

Package: r4subtrace (via r-universe)

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Title Traceability Engine for Clinical Submission Readiness

Version 0.1.1

Description Quantifies and explains end-to-end traceability between clinical submission artifacts (ADaM (Analysis Data Model) outputs, derivations, SDTM (Study Data Tabulation Model) sources, specs, code). Builds trace models from metadata and mapping sheets, computes trace levels, and emits standardized R4SUB (R for Regulatory Submission) evidence table rows via 'r4subcore'.

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URL <https://r4sub.github.io/r4subtrace/>,
<https://github.com/R4SUB/r4subtrace>

BugReports <https://github.com/R4SUB/r4subtrace/issues>

Depends R (>= 4.2)

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| build_trace_model | <i>Build a Trace Model</i> |
|-------------------|----------------------------|

Description

Constructs a directed trace model (nodes + edges + diagnostics) from ADaM metadata, SDTM metadata, and an optional mapping sheet.

Usage

```
build_trace_model(
  adam_meta,
  sdtm_meta,
  mapping = NULL,
  spec = NULL,
  config = trace_config_default()
)
```

Arguments

| | |
|-----------|--|
| adam_meta | A data.frame of ADaM variable metadata. Must contain dataset and variable columns. |
| sdtm_meta | A data.frame of SDTM variable metadata. Must contain dataset and variable columns. |
| mapping | An optional data.frame describing ADaM-to-SDTM mappings. Must contain adam_dataset, adam_var, sdtm_domain, sdtm_var. |
| spec | Reserved for future use (ADaM spec ingestion). |
| config | A trace_config object from trace_config_default() . |

Value

A list of class "trace_model" with elements:

- nodes: tibble of asset nodes (datasets and variables)
- edges: tibble of relationships between nodes
- diagnostics: list of tibbles (orphans, ambiguities, conflicts)
- config: the configuration used

Examples

```
adam_meta <- data.frame(
  dataset = "ADSL", variable = c("STUDYID", "USUBJID", "AGE"),
  label = c("Study ID", "Unique Subject ID", "Age")
)
sdm_meta <- data.frame(
  dataset = "DM", variable = c("STUDYID", "USUBJID", "AGE"),
  label = c("Study ID", "Unique Subject ID", "Age")
)
map <- data.frame(
  adam_dataset = "ADSL", adam_var = c("STUDYID", "USUBJID", "AGE"),
  sdm_domain = "DM", sdm_var = c("STUDYID", "USUBJID", "AGE")
)
tm <- build_trace_model(adam_meta, sdm_meta, mapping = map)
tm$nodes
tm$edges
```

compute_trace_levels *Compute Trace Levels for ADaM Variables*

Description

Assigns a traceability level (L0–L3) to each ADaM variable in the trace model based on available mapping, derivation text, and confidence scores.

Usage

```
compute_trace_levels(trace_model)
```

Arguments

trace_model A trace_model object from [build_trace_model\(\)](#).

Details

Trace levels:

- **L0:** No mapping and no derivation text.
- **L1:** Derivation text present but no SDTM mapping.
- **L2:** Mapping to SDTM variable/domain exists.
- **L3:** Mapping exists AND (confidence \geq threshold OR derivation text present alongside mapping).

Value

A tibble with columns: adam_dataset, adam_var, trace_level, has_mapping, has_derivation_text, n_candidates, max_confidence.

Examples

```
adam_meta <- data.frame(
  dataset = "ADSL", variable = c("STUDYID", "USUBJID", "AGE", "AGEGR1"),
  label = c("Study ID", "Unique Subject ID", "Age", "Age Group")
)
sdm_meta <- data.frame(
  dataset = "DM", variable = c("STUDYID", "USUBJID", "AGE"),
  label = c("Study ID", "Unique Subject ID", "Age")
)
map <- data.frame(
  adam_dataset = "ADSL", adam_var = c("STUDYID", "USUBJID", "AGE"),
  sdm_domain = "DM", sdm_var = c("STUDYID", "USUBJID", "AGE"),
  confidence = c(1.0, 1.0, 0.9)
)
tm <- build_trace_model(adam_meta, sdm_meta, mapping = map)
compute_trace_levels(tm)
```

print.trace_model *Print Trace Model*

Description

Print Trace Model

Usage

```
## S3 method for class 'trace_model'
print(x, ...)
```

Arguments

x A trace_model object.
 ... Ignored.

trace_config_default *Default Trace Configuration*

Description

Returns a list of default configuration values for trace model building and evidence emission.

Usage

```
trace_config_default(  
  severity_by_level = c(L0 = "high", L1 = "medium", L2 = "low", L3 = "info"),  
  result_by_level = c(L0 = "fail", L1 = "warn", L2 = "warn", L3 = "pass"),  
  confidence_threshold_L3 = 0.8,  
  uppercase_datasets = TRUE  
)
```

Arguments

`severity_by_level`
Named character vector mapping trace levels to severity.

`result_by_level`
Named character vector mapping trace levels to result.

