

Package ‘remoteoutcome’

November 17, 2025

Type Package

Title Program Evaluation with Remotely Sensed Variables

Version 1.0.0

Description Provides tools for estimating treatment effects using remotely sensed variables (RSVs) such as satellite images or mobile phone data. Implements the nonparametric methods developed in Rambachan, A., Singh, R., and Viviano, D. (2025) ``Program Evaluation with Remotely Sensed Outcomes" <[arXiv:2411.10959](https://arxiv.org/abs/2411.10959)>.

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Encoding UTF-8

LazyData true

LazyDataCompression xz

Depends R (>= 4.0.0)

Imports ranger (>= 0.17.0),
 dplyr,
 parallel,
 stats,
 utils

Suggests ggplot2,
 fixest,
 knitr,
 rmarkdown,
 kableExtra,
 latex2exp,
 stringr,
 tibble,
 tidyverse

VignetteBuilder knitr

RoxygenNote 7.3.2

URL <https://github.com/asheshrambachan/remoteoutcome>

BugReports <https://github.com/asheshrambachan/remoteoutcome/issues>

Contents

coef.rsv	2
confint.rsv	2
create_data_real	3
create_data_synth	4
pred_real_Ycons	6
print.rsv	8
remote_vars_p1	9
remote_vars_p2	10
rsv_estimate	11
smartcard_data	15
summary.rsv	17
vcov.rsv	17

Index

18

coef.rsv	<i>Extract coefficients from rsv objects</i>
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Description

Extract coefficients from rsv objects

Usage

```
## S3 method for class 'rsv'
coef(object, ...)
```

Arguments

object	An object of class "rsv".
...	Additional arguments (unused).

Value

The treatment effect coefficient.

confint.rsv	<i>Confidence intervals for rsv objects</i>
-------------	---

Description

Confidence intervals for rsv objects

Usage

```
## S3 method for class 'rsv'
confint(object, parm = "D", level = 0.95, ...)
```

Arguments

object	An object of class "rsv".
parm	Parameter name. Must be "D" (default).
level	Confidence level (default 0.95). Note: this returns the CI computed during estimation based on the alpha parameter. To change the confidence level, re-run <code>rsv_estimate()</code> with a different alpha.
...	Additional arguments (unused).

Value

A matrix with lower and upper confidence bounds.

create_data_real

*Create Real Experimental/Observational Split Dataset***Description**

Transforms `smartcard_data` into the real experimental/observational split where treatment is observed in "Experimental: Treated (2010)", "Experimental: Untreated (2011)", and "Experimental: Untreated (2012)" waves and outcomes are observed in the "Experimental: Untreated (2011)" and "Observational (N/A)" waves.

Usage

```
create_data_real(data)
```

Arguments

data	smartcard_data data frame included in the package.
------	--

Details

The function implements the real experimental design through the following steps:

1. Villages from "Experimental: Treated (2010)", "Experimental: Untreated (2011)", "Experimental: Untreated (2012)" waves are marked as `S_e = TRUE`
2. Villages from "Experimental: Untreated (2011)" and "Observational (N/A)" waves are marked as `S_o = TRUE`
3. Final sample indicator is created:
 - `S = "both"` if `S_e = TRUE` and `S_o = TRUE` (experimental and observational villages)
 - `S = "e"` if `S_e = TRUE` and `S_o = FALSE` (experimental only)
 - `S = "o"` if `S_e = FALSE` and `S_o = TRUE` (observational only)
4. Treatment visible only when `S = "e"` or "`both`"; outcomes visible only when `S = "o"` or "`both`"

Value

A data frame similar to `smartcard_data`, containing:

shrid2 SHRUG village identifier
spillover_20km Spillover indicator
S Sample indicator: "e" = experimental only, "o" = observational only, "both" = experimental and observational samples
D Treatment indicator, NA when not observed (only observed when S = "e" or "both")
Ycons, Ylowinc, Ymidinc Outcome variables, NA when not observed (only observed when S = "o" or "both")
clusters Cluster identifier (Subdistrict (mandal) name + District name in Andhra Pradesh)
luminosity_* VIIRS nighttime lights features
satellite_* MOSAIKS satellite feature

