Sampling RNA Secondary Structure Landscapes for Kinetics Simulations

Ronny Lorenz ronny@tbi.univie.ac.at

University of Vienna

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Secondary Structure Free Energy Landscapes

$$\mathcal{L} = (X, N : X \to \mathcal{P}(X), f : X \to \mathbb{R})$$

- X... Set of secondary structures
- N... Structures obtained by formation / opening of a base pair
- f . . . Free energy E(s) of structure s

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Describe dynamic process of state transition as Markov process with master equation

$$\frac{dp_i(t)}{dt} = \sum_{j \neq i} p_j(t) r_{ji} - p_i(t) r_{ij}$$

$$\frac{d}{dt} \vec{p}(t) = \mathbf{R} \vec{p}(t) \text{ with formal solution } \vec{p}(t) = e^{t \cdot \mathbf{R}} \cdot \vec{p}(0)$$

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- Focus on individual RNAs and perform Monte Carlo simulation, e.g. kinfold¹, Kinefold²
- Lump state space into macro states, e.g. barriers / treekin³

¹Flamm et al. 2001

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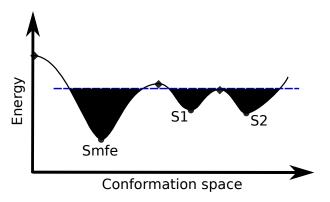
Still, vast numbers of trajectories or exhaustive enumeration of all states is required!

³Wolfinger et al. 2004

¹Flamm et al. 2001

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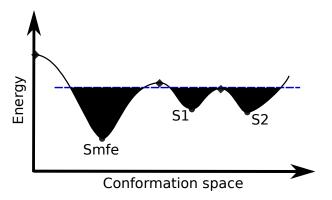
1. Exhaustive Enumeration⁴



- up to certain threshold δ above MFE
- · only applicable to short sequences

⁴Wuchty et al. 1999

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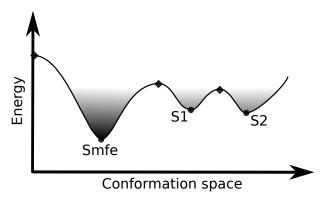


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Draw representative structure samples instead...

⁴Wuchty et al. 1999

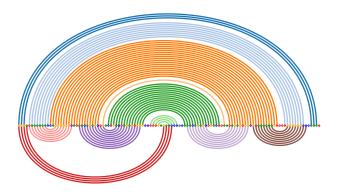
2. Boltzmann Sampling⁵



- obtain samples s with $p(s) = \frac{e^{-\frac{E(s)}{RT}}}{Q}$ and $Q = \sum_{S} e^{-\frac{E(s)}{RT}}$
- · dominated by low energy structures and highly redundant

⁵Ding et al. 2003

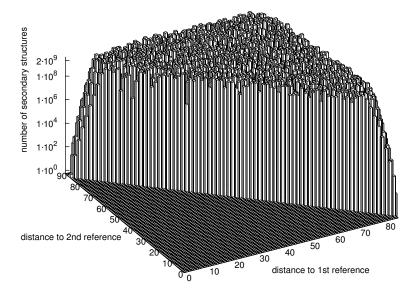
Example: $Q\beta$ replicase template SV11⁶



- artificial RNA sequence of 115 nt
- initially folds into metastable conformation
- metastable state is perfect template for $Q\beta$ replicase
- spontaneously refolds into very stable rod-like MFE structure
- metastable state > 30kcal/mol above MFE

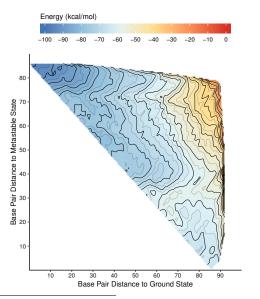
⁶Biebricher et al. 1992

Example: Qβ replicase template SV11
2D Projection of Secondary Structure Landscape⁷

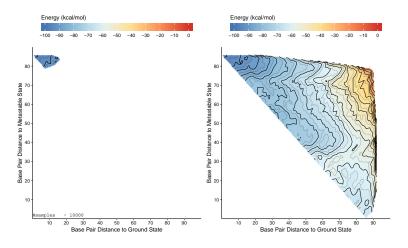


⁷Lorenz et al. 2009

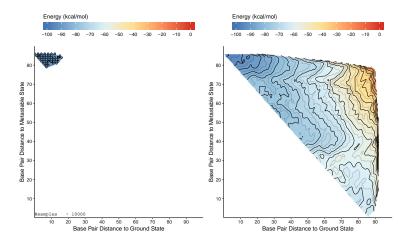
Example: Qβ replicase template SV11 2D Projection of Secondary Structure Landscape⁷



