Package 'cosmoGUI'

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Title GUI for constructing constraint sets used by the cosmo package

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Description cosmoGUI allows the user to interactively define constraint sets that can be used by the cosmo package to supervise the search for shared motifs in a set of DNA sequences. The constraints can be either adapted from a set of commonly used templates or defined from scratch.

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Depends tkWidgets, cosmo

License LGPL (>= 2)

URL http://cosmoweb.berkeley.edu/intro.html, http://www.bepress.com/ucbbiostat/paper209/

biocViews SequenceMatching, GUI

R topics documented:

`constraintBuilder` *GUI assistance for constructing constraint sets*

Description

This command opens a series of user-friendly pop-up windows that will help the user adapt sample constraints or build new constraints from scratch.

Usage

```
constraintBuilder()
```

Details

There are five sample constraints the user can modify: ICstep (the information content is a constant across the intervals), ICbound (the information content is bounded across each interval, V-shaped (the information content follows a symetric and continuous high-low-high), A-shaped (the information content follows a symetric and continuous low-high-low), Submotif (a segment of the motif is known).) The uiser also has the option of building a constraint set from scratch. The user will then be taken through a step-by-step construction (interval setup, palindromic intervals constraints, information content constraints, nucleotide frequencies constraints and submotif constraints.)

Value

The function returns an object of class `constraint set`, which can be passed to `cosmo()` as the `constraints` argument or plotted using the `plot()` function.

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Examples

```
#cs <- constraintBuilder()
#plot(cs)
```

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