See Also

[smartcard_data](#) for the input dataset structure, [create_data_synth](#) for creating synthetic sample splits

Examples

```
## Not run:
# Load complete dataset
data(smartcard_data, package = "remoteoutcome")

# Create real experimental/observational split
data_real <- create_data_real(smartcard_data)

# Sample membership distribution
table(data_real$S)

# Treatment and outcome overlap
with(data_real, table(observe_D = !is.na(D), observe_Y = !is.na(Ycons)))

## End(Not run)
```

Description

Transforms the complete dataset (`smartcard_data`) into a synthetic experimental/observational split where top 50 observational sample. This creates an artificial separation for testing RSV methods.

Usage

```
create_data_synth(data)
```

Arguments

data smartcard_data data frame included in the package.

Details

The function creates a synthetic experimental/observational split through the following steps:

1. Original experimental villages are marked as S_e = TRUE
2. Top 50
3. Final sample indicator is created:
 - S = "both" if S_e = TRUE and S_o = TRUE (experimental and observational villages)
 - S = "e" if S_e = TRUE and S_o = FALSE (experimental only)
 - S = "o" if S_e = FALSE and S_o = TRUE (observational only)
4. Treatment visible only when S = "e" or "both"; outcomes visible only when S = "o" or "both"

Value

A data frame similar to smartcard_data, containing:

shrid2 SHRUG village identifier

spillover_20km Spillover indicator

S Sample indicator: "e" = experimental only, "o" = observational only, "both" = experimental and observational samples

D Treatment indicator, NA when not observed (only observed when S = "e" or "both")

Ycons, Ylowinc, Ymidinc Outcome variables, NA when not observed (only observed when S = "o" or "both")

clusters Cluster identifier (Subdistrict (mandal) name + District name in Andhra Pradesh)

luminosity_* VIIRS nighttime lights features

satellite_* MOSAIKS satellite features

See Also

[smartcard_data](#) for the input dataset structure, [create_data_real](#) for creating real experimental splits

Examples

```
## Not run:
# Load complete dataset
data(smartcard_data, package = "remoteoutcome")

data_synth <- create_data_synth(smartcard_data)

# Sample distribution
table(data_synth$S)

# Treatment and outcome overlap
with(data_synth, table(observe_D = !is.na(D), observe_Y = !is.na(Ycons)))

## End(Not run)
```

<code>pred_real_Ycons</code>	<i>Predicted Values and Observations for Consumption Outcome (Real Sample Split)</i>
------------------------------	--

Description

Pre-computed predictions and observations from the RSV estimation procedure for the consumption outcome (`Ycons`) using the real experimental/observational sample split. This dataset allows users to run `rsv_estimate` with pre-fitted predictions, avoiding the computational cost of re-fitting random forest models.

Usage

`pred_real_Ycons`

Format

A data frame with 8,312 rows and 9 columns:

Y Binary outcome: consumption indicator (1 = bottom quartile, 0 = otherwise). NA for experimental-only observations where outcomes are not observed.

D Binary treatment indicator (1 = treated, 0 = control). NA for observational-only observations where treatment is not assigned.

S_e Experimental sample indicator: 1 if unit is in experimental sample (treatment observed), 0 otherwise.

S_o Observational sample indicator: 1 if unit is in observational sample (outcome observed), 0 otherwise.

pred_Y Predicted probability $P(Y = 1 | R, S_o = 1)$, where R includes VIIRS nighttime lights and MOSAIKS satellite features. Fitted using random forest on observational sample.

pred_D Predicted probability $P(D = 1 | R, S_e = 1)$. Fitted using random forest on experimental sample.

pred_S_e Predicted probability $P(S_e = 1 | R)$. Fitted using random forest on full sample.

pred_S_o Predicted probability $P(S_o = 1 | R)$. Fitted using random forest on full sample.

clusters Cluster identifier (subdistrict name + district name) for computing cluster-robust standard errors.

