs, e.g. attrition, density).
 Modules absent from the list are skipped.

Value

A data.frame with columns section, status, maps_to, detail.

cdm_connect*Connect to an OMOP CDM database*

Description

Opens a PostgreSQL connection via RPostgres and validates that the required clinical tables (person, observation_period, condition_occurrence, drug_exposure, measurement, visit_occurrence, death) exist in cdm_schema and the vocabulary tables (concept, concept_ancestor) exist in vocab_schema before returning. For split-schema CDMs (clinical and vocabulary in different schemas) pass vocab_schema; it defaults to cdm_schema for single-schema builds.

Usage

```
cdm_connect(  
  host = "localhost",  
  port = 5432,  
  dbname,  
  user,  
  password,  
  cdm_schema,  
  vocab_schema = cdm_schema  
)
```

Arguments

host	Database host. Default "localhost".
port	Database port. Default 5432.
dbname	Database name.
user	Database user.
password	Database password.
cdm_schema	Schema holding the clinical CDM tables.
vocab_schema	Schema holding the vocabulary tables. Defaults to cdm_schema.

Value

A live DBI connection to the CDM database.

Examples

```
## Not run:  
# Requires a live PostgreSQL OMOP CDM server and real credentials, so this  
# cannot be executed during checks. For a runnable, database-free demo of  
# the package, see example_cdm() and validate_cohort().  
con <- cdm_connect(  
  dbname = "omop", user = "me", password = "secret",  
  cdm_schema = "mimiciv_omop", vocab_schema = "vocab"
```

```
)
cdm_disconnect(con)

## End(Not run)
```

cdm_disconnect	<i>Disconnect from a CDM database</i>
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Description

Disconnect from a CDM database

Usage

```
cdm_disconnect(con)
```

Arguments

con A live DBI connection returned by `cdm_connect()`.

Value

Invisibly returns the result of `DBI::dbDisconnect()`.

Examples

```
# Works on any DBI connection, demonstrated here on the bundled in-memory
# DuckDB example CDM (no database server needed).
if (requireNamespace("duckdb", quietly = TRUE)) {
  con <- example_cdm()
  cdm_disconnect(con)
}
```

classify_status	<i>Classify a vector of module flags into a traffic-light status</i>
-----------------	--

Description

Flags are strings prefixed "FAIL:" or "WARN:" (see the module functions). Any FAIL -> "fail" (red); else any WARN -> "warn" (amber); else "pass" (green).

Usage

```
classify_status(flags)
```

Arguments

flags Character vector of flag messages (may be empty).

Value

A single string: "pass", "warn", or "fail".

example_cdm

Create a small in-memory OMOP CDM for examples and demos

Description

Builds a tiny synthetic OMOP CDM (20 persons) in an in-memory DuckDB database and returns a live connection. Every table rwevalidate queries for the concept, attrition, density, and covariate modules is populated, together with a cohort table that has the standard subject_id, cohort_definition_id, cohort_start_date, and cohort_end_date columns. The cohort table carries two arms so all four modules can be demonstrated: persons 1-10 are the target cohort (cohort_definition_id = 1) and persons 11-20 are a comparator (cohort_definition_id = 2). The clinical tables and a minimal vocabulary both live in the default main schema.

Usage

```
example_cdm()
```

Details

This exists so the package can be tried, and its examples can run, without a live database connection. It is a synthetic demo fixture, not a substitute for a real CDM. The duckdb package (a soft dependency) must be installed. The caller owns the returned connection and should close it with `cdm_disconnect()`.

Value

A live DBI connection to an in-memory DuckDB OMOP CDM.

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
  con <- example_cdm()
  attrition <- run_attrition(con, cdm_schema = "main",
                           cohort_table = "cohort", cohort_id = 1,
                           vocab_schema = "main")
  print(attrition$cohort_size)
  cdm_disconnect(con)
}
```

render_validation_report

Render the validation report (HTML) and write the JSON sidecar

Description

Renders the bundled R Markdown template to a self-contained HTML report and writes a machine-readable `validation_results.json` alongside it.

Usage

```
render_validation_report(
  results,
  output_dir,
  cdm_schema,
  cohort_id,
  package_version = as.character(utils::packageVersion("rwevalidate")),
  run_date = Sys.time(),
  quiet = TRUE
)
```

Arguments

<code>results</code>	Combined results list (e.g. <code>list(attrition = ..., density = ...)</code>), optionally <code>data_source = ...</code>).
<code>output_dir</code>	Directory to write the report into (created if needed).
<code>cdm_schema</code>	CDM schema name (for the report header / JSON).
<code>cohort_id</code>	Cohort definition id (for the report header / JSON).
<code>package_version</code>	Package version string. Defaults to the installed <code>rwevalidate</code> version.
<code>run_date</code>	Timestamp for the run. Defaults to <code>base::Sys.time()</code> .
<code>quiet</code>	Passed to <code>rmarkdown::render()</code> . Default TRUE.

Value

Invisibly, a list with `html`, `json`, and `check_summary`.

Description

Profiles an instantiated cohort: size, index-date distribution, prior observation coverage, and demographics at index. Maps to HARPER section 5 and RECORD-PE item 6. All thresholds are arguments.

Usage

