

Package: CGExplorer (via r-universe)

October 9, 2026

Type Package

Title Chemo-Genomic Screening Data Preprocessor and Visualizer

Version 0.3.2

Description An R package providing S4 data structures, analysis methods, and a Shiny application for preprocessing, quality control, and chemo-genomic interaction scoring of 384-well plate screening datasets generated by Tecan plate readers. Plate data is managed via a persistent local registry (PlateRegistry S4 object) that accumulates across sessions and survives package upgrades.

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Depends R (>= 4.1.0)

Imports methods, shiny (>= 1.7.0), shinydashboard, shinyjs, shinycssloaders, golem, dplyr, tidyr, readr, readxl, lubridate, stringr, plotly, DT, ggplot2, grDevices, RColorBrewer, tools, uuid

Suggests WriteXLS, ggrepel, testthat (>= 3.0.0)

Encoding UTF-8

LazyData false

Config/testthat/edition 3

URL <https://github.com/zqzneptune/CGExplorer>

BugReports <https://github.com/zqzneptune/CGExplorer/issues>

Config/roxygen2/version 8.1.0

Collate 'CGExplorer-package.R' 'app_server.R' 'app_ui.R' 'generics.R' 'classes.R' 'constructors.R' 'globals.R' 'methods.R' 'methods_batch.R' 'methods_plate.R' 'mod_batch_builder.R' 'mod_batch_overview.R' 'mod_data_upload.R' 'mod_layout_upload.R' 'mod_plate_card.R' 'mod_qc.R' 'mod_scoring.R' 'parsers.R' 'plotting.R' 'plotting_pdf.R' 'processing.R' 'run_app.R' 'scoring.R' 'staining_detect.R'

Config/pak/sysreqs cmake make libicu-dev libuv1-dev libssl-dev libx11-dev zlib1g-dev

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

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add_batch	<i>Add batch to registry</i>
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Description

Add batch to registry

Usage

```
add_batch(registry, batch, ...)
```

```
## S4 method for signature 'PlateRegistry'  
add_batch(registry, batch, ...)
```

Arguments

registry	PlateRegistry object
batch	Batch object
...	additional arguments

Methods (by class)

- add_batch(PlateRegistry): Add Batch object to PlateRegistry

add_layout	<i>Add layout to registry</i>
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Description

Add layout to registry

Usage

```
add_layout(registry, layout_name, layout_data, ...)
```

```
## S4 method for signature 'PlateRegistry'  
add_layout(registry, layout_name, layout_data, ...)
```

Arguments

registry	PlateRegistry object
layout_name	character name of layout
layout_data	data.frame of layout
...	additional arguments

Methods (by class)

- add_layout(PlateRegistry): Add layout to PlateRegistry

add_plate	<i>Add plate to registry</i>
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Description

Add plate to registry

Usage

```
add_plate(registry, plate, ...)

## S4 method for signature 'PlateRegistry'
add_plate(registry, plate, ...)
```

Arguments

registry	PlateRegistry object
plate	Plate object
...	additional arguments

Methods (by class)

- add_plate(PlateRegistry): Add Plate object to PlateRegistry

Batch-class	<i>S4 Class representing a Scoring Batch</i>
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Description

S4 Class representing a Scoring Batch

Slots

- uuid character.
- name character. User-assigned name.
- plate_uuids character. Ordered Plate UUIDs included in this batch.
- scores list. Scoring results per strategy/metric.
- scoring_params list. Params used in last score_batch().
- created_at POSIXct.

CGExplorer-generics	<i>S4 Generics for CGExplorer</i>
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Description

S4 Generics for CGExplorer

compute_relative_biofilm	<i>Compute relative biofilm</i>
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Description

Compute relative biofilm

Usage

```
compute_relative_biofilm(growth_m, biofilm_m)
```

Arguments

growth_m	data.frame growth metrics
biofilm_m	data.frame biofilm metrics

Value

data.frame joined and scored

detect_staining_jump	<i>Detect staining addition from a kinetic read</i>
----------------------	---

Description

Computes per-well OD delta between consecutive cycles. If the median plate-wide delta exceeds the threshold, flags that cycle as the start of the staining assay.

