

# Package ‘causalimages’

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**Title** causalimages: R Package for Causal Inference with Earth Observation, Bio-medical, and Social Science Images

**Version** 2.0

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**Description**

R Package for Causal Inference with Earth Observation, Bio-medical, and Social Science Images.

**Depends** R (>= 3.3.3)

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**Encoding** UTF-8

**LazyData** true

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**Imports** tensorflow

**RoxygenNote** 7.2.1

## R topics documented:

AnalyzeImageHeterogeneity . . . . .	1
SimulateImageSystem . . . . .	3
<b>Index</b>	<b>5</b>

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AnalyzeImageHeterogeneity
<i>AnalyzeImageHeterogeneity</i>

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## Description

Implements ...

**Usage**

```
AnalyzeImageHeterogeneity(
  obsW,
  obsY,
  X = NULL,
  imageKeys = NULL,
  transportabilityMat = NULL,
  lat = NULL,
  long = NULL,
  externalFigureKey = "",
  acquireImageRepFxn,
  acquireImageFxn_full = acquireImageRepFxn,
  TYPE = "variational_minimal",
  SimMode = F,
  nDepth_conv = 1,
  nDepth_dense = 1,
  plotResults = F,
  figuresPath = "./",
  kClust_est = 2,
  maxPoolSize = 2L,
  strides = 1L,
  nMonte_predictive = 10L,
  y_density = "normal",
  orthogonalize = F,
  compile = F,
  nMonte_variational = 5L,
  kernelWidth,
  nSGD = 400,
  nDenseWidth = 64L,
  nFilters = 7L
)
```

**Arguments**

DAG                    'DAG'.

**Value**

A list consisting of

- Items.

**References**

- References here

**Examples**

```
#set seed
set.seed(1)

#Generate data
x <- rnorm(100)
```

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SimulateImageSystem      *SimulateImageSystem*

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## Description

This function (1) generates simulated causal structures using images.

## Usage

```
SimulateImageSystem(dag = NULL, ...)
```

## Arguments

dag	( <i>character string</i> ) An input DAG specifying causal structure. This input should be of the form ‘ <b>i</b> -> <b>t</b> , <b>i</b> -> <b>y</b> , <b>t</b> -> <b>y</b> , ...’. Currently, only one node in a DAG can be an image (this should be labeled “ <b>i</b> ”). The non-image nodes can have arbitrary string labels. The image can be a confounder, effect moderator, effect mediator. If the image is to be used as a moderator, use the notation, <b>t</b> - <b>i</b> > <b>y</b> .
...	( <i>optional</i> ) In estimation mode, users input the data matrices associated with the non-image nodes of DAG and image node <b>i</b> . For example, if <b>x</b> is a DAG node, users must, in estimation mode, supply data to <b>x</b> in a form that can be coerced to a tensor.
treatment	( <i>character string, optional</i> ) In estimation mode, users specify the treatment variable here. If <b>treatment</b> is specified, users must provide other data inputs to the DAG (see ...).
image_pool	( <i>character string, optional</i> ) The path to where analysis specific images are located. This can be specified both in simulation and estimation mode. If not specified, the simulation uses a pool of Landsat images from Nigeria.
analysis_level	( <i>character string, default is ‘scene’</i> ) Defines the unit of analysis used in the simulation framework. This is ignored in estimation mode, where the unit of analysis is inferred from the data dimensions.
control	( <i>list</i> ) A list containing control parameters in the data generating process.

## Value

A list:

- In *simulation mode*, the function returns a list with as many elements as unique nodes in DAG. Each element represents the simulated data.
- In *estimation mode*, the function returns an estimated treatment effect with 95% confidence intervals.

## References

- CITES

**Examples**

```
#set seed
set.seed(1)

# Simulation mode
#simulatedData <- causalimage('r->i, i->t, t->y, r->y')
#print(names(simulatedData))

# Estimation mode
#estimatedResults <- causalimage('r->i, i->t, t->y, r->y', y=y, r=r, y=y', treatment='t')
#print( estimatedResults )
```

# Index

AnalyzeImageHeterogeneity, [1](#)

SimulateImageSystem, [3](#)