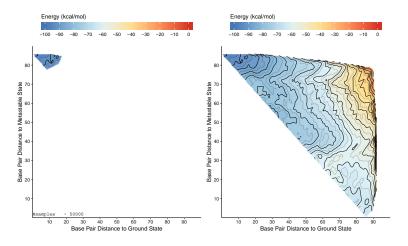
⁷Lorenz et al. 2009



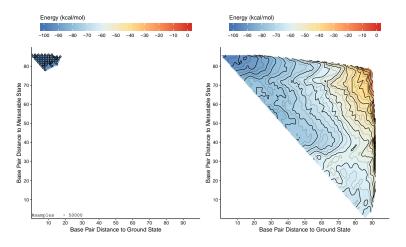
samples: 10,000, # local minima: 35



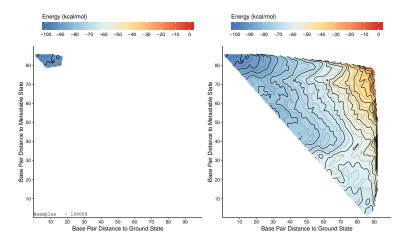
samples: 10,000, # local minima: 35



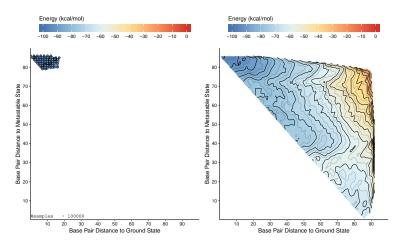
samples: 50,000 / # local minima: 49



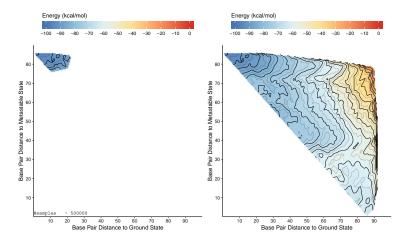
samples: 50,000 / # local minima: 49



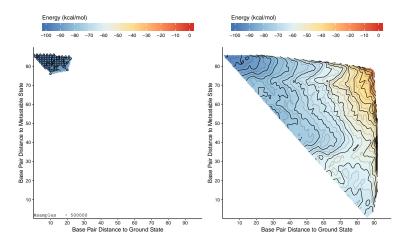
samples: 100,000 / # local minima: 58



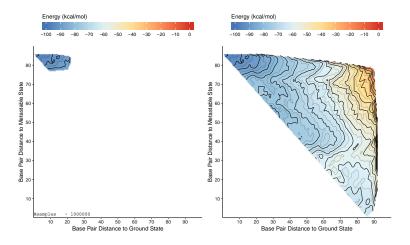
samples: 100,000 / # local minima: 58



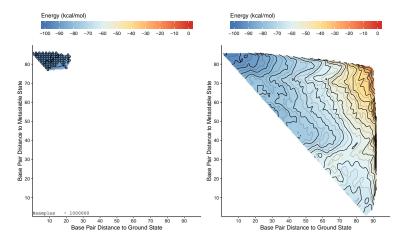
samples: 500,000 / # local minima: 101



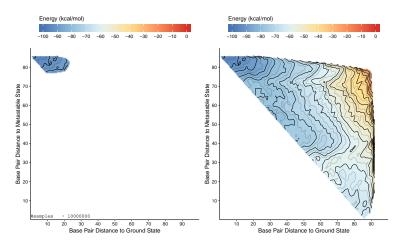
samples: 500,000 / # local minima: 101



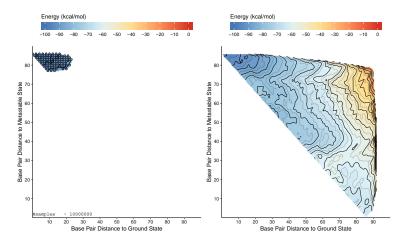
samples: 1,000,000 / # local minima: 132



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samples: 10,000,000 / # local minima: 259



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3. Restrict Conformation Space

- Local minima (RNAlocopt⁷)
- Flat structures (RNANR⁸)
- Local optimal stack configurations (RNASLOpt⁹)
- Shape abstraction (RNAShapes¹⁰)

drawbacks:

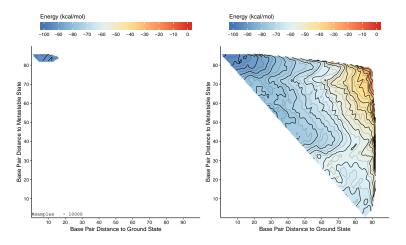
- · local optimal structures still grow exponentially
- rather high asymptotic time/memory complexities

⁷Lorenz WA et al. 2011

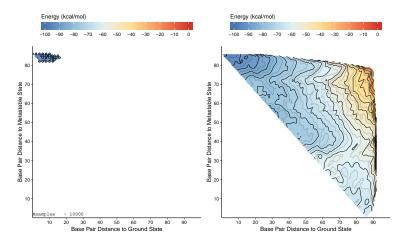
⁸Michalik et al. 2017

⁹Li et al. 2011

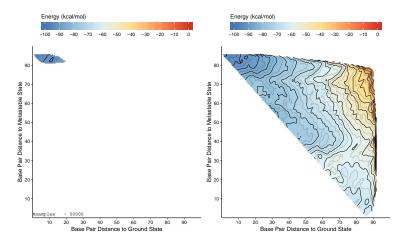
¹⁰Steffen et al. 2005



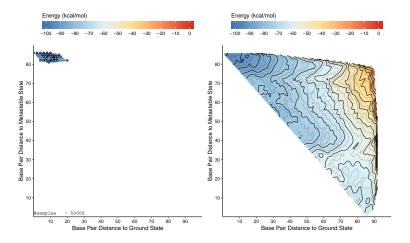
samples: 10,000, # local minima: 41



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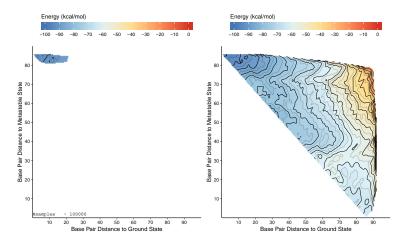


