Package ‘OmopStudyBuilder’

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Type Package

Title Build Reproducible Network Studies for OMOP Common Data Model

Version 0.1.0

Description Streamlines the setup and execution of network studies using the Observational Medical Outcomes Partnership (OMOP) Common Data Model (CDM). Creates standardised project structures with template code, manages dependencies with 'renv', provides code review utilities, and supports containerised execution with 'Docker' for reproducible multi-site studies. Includes 'GitHub' integration for collaboration and version control.

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URL `https://oxford-pharmacoepi.github.io/OmopStudyBuilder/`

Depends R (>= 4.1.0)

Imports cli, jsonlite, omopgenerics, rlang, whisker

Suggests dplyr, gert, getPass, gh, here, knitr, processx, purrr, renv, rmarkdown, scales, stringr, testthat

VignetteBuilder knitr

Encoding UTF-8

BugReports `https://github.com/oxford-pharmacoepi/OmopStudyBuilder/issues`

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NeedsCompilation no

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Repository CRAN

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Contents

`dockeriseStudy` *Build a Docker image for an OMOP study*

Description

Build a Docker image for an OMOP study

Usage

```
dockeriseStudy(
  image_name = NULL,
  path = ".",
  useRStudio = FALSE,
  r_version = NULL,
  snapshot = TRUE,
  github_token = NULL
)
```

Arguments

`image_name`	Name for the Docker image (default: auto-detected from directory)
`path`	Path to study directory (default: current directory)
`useRStudio`	Use RStudio Server base (TRUE) or r-ver base (FALSE, default)
`r_version`	R version override (default: auto-detected from renv.lock)
`snapshot`	Update renv.lock before building (default: TRUE)
`github_token`	Optional GitHub token for installing GitHub packages during build

Value

Image name (invisibly - already printed to console)

`initStudy` *Creates initial directory for an OMOP CDM network study*

Description

Creates initial directory for an OMOP CDM network study

Usage

```
initStudy(
  directory,
  diagnostics = TRUE,
  study = TRUE,
  studyTitle = NULL,
  studyLeads = NULL,
  studyDescription = NULL,
  repository = NULL,
  organisation = NULL,
  private = TRUE
)
```

Arguments

`directory`	Path to a directory that will be used as the root folder for the study. If it does not exist, it will be created. The directory must be empty if it already exists.
`diagnostics`	A single TRUE or FALSE value. If TRUE (the default), the function creates the ‘diagnosticsCode/‘ and ‘diagnosticsShiny/‘ folders using the package templates. If FALSE, these diagnostics folders are not created.
`study`	A single TRUE or FALSE value. If TRUE (the default), the function creates the ‘studyCode/‘ and ‘studyShiny/‘ folders using the package templates. If FALSE, these study folders are not created.
`studyTitle`	Character string with the study title. If NULL (default), uses the directory basename.
`studyLeads`	Character string with study leads. If NULL (default), leaves a placeholder.
`studyDescription`	Character string with study description. If NULL (default), leaves a placeholder.
`repository`	Optional GitHub repository name. If provided, creates a GitHub repository and links it to the study. Requires the `gh` and `gert` packages and GitHub authentication (for example via `GITHUB_PAT`).
`organisation`	Optional GitHub organisation name. If NULL (default), creates repository under your personal account. Only used when `repository` is provided.
`private`	Logical. If TRUE (default), creates a private GitHub repository. Only used when `repository` is provided.

Value

Project directory will be created

Examples

```
# Create a study called "SampleStudy" in a temporary directory
study_root <- file.path(tempdir(), "SampleStudy")
initStudy(study_root)

# Inspect the top-level contents
list.files(study_root)

# Create another study with custom metadata
study_root2 <- file.path(tempdir(), "DiabetesStudy")
initStudy(study_root2,
          studyTitle = "Diabetes Prevalence Study",
          studyLeads = "Dr. Smith, Dr. Jones")

## Not run:
# Create study with GitHub integration (requires GITHUB_PAT)
# Set PAT for current session:
Sys.setenv(GITHUB_PAT = "your_token_here")

study_root3 <- file.path(tempdir(), "GitHubStudy")
initStudy(
  directory = study_root3,
  repository = "my-omop-study",
  organisation = "oxford-pharmacoepi",
  private = TRUE
)

## End(Not run)
```

`linkGitHub` *Link study directory to GitHub repository*

Description

Creates a new GitHub repository and connects it to an existing study directory. Initializes git, creates .gitignore, commits all files, and pushes to GitHub.

