Package: phenoloom (via r-universe)

November 3, 2026

Type Package

Title CTTIR Spatial Biology Suite

Version 0.1.2

Description An installation framework for the CTTIR spatial biology suite. Declares 'segmantR', 'cellspecR', 'gatekeepR', and 'phenoscapR' as required dependencies so that standard package installation installs the suite and its required dependencies. Analysis functionality remains in the member packages; no additional functions or automatic attachment are provided.

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URL https://github.com/CTTIR/phenoloom, https://cttir.r-universe.dev/phenoloom

X-schema.org-keywords spatial-biology, multiplexed-imaging, cell-segmentation, phenotyping, installation

BugReports https://github.com/CTTIR/phenoloom/issues

Depends R (>= 4.1.0)

Imports segmantR, cellspecR, gatekeepR, phenoscapR

Remotes CTTIR/segmantR, CTTIR/cellspecR, CTTIR/gatekeepR, CTTIR/phenoscapR

Additional_repositories https://cttir.r-universe.dev

Encoding UTF-8

Language en-US

Config/pak/sysreqs libabsl-dev cmake libgdal-dev gdal-bin libgeos-dev make libpng-dev libuv1-dev libssl-dev libproj-dev python3 libsqlite3-dev libudunits2-dev zlib1g-dev

Repository https://cttir.r-universe.dev

Date/Publication 2026-11-03 13:13:28 UTC

RemoteUrl https://github.com/CTTIR/phenoloom

RemoteRef HEAD

RemoteSha b44b6a857d363f4f70317eeb6e8bdf5fa12fbe4b

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`phenoloom-package` *CTTIR Spatial Biology Suite*

Description

An installation framework for **segmantR**, **cellspecR**, **gatekeepR**, and **phenoscapR**, together with their required R package dependencies.

Details

Install from GitHub using `remotes::install_github("CTTIR/phenoloom", dependencies = NA)`. Required dependencies are installed recursively. Optional suggested packages, external segmentation environments, and model weights require separate setup. The required spatial packages include **sf** and **stars**; source builds need their documented native libraries. **imager** is optional in the tested **segmantR** 0.2.0. Consult each member's installation requirements for the chosen workflow and platform.

The metapackage exports no functions and does not attach its member packages. Use the installed packages directly through their own APIs, such as `cellspecR::cs_example()`.

GitHub installation follows the members' current default branches. Record the installed versions, source revisions and `sessionInfo()` with an analysis; pinning the metapackage alone does not pin its transitive dependencies. The README provides a recording recipe and a canonical cell-table write/read example. Synthetic software checks do not establish biological or clinical performance or qualify external segmentation engines.

Author(s)

R. Heller <raban.heller@charite.de>

See Also

https://github.com/CTTIR/phenoloom, https://r-spatial.github.io/sf/

Examples

```
x <- cellspecR::cs_example()
cellspecR::cs_assert_valid(x)
```

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