Details

Generation Process:

This dataset was generated using the following procedure:

1. Data preparation:

- Started with `data_real` (real experimental/observational split)
- Merged with satellite features (MOSAIKS 4,000-dimensional features)
- Constructed remotely sensed variable R from VIIRS nighttime lights (2012-2021) and MOSAIKS features

2. Sample indicators:

- $S_e = 1$ for units where treatment D and covariates R are both observed (experimental sample)
- $S_o = 1$ for units where outcome Y and covariates R are both observed (observational sample)
- Some units have both $S_e = 1$ and $S_o = 1$ (overlap sample)

3. Prediction fitting:

- Used method = "none" (no sample splitting - all data used for both training and prediction)
- Fitted four random forest models using ranger:
 - pred_Y: $P(Y = 1 | R, S_o = 1)$ fitted on observational sample
 - pred_D: $P(D = 1 | R, S_e = 1)$ fitted on experimental sample
 - pred_S_e: $P(S_e = 1 | R)$ fitted on full sample
 - pred_S_o: $P(S_o = 1 | R)$ fitted on full sample
- Random forest parameters: 100 trees, class weights c(10, 1) for pred_Y model (up-weighting rare outcome), seed = 42

4. Initial estimate:

- Computed theta_init (initial treatment effect estimate) on the training data using the predictions
- Stored as an attribute: attr(pred_real_Ycons, "theta_init")

Attribute

The dataset has one attribute:

theta_init Initial estimate of the treatment effect computed on the training data. This is used as a starting value in the RSV estimation procedure. Access with attr(pred_real_Ycons, "theta_init").

See Also

- [rsv_estimate](#) for using this dataset to estimate treatment effects
- [smartcard_data](#) for the underlying data without predictions
- vignette(package = "remoteoutcome") for examples

Examples

```
# Load the dataset
data("pred_real_Ycons", package = "remoteoutcome")

# Examine structure
str(pred_real_Ycons)

# Check sample sizes
table(S_e = pred_real_Ycons$S_e, S_o = pred_real_Ycons$S_o)

# View prediction distributions
summary(pred_real_Ycons[, c("pred_Y", "pred_D", "pred_S_e", "pred_S_o")])

# Access the initial treatment effect estimate
attr(pred_real_Ycons, "theta_init")

## Not run:
```

```

# Estimate treatment effect using pre-computed predictions
result <- rsv_estimate(
  Y = pred_real_Ycons$Y,
  D = pred_real_Ycons$D,
  S_e = pred_real_Ycons$S_e,
  S_o = pred_real_Ycons$S_o,
  pred_Y = pred_real_Ycons$pred_Y,
  pred_D = pred_real_Ycons$pred_D,
  pred_S_e = pred_real_Ycons$pred_S_e,
  pred_S_o = pred_real_Ycons$pred_S_o,
  method = "predictions",
  theta_init = attr(pred_real_Ycons, "theta_init"),
  se = TRUE,
  se_params = list(
    B = 1000,
    fix_seed = TRUE,
    clusters = pred_real_Ycons$clusters
  ),
  cores = 7
)

# View results
print(result)
confint(result)

## End(Not run)

```

print.rsv*Print method for rsv objects***Description**

Print method for rsv objects

Usage

```
## S3 method for class 'rsv'
print(x, ...)
```

Arguments

- x An object of class "rsv".
- ... Additional arguments (unused).

Description

First part of remote sensing features for villages in the Andhra Pradesh smartcard study. Contains VIIRS nighttime lights data (2012-2021) and the first 2,000 MOSAIKS satellite imagery features.

Usage

```
remote_vars_p1
```

Format

A data frame with 8,312 rows and 2,051 columns:

shrid2 SHRUG village identifier (unique) - merge key
luminosity_min.* Minimum VIIRS nighttime luminosity (2012-2021)
luminosity_max.* Maximum VIIRS nighttime luminosity (2012-2021)
luminosity_mean.* Mean VIIRS nighttime luminosity (2012-2021)
luminosity_sum.* Sum of VIIRS nighttime luminosity (2012-2021)
luminosity_num_cells.* Number of VIIRS grid cells per village (2012-2021)
satellite_* First 2,000 MOSAIKS satellite imagery features: convolutional neural network features extracted from Planet imagery (2019)

Details

This dataset contains 50 VIIRS nighttime lights features (5 statistics \times 10 years) and the first 2,000 of 4,000 MOSAIKS features. It must be merged with `smartcard_data` and `remote_vars_p2` to obtain the complete dataset for RSV estimation.

