

Package: harmorust (via r-universe)

October 31, 2026

Title 'Rust' Native Kernels for 'Harmony' Single-Cell Integration

Version 0.1.0

Description 'Rust' reimplement of the 'Harmony' integration loop (soft k-means, diversity penalty, mixture-of-experts ridge) with the same RunHarmony() signature used by the immunogenomics 'Harmony' R package. Designed to sit next to 'seurust': 'Seurat'/seurust' produce the PCA embedding, 'harmorust' corrects it. Installing from source builds the 'harmorust' CLI with Cargo and places it in the package 'bin' directory.

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URL <https://github.com/NebiliI/harmony-rs>,
<https://NebiliI.r-universe.dev/harmorust>

BugReports <https://github.com/NebiliI/harmony-rs/issues>

Encoding UTF-8

Depends R (>= 4.2)

Imports jsonlite, stats

Suggests Seurat (>= 4.1.1), SingleCellExperiment, ggplot2, seurust, testthat (>= 3.0.0)

SystemRequirements Cargo (Rust's package manager), rustc (>= 1.89)

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harmorust-package	<i>Rust Native Kernels for Harmony Single-Cell Integration</i>
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Description

Rust reimplementa-tion of the Harmony integration loop with the same RunHarmony() signature used by the immunogenomics Harmony R package. A source install compiles the harmorust CLI with Cargo and stores it in the package ‘bin’ directory.

Details

Package: harmorust
Version: 0.1.0
License: MIT

Typical workflow: Seurat or seurust produce a PCA embedding, then [RunHarmony](#) corrects batch effects.

Author(s)

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See Also

[RunHarmony](#), [harmony_options](#), [HarmonyConvergencePlot](#)

harmony_options	<i>Advanced Harmony options</i>
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Description

Same names as `harmony::harmony_options`.

Usage

```
harmony_options(  
  alpha = 0.2,  
  tau = 0,  
  block.size = 0.05,  
  max.iter.cluster = 4,  
  epsilon.cluster = 1e-3,  
  epsilon.harmony = 1e-2,  
  batch.prop.cutoff = 1e-5  
)
```

Arguments

<code>alpha</code>	Harmony2 automatic-lambda scale. Default 0.2.
<code>tau</code>	Softens theta for small batches. Default 0.
<code>block.size</code>	Fraction of cells updated per clustering block. (0, 1].
<code>max.iter.cluster</code>	Inner clustering iterations per Harmony round.
<code>epsilon.cluster</code>	Clustering convergence tolerance.
<code>epsilon.harmony</code>	Outer-loop convergence tolerance.
<code>batch.prop.cutoff</code>	Skip a batch in a cluster below this soft membership.

Value

An object of class `harmony_options`.

Examples

```
opts <- harmony_options(block.size = 0.1, max.iter.cluster = 5)
```

`HarmonyConvergencePlot`*Plot Harmony objective over clustering steps*

Description

Same role as the unexported `HarmonyConvergencePlot` helper in `immunogenomics/harmony`: visualise `objective_kmeans` across outer rounds.

Usage

```
HarmonyConvergencePlot(  
  harmonyObj,  
  round_start = 1,  
  round_end = Inf,  
  do_wrap = FALSE  
)
```

Arguments

<code>harmonyObj</code>	Object from <code>RunHarmony(..., return_object = TRUE)</code> .
<code>round_start</code>	First outer Harmony round to include (1-based).
<code>round_end</code>	Last outer Harmony round to include.
<code>do_wrap</code>	Facet by outer round when TRUE.

Value

A ggplot object.

See Also

[RunHarmony](#)

Examples

```
## Not run:  
obj <- RunHarmony(pca_matrix, meta_data, vars_use = "donor",  
  return_object = TRUE)  
HarmonyConvergencePlot(obj)  
  
## End(Not run)
```

Description

Drop-in companion to `harmony::RunHarmony()`. The default method matches Harmony's matrix API (`data_mat`, `meta_data`, `vars_use`). Seurat and SingleCellExperiment methods match the original package so a seurat-preprocessed object can be integrated without changing the rest of the workflow.

Usage

```
RunHarmony(...)

## Default S3 method:
RunHarmony(
  data_mat,
  meta_data,
  vars_use,
  theta = NULL,
  sigma = 0.1,
  lambda = NULL,
  nclust = NULL,
  max_iter = 10,
  early_stop = TRUE,
  ncores = 1,
  plot_convergence = FALSE,
  return_object = FALSE,
  verbose = TRUE,
  .options = harmony_options(),
  ...
)

## S3 method for class 'Seurat'
RunHarmony(
  object,
  group.by.vars,
  reduction.use = "pca",
  reduction = NULL,
  dims.use = NULL,
  reduction.save = "harmony",
  reduction.name = NULL,
  project.dim = TRUE,
  ...
)

## S3 method for class 'SingleCellExperiment'
```

```
RunHarmony(
  object,
  group.by.vars,
  dims.use = NULL,
  verbose = TRUE,
  reduction.save = "HARMONY",
  ...
)
```

Arguments

<code>object</code>	PCA matrix, Seurat object, or SingleCellExperiment.
<code>data_mat</code>	Cell embedding matrix (cells $\times$ PCs or PCs $\times$ cells).
<code>meta_data</code>	Data frame of covariates, or a batch vector.
<code>vars_use, group.by.vars</code>	Covariate name(s) Harmony should remove.
<code>theta</code>	Diversity penalty. Default 2 per covariate.
<code>sigma</code>	Soft k-means width. Default 0.1.
<code>lambda</code>	Ridge penalty. NULL enables Harmony2 automatic lambda.
<code>nclust</code>	Number of soft clusters. Default $\min(\text{round}(n/30), 100)$.
<code>max_iter</code>	Outer Harmony rounds. Default 10.
<code>early_stop</code>	Stop when the objective stalls. Default TRUE.
<code>ncores</code>	Rayon threads for the Rust kernel (RAYON_NUM_THREADS).
<code>plot_convergence</code>	Draw HarmonyConvergencePlot when TRUE.
<code>return_object</code>	Return a Harmony-like object instead of the matrix.
<code>verbose</code>	Print progress messages.
<code>.options</code>	Advanced options from harmony_options .
<code>reduction.use, reduction</code>	Name of the input reduction. Default "pca".
<code>reduction.save, reduction.name</code>	Name of the written reduction.
<code>dims.use</code>	Which PCs to correct.
<code>project.dim</code>	Project Harmony loadings (Seurat). Default TRUE.
<code>...</code>	Must be empty (legacy Harmony args are rejected).

Value

For the default method, a numeric matrix of corrected embeddings, or a Harmony-like object when `return_object = TRUE`. Seurat and SingleCellExperiment methods return the input object with a Harmony reduction added.

See Also

[harmony_options](#), [HarmonyConvergencePlot](#)

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