

# Package: SMITIDvisu (via r-universe)

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**Type** Package

**Title** Visualize Data for Host and Viral Population from 'SMITIDstruct' using 'HTMLwidgets'

**Version** 0.0.9

**Maintainer** Jean-Francois Rey <jean-francois.rey@inrae.fr>

**Description** Visualisation tools for 'SMITIDstruct' package. Allow to visualize host timeline, transmission tree, index diversities and variant graph using 'HTMLwidgets'. It mainly using 'D3JS' javascript framework.

**Date** 2021-02-08

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**Author** Jean-Francois Rey [aut, cre], Julien Boge [ctb]

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## Contents

SMITIDvisu-package . . . . .	2
createRainbowColors . . . . .	3
demo.SMITIDvisu.run . . . . .	4
df2geojson . . . . .	4
hostline . . . . .	5
maptt . . . . .	5
mapttProxy . . . . .	7
mapttSelectHost . . . . .	8
mstCompute . . . . .	9
mstVariant . . . . .	9
mstVariantProxy . . . . .	10
SMITIDvisu-shiny . . . . .	11
st . . . . .	11
st.dist113_2 . . . . .	12
st.dist113_all . . . . .	13
st.listTimeProp113 . . . . .	13
st.prop113_2 . . . . .	14
st.prop113_all . . . . .	14
timeLine . . . . .	15
timeLineProxy . . . . .	16
transmissionTree . . . . .	16
transmissionTreeProxy . . . . .	17
tt.edges . . . . .	18
tt.events . . . . .	19
tt.nodes . . . . .	19
updatemstVariant . . . . .	20
updateTimeLine . . . . .	21
updateTransmissionTree . . . . .	21
<b>Index</b>	<b>23</b>

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SMITIDvisu-package	<i>Visualize Data for Host and Viral Population from SMITIDstruct using HTMLwidgets</i>
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## Description

Visualisation tools for SMITIDstruct package. Allow to visualize host timeline, transmission tree, index diversities and variant graph using HTMLwidgets. It mainly using D3JS, noUiSlider and FileSaver javascript libraries.

## Details

Package: SMITIDvisu  
Type: Package  
Version: 0.0.9  
Date: 2021-02-08  
License: GPL (>=3)

## Author(s)

Jean-Francois Rey <jean-francois.rey@inrae.fr>  
Julien Boge <julien.boge.u@gmail.com>

## Examples

```
## Not run:  
library(SMITIDvisu)  
demo.SMITIDvisu.run()  
  
## End(Not run)
```

---

createRainbowColors *createRainbowColors Create a list of colors for each value v*

---

## Description

createRainbowColors Create a list of colors for each value v

## Usage

```
createRainbowColors(v)
```

## Arguments

v a vector of characters

## Value

a list of value=color

demo.SMITIDvisu.run     *demo.SMITIDvisu.run*

---

**Description**

run a demo to visualize data

**Usage**

```
demo.SMITIDvisu.run()
```

---

df2geojson                 *df2geojson*

---

**Description**

Transform a data frame into a string formatted in GeoJSON

**Usage**

```
df2geojson(df, multipleValuesByTime = c())
```

**Arguments**

**df**                         Data frame to convert in GeoJSON. It must contain at least columns 'id', 'time', 'X' and 'Y'. Additionnal columns will be added as features' properties.

**multipleValuesByTime**     Vector of strings indicating the df columns names which can contain several values by time.

**Value**

a geojson string

**Examples**

```
library(SMITIDvisu)
data(transmissiontree)
geojson <- df2geojson(tt.events, multipleValuesByTime = c('infectedby', 'probabilities'))
```

---

hostline	<i>A host infomation over time</i>
----------	------------------------------------

---

**Description**

kind of host time line

**Usage**

```
data("hostline")
```

**Format**

A data frame with 8 observations on the following 5 variables.

level a character vector

label a character vector

ID a character vector

timestart a character vector

timeend a character vector

**Examples**

```
data(hostline)
print(hostline)
```

---

maptt	<i>maptt</i>
-------	--------------

---

**Description**

Display a Transmission Tree over a map.