The data is split into two parts (`remote_vars_p1` and `remote_vars_p2`) due to size limits while still providing access to all 4,000 MOSAIKS features.

Source

- VIIRS nighttime lights: <https://dataverse.harvard.edu/api/access/datafile/10742856>
- MOSAIKS features: Rolf, E., Proctor, J., Carleton, T., Bolliger, I., Shankar, V., Ishihara, M., Recht, B., & Hsiang, S. (2021). A generalizable and accessible approach to machine learning with global satellite imagery. *Nature Communications*, 12, 4392. doi:[10.1038/s41467021-24638z](https://doi.org/10.1038/s41467021-24638z)

See Also

`smartcard_data` for base data, `remote_vars_p2` for remaining MOSAIKS features, `vignette("construct-remote-variables")` for instructions on generating these features

Examples

```
# Load all three datasets
data("smartcard_data", package = "remoteoutcome")
data("remote_vars_p1", package = "remoteoutcome")
data("remote_vars_p2", package = "remoteoutcome")
force(smartcard_data)
force(remote_vars_p1)
force(remote_vars_p2)

# Merge to create complete dataset
smartcard_data <- smartcard_data %>%
  inner_join(remote_vars_p1, by = "shrid2") %>%
  inner_join(remote_vars_p2, by = "shrid2")

# Check dimensions
dim(smartcard_data) # Should be 8,312 x 4,060

# Summary of VIIRS features
summary(remote_vars_p1[, grep("luminosity_mean", names(remote_vars_p1))])

# Summary of first 10 satellite features
summary(remote_vars_p1[, paste0("satellite_", 1:10)])
```

remote_vars_p2

Remote Sensing Variables: MOSAIKS Features (Part 2)

Description

Second part of remote sensing features for villages in the Andhra Pradesh smartcard study. Contains the remaining 2,000 MOSAIKS satellite imagery features (features 2001-4000).

Usage

```
remote_vars_p2
```

Format

A data frame with 8,312 rows and 2,001 columns:

shrid2 SHRUG village identifier (unique) - merge key

satellite_2001 to satellite_4000 Remaining 2,000 MOSAIKS satellite imagery features: convolutional neural network features extracted from Planet imagery (2019)

Details

This dataset contains the second half of the 4,000 MOSAIKS features. It must be merged with smartcard_data and remote_vars_p1 to obtain the complete dataset for RSV estimation.

The MOSAIKS features are high-dimensional representations of satellite imagery that capture various aspects of land use, development, vegetation, and built environment. These features are derived from applying convolutional neural networks to Planet imagery from 2019.

Source

MOSAIKS features: Rolf, E., Proctor, J., Carleton, T., Bolliger, I., Shankar, V., Ishihara, M., Recht, B., & Hsiang, S. (2021). A generalizable and accessible approach to machine learning with global satellite imagery. *Nature Communications*, 12, 4392. doi:10.1038/s4146702124638z

See Also

`smartcard_data` for base data, `remote_vars_p1` for VIIRS features and first 2000 MOSAIKS features, `vignette("construct-remote-vars", package = "remoteoutcome")` for instructions on generating these features

Examples

```
# Load all three datasets
data("smartcard_data", package = "remoteoutcome")
data("remote_vars_p1", package = "remoteoutcome")
data("remote_vars_p2", package = "remoteoutcome")
force(smartcard_data)
force(remote_vars_p1)
force(remote_vars_p2)

# Merge to create complete dataset
smartcard_data <- smartcard_data %>%
  inner_join(remote_vars_p1, by = "shrid2") %>%
  inner_join(remote_vars_p2, by = "shrid2")

# Check dimensions
dim(smartcard_data) # Should be 8,312 x 4,060

# Verify all 4,000 satellite features are present
satellite_cols <- grep("^satellite_", names(smartcard_data), value = TRUE)
length(satellite_cols) # Should be 4000

# Summary of last 10 satellite features
summary(remote_vars_p2[, paste0("satellite_", 3991:4000)])
```

Description

Estimates treatment effects using remotely sensed variables (RSVs) following Rambachan, Singh, and Viviano (2025). Implements Algorithm 1 from the main text for binary outcomes without pretreatment covariates.