`confidence_threshold_L3`
Numeric threshold for L3 classification. A mapping must have confidence \geq this value to qualify for L3.

`uppercase_datasets`
Logical; if TRUE, dataset and domain names are uppercased during canonicalization.

Value

A list of class "trace_config" with elements: `severity_by_level`, `result_by_level`, `confidence_threshold_L3`, `uppercase_datasets`.

Examples

```
cfg <- trace_config_default()  
cfg$severity_by_level  
  
# Override a single setting  
cfg2 <- trace_config_default(confidence_threshold_L3 = 0.9)
```

trace_indicator_scores

Compute Trace Indicator Scores

Description

Computes summary metrics from evidence rows generated by `trace_model_to_evidence()`. Returns key traceability indicators.

Usage

```
trace_indicator_scores(evidence)
```

Arguments

`evidence` A data.frame of evidence rows (must contain `indicator_id` and `metric_value` columns).

Value

A tibble with columns: `indicator`, `value`, `description`.

Examples

```
library(r4subcore)
ctx <- r4sub_run_context(study_id = "TEST001", environment = "DEV")
adam_meta <- data.frame(
  dataset = "ADSL", variable = c("STUDYID", "AGE", "AGEGR1"),
  label = c("Study ID", "Age", "Age Group")
)
sdtm_meta <- data.frame(
  dataset = "DM", variable = c("STUDYID", "AGE"),
  label = c("Study ID", "Age")
)
map <- data.frame(
  adam_dataset = "ADSL", adam_var = c("STUDYID", "AGE"),
  sdtm_domain = "DM", sdtm_var = c("STUDYID", "AGE")
)
tm <- build_trace_model(adam_meta, sdtm_meta, mapping = map)
ev <- trace_model_to_evidence(tm, ctx = ctx)
trace_indicator_scores(ev)
```

`trace_model_to_evidence`*Convert Trace Model to R4SUB Evidence*

Description

Emits evidence rows compatible with `r4subcore::validate_evidence()` for each ADaM variable's trace level, plus diagnostic rows for orphans, ambiguities, and conflicts.

Usage

```
trace_model_to_evidence(  
  trace_model,  
  ctx,  
  source_name = "r4subtrace",  
  source_version = NULL  
)
```

Arguments

`trace_model` A `trace_model` object from `build_trace_model()`.
`ctx` An `r4sub_run_context` from `r4subcore::r4sub_run_context()`.
`source_name` Character; the name of the evidence source.
`source_version` Character or `NULL`; version of the source.

Value

A `data.frame` of evidence rows passing `r4subcore::validate_evidence()`.

Examples

```
library(r4subcore)  
ctx <- r4sub_run_context(study_id = "TEST001", environment = "DEV")  
adam_meta <- data.frame(  
  dataset = "ADSL", variable = c("STUDYID", "AGE"),  
  label = c("Study ID", "Age")  
)  
sdtm_meta <- data.frame(  
  dataset = "DM", variable = c("STUDYID", "AGE"),  
  label = c("Study ID", "Age")  
)  
map <- data.frame(  
  adam_dataset = "ADSL", adam_var = c("STUDYID", "AGE"),  
  sdtm_domain = "DM", sdtm_var = c("STUDYID", "AGE")  
)  
tm <- build_trace_model(adam_meta, sdtm_meta, mapping = map)  
ev <- trace_model_to_evidence(tm, ctx = ctx)  
r4subcore::validate_evidence(ev)
```

| | |
|------------------|-------------------------------|
| validate_mapping | <i>Validate Trace Mapping</i> |
|------------------|-------------------------------|

Description

Checks that a mapping data.frame contains the required columns (adam_dataset, adam_var, sdtm_domain, sdtm_var) and canonicalizes names, trims whitespace, and optionally uppercases dataset/domain names.

Usage

```
validate_mapping(df, uppercase_datasets = TRUE)
```

Arguments

df A data.frame describing ADaM-to-SDTM variable mappings.
uppercase_datasets Logical; if TRUE, uppercases adam_dataset and sdtm_domain. Default TRUE.

Value

A tibble with canonicalized column names and values.

Examples

```
map <- data.frame(  
  ADAM_DATASET = "adsl", ADAM_VAR = "AGE",  
  SDTM_DOMAIN = "dm", SDTM_VAR = "AGE"  
)  
validate_mapping(map)
```

| | |
|-------------------|----------------------------------|
| validate_metadata | <i>Validate Dataset Metadata</i> |
|-------------------|----------------------------------|

Description

Checks that an ADaM or SDTM metadata data.frame contains the required columns (dataset, variable) and canonicalizes column names to lowercase.

Usage

```
validate_metadata(df, kind = c("adam", "sdtm"))
```

Arguments

`df` A data.frame of dataset metadata.
`kind` Character; "adam" or "sdm". Used in error messages only.

Value

A tibble with canonicalized column names.

Examples

```
meta <- data.frame(DATASET = "ADSL", VARIABLE = "SUBJID", LABEL = "Subject ID")
validate_metadata(meta, kind = "adam")
```

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