

# Package ‘SSVS’

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**Title** Functions for Stochastic Search Variable Selection (SSVS)

**Version** 2.2.0

**Description** Functions for performing stochastic search variable selection (SSVS) for binary and continuous outcomes and visualizing the results. SSVS is a Bayesian variable selection method used to estimate the probability that individual predictors should be included in a regression model. Using MCMC estimation, the method samples thousands of regression models in order to characterize the model uncertainty regarding both the predictor set and the regression parameters. For details see Bainter, McCauley, Wager, and Losin (2020) Improving practices for selecting a subset of important predictors in psychology: An application to predicting pain, *Advances in Methods and Practices in Psychological Science* 3(1), 66-80 <[DOI:10.1177/2515245919885617](https://doi.org/10.1177/2515245919885617)>.

**URL** <https://github.com/sabainter/SSVS>

**BugReports** <https://github.com/sabainter/SSVS/issues>

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**Imports** bayestestR, BoomSpikeSlab, checkmate, ggplot2, graphics, rlang, stats, dplyr, magrittr, gridExtra

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dat	<i>Example dataset for ssvs function @format A data frame with 74 records and 76 variables</i>
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## Description

Example dataset for ssvs function @format A data frame with 74 records and 76 variables

## Usage

dat

## Format

An object of class `data.frame` with 74 rows and 76 columns.

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imputed_affairs	<i>Imputed affairs Dataset</i>
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## Description

This dataset is a version of the `Affairs` dataset where random missing values were introduced, and multiple imputation was performed using the `mice` package.

## Usage

```
imputed_affairs
```

## Format

A data frame with 3005 rows and 12 variables

## Details

Random missingness was introduced into 10% of the values in the original `Affairs` dataset. Multiple imputation was then performed using the `mice` package with the following parameters:

- 5 multiple imputations ( $m = 5$ ).
- 50 iterations per imputation ( $maxit = 50$ ).
- Seed set to 123 for reproducibility.

The dataset included here is the first completed dataset resulting from the multiple imputation process.

## Source

Original dataset from `datasets::Affairs`, with missing values introduced and imputed.

## Examples

```
data(imputed_affairs)
head(imputed_affairs)
```

imputed\_mtcars      *Imputed mtcars Dataset*

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**Description**

This dataset is a version of the mtcars dataset where random missing values were introduced, and multiple imputation was performed using the mice package.

**Usage**

```
imputed_mtcars
```

**Format**

A data frame with 160 rows and 13 variables

**Details**

Random missingness was introduced into 10% of the values in the original mtcars dataset. Multiple imputation was then performed using the mice package with the following parameters:

- 5 multiple imputations ( $m = 5$ ).
- 50 iterations per imputation ( $\text{maxit} = 50$ ).
- Seed set to 123 for reproducibility.

The dataset included here is the first completed dataset resulting from the multiple imputation process.

**Source**

Original dataset from datasets::mtcars, with missing values introduced and imputed.

**Examples**

```
data(imputed_mtcars)
head(imputed_mtcars)
```

---

launch      *Run an interactive analysis tool (Shiny app) that lets you perform SSVS in a browser*

---

**Description**

Run an interactive analysis tool (Shiny app) that lets you perform SSVS in a browser

**Usage**

```
launch()
```

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plot.ssvs	<i>Plot results of an SSVS model</i>
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**Description**

Plot results of an SSVS model

**Usage**

```
## S3 method for class 'ssvs'
plot(x, threshold = 0.5, legend = TRUE, title = NULL, color = TRUE, ...)
```

**Arguments**

x	An ssvs result object obtained from <a href="#">ssvs()</a>
threshold	An MIP threshold to show on the plot, must be between 0-1. If NULL, no threshold is used.
legend	If TRUE, show a legend for the shapes based on the threshold. Ignored if threshold = NULL.
title	The title of the plot. Set to NULL to use a default title.
color	If TRUE, the data points will be colored based on the threshold.
...	Ignored

**Value**

Creates a plot of the inclusion probabilities by variable

**Examples**

```
outcome <- "qsec"
predictors <- c("cyl", "disp", "hp", "drat", "wt", "vs", "am", "gear", "carb", "mpg")
results <- ssvs(x = predictors, y = outcome, data = mtcars, progress = FALSE)
plot(results)
```

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plot.ssvs_mi	<i>Plot SSVS-MI Estimates and Marginal Inclusion Probabilities (MIP)</i>
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**Description**

This function creates a plot of SSVS-MI estimates with minimum and maximum and a plot for marginal inclusion probabilities (MIP) optional thresholds for highlighting significant predictors..

