

# Package ‘iStay’

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**Type** Package

**Title** Measuring ecological stability and synchrony

**Version** 0.1.0

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**Description** Provide simple functions to (i) calculate the order  $q$  of stability for single assemblage, (ii) calculate order  $q$  of stability and synchrony for multiple assemblages, and (iii) calculate stability of hierarchical data. This package also provide functions to plot stability (or synchrony) profile, and based on the diversity (or other) variable, analysis and plot the relationship between stability (and synchrony) and diversity (or other) variable.

**License** GPL ( $\geq 3$ )

**Imports** ggplot2,  
stringr,  
lmerTest,  
dplyr,  
ggpubr

**Encoding** UTF-8

**LazyData** true

**Depends** R ( $\geq 2.10$ )

**Suggests** knitr,  
rmarkdown

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

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iStay-package

*Measuring ecological stability and synchrony.***Description**

iStay (information-based measures of stability and related synchrony) is an R package for featuring a class of measures of community/ecosystem stability and related synchrony; the corresponding diversity-stability is also assessed if biodiversity data are available. The information-based measures of stability were developed based on the Hill-number parametrized by an order  $q > 0$ ; see Chao et al. (2024) for the relevant theory and methodological background. All measures are illustrated by using biomass temporal data from the Jena experiment (Wagg et al. 2022).

Specifically, iStay features the following measures separately for three cases:

- (1) For a single community, it computes stability measures of order  $q > 0$  and provides the stability profile which depicts the stability with respect to order  $q$ . When biodiversity data are available, the diversity-stability relationship is also assessed.
- (2) For multiple communities, it computes four measures (gamma, alpha and beta stability and synchrony) and provides the corresponding profiles. When biodiversity data are available, the diversity-stability and diversity-synchrony relationships are also assessed.
- (3) For hierarchies, it computes three measures (gamma, alpha, and normalized beta stability for data in each hierarchical level) of order  $q > 0$  and provides the stability profile which depicts the stability with respect to order  $q$ .

This package contains five main functions:

1. `Stay_Single` calculates stability of the time series data (like biomass, productivity, etc.) for single assemblage.
2. `Stay_Multiple` calculates Gamma, Alpha and Beta stability, and synchrony of the time series data (like biomass, productivity, etc.) for multiple assemblages.
3. `Stay_Hier` calculates stability of the time series data (like biomass, productivity, etc.) for hierarchical structure.
4. `ggStay_qprofile` provides to graph the  $q$ -profile of stability (and synchrony if is multiple assemblages) based on the output obtained from the function `Stay_Single`, `Stay_Multiple` or `Stay_Hier`.
5. `ggStay_analysis` provides to graph the relationships between stability (and synchrony if is multiple assemblages) and an additional diversity (or other) variable based on the output obtained from the function `Stay_Single` or `Stay_Multiple`.

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ggStay_analysis	<i>ggplot2 extension for a Stay_Single or Stay_Multiple object to analysis with an diversity (or other) variable.</i>
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## Description

ggStay\_analysis is a graphical function that based on the output from the function Stay\_Single or Stay\_Multiple. It provides to graph relationships between stability (and synchrony if is multiple assemblages) and an additional diversity (or other) variable .

## Usage

```
ggStay_analysis(output, x_variable, by_group = NULL, model = "LMM")
```

## Arguments

output	the output obtained from Stay_Single or Stay_Multiple and needs to combine with a column that sets as x_variable. Also, if by_group is not NULL, the output also need to combine with the column that sets as by_group.
x_variable	name of the column of diversity (or other) variable, that will use as the x-axis in the plot.
by_group	name of the column that is a categorical variable for plotting points with different color. And it is required if model = "LMM", model uses it as random effect for intercept and slope. Default is NULL.
model	specifying the fitting model, model = "lm" for linear model; model = "LMM" for linear mixed model with random effects for intercept and slope. Default is model = "LMM".

## Value

For an Stay\_Single object, this function return a figure of diversity (or other) variable vs. stability. For an Stay\_Multiple object, this function return a figure that is about diversity (or other) variable vs. (Gamma, Alpha, Beta) stability and synchrony.