```
run_attrition(
  con,
  cdm_schema,
  cohort_table,
  cohort_id,
  obs_window = c(-365, 0),
  vocab_schema = "vocab",
  obs_warn_pct = 70,
  obs_fail_pct = 50,
  attrition_warn_threshold = 0.5
)
```

Arguments

con	A live DBI connection (see cdm_connect()).
cdm_schema	Schema holding the clinical CDM tables (e.g. "mimic_cdm").
cohort_table	Cohort table, schema-qualified (e.g. "results.rwevalidate_test_cohort"). Must have columns subject_id, cohort_definition_id, cohort_start_date, cohort_end_date.
cohort_id	Integer cohort definition id to profile.
obs_window	Length-2 numeric c(pre, post) in days relative to index. The required prior-observation window is abs(obs_window[1]) days (default 365).
vocab_schema	Schema holding the vocabulary tables (concept). In this split-schema environment the clinical schema's concept table is empty, so the gender label is resolved from vocab_schema. Default "vocab".
obs_warn_pct, obs_fail_pct	Prior-observation coverage thresholds (percent of cohort with sufficient prior observation). Below obs_warn_pct flags WARN, below obs_fail_pct flags FAIL. Defaults 70 and 50.
attrition_warn_threshold	Reserved for stepwise inclusion-criteria attrition (single-criterion drop fraction). Not exercised in v0.1 because criteria lists are not yet a supported input. Default 0.5.

Details

This profiles the cohort as it was handed in. It reports the cohort-level counts that item 6 asks for, but it does not yet rebuild a step-by-step attrition flowchart (how many subjects each inclusion or exclusion criterion removed), because the cohort table does not carry the criteria that built it. Per-criterion attrition is planned for a later version.

Value

A named list:

cohort_size integer - distinct subjects in the cohort

index_date_summary data.frame of index_year, n

obs_coverage data.frame: cohort_n, n_sufficient, pct_sufficient, min_prior_days. cohort_n counts every cohort subject. A subject whose index date falls outside any observation period counts as insufficient prior observation rather than being dropped, so cohort_n matches cohort_size.

demographics data.frame: sex, mean_age, min_age, max_age, n

flags character vector of WARN:/FAIL: messages (empty if all pass)

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
  con <- example_cdm()
  res <- run_attrition(con, cdm_schema = "main", cohort_table = "cohort",
                      cohort_id = 1, vocab_schema = "main")

  res$cohort_size
  res$demographics
  cdm_disconnect(con)
}
```

run_concepts

Module 1 - Concept Coverage

Description

Profiles whether the cohort-defining concepts are present, well-mapped, and richly represented in the CDM. Maps to FDA RWE Relevance (are the data fit for the question?). This is the first module to read the vocabulary schema.

Usage

```
run_concepts(
  con,
  cdm_schema,
  cohort_table = NULL,
  cohort_id = NULL,
```



```

    concept_ids,
    domain = "condition",
    vocab_schema = "vocab",
    prevalence_warn_pct = 10,
    prevalence_fail_pct = 1,
    unmapped_warn_pct = 20
  )

```

Arguments

<code>con</code>	A live DBI connection (see <code>cdm_connect()</code>).
<code>cdm_schema</code>	Schema holding the clinical CDM tables.
<code>cohort_table</code>	Cohort table, schema-qualified. Optional and currently unused; reserved for cohort-restricted prevalence in a later version.
<code>cohort_id</code>	Integer cohort definition id. Optional and reserved, see <code>cohort_table</code> .
<code>concept_ids</code>	Numeric vector of cohort-defining seed concept id(s). Their descendants are expanded via <code>{vocab_schema}.concept_ancestor</code> .
<code>domain</code>	Domain the seed concepts live in; one of the names of the internal domain map ("condition", "drug", "measurement", "procedure"). Default "condition".
<code>vocab_schema</code>	Schema holding the vocabulary tables. Default "vocab".
<code>prevalence_warn_pct, prevalence_fail_pct</code>	Concept-prevalence thresholds (percent of CDM persons with at least one descendant record). Below warn flags WARN, below fail flags FAIL. Defaults 10 and 1.
<code>unmapped_warn_pct</code>	Per-domain unmapped-record threshold (percent mapped to <code>concept_id = 0</code>) above which a WARN is flagged. Default 20.