**Usage**

```
maptt(
  data,
  multipleValuesByTime = c(),
  circleRadius = 6,
  defaultNodeColor = "steelblue",
  nodeColorByState = list(),
  moveEdgeColor = "steelblue",
  color1 = "green",
  color2 = "red",
  nbColors = 10,
```

```

minWeight = 0,
maxWeight = 1,
weight1 = 0,
weight2 = 1,
autoFocus = TRUE,
keepOldFeatures = TRUE,
optionsControl = TRUE,
gradientControl = TRUE,
legend = TRUE,
width = NULL,
height = NULL,
elementId = NULL
)

```

### Arguments

<code>data</code>	Either a data frame that will be converted to a GeoJSON collection, or a string describing a valid GeoJSON collection. The data frame must contain at least columns 'id', 'time', 'X' and 'Y'. It can contain columns 'infectedby', 'probabilities'. Additional columns will be added as properties, but will do nothing in this implementation of maptt. See the 'df2geojson' function for more informations.
<code>multipleValuesByTime</code>	Vector of strings indicating the df columns names which can contain several values by time. Typically, you would use 'c('infectedby','probabilities')' if you have these values.
<code>circleRadius</code>	Numeric value specifying the radius of the nodes in pixels.
<code>defaultNodeColor</code>	String indicating the default color of nodes, if their status doesn't match with any color. Colors can be specified in hex.
<code>nodeColorByState</code>	List of strings, indicating the color scheme for each node state.
<code>moveEdgeColor</code>	String indicating the color of the edges representing the move of a node.
<code>color1</code>	String indicating the color corresponding to the minWeight value.
<code>color2</code>	String indicating the color corresponding to the maxWeight value.
<code>nbColors</code>	Number of colors for the color scheme using a gradient between color1 and color2. These colors will be used to represent the infection edges according to the infection probability. If no probability is used, the edge will use color2. Three intervals are created : color1 will be used for the probabilities between minWeight and weight1. Colors between color1 and color2 will be used for probabilities between weight1 and weight2. color2 will be used for probabilities between weight2 and maxWeight. This setting can be modified directly on the map if 'gradientControl' is activated.
<code>minWeight</code>	Minimal weight.
<code>maxWeight</code>	Maximal weight.

weight1	Lowest weight for the color scheme. This setting can be modified directly on the map if 'gradientControl' is activated.
weight2	Greatest weight for the color scheme. This setting can be modified directly on the map if 'gradientControl' is activated.
autoFocus	Boolean indicating if the map should focus at the displayed features at each time. This setting can be toggled directly on the map if 'optionsControl' is activated.
keepOldFeatures	Boolean indicating if old features should be displayed or not. Features are considered "old" if their last 'time' is prior to the current time displayed. This setting can be toggled directly on the map if 'optionsControl' is activated.
optionsControl	Boolean indicating if the options control should be displayed or not
gradientControl	Boolean indicating if the gradient control should be displayed or not
legend	Boolean indicating if the legend should be displayed or not
width	Numeric width for the area in pixels.
height	Numeric hieght for the area in pixels.
elementId	The element ID where the map is displayed

### Examples

```

library(SMITIDvisu)
data(transmissiontree)

maptt(tt.events, multipleValuesByTime = c('infectedby', 'probabilities'))

# In this example:
# - values lower than 20 will be yellow ;
# - values between 20 and 25 will use colors between yellow and red ;
# - values greater than 25 will be red.
maptt(tt.events,
  multipleValuesByTime = c('infectedby', 'probabilities'),
  color1 = 'yellow',
  color2 = 'red',
  nbColors = 10,
  minWeight = 0,
  maxWeight = 30,
  weight1 = 20,
  weight2 = 25
)

