

Package: grayleafspotdata (via r-universe)

September 19, 2026

Type Package

Title File Manifest for the S-BSST3199 Magnaporthe Colony Image Dataset

Version 0.1.0

Date 2026-08-19

Description Provides a machine-readable file and image manifest for the research data deposited in EMBL-EBI BioStudies under accession S-BSST3199 (a time-series petri-dish image dataset of Magnaporthe colonies from twelve plates, with associated morphometric analysis outputs produced by metrics-petri 3.0.0). The original research files are not bundled in this R package; they remain hosted by BioStudies. The manifest can be used in image-analysis and plant-pathology workflows, including workflows based on the 'grayleafspotr' software. Related research outputs are documented using their persistent identifiers.

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Encoding UTF-8

LazyData true

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URL <https://github.com/rotsl/grayleafspotdata>,
<https://www.ebi.ac.uk/biostudies/studies/S-BSST3199>,
<https://rotsl.r-universe.dev/>

BugReports <https://github.com/rotsl/grayleafspotdata/issues>

Depends R (>= 3.5.0)

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Repository <https://rotsl.r-universe.dev>

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RemoteUrl <https://github.com/rotsl/grayleafspotdata>

RemoteRef HEAD
RemoteSha 581493d4ef695aded79932f513053a3e643593ea

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grayleafspot_files	<i>Top-level deposited file manifest for S-BSST3199</i>
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Description

A machine-readable manifest of the six top-level research files deposited directly in the BioStudies record S-BSST3199 (excluding the macOS .DS_Store artifact). These are the files listed in the deposited SHA256SUMS.txt checksum file. SHA-256 values and file sizes are populated because BioStudies exposes them at this level.

Use this dataset to verify the integrity of the deposited archive without downloading every byte of raw_images.zip, or to locate each top-level file’s canonical BioStudies URL.

Format

A data frame with 6 rows and one row per deposited top-level file. Columns:

- file_id** Integer row identifier, 1 to 6.
- filename** Flattened filename as served by the BioStudies file URL endpoint (e.g. README.txt, metrics-petri-3.0.0.zip).
- relative_path** Path inside the BioStudies deposit as recorded in SHA256SUMS.txt (e.g. metadata/dataset_manifest.csv, software/metrics-petri-3.0.0.zip).
- extension** File extension, lowercased.
- media_type** Declared media type.
- file_size_bytes** File size in bytes, from the BioStudies files API.
- sha256** SHA-256 checksum from the deposited SHA256SUMS.txt, lowercase hexadecimal.
- study_accession** BioStudies accession, S-BSST3199.
- study_url** Canonical BioStudies study URL.
- biostudies_file_url** Direct BioStudies file URL.
- description** Description of the file as listed by the BioStudies files API.

Source

EMBL-EBI BioStudies accession S-BSST3199. Files API listing retrieved 2026-08-18 from <https://www.ebi.ac.uk/biostudies/api/v1/studies/S-BSST3199/files>. SHA-256 values retrieved 2026-08-18 from <https://www.ebi.ac.uk/biostudies/files/S-BSST3199/SHA256SUMS.txt>.

References

EMBL-EBI BioStudies accession S-BSST3199, DOI [doi:10.6019/SBSST3199](https://doi.org/10.6019/SBSST3199).

grayleafspot_images	<i>Image manifest for the S-BSST3199 Magnaporthe colony dataset</i>
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Description

A machine-readable manifest describing the 49 source image files associated with the research dataset deposited in EMBL-EBI BioStudies under accession S-BSST3199. The study is titled "Time-series Magnaporthe colony images from twelve petri dishes and morphometric analysis results generated using metrics-petri 3.0.0".

The original image files are not bundled with this R package. They remain available from the authoritative BioStudies record at <https://www.ebi.ac.uk/biostudies/studies/S-BSST3199>.

This manifest can be used on its own, or together with image-analysis software such as grayleafspotr. No R-level dependency on grayleafspotr is introduced.

Format

A data frame with 49 rows and one row per deposited source image. Columns:

file_id Integer row identifier, 1 to 49.

filename Original image filename as listed in `dataset_manifest.csv` (e.g. 20260204_P001_30JAN_WT_PCBM_CTRL_d05_T

relative_path Inferred path of the image inside the BioStudies deposit (e.g. `raw_images/30jan/20260204_P001_30JAN_WT`). Derived from the directory pattern of the related `metadata_file` value. Never an absolute path.

extension File extension, lowercased (e.g. `.jpg`).

media_type Declared media type (e.g. `image/jpeg`).

file_size_bytes File size in bytes. NA when not available from the deposited metadata. The 49 individual images are packaged inside `raw_images.zip`; per-image sizes are not exposed separately by the BioStudies record.

sha256 SHA-256 checksum as lowercase hexadecimal. NA for individual image rows because the BioStudies `SHA256SUMS.txt` only publishes top-level deposit checksums. Populate this column by re-running `data-raw/build_manifest.R` against a local copy of the dataset directory.

study_accession BioStudies accession, S-BSST3199.

study_repository Hosting repository name, EMBL-EBI BioStudies.

study_url Canonical BioStudies study URL.

biostudies_file_url Direct BioStudies file URL when one can be established. NA for individual image rows because the images are inside `raw_images.zip`, not directly retrievable per-image.

acquisition_group Acquisition group identifier as listed in `dataset_manifest.csv`: 30jan or 6feb.

- plate_id** Plate identifier as listed in `dataset_manifest.csv`: P001 for the 30 January group, P02 to P12 for the 6 February group.
- metadata_file** Path of the plate-level `image_metadata.csv` file as listed in `dataset_manifest.csv`.
- analysis_directory** Path of the plate-level analysis output directory as listed in `dataset_manifest.csv`.
- organism** Study-level organism. The BioStudies record identifies the colonies as *Magnaporthe*; propagated to all rows.
- metadata_source** Free-text provenance note describing where the per-row values were obtained from.
- local_manifest_source** Identifier of the local source directory used by `data-raw/build_manifest.R` when per-image checksums were computed. NA in the published build because the build was generated from the remote BioStudies record only.

Source

EMBL-EBI BioStudies accession S-BSST3199, file `dataset_manifest.csv`. Retrieved 2026-08-18 from https://www.ebi.ac.uk/biostudies/files/S-BSST3199/dataset_manifest.csv. Study landing page: <https://www.ebi.ac.uk/biostudies/studies/S-BSST3199>.

References

Related research outputs include:

- EMBL-EBI BioStudies accession S-BSST3199, DOI [doi:10.6019/SBSST3199](https://doi.org/10.6019/SBSST3199).
- Harvard Dataverse record DOI [doi:10.7910/DVN/SR2HBR](https://doi.org/10.7910/DVN/SR2HBR) (metrics-petri 3.0.0 software archive).
- Harvard Dataverse record DOI [doi:10.7910/DVN/7BJLIQ](https://doi.org/10.7910/DVN/7BJLIQ) (U-Net validation dataset for fungal colony segmentation).

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