Value

A named list:

prevalence data.frame: `n_with`, `n_total`, `pct`

ancestor_coverage data.frame: `total_descendants`, `present_descendants`, `pct_present`

mapping_by_domain data.frame: `domain`, `n_records`, `n_unmapped`, `pct_mapped`

flags character vector of WARN:/FAIL: messages

Examples

```

if (requireNamespace("duckdb", quietly = TRUE)) {
  con <- example_cdm()
  # 316139 = "Heart failure" (SNOMED), the seed concept in the demo CDM.
  res <- run_concepts(con, cdm_schema = "main", concept_ids = 316139,
                     domain = "condition", vocab_schema = "main")
  res$prevalence
  res$mapping_by_domain
  cdm_disconnect(con)
}

```

run_covariates

Module 4 - Covariate Feasibility

Description

Compares a target cohort against a comparator on baseline covariates: standardized mean differences (SMD love-plot data), a per-arm prevalence table, and a simple power calculation. Maps to HARPER Sec.4 (comparability). Runs only when a comparator_id is supplied.

Usage

```
run_covariates(
  con,
  cdm_schema,
  cohort_table,
  cohort_id,
  comparator_id,
  vocab_schema = "vocab",
  covariate_window = c(-365, 0),
  top_n = 20,
  smd_warn_threshold = 0.1,
  power_baseline_rate = 0.15,
  power_effect_rate = 0.3,
  power_sig_level = 0.05,
  power_warn_threshold = 0.8
)
```

Arguments

con	A live DBI connection (see cdm_connect()).
cdm_schema	Schema holding the clinical CDM tables.
cohort_table	Cohort table, schema-qualified, containing both arms.
cohort_id	Integer cohort definition id of the target arm.
comparator_id	Integer cohort definition id of the comparator arm.
vocab_schema	Schema holding the vocabulary tables. Default "vocab".
covariate_window	Length-2 numeric c(pre, post) days defining the baseline window relative to index for comorbidity/drug covariates. Default c(-365, 0).
top_n	Number of top conditions/drugs to profile. Default 20.
smd_warn_threshold	Absolute SMD above which a covariate is flagged imbalanced. Default 0.1 (standard).
power_baseline_rate, power_effect_rate	Assumed comparator and target event rates for the two-proportion power calculation. Defaults 0.15, 0.30.

power_sig_level

Significance level for the power calculation. Default 0.05.

power_warn_threshold

Power below this value flags a WARN. Default 0.80.

Value

A named list: `smd_table`, `prevalence_table`, `power`, `flags`.

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
  con <- example_cdm()
  # The demo CDM ships two arms: target = 1, comparator = 2.
  res <- run_covariates(con, cdm_schema = "main", cohort_table = "cohort",
                        cohort_id = 1, comparator_id = 2, vocab_schema = "main")
  res$smd_table
  res$power
  cdm_disconnect(con)
}
```

run_density

Module 3 - Temporal Data Density

Description

Profiles longitudinal data accrual around the index date: record density per patient per month across clinical domains, and follow-up completeness with a censoring-reason breakdown. Maps to FDA RWE Reliability (data accrual).

Usage

```
run_density(
  con,
  cdm_schema,
  cohort_table,
  cohort_id,
  obs_window = c(-365, 365),
  sparse_warn_min = 1
)
```

Arguments

<code>con</code>	A live DBI connection (see cdm_connect()).
<code>cdm_schema</code>	Schema holding the clinical CDM tables (e.g. "mimic_cdm").
<code>cohort_table</code>	Cohort table, schema-qualified.

cohort_id Integer cohort definition id.

obs_window Length-2 numeric c(pre, post) in days relative to index. Density is computed for records inside [index + pre, index + post]. Default c(-365, 365).

sparse_warn_min Minimum total records a domain must have within the window before it is considered present; domains below this flag WARN (likely missing/sparse domain). Default 1 (flag only truly empty domains).

Value

A named list:

density_by_domain data.frame: domain, months_from_index, n_patients, n_records, records_per_patient

followup_summary data.frame: one row per censoring_reason with n and median_followup_days (median over that group)

followup_detail per-subject data.frame: subject_id, effective_end_date, followup_days, censoring_reason

flags character vector of WARN:/FAIL: messages

Examples

