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# **riboconstruct Documentation**

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This module provides methods and techniques to generate riboswitch instances for a given model and evaluate these instances with respect to their folding behaviour.

`riboconstruct` is mainly based on two subpackages:

- `riboconstruct.riboswitch` provides methods to traverse and evaluate the space of riboswitch instances defined by the underlying model. A riboswitch instance fixes the different parts of the riboswitch model into a concrete setting by defining the size, structure or position of its elements.

The actual evaluation of a riboswitch instance is done using `riboconstruct.rna_f`.

- Once a riboswitch instance is fixed while iterating the riboswitch space, only the two structures and *some* of the bases are known. Therefore, a RNA sequence that is likely to fold into the structures has to be identified. The necessary methods are provided in `riboconstruct.inverse_folding`.

To generate and evaluate riboswitches the following subpackage can be used:

- `riboconstruct.eval_mp` provides methods to generate and evaluate a riboswitch model within given constraints. The methods are based on Python's `multiprocessing` and can be used to do the calculations on a `multiprocessing system` in parallel.

Besides, `riboconstruct` offers helper classes and functions e.g. to represent RNA structures or sequences:

- `riboconstruct.rna`
- `riboconstruct.helper`



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# Examples

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TODO: show examples how to use the code



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# Indices and tables

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- *genindex*
- *modindex*
- *search*