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**MLparameters***Compute Maximum Likelihood Parameters*

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**Description**

Computes the maximum likelihood parameters for a given tree topology.

**Usage**

```
MLparameters(x, tree, freq = NULL)
```

**Arguments**

<b>x</b>	a binary matrix whose rows are the (preferably unique) genetic profiles.
<b>tree</b>	the tree in matrix format.
<b>freq</b>	a vector whose length equals the number of rows of x, giving the frequency of each profile in the data.

**Value**

<b>p</b>	a vector of the maximum likelihood edge parameters (model probabilities).
<b>totloglik</b>	the likelihood at the ML parameters.

**Examples**

```
data(kidney)
MLparameters(kidney$x, freq = NULL, kidney$tree)
```

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**MLtopology***Compute Maximum Likelihood Tree Topology*

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**Description**

Tries to compute the maximum likelihood tree model for a given data set through stepwise leaf insertion and rearrangements.

**Usage**

```
MLtopology(x, verbose=FALSE)
```

**Arguments**

<b>x</b>	a binary matrix with rows representing tumors and columns representing genetic alterations.
<b>verbose</b>	a Boolean value indicating whether intermediate results of the algorithm are to be printed.

## Value

<code>tree</code>	the resulting tree in matrix format.
<code>p</code>	a vector of the maximum likelihood edge parameters (model probabilities).
<code>totloglik</code>	the likelihood of the tree model.

## Examples

```
data(kidney)
y <- MLtopology(kidney$x)
```

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<code>comp.freq</code>	<i>Compare Model Probabilities to Frequencies</i>
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## Description

Compares the model probabilities of single alterations and pairs to the observed frequencies and shows scatterplots for the comparisons.

## Usage

```
comp.freq(x, tree, p)
```

## Arguments

<code>x</code>	a binary data matrix with rows representing tumors and columns representing genetic alterations.
<code>tree</code>	the tree in matrix format.
<code>p</code>	a vector of edge parameters (model probabilities).

## Examples

```
data(kidney)
comp.freq(kidney$x, kidney$tree, kidney$p)
```

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<code>convert</code>	<i>Converts Matrix to Newick Format</i>
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### Description

Converts a tree from matrix to Newick format, assigning to each edge the negative log of the corresponding model probability.

### Usage

```
convert(tree, p, var.names)
```

### Arguments

<code>tree</code>	the tree in matrix format.
<code>p</code>	a vector of edge parameters (model probabilities).
<code>var.names</code>	a character vector of variable names.

### Value

a character vector of the tree in Newick format

### Examples

```
data(kidney)
convert(kidney$tree, kidney$p, colnames(kidney$x))
```

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<code>is.tree</code>	<i>Compare with Tree Format</i>
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### Description

tests whether a 2 x n matrix represents a rooted tree in the format accepted by the `oncomodel` package.

### Usage

```
is.tree(tree)
```

### Arguments

<code>tree</code>	a 2 x n matrix.
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## Details

In the accepted format, the columns of the integer matrix represent the edges of the tree, with the entry in the first row being closer to the root. The leaves have to be the smallest integers of the matrix. If an edge has a smaller column index than a second one, it may not be on the path from the second edge to the root (the order of the columns has to be compatible with the partial order of the edges of the tree).

## Examples

```
data(kidney)
is.tree(kidney$tree)
```

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<b>kidney</b>	<i>Cytogenetic data from kidney carcinoma</i>
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## Description

This data set contains cytogenetic data from 173 cases of renal clear cell carcinoma, covering 7 frequent chromosomal aberrations, as well as the corresponding maximum likelihood tree model.

## Usage

```
data(kidney)
```

## Format

A list with the following elements:

x the binary data matrix

tree the ML tree in matrix format

p the ML parameters

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<b>mrca</b>	<i>Most Recent Common Ancestor</i>
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## Description

Computes the most recent common ancestor node for a pair of nodes of a tree.

## Usage

```
mrca(x, y, tree)
```

### Arguments

<code>x</code>	a node of the tree.
<code>y</code>	a node of the tree.
<code>tree</code>	a tree in matrix format.

### Value

the most recent common ancestor node of `x` and `y`.

### Examples

```
data(kidney)
mrca(1,2, kidney$tree)
```

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<code>subtree</code>
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*Subtree*

### Description

Computes the subtree rooted at a given node.

### Usage

```
subtree(node, tree)
```

### Arguments

<code>node</code>	a node of the tree.
<code>tree</code>	a tree in matrix format.

### Value

the subtree rooted at the given node.

### Examples

```
data(kidney)
subtree(14, kidney$tree)
```