```
if (requireNamespace("duckdb", quietly = TRUE)) {
  con <- example_cdm()
  res <- run_density(con, cdm_schema = "main", cohort_table = "cohort",
                    cohort_id = 1)
  head(res$density_by_domain)
  res$followup_summary
  cdm_disconnect(con)
}
```

validate_cohort

Validate a patient cohort for real-world-evidence use

Description

One-call entry point: connects to the OMOP CDM (or uses a supplied connection), runs the attrition (Module 2) and temporal-density (Module 3) checks, and produces a self-contained HTML report plus a JSON sidecar aligned with FDA RWE and HARPER frameworks.

Usage

```
validate_cohort(
  cdm_schema,
  cohort_table,
  cohort_id = 1,
  con = NULL,
  vocab_schema = "vocab",
```

```

concept_ids = NULL,
concept_domain = "condition",
comparator_id = NULL,
obs_window = c(-365, 0),
density_window = c(-365, 365),
output_dir = "./validation_report",
host = "localhost",
port = 5432,
dbname = NULL,
user = NULL,
password = NULL,
render_html = TRUE,
quiet = TRUE
)

```

Arguments

cdm_schema	Schema holding the clinical CDM tables (e.g. "mimic_cdm").
cohort_table	Cohort table, schema-qualified (e.g. "results.rwevalidate_test_cohort").
cohort_id	Integer cohort definition id. Default 1.
con	Optional open DBI connection. If NULL (default) one is opened from the connection arguments and closed on exit.
vocab_schema	Schema holding the vocabulary tables. Default "vocab". Required because the clinical schema's concept table may be empty in split-schema builds.
concept_ids	Optional numeric vector of cohort-defining seed concept id(s). When supplied, Module 1 (concept coverage) runs and populates report Section 2. When NULL (default) Module 1 is skipped.
concept_domain	Domain the seed concepts live in ("condition", "drug", "measurement", "procedure"). Default "condition".
comparator_id	Optional integer cohort definition id of a comparator arm. When supplied, Module 4 (covariate feasibility) runs and populates report Section 5. When NULL (default) Module 4 is skipped.
obs_window	Length-2 numeric c(pre, post) days for attrition prior observation. Default c(-365, 0).
density_window	Length-2 numeric c(pre, post) days for density. Default c(-365, 365).
output_dir	Directory for the report + JSON. Default "./validation_report".
host, port, dbname, user, password	PostgreSQL connection arguments, used only when con is NULL.
render_html	Render the HTML report. Default TRUE. If Pandoc is unavailable, only the JSON sidecar is written (with a warning).
quiet	Passed to <code>rmarkdown::render()</code> . Default TRUE.

Details

Supply either an open con (e.g. for DuckDB testing) or PostgreSQL connection arguments (dbname, user, password, ...). Connections opened internally are closed on exit; a connection passed in via con is left open.

Against a live PostgreSQL OMOP CDM, a typical call looks like:

```
validate_cohort(
  cdm_schema = "mimic_cdm",
  cohort_table = "results.rwevalidate_test_cohort",
  cohort_id = 1,
  dbname = "FHIR", user = "me", password = "secret",
  vocab_schema = "vocab",
  output_dir = "./validation_report"
)
```

Value

Invisibly, a list with results (module outputs + data_source), report (paths + check summary), and flags (all collected flags).

Examples

```
# Runnable demo on a small in-memory DuckDB CDM (no database needed).
# render_html = FALSE writes only the JSON sidecar, so Pandoc is not required.
if (requireNamespace("duckdb", quietly = TRUE)) {
  con <- example_cdm()
  out <- validate_cohort(
    cdm_schema = "main",
    cohort_table = "cohort",
    cohort_id = 1,
    con = con,
    vocab_schema = "main",
    output_dir = tempfile("rwe_demo-"),
    render_html = FALSE
  )
  print(out$report$check_summary)
  cdm_disconnect(con)
}
```

write_results_json	<i>Write the JSON sidecar (no rendering)</i>
--------------------	--

Description

Exposed separately so results can be persisted even when Pandoc is unavailable for HTML rendering.

Usage

```
write_results_json(  
  results,  
  output_dir,  
  cdm_schema,  
  cohort_id,  
  package_version = as.character(utils::packageVersion("rwevalidate")),  
  run_date = Sys.time(),  
  check_summary = NULL  
)
```

Arguments

results	Combined results list (e.g. <code>list(attrition = ..., density = ...)</code> , optionally <code>data_source = ...</code>).
output_dir	Directory to write the report into (created if needed).
cdm_schema	CDM schema name (for the report header / JSON).
cohort_id	Cohort definition id (for the report header / JSON).
package_version	Package version string. Defaults to the installed rwevalidate version.
run_date	Timestamp for the run. Defaults to <code>base::Sys.time()</code> .
check_summary	Optional pre-built summary; rebuilt if NULL.

Value

The path to the written JSON file (invisibly).

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