* Execution mode ? `genmot: Generate motifs from a training set`

General options

* Family of species to consider ? `Eutherians`

* Width of the motifs ? `10`

* Allowed shift of a binding site position in orthologous species ?

`20`

Genmot options

* Evolutionary model used for motif generation ? `Felsenstein model`

* Threshold used for motif generation ? `11.0`

* Threshold used to scan training set sequences for display ? `8.0`

* Training set sequences coordinates ?

| paste | upload | | EDIT | CLEAR |

Enter your data below:

```
chr8   91462919 91464123 CYLD-SALL1
chr4   99040833 99042291 APG4C-FOXD3
chr14 118834760    118836087    SOX21-ABCC4
chr18 69658816 69660452 TCF4(intragenic)
chr6   138199417    138201368    MGST1-LMO3
chr12 51291542 51292872 FOXG1B-PRKD1
```

Scangen options

* Threshold used to scan the genome ? `8.0`

* Width of selected enhancers ? `1000`

* Number of motifs to consider at maximum ? `5`

* File containing a list of motif definitions ?

| paste | upload | | EDIT | CLEAR |

Enter your data below: