

Package: ConvergeR (via r-universe)

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Title Whitfield Convergence Score and Seurat Metadata Association

Version 0.99.0

Description Calculates the convergence score defined by Whitfield et al. 2026 (doi: 10.1158/0008-5472.CAN-25-4403). It allows visualization of this score alongside qualitative and quantitative Seurat object metadata via barplots and density curves, and runs appropriate statistical tests for associations.

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BugReports <https://github.com/pauldeboissier1/ConvergeR/issues>

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CalculateConvergedScore
Calculate Converged Score

Description

Computes a "convergence score" comparing two groups of Seurat module scores. Each group can be made of a single score or a combination of several scores; the underlying methodology is identical either way.

Usage

```
CalculateConvergedScore(
  seurat_obj,
  principal_score,
  other_scores,
  principal_name = "Principal",
  other_name = "Other",
  output_colname = "Converged_Score",
  direction_colname = NULL,
  color_colname = NULL,
  principal_color = "#2ecc71",
  other_color = "#e74c3c"
)
```

Arguments

seurat_obj	Seurat object. Its meta.data must already contain the score columns.
principal_score	Character. Name of one score, OR a character vector naming several scores.
other_scores	Character. Same as principal_score, but for the group compared against.
principal_name	Character. Human-readable label (default: "Principal").
other_name	Character. Human-readable label (default: "Other").
output_colname	Character. Name of the column for the score (default: "Converged_Score").
direction_colname	Character or NULL. Name of the interpretation column.

color_colname Character or NULL. Name of the hex color column.
principal_color Character. Hex color for principal group (default: "#2ecc71").
other_color Character. Hex color for other group (default: "#e74c3c").

Value

The same Seurat object, with the convergence score columns added to meta.data.

References

Whitfield HJ, Anderson ND, Burke C, Groot Koerkamp MJ, Parks C, Ogbonnah T, Wood Y, Piapi A, Robertson E, Watt E, White A, De Noon S, Kennedy J, Nagrecha R, Meister MT, Aladowicz E, Man YKS, Laspidea V, Trinh MK, Hodder A, Porter T, Lawrence JE, Tuck E, Nguyen T, Kelsey A, Flanagan AM, Hewitt R, Smeulders N, Slater O, Hutchinson JC, Sebire N, Shipley JM, Drost J, Straathof K, Behjati S. High-Risk Rhabdomyosarcomas Feature a Convergent Cell State. *Cancer Res.* 2026 Jul 14. doi: 10.1158/0008-5472.CAN-25-4403. PMID: 42446905.

Examples

```
# 1. Environment Setup and Data Preparation
seu_path <- system.file("extdata", "pbmc3k_subset.rds", package = "ConvergeR")
seu <- readRDS(seu_path)
seu <- Seurat::NormalizeData(seu, verbose = FALSE)

set.seed(42)
seu$age <- sample(20:70, ncol(seu), replace = TRUE)
seu$tumor_status <- sample(c("Primary", "Metastatic"), ncol(seu), replace = TRUE)
seu$treatment <- sample(c("Treated", "Untreated"), ncol(seu), replace = TRUE)
seu$SS <- paste0("Patient_", sample(1:5, ncol(seu), replace = TRUE))

# 2. Importing MSigDB Signatures and Scoring
if (requireNamespace("msigdb", quietly = TRUE)) {
  hs <- msigdb::msigdb(species = "Homo sapiens", category = "H")
  raw_group1 <- hs[hs$gs_name == "HALLMARK_INTERFERON_ALPHA_RESPONSE", ]$gene_symbol
  raw_group2 <- hs[hs$gs_name == "HALLMARK_INFLAMMATORY_RESPONSE", ]$gene_symbol

  group1_genes <- intersect(raw_group1, rownames(seu))
  group2_genes <- intersect(raw_group2, rownames(seu))

  seu <- Seurat::AddModuleScore(seu, features = list(group1_genes), name = "Score_IFN_")
  seu <- Seurat::AddModuleScore(seu, features = list(group2_genes), name = "Score_Inflam_")
  seu$Score_IFN <- seu$Score_IFN_1
  seu$Score_Inflam <- seu$Score_Inflam_1

# 3. Computing the Convergence Score
seu <- CalculateConvergedScore(
  seurat_obj = seu,
  principal_score = "Score_IFN",
  other_scores = "Score_Inflam",
  principal_name = "Interferon",
```

```

    other_name = "Inflammatory",
    output_colname = "Converged_Immune",
    principal_color = "#9b59b6",
    other_color = "#e67e22"
  )
}
```

PlotConvergenceCrossedProportion

Plot Convergence Crossed Proportion

Description

Draws a 100%-stacked barplot of cell proportions across categories of `x_var`, colored by a convergence-direction column, and separated (faceted) by a secondary categorical variable (`facet_var`).

Usage

```

PlotConvergenceCrossedProportion(
  seurat_obj,
  x_var,
  fill_var,
  facet_var,
  color_var = NULL,
  title = NULL,
  x_label = NULL
)
```

Arguments

<code>seurat_obj</code>	Seurat object whose meta.data holds <code>x_var</code> , <code>fill_var</code> , <code>facet_var</code> , and the color column.
<code>x_var</code>	Character. Name of the meta.data column used on the x-axis.
<code>fill_var</code>	Character. Name of the meta.data column used to fill the bars.
<code>facet_var</code>	Character. Name of the meta.data column used to facet the plot (e.g., "tumor_status").
<code>color_var</code>	Character or NULL. Name of the meta.data column holding the hex color.
<code>title</code>	Character or NULL. Plot title.
<code>x_label</code>	Character or NULL. X-axis label.

Value

A ggplot object.

Examples

```

seu_path <- system.file("extdata", "pbmc3k_subset.rds", package = "ConvergeR")
seu <- readRDS(seu_path)
set.seed(42)
seu$SS <- paste0("Patient_", sample(1:5, ncol(seu), replace = TRUE))
seu$tumor_status <- sample(c("Primary", "Metastatic"), ncol(seu), replace = TRUE)
seu$Score_IFN <- rnorm(ncol(seu))
seu$Score_Inflam <- rnorm(ncol(seu))

seu <- CalculateConvergedScore(
  seurat_obj = seu,
  principal_score = "Score_IFN",
  other_scores = "Score_Inflam",
  output_colname = "Converged_Immune"
)

b_cross <- PlotConvergenceCrossedProportion(
  seurat_obj = seu,
  x_var = "SS",
  fill_var = "Converged_Immune_Direction",
  facet_var = "tumor_status",
  title = "Immune Convergence split by Tumor Status",
  x_label = "Patient ID"
)
print(b_cross)

```

PlotConvergenceDensity

Plot Convergence Density

Description

Draws overlapping density curves of a continuous variable (`x_var`), split by a convergence-direction column (`fill_var`).

Usage

```

PlotConvergenceDensity(
  seurat_obj,
  x_var,
  fill_var,
  color_var = NULL,
  title = NULL,
  x_label = NULL,
  alpha = 0.6
)

```

Arguments

<code>seurat_obj</code>	Seurat object whose meta.data holds <code>x_var</code> , <code>fill_var</code> , and its matching color column.
<code>x_var</code>	Character. Name of the meta.data column holding the continuous variable (e.g. "age").
<code>fill_var</code>	Character. Name of the meta.data column used to fill the density curves.
<code>color_var</code>	Character or NULL. Name of the meta.data column holding the hex color.
<code>title</code>	Character or NULL. Plot title.
<code>x_label</code>	Character or NULL. X-axis label. Defaults to <code>x_var</code> .
<code>alpha</code>	Numeric. Transparency of the density fill, between 0 and 1 (default: 0.6).

Value

A ggplot object.

Examples

```

seu_path <- system.file("extdata", "pbmc3k_subset.rds", package = "ConvergeR")
seu <- readRDS(seu_path)
set.seed(42)
seu$age <- sample(20:70, ncol(seu), replace = TRUE)
seu$Score_IFN <- rnorm(ncol(seu))
seu$Score_Inflam <- rnorm(ncol(seu))

seu <- CalculateConvergedScore(
  seurat_obj = seu,
  principal_score = "Score_IFN",
  other_scores = "Score_Inflam",
  output_colname = "Converged_Immune"
)

PlotConvergenceDensity(
  seurat_obj = seu,
  x_var = "age",
  fill_var = "Converged_Immune_Direction",
  x_label = "Patient Age"
)

```

PlotConvergenceProportion

Plot Convergence Proportion

Description

Draws a 100%-stacked barplot of cell proportions across categories of `x_var`, colored by a convergence-direction column (`fill_var`). The color mapping is extracted automatically from meta.data based on the color column generated by `CalculateConvergedScore()`.

Usage

```
PlotConvergenceProportion(
  seurat_obj,
  x_var,
  fill_var,
  color_var = NULL,
  title = NULL
)
```

Arguments

<code>seurat_obj</code>	Seurat object whose meta.data holds both <code>fill_var</code> and its matching color column.
<code>x_var</code>	Character. Name of the meta.data column used on the x-axis (e.g. a patient identifier).
<code>fill_var</code>	Character. Name of the meta.data column used to fill the bars.
<code>color_var</code>	Character or NULL. Name of the meta.data column holding the hex color. Defaults to <code>paste0(fill_var, "_Color")</code> .
<code>title</code>	Character or NULL. Plot title. Defaults to <code>x_var</code> .