Usage

```
linkGitHub(
  directory,
  repository,
  organisation = NULL,
  private = TRUE,
  description = NULL
)
```

Arguments

`directory`	Path to study directory
`repository`	GitHub repository name (will be sanitised if needed)
`organisation`	GitHub organisation name. If NULL (default), creates repo under your personal account
`private`	Logical. If TRUE (default), creates a private repository
`description`	Repository description. If NULL, auto-generated from directory name

Value

GitHub repository URL (invisibly)

Requirements

- **GitHub authentication**: Set up via GITHUB_PAT, gh CLI, or git credentials
- **R package 'gh'**: Install with `install.packages("gh")`
- **R package 'gert'**: Install with `install.packages("gert")`

Authentication

This function needs credentials for both:

- **GitHub API access**: used by `gh` to check your account and create the repository
- **Git transport authentication**: used by `gert` to push the local repository to GitHub

Recommended setup:

- **GITHUB_PAT environment variable**: recommended for HTTPS authentication and works for both GitHub API calls and Git pushes to GitHub
- **Stored Git credentials**: credentials in your OS credential store or Git credential helper can also work for both the API and push steps
- **gh CLI**: may help set up GitHub authentication, but you may still need Git credentials available for the final push
- **SSH**: supported when your remote/auth setup is configured accordingly

To create a Personal Access Token (PAT):

1. Visit `https://github.com/settings/tokens`
2. Generate a token with `repo` scope
3. Set for current session: `Sys.setenv(GITHUB_PAT = "your_token_here")`
4. Or add to .Renviron: `GITHUB_PAT='your_token_here'` and restart R

Examples

```
## Not run:
library(OmopStudyBuilder)
library(here)

# Authenticate (choose one method):
# 1. Set GITHUB_PAT for current session
Sys.setenv(GITHUB_PAT = "your_token_here")
# 2. Or use gh CLI: gh auth login

# Create repo under personal account
linkGitHub(
  directory = here::here(),
  repository = "my-omop-study"
)

# Create repo under organisation
linkGitHub(
  directory = here::here(),
  repository = "diabetes-study",
  organisation = "oxford-pharmacoepi",
  private = TRUE
)

## End(Not run)
```

`pushDockerImage` *Push a Docker image to Docker Hub*

Description

Push a Docker image to Docker Hub

Usage

```
pushDockerImage(
  image_name = NULL,
  repo,
  tag = "latest",
  username = NULL,
  password = NULL,
  logout = TRUE
)
```

Arguments

`image_name`	Name of Docker image to push (default: auto-detected from directory)
`repo`	Docker Hub repository (e.g., "username/repo" or "repo")

`tag`	Tag to push (default: "latest")
`username`	Docker Hub username (prompted if NULL)
`password`	Docker Hub password or token (prompted if NULL, hidden input)
`logout`	If TRUE, logs out after pushing

Value

Pushed image reference (invisibly)

`reviewStudy` *Review a study directory*

Description

Summarises the code and/or renv dependencies in a study directory.

Usage

```
reviewStudy(dir, code = TRUE, dependencies = TRUE, type = "analysis")
```

Arguments

`dir`	Path to the study directory.
`code`	If ‘TRUE‘, summarises R, JSON, CSV, and Excel files found in the directory.
`dependencies`	If ‘TRUE‘, summarises the renv.lock dependencies.
`type`	Whether the R project is for analysis code or study reporting. Only used when ‘dependencies = TRUE‘.

Value

Invisibly returns ‘NULL‘. Called for its side effects of printing summaries to the console.

`runRStudio` *Run RStudio Server for interactive study execution*

Description

Note: The Docker image must include RStudio Server (i.e., be built with ‘dockeriseStudy(useRStudio = TRUE)‘ which uses a ‘rocker/rstudio‘ base image).

Usage

```
runRStudio(
  image_name = NULL,
  results_path = "./results",
  env_file = NULL,
  port = 8787,
  password = NULL
)
```

Arguments

`image_name`	Name of Docker image to run (default: auto-detected from directory)
`results_path`	Path to save results (default: "./results")
`env_file`	Optional path to a .env file (passed to Docker via –env-file). If NULL and a ‘.env‘ file exists in the current working directory, it will be used automatically.
`port`	Port for RStudio Server (default: 8787, auto-finds next available if busy)
`password`	RStudio password (default: auto-generated and displayed)

Value

Container ID (invisibly)

`runStudy` *Run study in automated mode with real-time log streaming*

Description

Run study in automated mode with real-time log streaming

Usage

```
runStudy(
  image_name = NULL,
  results_path = "./results",
  env_file = NULL,
  data_path = NULL,
  script_path = "codeToRun.R"
)
```

Arguments

`image_name`	Name of Docker image to run (default: auto-detected from directory)
`results_path`	Path to save results (default: "./results")
`env_file`	Optional path to a .env file (passed to Docker via –env-file). If NULL and a ‘.env‘ file exists in the current working directory, it will be used automatically.
`data_path`	Optional path to data directory (mounted at /data)
`script_path`	Path to R script to execute (default: "codeToRun.R")

Value

Exit status (0 = success, non-zero = failure)

`stopStudy` *Stop a running OmopStudyBuilder container (automated or RStudio)*

Description

Stops containers started by `runStudy()` and/or `runRStudio()`. By default it stops containers for the image inferred from the current directory name.

Usage

```
stopStudy(
  container = NULL,
  image_name = NULL,
  mode = c("any", "rstudio", "run"),
  all = FALSE
)
```

Arguments

`container`	Optional container name or ID to stop directly.
`image_name`	Optional Docker image name. Defaults to current directory name.
`mode`	Which container(s) to stop: "any" (default), "rstudio", or "run".
`all`	If TRUE, stops all running containers started by OmopStudyBuilder.

Value

TRUE if at least one container was stopped (invisibly)

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