## Examples

```
data("Jena_plot_biomass_data")
data("Jena_species_biomass_data")
data("Jena_hierarchical_biomass_data")
data("Jena_hierarchical_mat")

## Single assemblage
# Stability of each single plot
single_plot <- do.call(rbind, Jena_plot_biomass_data)
output_single_plot_div <- Stay_Single(data = single_plot, order.q = c(1,2), Alltime = TRUE)
output_single_plot_div <- data.frame(output_single_plot_div,
                                   log2_sowndiv = log2(as.numeric(do.call(rbind,
                                   strsplit(output_single_plot_div[,1], "[.]+"))[,2])),
                                   block = do.call(rbind,
                                   strsplit(output_single_plot_div[,1], "[.]+"))[,1])

ggStay_analysis(output=output_single_plot_div, x_variable="log2_sowndiv",
```

```

      by_group = "block", model = "LMM")

# Stability of each single species
single_species <- do.call(rbind, Jena_species_biomass_data)
output_single_species_div <- Stay_Single(data = single_species,
                                         order.q = c(1,2), Alltime = TRUE)
output_single_species_div <- data.frame(output_single_species_div,
                                       log2_sowndiv = log2(as.numeric(do.call(rbind, strsplit(output_single_species_div[,1], "[
                                       block=do.call(rbind, strsplit(output_single_species_div[,1], "[._]+"))[,2])

ggStay_analysis(output = output_single_species_div, x_variable = "log2_sowndiv", by_group = "block", model = "

## Multiple assemblages
# Stability of multiple plots
multiple_plot <- Jena_plot_biomass_data
output_multi_plot_div <- Stay_Multiple(data = multiple_plot, order.q = c(1,2), Alltime = TRUE)
output_multi_plot_div <- data.frame(output_multi_plot_div,
                                   log2_sowndiv = log2(as.numeric(do.call(rbind, strsplit(output_multi_plot_div[, 1], "-"))
                                   block = do.call(rbind, strsplit(output_multi_plot_div[, 1], "-"))[, 1])

ggStay_analysis(output = output_multi_plot_div, x_variable= "log2_sowndiv",
               by_group = "block", model = "LMM")

# Stability of multiple species in plot
multiple_species <- Jena_species_biomass_data
output_multi_species_div <- Stay_Multiple(data = multiple_species,
                                         order.q = c(1,2), Alltime = TRUE)
output_multi_species_div <- data.frame(output_multi_species_div,
                                       log2_sowndiv = log2(as.numeric(do.call(rbind,
                                       strsplit(output_multi_species_div[,1], "-"))[,3])),
                                       block=do.call(rbind,
                                       strsplit(output_multi_species_div[,1], "-"))[,2])

ggStay_analysis(output = output_multi_species_div, x_variable = "log2_sowndiv",
               by_group = "block", model = "LMM")

```

---

ggStay\_qprofile

*ggplot2 extension for a Stay\_Single, Stay\_Multiple or Stay\_Hier object with q-profile.*


---

## Description

ggStay\_qprofile is a graphical function that based on the output from the function Stay\_Single, Stay\_Multiple or Stay\_Hier. It provides to graph the q-profile of stability (and synchrony if is multiple assemblages).

## Usage

```
ggStay_qprofile(output)
```

## Arguments

output                      the output obtained from Stay\_Single, Stay\_Multiple or Stay\_Hier.

**Value**

For a `Stay_Single` object, this function return a figure of q-profile for stability . For a `Stay_Multiple` object, this function return a figure that contains q-profile for (Gamma, Alpha, Beta) stability and synchrony. For a `Stay_Hier` object, this function return a figure that contains q-profile for gamma stability of highest hierarchical level and alpha stability of other hierarchical level. And it also provides a figure about the relationship between each decomposition of overall stability and the synchrony of each hierarchical level and order.q.

**Examples**

```
data("Jena_plot_biomass_data")
data("Jena_species_biomass_data")
data("Jena_hierarchical_biomass_data")
data("Jena_hierarchical_mat")

## Single assemblage
# Stability of each single plot
single_plot <- do.call(rbind, Jena_plot_biomass_data)
output_single_plot_q <- Stay_Single(data=single_plot[c(12,65),],
                                   order.q=seq(0.1,2,0.1), Alltime=TRUE)
ggStay_qprofile(output=output_single_plot_q)

# Stability of each single species
single_species <- do.call(rbind, Jena_species_biomass_data)
output_single_species_q <- Stay_Single(data=single_species[c(41,45),],
                                       order.q=seq(0.1,2,0.1), Alltime=TRUE)
ggStay_qprofile(output=output_single_species_q)

## Multiple assemblages
# Stability of multiple plots
multiple_plot <- Jena_plot_biomass_data
output_multi_plot_q <- Stay_Multiple(data=multiple_plot[c(1,13)],
                                    order.q=seq(0.1,2,0.1), Alltime=TRUE)
ggStay_qprofile(output=output_multi_plot_q)

# Stability of multiple species in plot
multiple_species <- Jena_species_biomass_data
output_multi_species_q <- Stay_Multiple(data=multiple_species[c(4,69)],
                                       order.q=seq(0.1,2,0.1), Alltime=TRUE)
ggStay_qprofile(output=output_multi_species_q)

## Hierarchies
output_hier_q <- Stay_Hier(data=Jena_hierarchical_biomass_data,
                          mat=Jena_hierarchical_mat,
                          order.q=seq(0.1,2,0.1), Alltime=TRUE)
ggStay_qprofile(output=output_hier_q)
```

