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 with partition function and pair probabilities.

–partfunc and –MEA can not be used at the same time

- ▶ Start `RNAfold` using --partfunc and --MEA
- ▶ Look into the output

Goal: Use SHAPE-directed `RNAfold` to do a structure prediction
problem with shape files

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

Goal: Use `RNApvmin` to assist the SHAPE directed `RNAfold`.
not tested

- Use `RNApvmin` with the rna.shape file and rna.seq to create a vector.csv
- Start `RNAfold` using the vector.csv as shape file and --shapeMethod=W
- Compare the output with the other shape method

Goal: Use `RNAcofold` to predict the co-folding of two sequences. –partfunc does not make an rna structure eps, without –partfunc two eps outputs are generated, one is empty

- ▶ 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.
not installed yet

- ▶ 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`
-d and -m are both activated by default
rnaz output is treated as fasta file and inmportant information is
missing

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