

Package: PhysioAnnotationHub (via r-universe)

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Type Package

Title Anatomical and Clinical Knowledge Graph for Physiological Data

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Description Centralized annotation hub providing anatomical ontology, muscle/bone metadata, nerve innervation, clinical codes (ICD-10, ICF), and knowledge graph queries for the physio-ecosystem.

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<https://x-biosignal.r-universe.dev/PhysioAnnotationHub>,
<https://x-biosignal.github.io/PhysioAnnotationHub/>

BugReports <https://github.com/x-biosignal/PhysioAnnotationHub/issues>

Repository <https://x-biosignal.r-universe.dev>

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getBoneAnnotation	<i>Get bone annotations</i>
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Description

Get bone annotations

Usage

getBoneAnnotation(bones = NULL, hub = NULL, fuzzy = TRUE)

Arguments

- bones Character vector of bone names (NULL for all)
- hub AnnotationHub object
- fuzzy Logical; use fuzzy matching (default TRUE)

Value

data.frame of bone annotations

Examples

getBoneAnnotation("Occipital")

getClinicalCodes	<i>Get clinical codes for muscles</i>
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Description

Get clinical codes for muscles

Usage

```
getClinicalCodes(muscles, system = c("icd10", "icf"), hub = NULL)
```

Arguments

muscles	Character vector of muscle names
system	Character; "icd10" or "icf" (default "icd10")
hub	AnnotationHub object

Value

data.frame of matching clinical codes

Examples

```
getClinicalCodes("Rectus abdominis", system = "icd10")
```

getCoreSet	<i>Retrieve a published ICF Core Set</i>
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Description

Returns the categories of a published WHO ICF Core Set for a health condition. Currently the Brief ICF Core Set for Stroke (Geyh 2004) is bundled; the data are the officially published category lists, not derived.

Usage

```
getCoreSet(condition, level = c("brief", "comprehensive"), hub = NULL)
```

Arguments

condition	Condition name (e.g. "Stroke"); case-insensitive.
level	"brief" or "comprehensive" (default "brief").
hub	Optional PhysioAnnotationHub.

Value

A data frame of ICF categories (icf_code, category_title, component, ...) for the requested Core Set.

References

Geyh et al. 2004, ICF Core Sets for Stroke; ICF Research Branch.

See Also

[icfCategories()], [tagICF()]

Examples

```
getCoreSet("Stroke")
```

getMuscleAnnotation	<i>Get muscle annotations</i>
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Description

Get muscle annotations

Usage

```
getMuscleAnnotation(muscles = NULL, hub = NULL, fuzzy = TRUE)
```

Arguments

muscles	Character vector of muscle names (NULL for all)
hub	AnnotationHub object
fuzzy	Logical; use fuzzy matching (default TRUE)

Value

data.frame of muscle annotations

Examples

```
getMuscleAnnotation("Trapezius")
nrow(getMuscleAnnotation()) # the whole muscle table
```

getNerveAnnotation	<i>Get nerve annotations</i>
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Description

Get nerve annotations

Usage

```
getNerveAnnotation(nerves = NULL, hub = NULL)
```

Arguments

nerves	Character vector of nerve names (NULL for all)
hub	AnnotationHub object

Value

data.frame of nerve annotations

Examples

```
getNerveAnnotation("Accessory")
```

icfCategories	<i>Look up ICF category titles</i>
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Description

Resolves ICF category codes to their titles (across the hub's Core-Set, metric-link, and clinical ICF tables).

Usage

```
icfCategories(codes, hub = NULL)
```

Arguments

codes	A character vector of ICF codes (e.g. c("b730", "d450")).
hub	Optional PhysioAnnotationHub.

Value

A data frame with icf_code and title (NA title for an unknown code).

See Also

[getCoreSet()], [tagICF()]

Examples

```
icfCategories(c("b730", "d450"))
```

kgEnrichment

Functional enrichment analysis for a set of muscles

Description

Tests whether a set of muscles is enriched for specific annotations (actions, innervation, body regions) compared to the full set.