**Usage**

```
## S3 method for class 'ssvs_mi'
plot(
  x,
  type = "both",
  threshold = 0.5,
  legend = TRUE,
  est_title = NULL,
  mip_title = NULL,
  color = TRUE,
  ...
)
```

**Arguments**

x	An ssvs result object obtained from <code>ssvs_mi()</code>
type	Defaults to "both", can change to "estimate" or "MIP".
threshold	A numeric value (between 0 and 1) specifying the MIP threshold to highlight significant predictors. Defaults to 0.5.
legend	Logical indicating whether to include a legend for the threshold. Defaults to TRUE.
est_title	A character string specifying the plot title. Defaults to "SSVS-MI estimates".
mip_title	A character string specifying the plot title. Defaults to "Multiple Inclusion Probability for SSVS-MI".
color	Logical indicating whether to use color to highlight thresholds. Defaults to TRUE.
...	Ignored

**Value**

Two ggplot2 objects representing the plot of SSVS estimates and the plot of MIP with thresholds.

**Examples**

```
data(imputed_mtcars)
outcome <- 'qsec'
predictors <- c('cyl', 'disp', 'hp', 'drat', 'wt', 'vs', 'am', 'gear', 'carb', 'mpg')
imputation <- '.imp'
results <- ssvs_mi(data = imputed_mtcars, y = outcome, x = predictors, imp = imputation)
plot(results)
```

## Description

For continuous outcomes, a basic Gibbs sampler is used. For binary outcomes, `BoomSpikeSlab::logit.spike()` is used.

## Usage

```
ssvs(  
  data,  
  y,  
  x,  
  continuous = TRUE,  
  prior.probs = 0.5,  
  inprob = NULL,  
  force.in = NULL,  
  runs = 20000,  
  burn = 5000,  
  a1 = 0.01,  
  b1 = 0.01,  
  prec.beta = 0.1,  
  progress = TRUE  
)
```

## Arguments

<code>data</code>	The dataframe used to extract predictors and response values
<code>y</code>	The response variable
<code>x</code>	The set of predictor variables
<code>continuous</code>	If TRUE, treat the response variable as continuous. If FALSE, treat the response variable as binary.
<code>prior.probs</code>	Numeric vector or scalar specifying the prior probability that each predictor variable is included in the model. If a scalar, the value is replicated for all variables. If a vector, must have length equal to <code>length(x)</code> . Each value must be between 0 and 1. Setting a prior probability to 1.0 forces that variable to always be included. The default prior inclusion probability is .5 for all predictors. The prior inclusion probabilities will influence the magnitude of the marginal inclusion probabilities (MIPs), but the relative pattern of MIPs is expected to remain fairly consistent.
<code>inprob</code>	<b>Deprecated;</b> use <code>prior.probs</code> instead. If provided, this overrides <code>prior.probs</code> (with a warning).

<code>force.in</code>	Character vector specifying variables that should always be included in the model. This is a convenience parameter that sets <code>prior.probs = 1.0</code> for the specified variables. If both <code>prior.probs</code> and <code>force.in</code> are provided, <code>force.in</code> takes precedence and will override probabilities for those variables. Default is <code>NULL</code> .
<code>runs</code>	Total number of iterations (including burn-in). Results are based on the Total - Burn-in iterations.
<code>burn</code>	Number of burn-in iterations. Burn-in iterations are discarded warmup iterations used to achieve MCMC convergence. You may increase the number of burn-in iterations if you are having convergence issues.
<code>a1</code>	Prior parameter for Gamma(a,b) distribution on the precision (1/variance) residual variance. Only used when <code>continuous = TRUE</code> .
<code>b1</code>	Prior parameter for Gamma(a,b) distribution on the precision (1/variance) residual variance. Only used when <code>continuous = TRUE</code> .
<code>prec.beta</code>	Prior precision (1/variance) for beta coefficients. Only used when <code>continuous = TRUE</code> .
<code>progress</code>	If <code>TRUE</code> , show progress of the model creation. When <code>continuous = TRUE</code> , progress plots will be created for every 1000 iterations. When <code>continuous = FALSE</code> , 10 progress messages will be printed. Only used when <code>continuous = TRUE</code> .

### Value

An `ssvs` object that can be used in `summary()` or `plot()`.