```

---

mapttProxy

*mapttProxy*

---

### Description

get mapttProxy

**Usage**

```
mapttProxy(mapttId, session = shiny::getDefaultReactiveDomain())
```

**Arguments**

mapttId	widget instance identifier
session	shiny session

**Examples**

```
## Not run:  
library(SMITIDvisu)  
## server.R  
mapttProxy <- mapttProxyProxy("mapttOutput")  
  
## End(Not run)
```

---

mapttSelectHost	<i>mapttSelectHost</i>
-----------------	------------------------

---

**Description**

select a host on a MapTT instance

**Usage**

```
mapttSelectHost(mapttProxy, hostId)
```

**Arguments**

mapttProxy	mapttProxy instance
hostId	the id of the host to select

**See Also**

[maptt](#)

**Examples**

```
## Not run:  
library(SMITIDvisu)  
data(transmissiontree)  
## server.R  
mapttProxy("mapttOutput") %>% mapttSelectHost()  
  
## End(Not run)
```



---

mstCompute	<i>compute the minimum spanning tree</i>
------------	--

---

**Description**

compute the minimum spanning tree of a matrix representing edges between nodes (of a graph)

**Usage**

```
mstCompute(mat)
```

**Arguments**

mat	weighted matrix representing nodes connection (edges weight)
-----	--

**Value**

a matrix with 1 if nodes are linked, 0 otherwise.

---

mstVariant	<i>mstVariant</i>
------------	-------------------

---

**Description**

Draw Variants genotypes distances as a graph using Minimum Spanning Tree algorithm.

**Usage**

```
mstVariant(
  mat,
  prop,
  node.prop = NULL,
  width = NULL,
  height = NULL,
  elementId = NULL
)
```

**Arguments**

mat	a distance matrix between sequence of variants (integer distance no floating values)
prop	a data.frame for variants sequences proportions and count (see details)
node.prop	list of variants with proportions and time (default NULL)
width	numeric width for the area in pixels.
height	numeric hieght for the area in pixels.
elementId	the element ID where is draw

## Details

**mat** is a simple distance matrix with interger values, row and lines contain a unique identifier of each variant sequences. **prop** is a data.frame where each row is a variant sequence, it have to contain in columns factor "ID", "proportion" and "count". "ID" is a unique identifier matching matrix value identifier, "proportion" is the proportions of the variant sequence and "count" the number of variant sequence in a varions set. **node.prop** is a list with name that matching **mat** identifier and **prop** "ID". Each list element contains a subvector time (Julian or timestamp) and value (proportions). That allow to draw variants proportions over time.

## Examples

```
library(SMITIDvisu)
data(st)
mstV <- mstVariant(st.dist113_all,st.prop113_all, st.listTimeProp113)
## Not run:
## export as standalone html file
htmlwidgets::saveWidget(mstV, "mstVariant.html")
browseURL("mstVariant.html")

## End(Not run)
```

---

mstVariantProxy

*mstVariantProxy*

---

## Description

get mstVariantProxy

## Usage

```
mstVariantProxy(mstVid, session = shiny::getDefaultReactiveDomain())
```

## Arguments

mstVid	widget instance identifier
session	shiny session

## Examples

```
## Not run:
library(SMITIDvisu)
## server.R
mstVariantProxy <- mstVaraintProxy("mstvariantoutput")

## End(Not run)
```

---

SMITIDvisu-shiny      *Shiny bindings for visualisation widgets*

---

### Description

Output and render functions for using visualisation widgets within Shiny applications and interactive Rmd documents.

### Usage

```
mapttOutput(outputId, width = "100%", height = "400px")
renderMaptt(expr, env = parent.frame(), quoted = FALSE)
mstVariantOutput(outputId, width = "100%", height = "600px")
rendermstVariant(expr, env = parent.frame(), quoted = FALSE)
timeLineOutput(outputId, width = "100%", height = "400px")
renderTimeLine(expr, env = parent.frame(), quoted = FALSE)
transmissionTreeOutput(outputId, width = "100%", height = "500px")
renderTransmissionTree(expr, env = parent.frame(), quoted = FALSE)
```

### Arguments

outputId	output variable to read from
width, height	Must be a valid CSS unit (like "100%", "400px", "auto") or a number, which will be coerced to a string and have "px" appended.
expr	An expression that generates a networkD3 graph
env	The environment in which to evaluate expr.
quoted	Is expr a quoted expression (with quote())? This is useful if you want to save an expression in a variable.