Usage

```
detect_staining_jump(df, threshold = 0.3)
```

Arguments

df	data.frame with Plate, Row, Column, DateTime, Time_Hours, OD_Raw
threshold	numeric, OD jump threshold (default 0.3)

Value

A list with 'has_staining', 'jump_cycle', 'jump_time', 'staining_hr'

export_batch_growth_curves_pdf

Export per-strain growth curves for a batch to a multi-page PDF

Description

Writes one page per strain (WT/control strains first, then mutants alphabetically). Each page has one facet per plate in the batch and one line per well, coloured by well ID.

Usage

```
export_batch_growth_curves_pdf(
  registry,
  batch_name,
  file,
  mode = c("raw", "corrected"),
  strains = NULL,
  progress = NULL
)
```

Arguments

registry	PlateRegistry
batch_name	character. Name of a batch in registry@batches.
file	character. Output PDF path.
mode	"raw" (raw OD values from the growth assay, as read) or "corrected" (OD_Raw minus the plate blank median at each timepoint, with no floor or clipping). Values are never normalized or rescaled; all wells, including blanks, are plotted in both modes. Staining reads are excluded.
strains	optional character vector restricting which strains are drawn.
progress	optional function(i, n, strain) called after each page.

Value

Invisibly, the number of pages written.

`extract_biofilm_metrics`*Extract biofilm metrics*

Description

Extract biofilm metrics

Usage

```
extract_biofilm_metrics(df)
```

Arguments

df data.frame corrected

Value

data.frame of biofilm metrics

`extract_growth_metrics`*Extract growth metrics*

Description

Extract growth metrics

Usage

```
extract_growth_metrics(df, growth_threshold = 0.02)
```

Arguments

df data.frame corrected
growth_threshold
 numeric, threshold for valid growth

Value

data.frame of metrics

get_layout	<i>Get layout from registry</i>
------------	---------------------------------

Description

Get layout from registry

Usage

```
get_layout(registry, layout_name, ...)

## S4 method for signature 'PlateRegistry'
get_layout(registry, layout_name, ...)
```

Arguments

registry	PlateRegistry object
layout_name	character name of layout
...	additional arguments

Methods (by class)

- `get_layout(PlateRegistry)`: Get layout from PlateRegistry

load_registry	<i>Load a PlateRegistry from RDS</i>
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Description

Load a PlateRegistry from RDS

Usage

```
load_registry(path)
```

Arguments

path	character. Path to the RDS file or directory containing cgexplorer_registry.rds.
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Value

A [PlateRegistry-class](#) object loaded from disk.

merge_plates	<i>Merge plates in registry</i>
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Description

Merge plates in registry

Usage

```
merge_plates(registry, uuids, ...)  
  
## S4 method for signature 'PlateRegistry'  
merge_plates(registry, uuids, ...)
```

Arguments

registry	PlateRegistry object
uuids	character vector of plate UUIDs
...	additional arguments

Methods (by class)

- merge_plates(PlateRegistry): Merge multiple plates in PlateRegistry

new_batch	<i>Constructor for Batch</i>
-----------	------------------------------

Description

Constructor for Batch

Usage

```
new_batch(name, plate_uuids)
```

Arguments

name	character. Name of the batch.
plate_uuids	character vector. UUIDs of plates included in this batch.

Value

A [Batch-class](#) object.

new_plate	<i>Constructor for Plate</i>
-----------	------------------------------

Description

Constructor for Plate

Usage

```
new_plate(slot_id, growth_data, layout, timezone = "America/Halifax")
```

Arguments

- slot_id character. Unique identifier for the plate slot (e.g. "S1L1").
- growth_data data.frame. Raw growth assay readings.
- layout data.frame. Well layout definition.
- timezone character. Timezone string, defaults to "America/Halifax".