### Examples

```
# Example 1: Continuous response variable, uniform prior
outcome <- "qsec"
predictors <- c("cyl", "disp", "hp", "drat", "wt", "vs", "am", "gear", "carb", "mpg")
results <- ssvs(data = mtcars, x = predictors, y = outcome,
  prior.probs = .5, #same for all predictors
  progress = FALSE)

#' # Example 2: Continuous response variable, variable-specific priors
outcome <- "mpg"
predictors <- c("cyl", "disp", "hp", "wt")
prior.probs = c(0.7, 0.5, 0.2, 0.2) # Different prior probability for each
results <- ssvs(data = mtcars, x = predictors, y = outcome,
  progress = FALSE)

# Example 3: Binary response variable
library(AER)
data(Affairs)
Affairs$hadaffair[Affairs$affairs > 0] <- 1
Affairs$hadaffair[Affairs$affairs == 0] <- 0
outcome <- "hadaffair"
predictors <- c("gender", "age", "yearsmarried", "children", "religiousness",
  "education", "occupation", "rating")
results <- ssvs(data = Affairs, x = predictors, y = outcome, continuous = FALSE, progress = FALSE)
```

```
#' # Example 4: Binary response variable with forced inclusion of select predictors
library(AER)
data(Affairs)
Affairs$hadaffair[Affairs$affairs > 0] <- 1
Affairs$hadaffair[Affairs$affairs == 0] <- 0
outcome <- "hadaffair"
predictors <- c("gender", "age", "yearsmarried", "children", "religiousness",
"education", "occupation", "rating")
results <- ssvs(data = Affairs, x = predictors, y = outcome, force.in = c("children", "rating"),
continuous = FALSE, progress = FALSE)
```

---

ssvs\_mi

*Perform SSVS on Multiply Imputed Datasets*


---

### Description

This function performs Stochastic Search Variable Selection (SSVS) analysis on multiply imputed datasets for a given set of predictors and a response variable. It supports continuous response variables and calculates aggregated results across multiple imputations.

### Usage

```
ssvs_mi(
  data,
  y,
  x,
  imp,
  imp_num = 5,
  interval = 0.9,
  continuous = TRUE,
  progress = FALSE
)
```

### Arguments

data	A dataframe containing the variables of interest, including an <code>.imp</code> column for imputation identifiers.
y	The response variable (character string).
x	A vector of predictor variable names.
imp	The imputation variable.
imp_num	The number of imputations to process (default is 5).
interval	Confidence interval level for summary results (default is 0.9).
continuous	If TRUE, treat the response variable as continuous. If FALSE, treat the response variable as binary.
progress	Logical indicating whether to display progress (default is FALSE).

**Value**

An `ssvs_mi` object containing aggregated results across imputations that can be used in `summary()`.

**Examples**

```
# example 1: continuous response variable
data(imputed_mtcars)
outcome <- 'qsec'
predictors <- c('cyl', 'disp', 'hp', 'drat', 'wt', 'vs', 'am', 'gear', 'carb', 'mpg')
imputation <- '.imp'
results <- ssvs_mi(data = imputed_mtcars, y = outcome, x = predictors, imp = imputation)

# example 2: binary response variable
data(imputed_affairs)
outcome <- "hadaffair"
predictors <- c("gender", "age", "yearsmarried", "children", "religiousness",
"education", "occupation", "rating")
imputation <- '.imp'
results <- ssvs_mi(data = imputed_affairs, x = predictors, y = outcome,
continuous = FALSE, imp = imputation)
```

---

summary.ssvs

*Summarize results of an SSVS model*


---

**Description**

Summarize results from SSVS including marginal inclusion probabilities, Bayesian model averaged parameter estimates, and 95% highest posterior density credible intervals. Estimates and credible intervals are based on standardized X variables.

**Usage**

```
## S3 method for class 'ssvs'
summary(object, interval = 0.89, threshold = 0, ordered = FALSE, ...)
```

**Arguments**

<code>object</code>	An SSVS result object obtained from <code>ssvs()</code>
<code>interval</code>	The desired probability for the credible interval, specified as a decimal
<code>threshold</code>	Minimum MIP threshold where a predictor will be shown in the output, specified as a decimal
<code>ordered</code>	If TRUE, order the results based on MIP (in descending order)
<code>...</code>	Ignored

**Value**

A dataframe with results

## Examples

```
outcome <- "qsec"
predictors <- c("cyl", "disp", "hp", "drat", "wt", "vs", "am", "gear", "carb", "mpg")
results <- ssvs(data = mtcars, x = predictors, y = outcome, progress = FALSE)
summary(results, interval = 0.9, ordered = TRUE)
```

---

summary.ssvs\_mi

*Calculate Summary Statistics for SSVS-MI Results*

---

## Description

Computes summary statistics (average, minimum, and maximum) for beta coefficients, MIP and average nonzero beta coefficients from an SSVS result object.

## Usage

```
## S3 method for class 'ssvs_mi'
summary(object, ...)
```

## Arguments

object            An ssvs\_mi result object obtained from `ssvs_mi()`  
...               Ignored

## Value

A data frame with results

## Examples

```
data(imputed_mtcars)
outcome <- 'qsec'
predictors <- c('cyl', 'disp', 'hp', 'drat', 'wt', 'vs', 'am', 'gear', 'carb', 'mpg')
imputation <- '.imp'
results <- ssvs_mi(data = imputed_mtcars, y = outcome, x = predictors, imp = imputation)
summary_MI <- summary(results)
print(summary_MI)
```

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