Usage

```
rsv_estimate(
  Y = NULL,
  D = NULL,
  S_e = NULL,
  S_o = NULL,
  R = NULL,
```

```

pred_Y = NULL,
pred_D = NULL,
pred_S_e = NULL,
pred_S_o = NULL,
theta_init = NULL,
eps = 0.01,
method = c("crossfit", "split", "none", "predictions"),
ml_params = list(),
se = TRUE,
se_params = list(),
cores = 1
)

```

Arguments

Y	Outcome variable (binary, NA where not observed).
D	Treatment indicator (binary, NA where not observed).
S_e	Experimental sample indicator (0 or 1).
S_o	Observational sample indicator (0 or 1).
R	Remotely sensed variable. Required if predictions are not provided.
pred_Y	(Optional) Predicted $P(Y R, S_o = 1)$, $\text{PRED}_Y(R)$. If provided, other predictions must also be provided.
pred_D	(Optional) Predicted $P(D R, S_e = 1)$, $\text{PRED}_D(R)$.
pred_S_e	(Optional) Predicted $P(S_e = 1 R)$, $\text{PRED}_{S_e}(R)$.
pred_S_o	(Optional) Predicted $P(S_o = 1 R)$, $\text{PRED}_{S_o}(R)$.
theta_init	Initial estimate of the treatment effect on the train data.
eps	Small constant for numerical stability of sigma2 estimate (default 1e-2).
method	Prediction fitting method; one of "split" (default), "crossfit", or "none". "split" = simple sample split; "crossfit" = K-fold cross-fitting; "none" = use all data for training/testing.
ml_params	List of parameters for random forest: ntree Number of trees classwt_Y Class weights for pred_Y model; default c(10, 1) seed User specified seed passed to each ranger function for reproducibility; default NULL nfolds Number of folds for cross-fitting (default 5). train_ratio Proportion for training in sample split (default 0.5).
se	Logical; compute standard errors via bootstrap? (default TRUE).
se_params	List of bootstrap parameters: B Number of bootstrap replications (default 1000) fix_seed If TRUE, deterministic seeding is used with ‘set.seed(b)’ for the *b*-th replication (default FALSE) clusters Clusters for the bootstrap. If NULL, uses individual-level bootstrap
cores	Number of cores used by either ‘ranger‘ or bootstrap replications; default 1

Details

The function supports two interfaces:

1. Provide fitted predictions pred_Y, pred_D, pred_S_e, pred_S_o directly.
2. Provide raw data (Y, D, S, R) and the function fits predictions using random forests.

The function also supports sample splitting and K-fold cross-fitting for prediction fitting.

Value

A list of class "rsv" with components:

- coef** Treatment effect estimate.
- se** Standard error (if se = TRUE).
- denominator_se** Standard error of the denominator of the treatment effect (if se = TRUE)
- n_obs** Sample size in observational sample.
- n_exp** Sample size in experimental sample.
- n_both** Sample size in both samples.
- numerator** Numerator of the treatment effect estimate
- denominator** Denominator of the treatment effect estimate
- method** Prediction fitting method used.
- call** The matched call.