---

st      *A SMITIDstruct package variable.*

---

### Description

A SMITIDstruct package variable from simul-chain as a list. The list is a set of HostSet, ViralPopset and an index

**Usage**

```
data("st")
```

**Format**

The format is: List of 3 \$ :List of 21 .. ..- attr(\*, "class")= chr "HostSet" \$ :List of 20 .. ..- attr(\*, "class")= chr "ViralPopSet" \$ :'data.frame': 79 obs. of 3 variables: ..\$ TIME : chr [1:79] "0" "0" "1.26" "1.35" ... ..\$ ID\_HOST : chr [1:79] "1" "2" "2" "2" ... ..\$ EVENTCODE: chr [1:79] "000011" "000110" "001000" "001000" ...

**Examples**

```
data(st)
## maybe str(st) ; plot(st) ...
```

---

```
st.dist113_2
```

*Distance matrix of observed variants sequences of a host 113 at time 2 from simulation.*

---

**Description**

Levenshtein Distance matrix with rows and cols label as sequences ID.

**Usage**

```
data("st")
```

**Format**

The format is: num [1:23, 1:23] 0 1 1 1 2 1 1 1 1 2 ...

**Examples**

```
data(st)
```

---

st.dist113_all	<i>Distance matrix of observed variants sequences of a host 113 at time 2, 3 and 4 from simulation.</i>
----------------	---

---

**Description**

Levenshtein Distance matrix with rows and cols label as sequences ID. Unique sequence variants observed on host 113 at time 2, 3 and 4 from a simulation.

**Usage**

```
data("st")
```

**Format**

The format is: num [1:51, 1:51] 0 1 1 1 1 1 3 1 1 1 ...

**Examples**

```
data(st)
```

---

st.listTimeProp113	<i>List of variants ID with subvector for time and value.</i>
--------------------	---

---

**Description**

A list indexed by variants sequences ID. Each element contain a time and value vector for time of observation and proportions observed at this time.

**Usage**

```
data("st")
```

**Examples**

```
data(st)
```

---

st.prop113_2	<i>Variants proportions and count for host 113 at time 2 from simulation.</i>
--------------	---

---

**Description**

A data.frame with label "ID", "proportion" and "count" for an host 113 at time 2 from simulation. Each row is a sequence.

**Usage**

```
data("st")
```

**Format**

A data frame with 23 observations on the following 3 variables.

ID a character vector

proportion a numeric vector

count a numeric vector

**Examples**

```
data(st)
```

---

st.prop113_all	<i>Variants proportions and count for an host 113 at time 2, 3 and 4 from simulation.</i>
----------------	---

---

**Description**

A data.frame with label "ID", "proportion" and "count" for an host 113 at time 2, 3 and 4 from simulation. Each row is a sequence.

**Usage**

```
data("st")
```

**Format**

A data frame with 51 observations on the following 3 variables.

ID a character vector

proportion a numeric vector

count a numeric vector

**Examples**

```
data(st)
```

---

timeLine	<i>timeLine</i>
----------	-----------------

---

## Description

Draw a host time line. Time use timestamp or Date in ISO format.