Value

A ggplot object.

Examples

```
seu_path <- system.file("extdata", "pbmc3k_subset.rds", package = "ConvergeR")
seu <- readRDS(seu_path)
set.seed(42)
seu$SS <- paste0("Patient_", sample(1:5, ncol(seu), replace = TRUE))

# Simulate fast scores to ensure example runs efficiently
seu$Score_IFN <- rnorm(ncol(seu))
seu$Score_Inflam <- rnorm(ncol(seu))

seu <- CalculateConvergedScore(
  seurat_obj = seu,
  principal_score = "Score_IFN",
  other_scores = "Score_Inflam",
  output_colname = "Converged_Immune"
)

p <- PlotConvergenceProportion(
  seurat_obj = seu,
  x_var = "SS",
  fill_var = "Converged_Immune_Direction",
  title = "Immune Convergence by Patient"
)
print(p)
```

TestConvergenceScore *Test Convergence Score*

Description

Runs a statistical test between a numeric convergence score and another variable, automatically choosing the appropriate test (Spearman, Wilcoxon, or Kruskal-Wallis).

Usage

```
TestConvergenceScore(
  seurat_obj,
  score_var,
  test_var,
  level = c("cell", "patient"),
  patient_id_var = NULL
)
```

Arguments

seurat_obj	Seurat object whose meta.data holds score_var and test_var.
score_var	Character. Name of the meta.data column holding the numeric score.
test_var	Character. Name of the meta.data column to test the score against.
level	Character. Either "cell" (default) or "patient" (pseudobulk aggregation).
patient_id_var	Character. Name of the meta.data column identifying patients (required if level = "patient").

Value

The underlying htest object (invisibly). A message is printed summarizing the results.

Examples

```
seu_path <- system.file("extdata", "pbmc3k_subset.rds", package = "ConvergeR")
seu <- readRDS(seu_path)
set.seed(42)
seu$SS <- paste0("Patient_", sample(1:5, ncol(seu), replace = TRUE))
seu$age <- sample(20:70, ncol(seu), replace = TRUE)
seu$Score_IFN <- rnorm(ncol(seu))
seu$Score_Inflam <- rnorm(ncol(seu))

seu <- CalculateConvergedScore(
  seurat_obj = seu,
  principal_score = "Score_IFN",
  other_scores = "Score_Inflam",
  output_colname = "Converged_Immune"
)
```

```
TestConvergenceScore(  
  seurat_obj = seu,  
  score_var = "Converged_Immune",  
  test_var = "age",  
  level = "patient",  
  patient_id_var = "SS"  
)
```

TestMultivariateConvergence
Test Multivariate Convergence

Description

Fits a multivariate linear model (lm) to test a numeric convergence score against multiple covariates simultaneously, correcting for confounding factors.

Usage

```
TestMultivariateConvergence(  
  seurat_obj,  
  score_var,  
  test_vars,  
  level = c("cell", "patient"),  
  patient_id_var = NULL  
)
```

Arguments

seurat_obj	Seurat object whose meta.data holds the variables.
score_var	Character. Name of the meta.data column holding the numeric score.
test_vars	Character vector. Names of the meta.data columns to include in the model.
level	Character. Either "cell" (default) or "patient" (pseudobulk aggregation).
patient_id_var	Character. Name of the meta.data column identifying patients (required if level = "patient").

Value

The summary.lm() object (invisibly). A detailed message is printed summarizing the model.

Examples

```
seu_path <- system.file("extdata", "pbmc3k_subset.rds", package = "ConvergeR")
seu <- readRDS(seu_path)
set.seed(42)
seu$SS <- paste0("Patient_", sample(1:5, ncol(seu), replace = TRUE))
seu$age <- sample(20:70, ncol(seu), replace = TRUE)
seu$tumor_status <- sample(c("Primary", "Metastatic"), ncol(seu), replace = TRUE)
seu$treatment <- sample(c("Treated", "Untreated"), ncol(seu), replace = TRUE)
seu$Score_IFN <- rnorm(ncol(seu))
seu$Score_Inflam <- rnorm(ncol(seu))

seu <- CalculateConvergedScore(
  seurat_obj = seu,
  principal_score = "Score_IFN",
  other_scores = "Score_Inflam",
  output_colname = "Converged_Immune"
)

TestMultivariateConvergence(
  seurat_obj = seu,
  score_var = "Converged_Immune",
  test_vars = c("age", "tumor_status", "treatment"),
  level = "patient",
  patient_id_var = "SS"
)
```

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