

get_significant_associations.R

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

Description

Identifies significant species associations based on support and mean values.

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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`get_significant_associations`, [1](#)