Value

A [Plate-class](#) object.

new_registry	<i>Constructor for PlateRegistry</i>
--------------	--------------------------------------

Description

Constructor for PlateRegistry

Usage

```
new_registry(project_name = "Untitled Project", project_dir = getwd())
```

Arguments

- project_name character. Project display name.
- project_dir character. Path to project directory storing registry.

Value

A [PlateRegistry-class](#) object.

parse_plate_layout	<i>Parse 96 or 384 well Plate Layout</i>
--------------------	--

Description

Parse 96 or 384 well Plate Layout

Usage

```
parse_plate_layout(filepath)
```

Arguments

filepath character.

Value

A list containing format info and the parsed data.frame.

parse_tecan_txt	<i>Parse Tecan Plate Reader output (.txt)</i>
-----------------	---

Description

Parse Tecan Plate Reader output (.txt)

Usage

```
parse_tecan_txt(filepath)
```

Arguments

filepath character.

Value

A data.frame with Plate, DateTime, Row, Column, OD

Plate-class	<i>S4 Class representing a Chemo-Genomic Plate</i>
-------------	--

Description

S4 Class representing a Chemo-Genomic Plate

Slots

uuid character. Internal UUID.
 slot_id character. E.g. "S1L1".
 label character. User-facing name.
 treatment character. E.g. "NoDrug", "Drug1".
 replicate integer. Biological replicate number.
 media character. Growth media label.
 layout data.frame. Well map.
 assays list. Named list of assay data.frames (growth, final, staining).
 staining_hr numeric. Hours post t0 when staining was performed (NA if unknown).
 staining_confirmed logical. TRUE after user confirms staining detection.
 t0 POSIXct. Earliest DateTime in assays\$growth.
 t_end POSIXct. Latest DateTime across all non-NULL assays.
 timezone character. Timezone, fixed to "America/Halifax".
 metrics list. Populated by compute_metrics().
 qc_flags list. QC results.
 provenance list. Audit trail records.
 is_merged logical. TRUE if created from merge_plates().

PlateRegistry-class	<i>S4 Class representing the Project Plate Registry</i>
---------------------	---

Description

S4 Class representing the Project Plate Registry

Slots

plates list. Named list: UUID -> Plate S4 object.

batches list. Named list: batch_name -> Batch S4 object.

layouts list. Named layout registry.

project_name character. User-assigned project name.

project_dir character. Absolute path to directory holding registry.rds.

schema_version character. Package version at save time.

created_at POSIXct.

modified_at POSIXct.

plot_multi_strain_growth_curves
Plot Multi-Strain Growth Curves

Description

Plot Multi-Strain Growth Curves

Usage

```
plot_multi_strain_growth_curves(
  df,
  selected_genes = NULL,
  use_raw_od = FALSE,
  color_by = "strain"
)
```

Arguments

df	data.frame containing Time_Hours, OD_Corrected, OD_Raw, Gene, Type, Rep_Suffix, Row, Column
selected_genes	character vector of selected genes/strains
use_raw_od	logical. TRUE for OD_Raw, FALSE for OD_Corrected
color_by	character. "strain", "replicate", or "type"

Value

plotly object

plot_plate_qc_layout *Plot Plate QC Layout*

Description

Plot Plate QC Layout

Usage

```
plot_plate_qc_layout(
  plate,
  metric = "Growth_Endpoint_OD",
  colorscale = "plasma",
  cmin = NULL,
  cmax = NULL
)
```

Arguments

plate	Plate object
metric	character. Column name in metrics to plot.
colorscale	character. Color scheme key.
cmin	numeric. Minimum value for color scale.
cmax	numeric. Maximum value for color scale.