## Usage

```
timeLine(  
  data,  
  title,  
  color = NULL,  
  width = NULL,  
  height = NULL,  
  elementId = NULL  
)
```

## Arguments

data	a data.frame that represent hosts status in time with ID, status and time in columns
title	a title as character
color	list of color for timeline elements
width	numeric width for the area in pixels.
height	numeric height for the area in pixels.
elementId	the element ID where is draw

## Examples

```
library(SMITIDvisu)  
data(hostline)  
tl <- timeLine(hostline,  
               title="Example host 113",  
               color=list("infected"="red", "offspring"="green",  
                           "alive"="blue", "inf"="orange",  
                           "dead"="black", "Obs"="purple"))  
  
## Not run:  
## export as standalone html file  
htmlwidgets::saveWidget(tl, "timeline.html")  
browseURL("timeline.html")  
  
## End(Not run)
```

timeLineProxy            *timeLineProxy* get an instance of a timeline

---

### Description

timeLineProxy get an instance of a timeline

### Usage

```
timeLineProxy(tlid, session = shiny::getDefaultReactiveDomain())
```

### Arguments

tlid	a timeline instance id
session	shiny session

### Value

an object of class timeline\_proxy

### Examples

```
## Not run:
## server.R
## output server variable
output$timeline <- renderTimeLine({
  timeLine(data.frame(), "")
})
## ui.R
timeLineOutput("timeline")
## server.R
tlproxy <- timeLineProxy("timeline")

## End(Not run)
```

---

transmissionTree            *transmissionTree*

---

### Description

Draw a transmission tree over the time. Time use timestamp or Date in ISO format ("



**Usage**

```
transmissionTree(
  nodes,
  edges,
  nodes.color = NULL,
  width = NULL,
  height = NULL,
  elementId = NULL
)
```

**Arguments**

nodes	a data.frame that represent hosts status in time with ID, status and time in columns
edges	a data.frame that represent transmission link between hosts (pathogens) with ID, source, target and time in columns
nodes.color	a list of color for nodes status "status"="color"
width	numeric width for the area in pixels.
height	numeric hieght for the area in pixels.
elementId	the element ID where is draw

**Examples**

```
library(SMITIDvisu)
data(transmissiontree)
tt <- transmissionTree(tt.nodes,tt.edges, nodes.color = list("default"="black","Inf"="red"))
## Not run:
## export as standalone html file
htmlwidgets::saveWidget(tt, "transTree.html")
browseURL("transTree.html")

## End(Not run)
```

---

transmissionTreeProxy *transmissionTreeProxy*

---

**Description**

get transmissionTreeProxy

**Usage**

```
transmissionTreeProxy(ttid, session = shiny::getDefaultReactiveDomain())
```

**Arguments**

ttid            widget instance identifier  
session        shiny session

**Examples**

```
## Not run:  
library(SMITIDvisu)  
## server.R  
transmissionTreeProxy <- transmissionTreeProxyProxy("transmissionTreeoutput")  
  
## End(Not run)
```

---

tt.edges                      *Pathogen link over the time*

---

**Description**

A data.frame of all transmission links between hosts (pathogens). Five columns ID, source, target, time and weight.

**Usage**

```
data("transmissiontree")
```

**Format**

A data frame with 13 observations on the following 5 variables.

ID a numeric vector

source a character vector

target a factor with levels 113 104 116 115 111 109 105 108 106 112

time a character vector

weight a character vector

**Examples**

```
data(transmissiontree)  
print(tt.edges)
```

---

tt.events	<i>Data.frame of hosts events information by time. Fake data.</i>
-----------	---

---

**Description**

Fake simulated data of hosts events over the time.

**Usage**

```
data("transmissiontree")
```

**Format**

A data frame with 63 observations on the following 7 variables.

id a character vector

time a character vector

status a character vector

infectedby a character vector

probabilities a character vector

X a numeric vector

Y a numeric vector

**Examples**

```
data(transmissiontree)
print(tt.events)
```

---

tt.nodes	<i>Host list with there status over the time.</i>
----------	---

---

**Description**

a data.frame of all the hosts identify by there ID. Three colums is use ID, status and time

**Usage**

```
data("transmissiontree")
```

**Format**

A data frame with 47 observations on the following 3 variables.