samples: 50,000, # local minima: 61



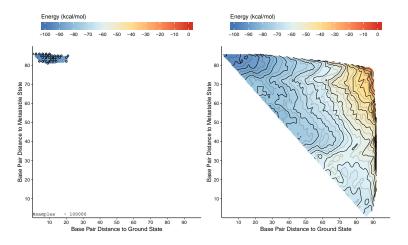
samples: 50,000, # local minima: 61

RNAlocopt Boltzmann sampling



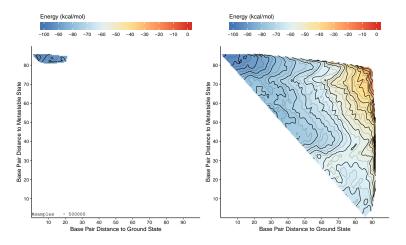
samples: 100,000, # local minima: 72

RNAlocopt Boltzmann sampling



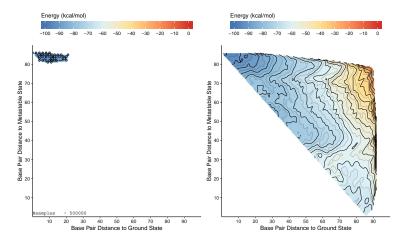
samples: 100,000, # local minima: 72

RNAlocopt Boltzmann sampling



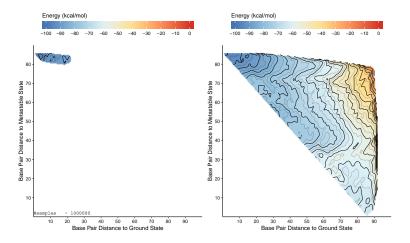
samples: 500,000, # local minima: 107

RNAlocopt Boltzmann sampling



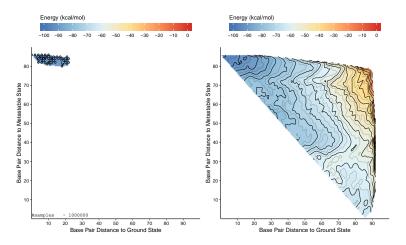
samples: 500,000, # local minima: 107

RNAlocopt Boltzmann sampling



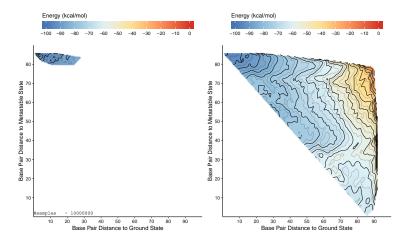
samples: 1,000,000, # local minima: 130

RNAlocopt Boltzmann sampling



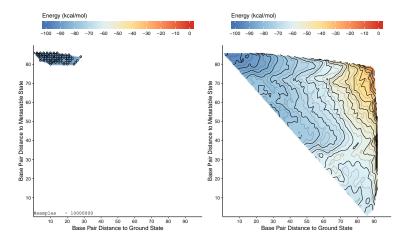
samples: 1,000,000, # local minima: 130

RNAlocopt Boltzmann sampling



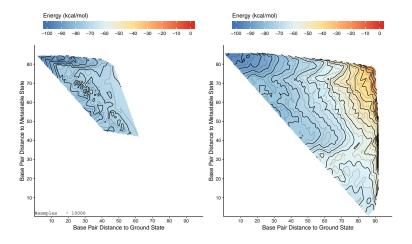
samples: 10,000,000, # local minima: 272

RNAlocopt Boltzmann sampling



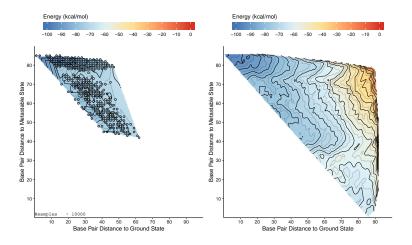
samples: 10,000,000, # local minima: 272

RNANR non-redundant Boltzmann sampling



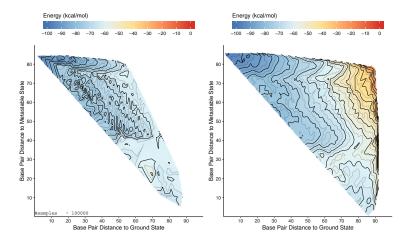
samples: 10,000, # local minima: 10,000

RNANR non-redundant Boltzmann sampling



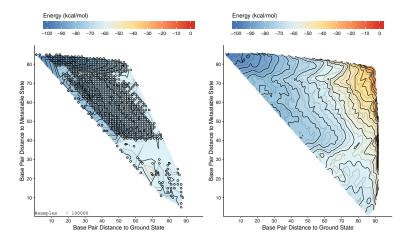
samples: 10,000, # local minima: 10,000

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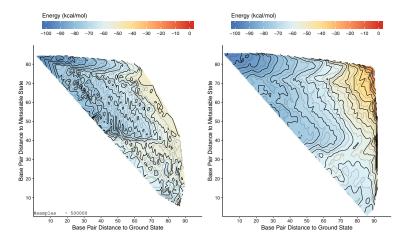
samples: 100,000, # local minima: 100,000

RNANR non-redundant Boltzmann sampling



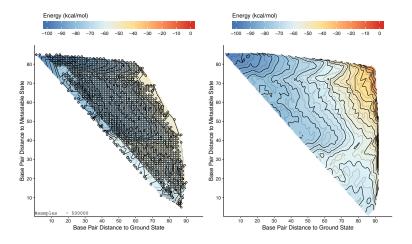
samples: 100,000, # local minima: 100,000

RNANR non-redundant Boltzmann sampling



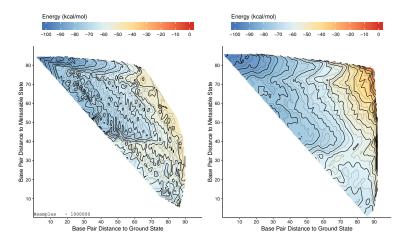
samples: 500,000, # local minima: 500,000

RNANR non-redundant Boltzmann sampling



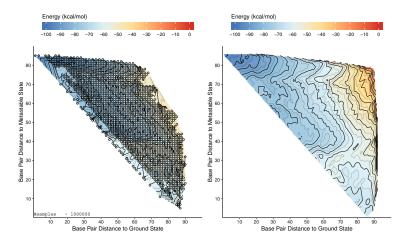
samples: 500,000, # local minima: 500,000

RNANR non-redundant Boltzmann sampling



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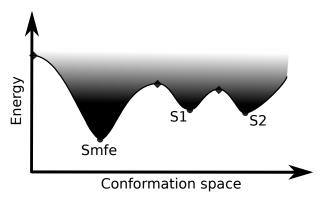
RNANR non-redundant Boltzmann sampling



samples: 1,000,000, # local minima: 1,000,000

Sampling Strategies

4. Elevated Temperature Boltzmann Sampling

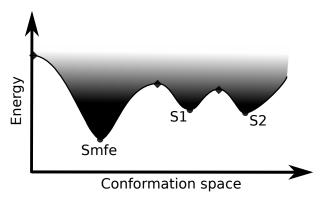


- iteratively draw samples at different $T = \xi \cdot T_0, \, \xi > 1$
- RNAlocmin¹¹

¹¹Kucharik et al. 2014

Sampling Strategies

4. Elevated Temperature Boltzmann Sampling

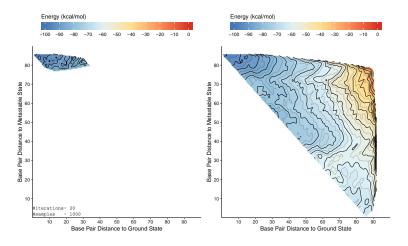


- iteratively draw samples at different $T = \xi \cdot T_0, \, \xi > 1$
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Samples are drawn from uniform distribution for $T \to \infty$

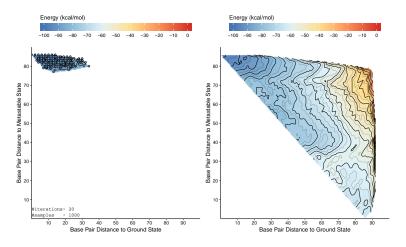
¹¹Kucharik et al. 2014

RNAlocmin temperature elevation scheme Boltzmann sampling



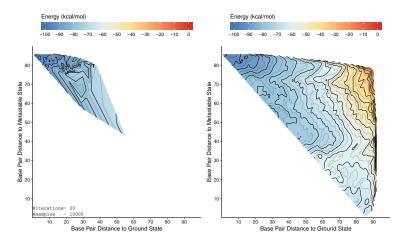
iterations: 20, # samples: 1,000, # local minima: 528

