

# get\_significant\_associations.R

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get_significant_associations	
	<i>Get Significant Species Associations</i>

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## Description

Identifies significant species associations based on support and mean values for each error level.

## Usage

```
get_significant_associations(data_source, alpha = 0.05)
```

## Arguments

data_source	A list containing association matrices from a fitted Hmsc model. Generally, this is the output of the function <code>get_species_association()</code> .
alpha	Significance level for support threshold (default: 0.05).

## Value

A vector of significant association values.

## See Also

[`get_species_association()`]

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