

Package: **cpgdirectionData** (via **r-universe**)

October 1, 2026

Type Package

Title Data Layers for the cpgdirection Package (ExperimentHub)

Version 0.99.1

Description ExperimentHub companion to the cpgdirection package.

Serves the eight data layers too large to ship inside a Bioconductor software package: the three tissue catalogue lookup tables (blood, nasal epithelium, solid tissue; hg19), the SMR causal-direction table, the EPIC v2 hg19 probe positions, the brain SMR directions, the genome-wide saliva bridge scores, and the multi-source EPIC v2 probe-to-gene annotation (five cross-validated annotation tracks with per-track support flags). Each resource is a serialized data.frame retrieved from ExperimentHub on first use and cached locally thereafter. The cpgdirection package consumes these resources transparently; direct use is possible through the accessors documented here.

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Encoding UTF-8

Depends R (>= 4.5.0), ExperimentHub

Imports AnnotationHub

Suggests testthat (>= 3.0.0), knitr, rmarkdown, cpgdirection

VignetteBuilder knitr

biocViews ExperimentData, ExperimentHub, Homo_sapiens_Data, MicroarrayData, MethylationArrayData, TissueMicroarrayData, Tissue, Genome

URL <https://github.com/teindor/cpgdirection>,
<https://doi.org/10.5281/zenodo.22225164>

BugReports <https://github.com/teindor/cpgdirection/issues>

Config/roxygen2/version 8.1.0

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository <https://biocstaging.r-universe.dev>
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cpgdData	<i>Retrieve one cpgdirection data layer</i>
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Description

Fetches the named resource from ExperimentHub (cached locally by the Hub after the first download), or from a local directory when `options(cpgdirectionData.local = "<dir>")` is set – the directory must hold the resource as "`<name>.rds`". The local mode serves air-gapped machines and lets the `cpgdirection` stack run against a data snapshot pinned for a specific analysis.

Usage

`cpgdData(name)`

Arguments

`name` One of `cpgdData_resources()`\$name.

Value

A `data.frame`.

Examples

```
# The default retrieval is ExperimentHub (cached after first use):
# pos <- cpgdData("cpg_positions_hg19")
# The local mode serves the same files from a directory, demonstrated
# here with a stand-in so the example runs without network access:
d <- tempfile(); dir.create(d)
saveRDS(data.frame(cpg_id = "cg000000029", chr = "chr16", pos = 53434200L),
        file.path(d, "cpg_positions_hg19.rds"))
old <- options(cpgdirectionData.local = d)
```

```
pos <- cpgdData("cpg_positions_hg19")
head(pos)
options(old)
```

cpgdData_resources	<i>The data layers this package serves</i>
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Description

The data layers this package serves

Usage

```
cpgdData_resources()
```

Value

A data.frame with one row per resource: name (the identifier accepted by [cpgdData](#)), title (the ExperimentHub title), description and genome.

Examples

```
cpgdData_resources()
```

cpgdirectionData	<i>cpgdirectionData: data layers for the cpgdirection package</i>
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Description

ExperimentHub companion to **cpgdirection**. Bioconductor software packages are capped at 5 MB per file; the eight data layers served here are larger than that, so they live on the Hub and are fetched on first use (then cached locally by ExperimentHub). The **cpgdirection** package retrieves them transparently through its data backend; direct access goes through [cpgdData](#) or the named accessors.

Details

Provenance: the layers are built by the scripts under `inst/scripts/` from the sources documented there (the cpgdirection catalogues and SMR analyses; the Illumina EPIC-8v2-0_A2 manifest; the Zhou lab SeSAmE EPIC v2 annotation and masks; the Exeter EPIC v2 re-annotation, Zenodo record 15181885; the Garvan EPICv2manifest cross-hybridization evidence).

Author(s)

Maintainer: Tsachi Ein-Dor <teindor@runi.ac.il> ([ORCID](#)) [funder]

Authors:

- Tsachi Ein-Dor <teindor@runi.ac.il> ([ORCID](#)) [funder]

See Also

Useful links:

- <https://github.com/teindor/cpgdirection>
- Report bugs at <https://github.com/teindor/cpgdirection/issues>

layer-accessors

Named accessors for the individual data layers

Description

Convenience wrappers around [cpgdData](#), one per resource. `getBloodLookup()`, `getNasalEpitheliumLookup()` and `getSolidTissueLookup()` return the per-tissue catalogue tables; `getSmrDirections()` the SMR causal directions; `getCpgPositionsHg19()` the EPIC v2 hg19 probe positions; `getBrainDirections()` the brain SMR directions; `getSalivaBridgeScores()` the saliva-bridge scores; and `getEpicv2ProbeGeneAnnotation()` the multi-source probe-to-gene annotation.

Usage

```
getBloodLookup()

getNasalEpitheliumLookup()

getSolidTissueLookup()

getSmrDirections()

getCpgPositionsHg19()

getBrainDirections()

getSalivaBridgeScores()

getEpicv2ProbeGeneAnnotation()
```

Value

A data.frame; see [cpgdData_resources](#) for the per-resource description.

Examples

```
# Hub retrieval (default): pos <- getCpgPositionsHg19()
# Local-mode stand-in so the example runs without network access:
d <- tempfile(); dir.create(d)
saveRDS(data.frame(cpg_id = "cg00000029", chr = "chr16", pos = 53434200L),
        file.path(d, "cpg_positions_hg19.rds"))
old <- options(cpgdirectionData.local = d)
head(getCpgPositionsHg19())
options(old)
```

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