Value

plotly object

plot_replicate_growth_curves
Plot Replicate Growth Curves

Description

Plot Replicate Growth Curves

Usage

```
plot_replicate_growth_curves(replicate_data, stain_hr = 26)
```

Arguments

replicate_data	data.frame containing Time_Hours, OD_Raw or OD_Corrected, Row, Column, Gene, Rep_Suffix
stain_hr	numeric staining hour threshold

Value

plotly object

remove_batch	<i>Remove batch from registry</i>
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Description

Remove batch from registry

Usage

```
remove_batch(registry, batch_name, ...)

## S4 method for signature 'PlateRegistry'
remove_batch(registry, batch_name, ...)
```

Arguments

registry	PlateRegistry object
batch_name	character batch name
...	additional arguments

Methods (by class)

- remove_batch(PlateRegistry): Remove Batch object from PlateRegistry

remove_layout	<i>Remove layout from registry</i>
---------------	------------------------------------

Description

Remove layout from registry

Usage

```
remove_layout(registry, layout_name, ...)

## S4 method for signature 'PlateRegistry'
remove_layout(registry, layout_name, ...)
```

Arguments

registry	PlateRegistry object
layout_name	character name of layout
...	additional arguments

Methods (by class)

- remove_layout(PlateRegistry): Remove layout from PlateRegistry

remove_plate	<i>Remove plate from registry</i>
--------------	-----------------------------------

Description

Remove plate from registry

Usage

```
remove_plate(registry, uuid, ...)

## S4 method for signature 'PlateRegistry'
remove_plate(registry, uuid, ...)
```

Arguments

registry	PlateRegistry object
uuid	character plate UUID
...	additional arguments

Methods (by class)

- remove_plate(PlateRegistry): Remove Plate object from PlateRegistry

run_cgexplorer_app	<i>Run the Shiny Application</i>
--------------------	----------------------------------

Description

Run the Shiny Application

Usage

```
run_cgexplorer_app(...)
```

Arguments

...	arguments to pass to golem_opts.
-----	----------------------------------

save_registry	<i>Save registry to disk</i>
---------------	------------------------------

Description

Save registry to disk

Usage

```
save_registry(registry, ...)  
  
## S4 method for signature 'PlateRegistry'  
save_registry(registry, ...)
```

Arguments

registry	PlateRegistry object
...	additional arguments

Methods (by class)

- save_registry(PlateRegistry): Save PlateRegistry to RDS file

score_batch_dataset	<i>Standardized Scoring Engine</i>
---------------------	------------------------------------

Description

Standardized Scoring Engine

Usage

```
score_batch_dataset(  
  pheno_df,  
  strategy_type = c("NoDrug_Plates", "NoDrug_Wells"),  
  metrics,  
  control_drug = "NoDrug"  
)
```

Arguments

pheno_df	data.frame containing aggregated phenotypic metrics across a batch
strategy_type	character, either "NoDrug_Plates" or "NoDrug_Wells"
metrics	character vector of target metrics
control_drug	character, name of control treatment

Value

data.frame of scores

subtract_plate_blanks	<i>Subtract blanks at the plate level</i>
-----------------------	---

Description

Subtract blanks at the plate level

Usage

```
subtract_plate_blanks(df, blank_threshold = 0.05)
```

Arguments

df	data.frame with Row, Column, Time_Hours, OD_Raw, Type, Is_Stained
blank_threshold	numeric, threshold for bad blanks

Value

list with corrected 'data' and 'removed_blanks'

update_plate	<i>Update plate in registry</i>
--------------	---------------------------------

Description

Update plate in registry

Usage

```
update_plate(registry, plate, ...)

## S4 method for signature 'PlateRegistry'
update_plate(registry, plate, ...)
```

Arguments

registry	PlateRegistry object
plate	Plate object
...	additional arguments

Methods (by class)

- update_plate(PlateRegistry): Update Plate object in PlateRegistry

validate_batch_plates *Validate plate eligibility and layout uniformity for a batch*

Description

Validate plate eligibility and layout uniformity for a batch

Usage

```
validate_batch_plates(registry, uuids)
```

Arguments

registry	PlateRegistry
uuids	character vector of plate UUIDs

Value

TRUE if valid, otherwise throws an error

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