Examples

```
## Not run:
library(dplyr)
library(remoteoutcome)

# Example data: data_real (included in package)
path_to_satellite_features <- "path/to/satellite_features.rds"
satellite_features <- readRDS(path_to_satellite_features) %>%
  select(-contains("lat"), -contains("lon"))
data("data_real", package = "remoteoutcome")
data_real <- inner_join(data_real, satellite_features, by = "shrid2")

Y <- data_real$Ycons # binary outcome
D <- data_real$D # binary treatment
R <- data_real %>% select(
  starts_with("luminosity"),
  starts_with("satellite"))
) # remotely sensed variable
S_e <- !is.na(D) & (rowSums(is.na(R)) == 0) # experimental sample indicator (Observe D, R)
S_o <- !is.na(Y) & (rowSums(is.na(R)) == 0) # observational sample indicator (Observe Y, R)
clusters <- data_real$clusters # Subdistrict-level cluster identifiers

# Example 1: No sample splitting
result <- rsv_estimate(
  Y = Y, D = D, S_e = S_e, S_o = S_o, R = R,
  method = "none",
  ml_params = list(seed = 42),
  se_params = list(fix_seed = TRUE, clusters = clusters),
  cores = 7
```

```

)
print(result)

# Example 2: With sample splitting
result <- rsv_estimate(
  Y = Y, D = D, S_e = S_e, S_o = S_o, R = R,
  method = "split",
  ml_params = list(train_ratio = 0.5, seed = 42),
  se_params = list(fix_seed = TRUE, clusters = clusters),
  cores = 7
)
print(result)

# Example 3: With cross fitting
result <- rsv_estimate(
  Y = Y, D = D, S_e = S_e, S_o = S_o, R = R,
  method = "crossfit",
  ml_params = list(nfold = 5, seed = 42),
  se_params = list(fix_seed = TRUE, clusters = clusters),
  cores = 7
)
print(result)

# Example 4: Custom ML parameters
result <- rsv_estimate(
  Y = Y,
  D = D,
  S_e = S_e,
  S_o = S_o,
  R = R,
  eps = 1e-2,
  method = "none",
  ml_params = list(      # Customize random forest parameters:
    ntree = 100,          # Number of trees
    classwt_Y = c(10, 1), # Class weights for PRED_Y model
    seed = 42,            # A random seed for each RF for reproducibility
  ),
  se = TRUE,
  se_params = list(      # Customize cluster-bootstrap standard errors:
    B = 1000,             # Number of bootstrap replications
    clusters = clusters, # Cluster identifiers for clustered sampling
    fix_seed = TRUE,       # Enables deterministic seeding for reproducibility
  ),
  cores = 7
)
print(result)

# Example 5: User provides fitted predictions
# Example data: pred_real_Ycons (included in package)
data("pred_real_Ycons", package = "remoteoutcome")

result <- rsv_estimate(
  Y = pred_real_Ycons$Y,
  D = pred_real_Ycons$D,
  S_e = pred_real_Ycons$S_e,
  S_o = pred_real_Ycons$S_o,
  pred_Y = pred_real_Ycons$pred_Y,
)

```

```

pred_D = pred_real_Ycons$pred_D,
pred_S_e = pred_real_Ycons$pred_S_e,
pred_S_o = pred_real_Ycons$pred_S_o,
method = "predictions",
theta_init = attr(pred_real_Ycons, "theta_init"),
# ml_params = list(
#   train_ratio = 0.2,    # If theta_init is not provided, 20% of the data
#   # will be used to estimate theta_init.
#   seed = 42            # A random seed for each RF for reproducibility
# ),
se = TRUE,
se_params = list(B = 1000, fix_seed = TRUE, clusters = pred_real_Ycons$clusters),
cores = 7
)
print(result)

## End(Not run)

```

smartcard_data*Andhra Pradesh Smartcard Study Data***Description**

Base dataset from Muralidharan et al.'s smartcard study in Andhra Pradesh, India, merged with SECC socioeconomic data. This dataset contains all villages with treatment assignment and outcomes, but excludes remote sensing features to reduce file size.