RNAlocmin temperature elevation scheme Boltzmann sampling



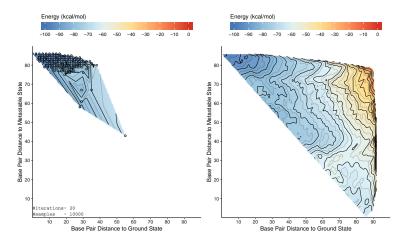
iterations: 20, # samples: 1,000, # local minima: 528

RNAlocmin temperature elevation scheme Boltzmann sampling



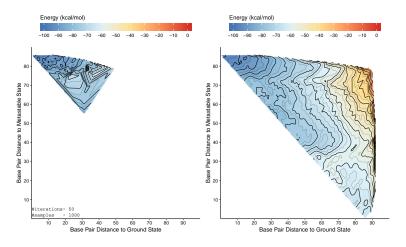
iterations: 20, # samples: 10,000, # local minima: 2,283

RNAlocmin temperature elevation scheme Boltzmann sampling



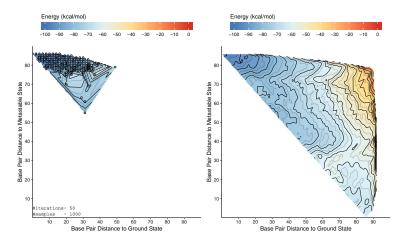
iterations: 20, # samples: 10,000, # local minima: 2,283

RNAlocmin temperature elevation scheme Boltzmann sampling



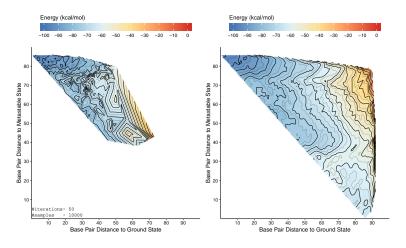
iterations: 50, # samples: 1,000, # local minima: 2,669

RNAlocmin temperature elevation scheme Boltzmann sampling



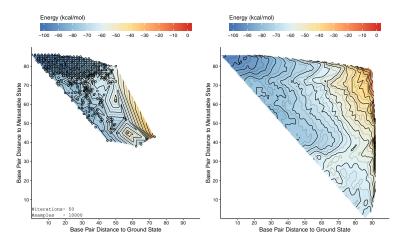
iterations: 50, # samples: 1,000, # local minima: 2,669

RNAlocmin temperature elevation scheme Boltzmann sampling



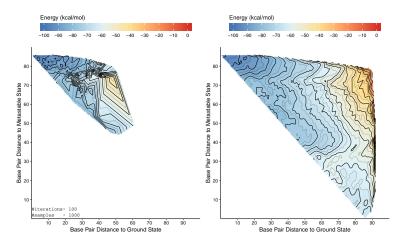
iterations: 50, # samples: 10,000, # local minima: 14,092

RNAlocmin temperature elevation scheme Boltzmann sampling



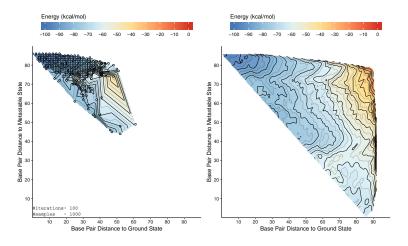
iterations: 50, # samples: 10,000, # local minima: 14,092

RNAlocmin temperature elevation scheme Boltzmann sampling



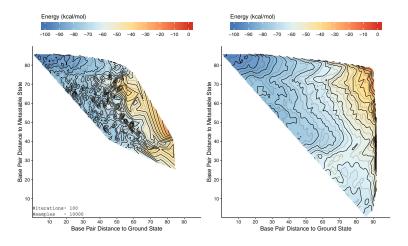
iterations: 100, # samples: 1,000, # local minima: 6,422

RNAlocmin temperature elevation scheme Boltzmann sampling



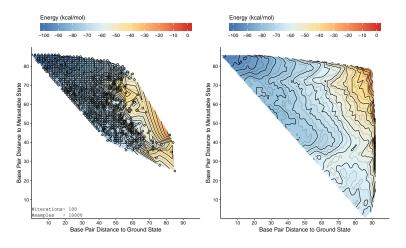
iterations: 100, # samples: 1,000, # local minima: 6,422

RNAlocmin temperature elevation scheme Boltzmann sampling



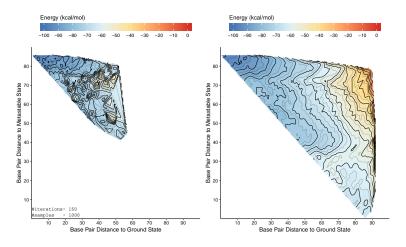
iterations: 100, # samples: 10,000, # local minima: 51,470

RNAlocmin temperature elevation scheme Boltzmann sampling



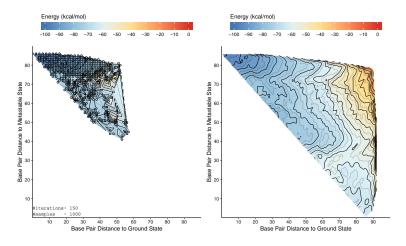
iterations: 100, # samples: 10,000, # local minima: 51,470

RNAlocmin temperature elevation scheme Boltzmann sampling



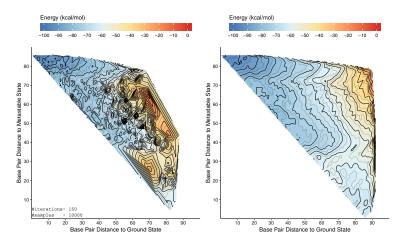
iterations: 150, # samples: 1,000, # local minima: 12,741

RNAlocmin temperature elevation scheme Boltzmann sampling



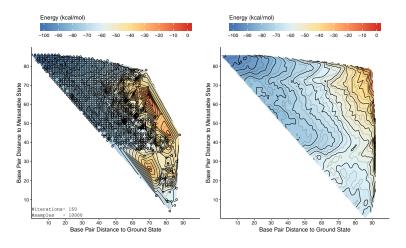
iterations: 150, # samples: 1,000, # local minima: 12,741

