

# Package: lyubishchev (via r-universe)

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**Type** Package

**Title** Quantitative Taxonomy Methods of A.A. Lyubishchev (1943)

**Version** 0.1.0

**Description** Implements the multivariate classification methods of Alexander Alexandrovich Lyubishchev (1890-1972), as described in his 1943 manuscript 'Programma obshchey sistematiki' Lyubishchev (1943) <https://www.zin.ru/animalia/coleoptera/rus/lyubis05.htm> and published in Lyubishchev (1962) <https://www.jstor.org/stable/2527894>. Provides `divergence_coefficient()` for measuring separation between groups on continuous features, `scatter_ellipse()` for fitting covariance ellipses per class, `transgression()` for detecting ellipse overlap, and `classify()` for Bayesian posterior classification. These methods predate and are more general than the binary-character similarity coefficients of Sokal and Sneath (1963) that appear in other R packages.

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**Encoding** UTF-8

**RoxygenNote** 7.3.1

**Suggests** testthat (>= 3.0.0), knitr, rmarkdown, ggplot2

**VignetteBuilder** knitr

**URL** <https://github.com/AkzhanBerdi/lyubishchev-r>

**BugReports** <https://github.com/AkzhanBerdi/lyubishchev-r/issues>

**NeedsCompilation** no

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**Repository** <https://akzhanberdi.r-universe.dev>

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classify	<i>Classify a Specimen by Multivariate Posterior Probability</i>
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### Description

Assigns posterior class probabilities to a new specimen using the Edgeworth-Pearson multivariate Gaussian likelihood for each class scatter ellipse. For each class the log-likelihood of the specimen under a multivariate normal with the class mean and covariance is computed, and a softmax over the per-class log-likelihoods yields posterior probabilities.

### Usage

```
classify(specimen, ellipses)
```

### Arguments

specimen	A numeric vector of feature values for a single observation.
ellipses	A named list of scatter ellipses as returned by <a href="#">scatter_ellipse</a> .

### Details

The log-likelihood for class  $k$  is

$$-\frac{1}{2} (p \log 2\pi + \log |\Sigma_k| + (x - \mu_k)^\top \Sigma_k^{-1} (x - \mu_k))$$

where  $p$  is the number of features,  $\mu_k$  and  $\Sigma_k$  are the class mean and covariance, and  $x$  is the specimen.

### Value

A named list with one element per class. Each element is a list with components:

- mahalanobis\_distance** Squared Mahalanobis distance from the specimen to the class centroid.
- log\_likelihood** Multivariate Gaussian log-likelihood of the specimen under the class.
- posterior** Posterior probability of the class (softmax over the per-class log-likelihoods). Posteriors sum to 1 across classes.

### References

Lubischew, A.A. (1962). On the use of discriminant functions in taxonomy. *Biometrics*, 18(4), 455-477.

**See Also**[scatter\\_ellipse](#)**Examples**

```
ellipses <- scatter_ellipse(iris[, 1:4], iris$Species)
specimen <- c(5.1, 3.5, 1.4, 0.2)
result <- classify(specimen, ellipses)
sapply(result, function(r) r$posterior)
```

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 divergence\_coefficient

*Lyubishchev's Divergence Coefficient*


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**Description**

Computes Lyubishchev's divergence coefficient  $D$  between two groups measured on one or more continuous features. The coefficient summarises the standardised separation between the group means, summed across features:

$$D = \sum_j \frac{(M_{1j} - M_{2j})^2}{\sigma_{1j}^2 + \sigma_{2j}^2}$$

where  $M_{ij}$  and  $\sigma_{ij}^2$  are the mean and (sample) variance of feature  $j$  in group  $i$ . Features whose pooled variance is zero are skipped to avoid division by zero.