Usage

```
smartcard_data
```

Format

A data frame with 8,312 rows and 10 columns:

shrid2 SHRUG village identifier (unique)

spillover_20km Logical indicator for spillover-affected villages (within 20km of villages with different treatment status). Identified using maximum bipartite matching and Konig's theorem to find the maximum independent set.

tot_p Total population from SECC census

tot_f Total number of families from SECC census

Sample (Smartcard) Factor indicating sample assignment: "Experimental: Treated (2010)", "Experimental: Untreated (2011)", "Experimental: Untreated (2012)", or "Observational (N/A)"

D Treatment indicator: 1 if "Experimental: Treated (2010)" wave, 0 if "Experimental: Untreated (2011)" or "Experimental: Untreated (2012)" waves, NA if "Observational (N/A)" wave

Ycons Binary outcome: 1 if village consumption is in bottom quartile (<= 18,946.61 rupees per capita), 0 otherwise

Ylowinc Binary outcome: 1 if no households earn less than 5,000 rupees, 0 otherwise

Ymidinc Binary outcome: 1 if no households earn more than 10,000 rupees, 0 otherwise

clusters Cluster identifier (subdistrict name + district name in Andhra Pradesh)

Details

This dataset must be merged with `remote_vars_p1` and `remote_vars_p2` to obtain the complete data with remote sensing features required for RSV estimation. The remote sensing variables are stored separately due to file size limits.

Source

- Study data: Muralidharan, K., Niehaus, P., & Sukhtankar, S. (2016). Building State Capacity: Evidence from Biometric Smartcards in India. *American Economic Review*, 106(10), 2895-2929. [doi:10.1257/aer.20141346](https://doi.org/10.1257/aer.20141346)
- SHRUG location data: Asher, S., Lunt, T., Matsuura, R., & Novosad, P. (2021). <https://dataverse.harvard.edu/api/access/datafile/10742739>
- SECC Consumption: <https://dataverse.harvard.edu/api/access/datafile/10742743>
- SECC Income: <https://dataverse.harvard.edu/api/access/datafile/10742876>

See Also

`remote_vars_p1`, `remote_vars_p2` for remote sensing features

Examples

```
# Load all three datasets
data("smartcard_data", package = "remoteoutcome")
data("remote_vars_p1", package = "remoteoutcome")
data("remote_vars_p2", package = "remoteoutcome")
force(smartcard_data)
force(remote_vars_p1)
force(remote_vars_p2)

# Merge to create complete dataset
smartcard_data <- smartcard_data %>%
  inner_join(remote_vars_p1, by = "shrid2") %>%
  inner_join(remote_vars_p2, by = "shrid2")

# Summary statistics
table(smartcard_data$D, useNA = "ifany")
table(smartcard_data$`Sample (Smartcard)`)

## Not run:
# Use with RSV estimation
Y <- smartcard_data$Ycons
D <- smartcard_data$D
R <- smartcard_data %>%
  select(starts_with("luminosity_"), starts_with("satellite_"))
S_e <- !is.na(D) & (rowSums(is.na(R)) == 0)
S_o <- !is.na(Y) & (rowSums(is.na(R)) == 0)
clusters <- smartcard_data$clusters

result <- rsv_estimate(
  Y = Y, D = D, S_e = S_e, S_o = S_o, R = R,
  method = "split",
  se_params = list(clusters = clusters)
)
## End(Not run)
```

`summary.rsv`

Summary method for rsv objects

Description

Summary method for rsv objects

Usage

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

Arguments

object	An object of class "rsv".
...	Additional arguments (unused).

`vcov.rsv`

Extract variance-covariance matrix from rsv objects

Description

Extract variance-covariance matrix from rsv objects

Usage

```
## S3 method for class 'rsv'  
vcov(object, ...)
```

Arguments

object	An object of class "rsv".
...	Additional arguments (unused).

Value

A 1x1 matrix containing the variance of the treatment effect.

Index

* datasets

`pred_real_Ycons`, 6
`remote_vars_p1`, 9
`remote_vars_p2`, 10
`smartcard_data`, 15

`coef.rsv`, 2
`confint.rsv`, 2
`create_data_real`, 3, 5
`create_data_synth`, 4, 4

`pred_real_Ycons`, 6
`print.rsv`, 8

`remote_vars_p1`, 9, 11, 16
`remote_vars_p2`, 9, 10, 16
`rsv_estimate`, 6, 7, 11

`smartcard_data`, 4, 5, 7, 9, 11, 15
`summary.rsv`, 17

`vcov.rsv`, 17