RNAlocmin temperature elevation scheme Boltzmann sampling



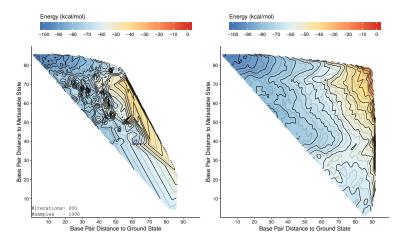
iterations: 150, # samples: 10,000, # local minima: 97,756

RNAlocmin temperature elevation scheme Boltzmann sampling



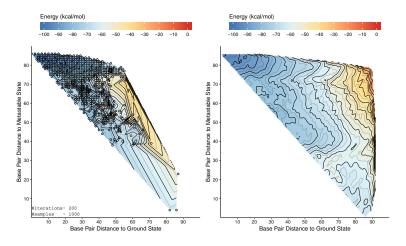
iterations: 150, # samples: 10,000, # local minima: 97,756

RNAlocmin temperature elevation scheme Boltzmann sampling



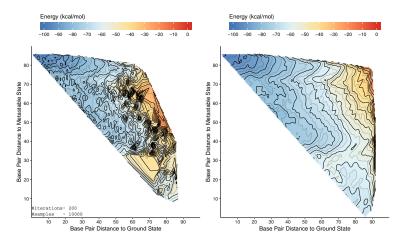
iterations: 200, # samples: 1,000, # local minima: 18,221

RNAlocmin temperature elevation scheme Boltzmann sampling



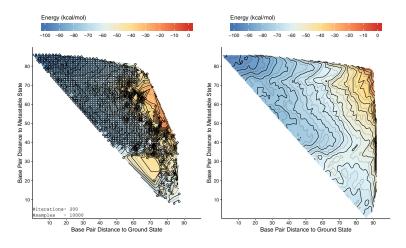
iterations: 200, # samples: 1,000, # local minima: 18,221

RNAlocmin temperature elevation scheme Boltzmann sampling



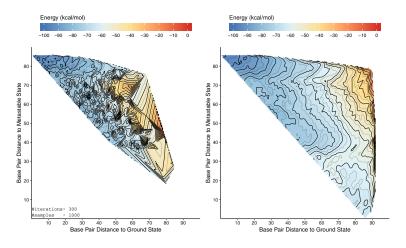
iterations: 200, # samples: 10,000, # local minima: 145,391

RNAlocmin temperature elevation scheme Boltzmann sampling



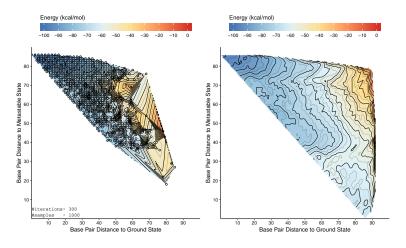
iterations: 200, # samples: 10,000, # local minima: 145,391

RNAlocmin temperature elevation scheme Boltzmann sampling



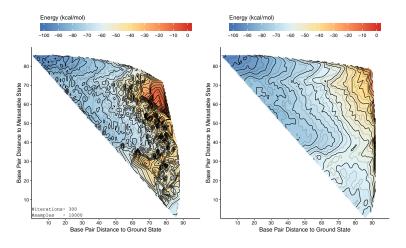
iterations: 300, # samples: 1,000, # local minima: 32,569

RNAlocmin temperature elevation scheme Boltzmann sampling



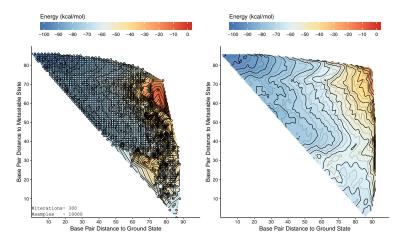
iterations: 300, # samples: 1,000, # local minima: 32,569

RNAlocmin temperature elevation scheme Boltzmann sampling



iterations: 300, # samples: 10,000, # local minima: 260,994

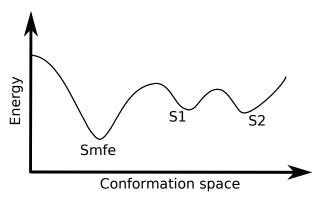
RNAlocmin temperature elevation scheme Boltzmann sampling



iterations: 300, # samples: 10,000, # local minima: 260,994

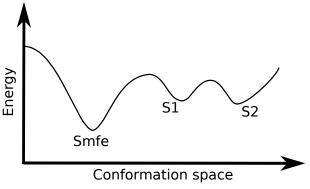
Sampling Strategies

5. Sampling with Guiding Potentials (RNAxplorer)¹²



¹²Entzian et al. (manuscript in preparation)

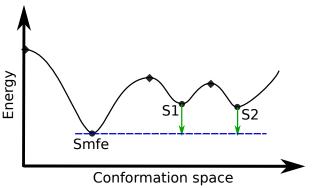
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•
$$p(s) = \frac{exp(-\beta E(s))}{Z}$$

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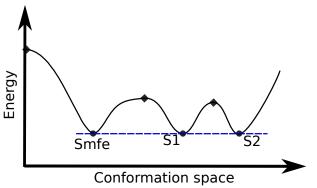


•
$$p(s) = \frac{exp(-\beta E(s))}{7}$$

•
$$E(s_{mfe}) = [E(s_1) + \hat{E}(s_1)] = [E(s_2) + \hat{E}(s_2)]$$

¹²Entzian et al. (manuscript in preparation)

5. Sampling with Guiding Potentials (RNAxplorer)¹²



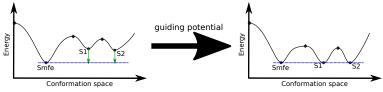
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5. Sampling with Guiding Potentials (RNAxplorer)¹²

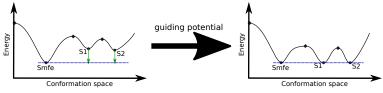


Guiding potential needs to allow for efficiently:

- computing partition function Q
- · sampling from distorted energy ensemble

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- · sampling from distorted energy ensemble

Make use of soft constraints feature of ViennaRNA Package 13

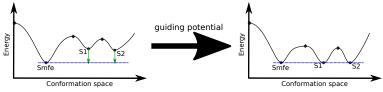
$$E(s_{mfe}) = [E(s_1) + \hat{E}(s_1)] = [E(s_2) + \hat{E}(s_2)]$$