---

Jena\_hierarchical\_biomass\_data

*Hierarchical biomass data of Jena experiment*


---

**Description**

This data includes the biomass time series of every plant species in each plot. For each plot, there are 1, 2, 4, 8 or 16 plant species. Total are 462 plant species which is equal to the number of row for this data. And since the biomass of each species in 2004 was not recorded in the Jena experiment, the number of columns in this data is 16, namely 2003 and 2005-2019.

**Usage**

```
data(Jena_hierarchical_biomass_data)
```

**Format**

Jena\_hierarchical\_biomass\_data is a species-by-time data.frame. The row of data is all the plant species in each plots, and the columns are the years in which biomass was recorded.

**References**

Wagg, C., Roscher, C., Weigelt, A. et al. (2022) Biodiversity–stability relationships strengthen over time in a long-term grassland experiment. Nature Communications 13, 7752.

---

Jena_hierarchical_mat	<i>Hierarchical</i>	<i>structure</i>	<i>matrix</i>	<i>corresponding</i>	<i>to</i>
	Jena_hierarchical_data				

---

**Description**

This dataset includes three columns which are "block", "plot" and "species" the hierarchical level of Jena experiment. Each row of this data is corresponding to the same row in Jena\_hierarchical\_data, and record the names of block, plot and species that the row belongs to.

**Usage**

```
data(Jena_hierarchical_mat)
```

**Format**

Jena\_hierarchical\_mat is a data.frame with "block", "plot" and "species" three columns and 462 rows which is same as the number of rows in Jena\_hierarchical\_data.

**References**

Wagg, C., Roscher, C., Weigelt, A. et al. (2022) Biodiversity–stability relationships strengthen over time in a long-term grassland experiment. Nature Communications 13, 7752.

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`Jena_plot_biomass_data`*17-years biomass data of plots in Jena experiment*

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**Description**

In Jena experiment, there are 4 blocks (B1, B2, B3, B4) with a total of 76 plots. For each plot 1, 2, 4, 8 or 16 plants are sown. There are approximately 3 or 4 plots in each block for each number of plant species planted. The set includes 20 lists that are combinations of four blocks and number of five different plant species planted. In each list, it is a plots/assemblages by time dataframe. For example, the list "B1\_16" is a dataframe that contains the 17-year biomass of all plants in the plots, which are in block B1 and has been sown with 16 plant species.

**Usage**

```
data(Jena_plot_biomass_data)
```

**Format**

`Jena_plot_biomass_data` contains 20 lists. Each list is a dataframe that the rows are plots/assemblages and the columns are the time. For each row, it record the biomass of the plot/assemblage during the time.

**References**

Wagg, C., Roscher, C., Weigelt, A. et al. (2022) Biodiversity–stability relationships strengthen over time in a long-term grassland experiment. *Nature Communications* 13, 7752.

---

`Jena_species_biomass_data`*16-years biomass data of each speices in the plot in Jena experiment  
(except 2004)*

---

**Description**

In Jena experiment, there are 4 blocks (B1, B2, B3, B4) with a total of 76 plots. For each plot 1, 2, 4, 8 or 16 plants are sown. There are approximately 3 or 4 plots in each block for each number of plant species planted. This data includes 76 lists which are corresponding to 76 plots. In each list, it is a species by time dataframe that record the biomass of each species sown in the plot. However, because Jena experiment only records the total biomass of all species in the plot, biomass of each species are unknown in 2004, the time length of data is about 16-years except 2004.

**Usage**

```
data(Jena_species_biomass_data)
```

## Format

Jena\_species\_biomass\_data contains 76 lists. Each list is a dataframe that the rows are species and the columns are the time. For each row, it record the biomass of each species during the time.

## References

Wagg, C., Roscher, C., Weigelt, A. et al. (2022) Biodiversity–stability relationships strengthen over time in a long-term grassland experiment. Nature Communications 13, 7752.