**Usage**

```
divergence_coefficient(a, b)
```

**Arguments**

- |   |   |
|---|---|
| a | A numeric matrix or data frame for the first group, with one row per observation and one column per feature. A numeric vector is treated as a single-feature group. |
| b | A numeric matrix or data frame for the second group, with the same columns (features) as a.   |

**Details**

This is the measure described in Lyubishchev's 1943 manuscript and later published in English by Lubishev (1962). It predates and is more general than the binary-character similarity coefficients of Sokal and Sneath (1963), operating directly on continuous measurements.

**Value**

A single numeric value, the divergence coefficient  $D$ . Larger values indicate greater separation between the groups.

## References

- Lyubishchev, A.A. (1943). Programma obshchey sistematiki [Program of General Systematics]. Manuscript, 22 November 1943.
- Lubischew, A.A. (1962). On the use of discriminant functions in taxonomy. *Biometrics*, 18(4), 455-477.

## Examples

```
setosa <- as.matrix(iris[iris$Species == "setosa", 1:4])
versicolor <- as.matrix(iris[iris$Species == "versicolor", 1:4])
divergence_coefficient(setosa, versicolor)
```

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scatter\_ellipse      *Fit Scatter Ellipses per Class*

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## Description

Fits a covariance ellipse to each class in a labelled multivariate data set. For every class the function computes the centroid (mean vector), the feature covariance matrix and the sample size. These ellipses are the building blocks for [transgression](#) and [classify](#).

## Usage

```
scatter_ellipse(X, y)
```

## Arguments

- |   |  |
|---|--|
| X | A numeric matrix or data frame of observations, with one row per observation and one column per feature. |
| y | A vector of class labels of length nrow(X). May be a factor, character or numeric vector.                |

## Value

A named list with one element per class. Each element is itself a list with components:

- mean** Numeric vector of feature means for the class.
- cov** Feature covariance matrix for the class.
- n\_samples** Integer count of observations in the class.

The names of the list are the class labels (coerced to character).

## References

- Lubischew, A.A. (1962). On the use of discriminant functions in taxonomy. *Biometrics*, 18(4), 455-477.

**See Also**

[transgression](#), [classify](#)

**Examples**

```
ellipses <- scatter_ellipse(iris[, 1:4], iris$Species)
ellipses[["setosa"]]$mean
ellipses[["setosa"]]$n_samples
```

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transgression

*Detect Overlap (Transgression) Between Two Scatter Ellipses*


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**Description**

Tests whether two class scatter ellipses overlap, in Lyubishchev's sense of "transgression" between groups. The centroids are compared using the squared Mahalanobis distance under the pooled covariance of the two classes, and that distance is compared against a chi-squared threshold with degrees of freedom equal to the number of features. When the Mahalanobis distance is below the threshold the groups are deemed to transgress (overlap).

**Usage**

```
transgression(ellipses, class_a, class_b, confidence = 0.95)
```

**Arguments**

<code>ellipses</code>	A named list of scatter ellipses as returned by <a href="#">scatter_ellipse</a> .
<code>class_a</code>	Name (character) of the first class in ellipses.
<code>class_b</code>	Name (character) of the second class in ellipses.
<code>confidence</code>	Confidence level for the chi-squared threshold, between 0 and 1. Defaults to 0.95.

**Value**

A list with components:

**mahalanobis\_distance** Squared Mahalanobis distance between the two centroids under the pooled covariance.

**threshold** Chi-squared threshold at the requested confidence with degrees of freedom equal to the number of features.

**transgression** Logical; TRUE when the distance is below the threshold (the ellipses overlap).

**separation\_ratio** Ratio of the Mahalanobis distance to the threshold. Values above 1 indicate well-separated groups.

**References**

Lubischew, A.A. (1962). On the use of discriminant functions in taxonomy. *Biometrics*, 18(4), 455-477.

**See Also**

[scatter\\_ellipse](#)

**Examples**

```
ellipses <- scatter_ellipse(iris[, 1:4], iris$Species)
transgression(ellipses, "versicolor", "virginica")
```

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