ID a character vector

status a character vector

time a character vector

**Examples**

```
data(transmissiontree)
print(tt.nodes)
```

---

updateMstVariant      *updateMstVariant*

---

**Description**

update (redraw) an instance on mstVariant

**Usage**

```
updateMstVariant(mstVProxy, mat, prop, propTime = NULL)
```

**Arguments**

mstVProxy	mstVaraintProxy instance
mat	distance matrix
prop	proportions data.frame
propTime	list of each variant by time and proportions

**See Also**

[mstVariant](#)

**Examples**

```
## Not run:
library(SMITIDvisu)
data(mstVariant)
## server.R
mstVaraintProxy("mstvariantoutput") %>% updateMstVariant(st.dist, st.prop)

## End(Not run)
```

---

updateTimeLine	<i>updateTimeLine</i>
----------------	-----------------------

---

**Description**

updateTimeLine

**Usage**

```
updateTimeLine(tlProxy, data, title)
```

**Arguments**

tlProxy	a timeline proxy instance
data	new data
title	new title

**See Also**

[timeLine](#)

**Examples**

```
## Not run:
## server.R
## output server variable
output$timeline <- renderTimeLine({
  timeLine(data.frame(), "")
})
## ui.R
timeLineOutput("timeline")
## server.R
timeLineProxy("timeline") %>% updateTimeLine(newtimeline, "newId")

## End(Not run)
```

---

updateTransmissionTree	<i>updateTransmissionTree</i>
------------------------	-------------------------------

---

**Description**

update (redraw) an instance of a transmissionTree

**Usage**

```
updateTransmissionTree(TTProxy, nodes, edges, options = NULL)
```

**Arguments**

TTProxy	transmissionTreeProxy instance
nodes	a data.frame that represent hosts status in time with ID, status and time in columns
edges	a data.frame that represent transmission link between hosts (pathogens) with ID, source, weight, target and time in columns
options	transmissionTree new options

**See Also**

[transmissionTree](#)

**Examples**

```
## Not run:  
library(SMITIDvisu)  
data(transmissionTree)  
## server.R  
transmissionTreeProxy("transmissionTreeoutput") %>% updatetransmissionTree(tt.nodes,tt.edges)  
  
## End(Not run)
```

# Index

## \* datasets

- hostline, [5](#)
- st, [11](#)
- st.dist113\_2, [12](#)
- st.dist113\_all, [13](#)
- st.listTimeProp113, [13](#)
- st.prop113\_2, [14](#)
- st.prop113\_all, [14](#)
- tt.edges, [18](#)
- tt.events, [19](#)
- tt.nodes, [19](#)

createRainbowColors, [3](#)

demo.SMITIDvisu.run, [4](#)

df2geojson, [4](#)

hostline, [5](#)

maptt, [5](#), [8](#)

mapttOutput (SMITIDvisu-shiny), [11](#)

mapttProxy, [7](#)

mapttSelectHost, [8](#)

mstCompute, [9](#)

mstVariant, [9](#), [20](#)

mstVariantOutput (SMITIDvisu-shiny), [11](#)

mstVariantProxy, [10](#)

renderMaptt (SMITIDvisu-shiny), [11](#)

rendermstVariant (SMITIDvisu-shiny), [11](#)

renderTimeLine (SMITIDvisu-shiny), [11](#)

renderTransmissionTree  
(SMITIDvisu-shiny), [11](#)

SMITIDvisu (SMITIDvisu-package), [2](#)

SMITIDvisu-package, [2](#)

SMITIDvisu-shiny, [11](#)

st, [11](#)

st.dist113\_2, [12](#)

st.dist113\_all, [13](#)

st.listTimeProp113, [13](#)

st.prop113\_2, [14](#)

st.prop113\_all, [14](#)

timeLine, [15](#), [27](#)

timeLineOutput (SMITIDvisu-shiny), [11](#)

timeLineProxy, [16](#)

transmissionTree, [16](#), [22](#)

transmissionTreeOutput  
(SMITIDvisu-shiny), [11](#)

transmissionTreeProxy, [17](#)

tt.edges, [18](#)

tt.events, [19](#)

tt.nodes, [19](#)

updateMstVariant, [20](#)

updateTimeLine, [21](#)

updateTransmissionTree, [21](#)