

# Package ‘aop’

June 17, 2015

**Type** Package

**Title** Adverse Outcome Pathway Analysis

**Version** 0.99.5

**Date** 2015-06-16

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**Description** Provides tools for analyzing adverse outcome pathways (AOPs) that are either 1) developed in and exported from Cytoscape or 2) already exist in R as a graph object.

**License** CC0

**Suggests** RUnit, BiocGenerics, knitr, rmarkdown

**Imports** graph (>= 1.38.3), rjson (>= 0.2.14), igraph (>= 0.7.1), Rgraphviz (>= 2.10.0), methods

**VignetteBuilder** knitr

**Collate** 'aopCytoscape\_Class.R' 'aop\_cytoscape\_methods.R'  
'aop\_graph\_analysis.R'

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2015-06-17 00:45:52

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`aop_backdoor`*Backdoor Causal Network Analysis for AOPs*

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**Description**

Performs a backdoor causal network analysis to identify nodes/key events which are sufficient to infer causality.

**Usage**

```
aop_backdoor(aop_graph, ke_coord, ao_coord, measureable_nodes = NULL)
```

**Arguments**

<code>aop_graph</code>	a graphNEL object that encodes the AOP. Typically, this would be output from the <code>convert_aop_to_graph</code> function.
<code>ke_coord</code>	typically this is the molecular initiating event node, but really, this is any node that you want as the starting/source point. For instance, this is normally the point at which exposure to a stressor is going to enter the AOP.
<code>ao_coord</code>	typically this is the adverse outcome node.
<code>measureable_nodes</code>	this param is not used yet. In the future this node will be a vector of the nodes where an assay is available to measure the node. In a future release this param will focus the backdoor algorithm on finding only those nodes for which measurements can actually be taken, as opposed to causal nodes regardless of our ability to measure them. This allows for the assumption that AOP key events may or may not be measureable.

**Details**

This function performs Pearl's backdoor analysis. Whereas Pearl was interested in identifying nodes which need to be measured to make a causal statement, we are interested in identifying those nodes/key events which need to be measured to say that an adverse outcome is likely to occur. It's essentially the same thing as Pearl, only a slightly different interpretation.

**Value**

`causal_nodes` vector a vector of the names of the causal nodes.

**Examples**

```
steatosis_json_file <- system.file("extdata", "steatosis_aop_json.cyjs",  
  package = "aop")  
steatosis_aop <- convert_cytoscape_to_aop(steatosis_json_file)  
steatosis_aop_graph <- convert_aop_to_graph(steatosis_aop)  
aop_backdoor(steatosis_aop_graph, "391", "388")
```

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aop\_cytoscape-class    *aop\_cytoscape class*

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**Description**

Creates an object of class aop\_cytoscape

**Slots**

name: Object of class "character", containing the name of the AOP.

nodes: Object of class "list", containing the list of nodes.

edges: Object of class "list", containing the list of edges.

**Author(s)**

Lyle D. Burgoon

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convert\_aop\_to\_graph    *Convert AOP to Graph*

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**Description**

Converts an AOP (encoded as aop\_cytoscape object) to a graphNEL object.

**Usage**

```
convert_aop_to_graph(aop)
```

**Arguments**

aop                    an object of class aop\_cytoscape.

**Details**

This function converts an aop\_cytoscape object to a graphNEL object. This allows us to perform graph-based analyses of the AOP.

**Value**

aop\_graph a graphNEL object representation of the AOP

## Examples

```
library(graph)
steatosis_json_file <- system.file("extdata", "steatosis_aop_json.cyjs",
package = "aop")
steatosis_aop <- convert_cytoscape_to_aop(steatosis_json_file)
steatosis_aop_graph <- convert_aop_to_graph(steatosis_aop)
plot(steatosis_aop_graph)
```

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convert\_cytoscape\_to\_aop

*Convert Cytoscape Graph to an AOP*

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## Description

Converts a cytoscape JSON file to an aop\_cytoscape-class object.

## Usage

```
convert_cytoscape_to_aop(file)
```

## Arguments

file            a Cytoscape JSON file.

## Details

This function converts a JSON file exported from Cytoscape into a aop\_cytoscape-class object. Once an aop\_cytoscape-class object, we can perform conversion to a graphNEL object, and then perform graph-based analyses.

## Value

aop a aop\_cytoscape-class object.

## Examples

```
steatosis_json_file <- system.file("extdata", "steatosis_aop_json.cyjs",
package = "aop")
steatosis_aop <- convert_cytoscape_to_aop(steatosis_json_file)
```

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getAOPNodeName	<i>Get Node Name from ID</i>
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**Description**

Given an id, this method returns an aop\_cytoscape node name.

**Usage**

```
getAOPNodeName(theObject, id)

## S4 method for signature 'aop_cytoscape'
getAOPNodeName(theObject, id)
```

**Arguments**

theObject	is an AOP as an object of class aop_cytoscape.
id	an object of class character such as "389".

**Value**

the name of the node

**Examples**

```
library(graph)
steatosis_json_file <- system.file("extdata", "steatosis_aop_json.cyjs",
package = "aop")
steatosis_aop <- convert_cytoscape_to_aop(steatosis_json_file)
getAOPNodeName(steatosis_aop, "389")
```

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