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Stay_Hier	<i>Calculate stability of the time series data for hierarchical structure.</i>
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---

## Description

Stay\_Hier is a function that calculate stability of the time series data (like biomass, productivity, etc.) for hierarchical structure.

## Usage

```
Stay_Hier(
  data,
  mat,
  order.q = c(1, 2),
  Alltime = TRUE,
  start_T = NULL,
  end_T = NULL
)
```

## Arguments

data	can be input as data.frame (assemblages by times).
mat	hierarchical structure of data.
order.q	a numerical vector specifying the orders of stability. Default is c(1,2).
Alltime	TRUE or FALSE, to decide whether to use all the times in the data.
start_T	(argument only for Alltime = FALSE) a positive integer specifying the start column of time in the data.
end_T	(argument only for Alltime = FALSE) a positive integer specifying the end column of time in the data.

## Value

a dataframe with columns "Hier", "Order\_q", and stability "Gamma", "Alpha", "Beta" and "Synchrony".



**Examples**

```
data("Jena_hierarchical_biomass_data")
data("Jena_hierarchical_mat")
output_hier <- Stay_Hier(data=Jena_hierarchical_biomass_data, mat=Jena_hierarchical_mat,
                        order.q=c(1,2), Alltime=TRUE)

output_hier
```

---

Stay_Multiple	<i>Calculate stability and synchrony of the time series data for multiple assemblages.</i>
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---

**Description**

Stay\_Multiple is a function that calculate (Gamma, Alpha and Beta) stability and synchrony of the time series data (like biomass, productivity, etc.) for multiple assemblages.

**Usage**

```
Stay_Multiple(
  data,
  order.q = c(1, 2),
  Alltime = TRUE,
  start_T = NULL,
  end_T = NULL
)
```

**Arguments**

data	can be input as a data.frame/matrix (assemblages by times), or a list of data.frames with each dataframe representing a assemblages-by-times data.
order.q	a numerical vector specifying the orders of stability and synchrony. Default is c(1,2).
Alltime	TRUE or FALSE, to decide whether to use all the times in (every) dataframe.
start_T	(argument only for Alltime = FALSE) a positive integer specifying the start column of time in (every) dataframe.
end_T	(argument only for Alltime = FALSE) a positive integer specifying the end column of time in (every) dataframe.

**Value**

a dataframe with columns "Site", "Order\_q", "Gamma", "Alpha", "Beta" and "Synchrony".

**Examples**

```
# Stability of multiple plots
data("Jena_plot_biomass_data")
multiple_plot <- Jena_plot_biomass_data
output_multi_plot <- Stay_Multiple(data=multiple_plot, order.q=c(1,2), Alltime=TRUE)
output_multi_plot
```

```
# Stability of multiple species in each plot
data("Jena_species_biomass_data")
multiple_species <- Jena_species_biomass_data
output_multi_species <- Stay_Multiple(data=multiple_species, order.q=c(1,2), Alltime=TRUE)
output_multi_species
```

---

Stay\_Single

---

*Calculate stability of the time series data for single assemblage.*


---

## Description

Stay\_Single is a function that calculate stability of the time series data (like biomass, productivity, etc.) for single assemblage.

## Usage

```
Stay_Single(
  data,
  order.q = c(1, 2),
  Alltime = TRUE,
  start_T = NULL,
  end_T = NULL
)
```

## Arguments

data	can be input as a vector of time series data, or data.frame (assemblages by times).
order.q	a numerical vector specifying the orders of stability. Default is c(1,2).
Alltime	TRUE or FALSE, to decide whether to use all the times in the data.
start_T	(argument only for Alltime = FALSE) a positive integer specifying the start column of time in the data.
end_T	(argument only for Alltime = FALSE) a positive integer specifying the end column of time in the data.

## Value

a dataframe with columns "Plot/Community", "Order\_q" and "Stability".

## Examples

```
# Stability of each single plot
data("Jena_plot_biomass_data")
single_plot <- do.call(rbind, Jena_plot_biomass_data)
output_single_plot <- Stay_Single(data=single_plot, order.q=c(1,2), Alltime=TRUE)
output_single_plot

# Stability of each single species in each plot
data("Jena_species_biomass_data")
```

```
single_species <- do.call(rbind, Jena_species_biomass_data)
output_single_species <- Stay_Single(data=single_species, order.q=c(1,2), Alltime=TRUE)
output_single_species
```

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