

# 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

**License** LGPL (>= 2)

**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.

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**Examples**

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

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\*Topic **misc**

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