 $\hat{E}(s) = d_{BP}(s, s_1) \cdot w_1 + d_{BP}(s, s_2) \cdot w_2$

¹²Entzian et al. (manuscript in preparation)

¹³Lorenz et al. 2016

5. Sampling with Guiding Potentials (RNAxplorer)¹²



Guiding potential needs to allow for efficiently:

- computing partition function Q
- · sampling from distorted energy ensemble

Make use of soft constraints feature of ViennaRNA Package 13

$$E(s_{mfe}) = [E(s_1) + \hat{E}(s_1)] = [E(s_2) + \hat{E}(s_2)]$$

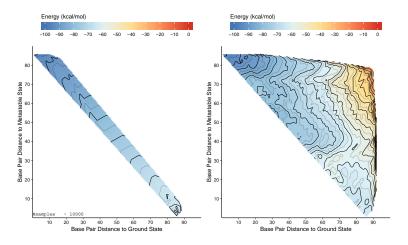
$$\hat{E}(s) = d_{BP}(s, s_1) \cdot w_1 + d_{BP}(s, s_2) \cdot w_2$$

How to choose reference structures s_x ?

¹²Entzian et al. (manuscript in preparation)

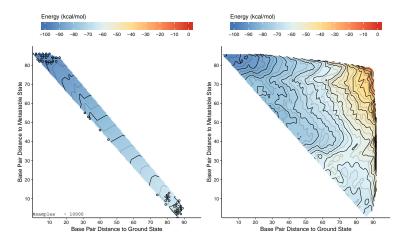
¹³Lorenz et al. 2016

RNAxplorer attraction scheme Boltzmann sampling



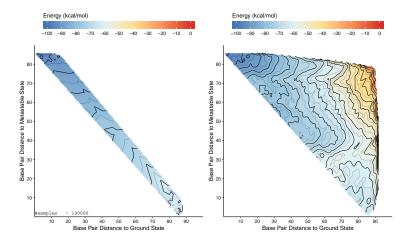
references: 2, # samples: 10,000, # local minima: 86

RNAxplorer attraction scheme Boltzmann sampling



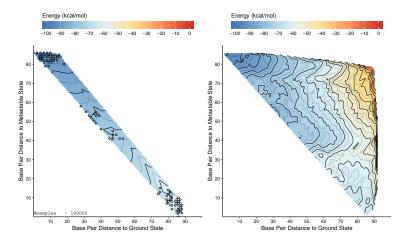
references: 2, # samples: 10,000, # local minima: 86

RNAxplorer attraction scheme Boltzmann sampling



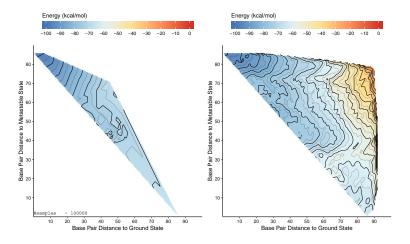
references: 2, # samples: 100,000, # local minima: 167

RNAxplorer attraction scheme Boltzmann sampling



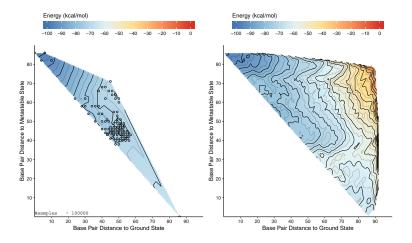
references: 2, # samples: 100,000, # local minima: 167

RNAxplorer attraction scheme Boltzmann sampling



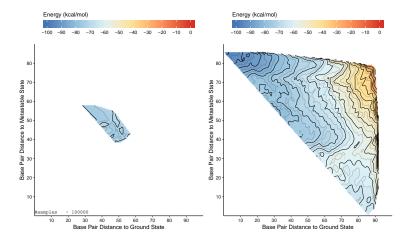
references: 3, # samples: 100,000, # local minima: 182

RNAxplorer attraction scheme Boltzmann sampling



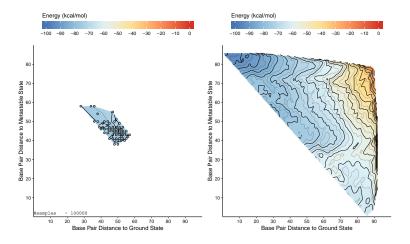
references: 3, # samples: 100,000, # local minima: 182

RNAxplorer attraction scheme Boltzmann sampling



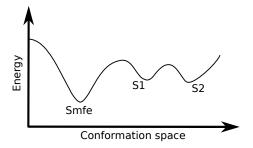
references: 4, # samples: 100, 000, # local minima: 143

RNAxplorer attraction scheme Boltzmann sampling

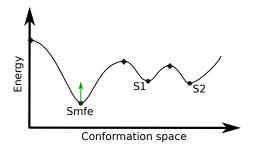


references: 4, # samples: 100, 000, # local minima: 143

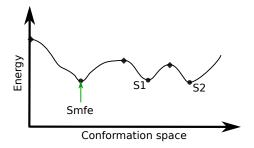
5b. Sampling with (repellent) Guiding Potentials



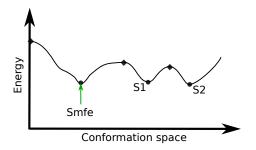
5b. Sampling with (repellent) Guiding Potentials



5b. Sampling with (repellent) Guiding Potentials



5b. Sampling with (repellent) Guiding Potentials

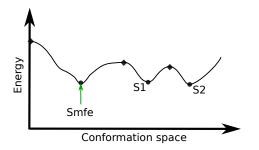


- · draw samples and determine corresponding local minima
- add most over-represented local minimum s_m to list L
- assign $\hat{E}(s)$ according to structures in L, e.g.

$$\begin{array}{l} \hat{E}(s) = \sum_{s_m \in L} w(s_m) \cdot \frac{|s \cap s_m|}{|s_m|} \\ \hat{E}(s) = \sum_{s_m \in L} w(s_m) \cdot (d_{BP}^{max}(s_m) - d_{BP}(s, s_m)) \end{array}$$

. . .

5b. Sampling with (repellent) Guiding Potentials

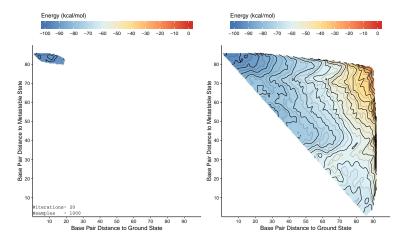


- · draw samples and determine corresponding local minima
- add most over-represented local minimum s_m to list L
- assign $\hat{E}(s)$ according to structures in L, e.g.

$$\begin{aligned} \hat{E}(s) &= \sum_{s_m \in L} w(s_m) \cdot \frac{|s \cap s_m|}{|s_m|} \\ \hat{E}(s) &= \sum_{s_m \in L} w(s_m) \cdot (d_{BP}^{max}(s_m) - d_{BP}(s, s_m)) \end{aligned}$$

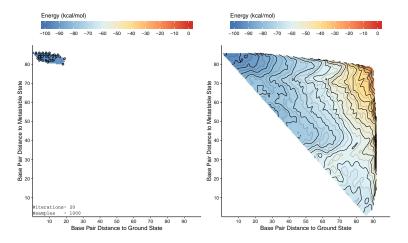
Choose moderate weighting factors, e.g. $w(s_m) = \gamma RT$

RNAxplorer repulsion scheme Boltzmann sampling



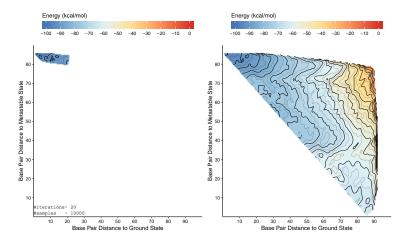
iterations: 20, # samples: 1,000, # local minima: 52

RNAxplorer repulsion scheme Boltzmann sampling



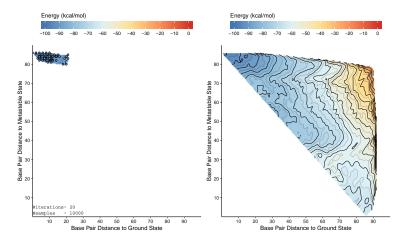
iterations: 20, # samples: 1,000, # local minima: 52

RNAxplorer repulsion scheme Boltzmann sampling



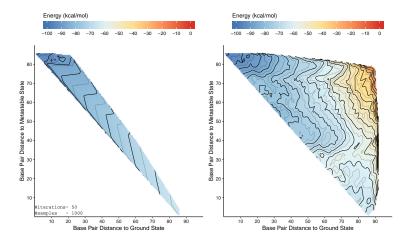
iterations: 20, # samples: 10,000, # local minima: 97

RNAxplorer repulsion scheme Boltzmann sampling



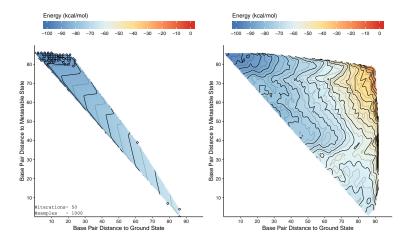
iterations: 20, # samples: 10,000, # local minima: 97

RNAxplorer repulsion scheme Boltzmann sampling



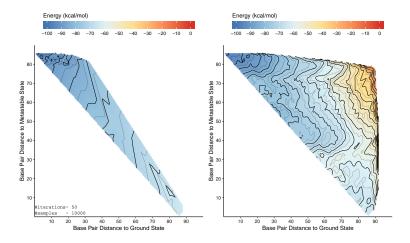
iterations: 50, # samples: 1,000, # local minima: 133

RNAxplorer repulsion scheme Boltzmann sampling



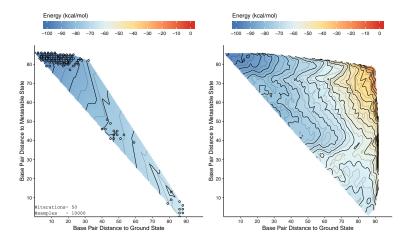
iterations: 50, # samples: 1,000, # local minima: 133

RNAxplorer repulsion scheme Boltzmann sampling



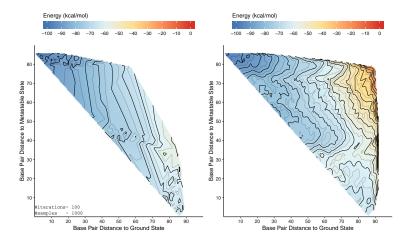
iterations: 50, # samples: 10,000, # local minima: 320

RNAxplorer repulsion scheme Boltzmann sampling



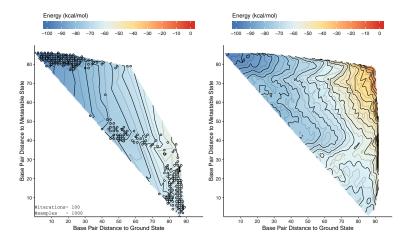
iterations: 50, # samples: 10,000, # local minima: 320

RNAxplorer repulsion scheme Boltzmann sampling



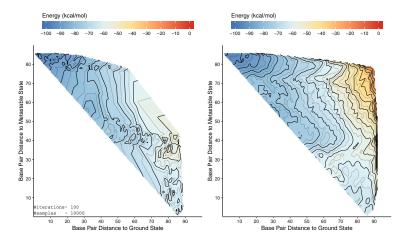
iterations: 100, # samples: 1,000, # local minima: 765

RNAxplorer repulsion scheme Boltzmann sampling



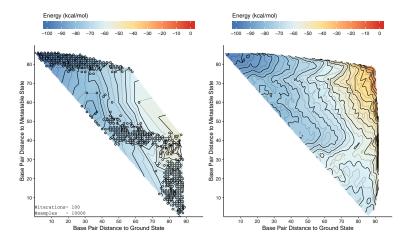
iterations: 100, # samples: 1,000, # local minima: 765

RNAxplorer repulsion scheme Boltzmann sampling



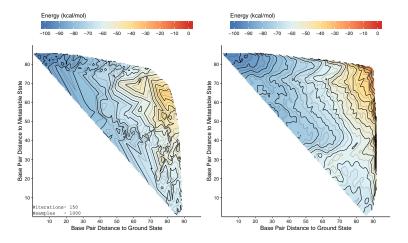
iterations: 100, # samples: 10,000, # local minima: 2,549

