

Package: CrossDomainAdjust (via r-universe)

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Type Package

Title Lambda-Controlled Cross-Domain Feature Adjustment

Version 0.1.1

Description Provides cross-domain feature adjustment methods for biological and other tabular data. Domain labels define group centroids, and singular value decomposition of their offsets from a common anchor estimates a domain-shift subspace. An orthogonal projection removes a user-controlled fraction of each sample's component in that subspace. A correction strength of zero preserves the input; a strength of one removes the entire learned subspace component. Intermediate values provide partial correction. The fitted transformation can be applied to new samples without refitting.

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Author Weikaixin Kong [aut, cre]

Maintainer Weikaixin Kong <weikaixin.kong@aalto.fi>

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fit_domain_projector *Fit a Cross-Domain Feature Projector*

Description

Learns the low-dimensional subspace spanned by domain centroid differences and stores the orthogonal projection matrix for that subspace. For K domains, the learned domain-shift subspace has rank at most $K - 1$ when the anchor is in the affine hull of the centroids, including both built-in anchors. An arbitrary custom anchor can give rank K , subject to the number of features.

Usage

```
fit_domain_projector(x, domain, anchor = "domain_mean")
```

Arguments

<code>x</code>	Numeric matrix or data frame with samples in rows and features in columns.
<code>domain</code>	Character or factor vector giving the domain label for each row of <code>x</code> .
<code>anchor</code>	Character string or named numeric vector. Use "domain_mean" for the equal-weight mean of domain centroids, matching $(\mu_1 + \dots + \mu_K) / K$. Use "sample_mean" for the sample-size-weighted feature mean. A named numeric vector can also be supplied as a custom projection anchor.

Value

An object of class "domain_projector".

Examples

```
set.seed(1)
x <- rbind(
  matrix(rnorm(20), nrow = 5),
  matrix(rnorm(20) + 1, nrow = 5),
  matrix(rnorm(20) - 1, nrow = 5)
)
colnames(x) <- paste0("feature_", seq_len(ncol(x)))
domain <- rep(c("A", "B", "C"), each = 5)

projector <- fit_domain_projector(x, domain, anchor = "domain_mean")
projector
```

project_features	<i>Project Features with a Fitted Cross-Domain Projector</i>
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Description

Corrects feature values by removing a lambda-controlled fraction of the learned domain-shift projection component: $x_{\text{corrected}} = x - \lambda * ((x - \text{anchor}) \% \% P)$. $\lambda = 0$ returns the original features. $\lambda = 1$ fully projects away the learned cross-domain subspace.

Usage

```
project_features(projector, x, lambda = 1)
```

Arguments

projector	A "domain_projector" returned by <code>fit_domain_projector()</code> .
x	Numeric matrix, data frame, or named numeric vector of feature values.
lambda	Numeric scalar in $[0, 1]$.

Value

A numeric matrix with corrected features.

Examples

```
set.seed(2)
x <- rbind(
  matrix(rnorm(20), nrow = 5),
  matrix(rnorm(20) + 1, nrow = 5)
)
colnames(x) <- paste0("feature_", seq_len(ncol(x)))
domain <- rep(c("A", "B"), each = 5)

projector <- fit_domain_projector(x, domain)
project_features(projector, x, lambda = 0)
project_features(projector, x, lambda = 0.5)
project_features(projector, x, lambda = 1)
```

project_new_sample	<i>Project One New Sample</i>
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Description

Convenience wrapper for correcting a single named feature vector.

Usage

```
project_new_sample(projector, sample, domain = NULL, lambda = 1)
```

Arguments

projector	A "domain_projector" returned by <code>fit_domain_projector()</code> .
sample	Named numeric vector, one-row data frame, or one-row matrix.
domain	Optional source-domain label for the sample. If supplied, it must match one of the training domains.
lambda	Numeric scalar in $[0, 1]$.

Value

A named numeric vector of corrected features.

Examples

```
set.seed(3)
x <- rbind(
  matrix(rnorm(20), nrow = 5),
  matrix(rnorm(20) + 1, nrow = 5)
)
colnames(x) <- paste0("feature_", seq_len(ncol(x)))
domain <- rep(c("A", "B"), each = 5)

projector <- fit_domain_projector(x, domain)
new_sample <- setNames(rnorm(ncol(x)) + 1, colnames(x))
project_new_sample(projector, new_sample, domain = "B", lambda = 0.8)
```

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