

Package ‘cosmoGUI’

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Title GUI for constructing constraint sets used by the cosmo package

Version 1.24.0

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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

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

biocViews SequenceMatching, GUI

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constraintBuilder	<i>GUI assistance for constructing constraint sets</i>
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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 symmetric and continuous high-low-high), A-shaped (the information content follows a symmetric and continuous low-high-low), Submotif (a segment of the motif is known.) The user 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.

Author(s)

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Examples

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

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