Usage

```
kgEnrichment(
  muscles,
  annotation_type = c("action", "nerve", "body_region", "spinal_level"),
  hub = NULL
)
```

Arguments

muscles	Character vector of muscle names (query set)
annotation_type	Character; "action", "nerve", "body_region", "spinal_level"
hub	AnnotationHub object

Value

data.frame with term, count, expected, fold_enrichment, p_value

Examples

```
kgEnrichment(
  c("Trapezius", "Latissimus Dorsi", "Serratus Posterior Superior"),
  annotation_type = "body_region"
)
```

kgNeighbors	<i>Get KG neighbors of an entity</i>
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Description

Get KG neighbors of an entity

Usage

```
kgNeighbors(entity, depth = 1, hub = NULL)
```

Arguments

- | | |
|--------|--------------------------------------|
| entity | Character; entity name |
| depth | Integer; traversal depth (default 1) |
| hub | AnnotationHub object |

Value

data.frame of all triples within depth hops

Examples

```
head(kgNeighbors("Trapezius"))
```

kgShortestPath	<i>Find shortest path between two entities in the KG</i>
----------------	--

Description

Find shortest path between two entities in the KG

Usage

```
kgShortestPath(from, to, hub = NULL, max_depth = 5)
```

Arguments

- | | |
|-----------|---|
| from | Character; source entity name |
| to | Character; target entity name |
| hub | AnnotationHub object |
| max_depth | Integer; maximum search depth (default 5) |

Value

List with path (entities), predicates, and depth

Examples

```
kgShortestPath("Trapezius", "External Occipital Protuberance")
```

linkInstrumentToICF	<i>Link a clinical instrument to its ICF categories</i>
---------------------	---

Description

Like [tagICF()] but returns a data frame with the ICF code and its title, suitable for annotating a clinical outcome measure.

Usage

```
linkInstrumentToICF(instrument_id, hub = NULL)
```

Arguments

instrument_id	A clinical instrument identifier (e.g. "berg", "fma_ue").
hub	Optional PhysioAnnotationHub.

Value

A data frame with instrument_id, icf_code, icf_title (zero rows, with a warning, if unmapped).

See Also

[tagICF()]

Examples

```
linkInstrumentToICF("berg")
```

loadAnnotationHub	<i>Load the PhysioAnnotationHub</i>
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Description

Loads all annotation data into a cached environment for fast repeated queries.

Usage

```
loadAnnotationHub(reload = FALSE)
```

Arguments

reload	Logical; force reload even if cached (default FALSE)
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Value

An AnnotationHub object (list) with muscle, bone, nerve, kg, clinical data

Examples

```
hub <- loadAnnotationHub()
hub
```

print.PhysioAnnotationHub	<i>Print method for PhysioAnnotationHub</i>
---------------------------	---

Description

Print method for PhysioAnnotationHub

Usage

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

Arguments

x	A PhysioAnnotationHub object
...	Additional arguments (ignored)

Value

Invisibly returns x

queryKG

Query the Knowledge Graph by triple pattern

Description

Query the Knowledge Graph by triple pattern

Usage

```
queryKG(
  subject = NULL,
  predicate = NULL,
  object = NULL,
  hub = NULL,
  exact = FALSE
)
```

Arguments

subject	Character or NULL; entity name pattern (grep)
predicate	Character or NULL; relation type (exact or grep)
object	Character or NULL; target entity pattern (grep)
hub	AnnotationHub object (loaded if NULL)
exact	Logical; use exact matching instead of grep (default FALSE)

Value

data.frame of matching triples

Examples

```
# All triples with Trapezius as the subject:
head(queryKG(subject = "Trapezius"))
```

tagICF

Tag a metric or instrument with ICF categories

Description

Returns the WHO ICF category codes linked to a physiological metric or clinical instrument, using the packaged metric-to-ICF map (built with the Cieza 2005 ICF linking rules). Matching is case-insensitive.

Usage

```
tagICF(metric, hub = NULL)
```

Arguments

<code>metric</code>	A metric / instrument identifier (e.g. "gait_speed", "FMA_UE", "HRV").
<code>hub</code>	Optional <code>PhysioAnnotationHub</code> (loaded on demand otherwise).

Value

A character vector of ICF codes (empty, with a warning, if unmapped).

References

WHO ICF; Cieza et al. 2005 (ICF linking rules).

See Also

[`linkInstrumentToICF()`], [`getCoreSet()`], [`icfCategories()`]

Examples

```
tagICF("gait_speed")
tagICF("FMA_UE")
```

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