

# de.NBI and its Galaxy interface for RNA folding

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You can download the pdfs you will need today here

[http://www.bioinf.uni-leipzig.de/~fall/RNA\\_folding\\_workshop-presentation.pdf](http://www.bioinf.uni-leipzig.de/~fall/RNA_folding_workshop-presentation.pdf)

<http://www.bioinf.uni-leipzig.de/~fall/Exercises.pdf>

**Goal:** Use RNAfold to do a simple structure prediction.

- ▶ Upload the file `rna.fa` into your Galaxy session.
- ▶ Start RNAfold with standard parameters
- ▶ Look into the output

**Goal:** Use RNAfold to do a structure prediction using the partition function

- ▶ Start RNAfold using --partfunc
- ▶ Look into the output

**Goal:** Use SHAPE-directed RNAfold to do a structure prediction

- ▶ Upload the file `rna.shape` into your Galaxy session.
- ▶ Start RNAfold using the shape file and `--shapeMethod=D`
- ▶ Look into the output

**Goal:** Use RNACofold to predict the cofolding of two sequences.

- ▶ Upload the file `cofold.txt` into your Galaxy session. (Look at it)
- ▶ Start RNACofold using `cofold.txt` with the `--partfunc` option
- ▶ Look at the output.

**Goal:** Use RNAduplex to predict *only* intermolecular base pairs of two sequences.

- ▶ Upload the file duplex.txt into your Galaxy session. (Look at it)
- ▶ Start RNAduplex using duplex.seq with standard parameter
- ▶ Look at the output.

**Goal:** Use RNAup to test the RNAduplex result.

- ▶ Start RNAup using duplex.txt with --include\_both
- ▶ Look at the output and compare it with the RNAduplex result.

**Bonus exercises:**

- ▶ Use RNAcofold for duplex.seq, as well (you have to edit the file)



**Goal:** Use RNAalifold to predict the consensus structure

- ▶ Upload the clustal file `alifold.aln` into your Galaxy session.
- ▶ Edit the data type of `alifold.aln` to 'clustal'
- ▶ Use RNAalifold with the `alifold.aln` and `--partfunc` (Calculate partition function: 1)
- ▶ (Download the output) and look at it
- ▶ Bonus: Fold the sequences (`alifold.fa`) individually (RNAfold) and compare the results.

**Goal:** Use RNAalifold to predict *and visualize* the consensus structure

- ▶ Use RNAalifold with alifold.aln and --color and --aln
- ▶ (Download the output) and look at it

**Goal:** Use RNACode to predict coding sequences in a MAF alignment.

- ▶ Upload the file `oskar.27way.rnacode.maf` into your Galaxy session.
- ▶ (Change its data type to maf)
- ▶ Use RNACode with the maf file
- ▶ (Download the output) and look at it

**Goal:** Use RNAz

- ▶ Upload the file `oskar.27way.rnaz.maf` into your Galaxy session.
- ▶ Use RNAz with the maf file
- ▶ (Download the output) and look at it