RNAxplorer repulsion scheme Boltzmann sampling



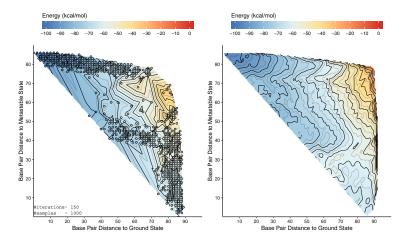
iterations: 100, # samples: 10,000, # local minima: 2,549

RNAxplorer repulsion scheme Boltzmann sampling



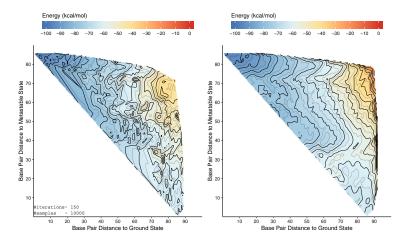
iterations: 150, # samples: 1,000, # local minima: 3,781

RNAxplorer repulsion scheme Boltzmann sampling



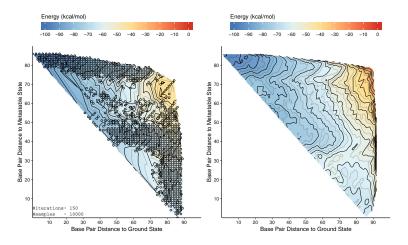
iterations: 150, # samples: 1,000, # local minima: 3,781

RNAxplorer repulsion scheme Boltzmann sampling



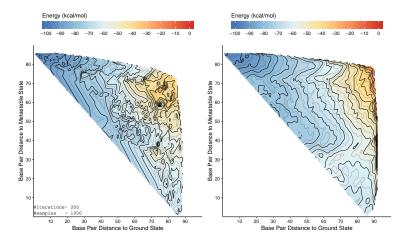
iterations: 150, # samples: 10,000, # local minima: 15,041

RNAxplorer repulsion scheme Boltzmann sampling



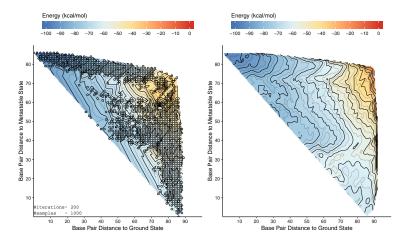
iterations: 150, # samples: 10,000, # local minima: 15,041

RNAxplorer repulsion scheme Boltzmann sampling



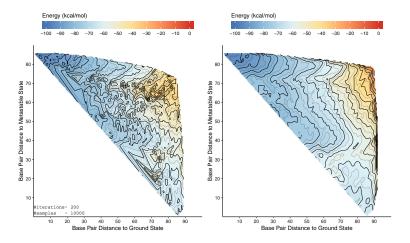
iterations: 200, # samples: 1,000, # local minima: 13,066

RNAxplorer repulsion scheme Boltzmann sampling



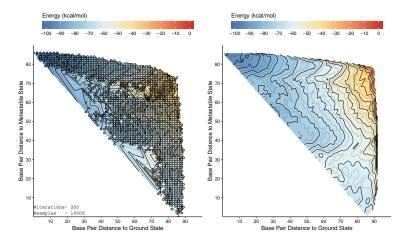
iterations: 200, # samples: 1,000, # local minima: 13,066

RNAxplorer repulsion scheme Boltzmann sampling



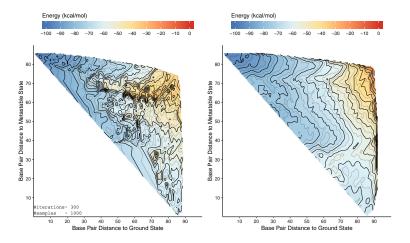
iterations: 200, # samples: 10,000, # local minima: 57,296

RNAxplorer repulsion scheme Boltzmann sampling



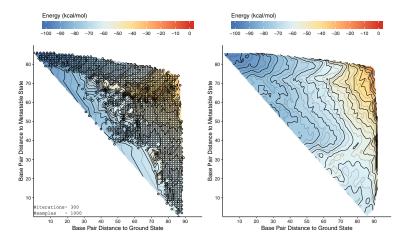
iterations: 200, # samples: 10,000, # local minima: 57,296

RNAxplorer repulsion scheme Boltzmann sampling



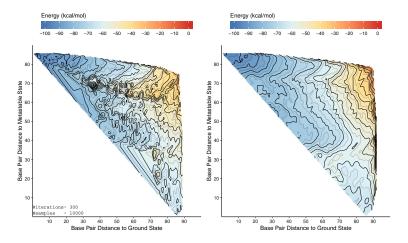
iterations: 300, # samples: 1,000, # local minima: 61,952

RNAxplorer repulsion scheme Boltzmann sampling



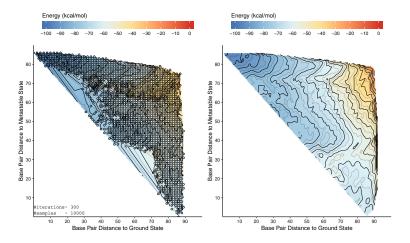
iterations: 300, # samples: 1,000, # local minima: 61,952

RNAxplorer repulsion scheme Boltzmann sampling



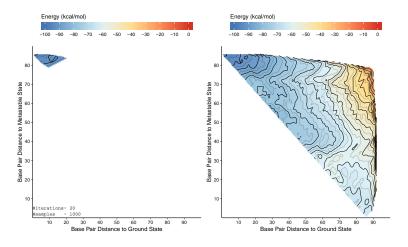
iterations: 300, # samples: 10,000, # local minima: 309,669

RNAxplorer repulsion scheme Boltzmann sampling



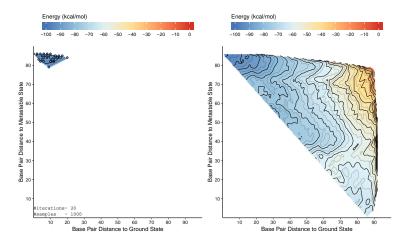
iterations: 300, # samples: 10,000, # local minima: 309,669

RNAxplorer repulsion scheme Boltzmann sampling (distance)



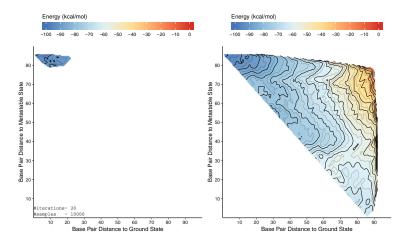
iterations: 20, # samples: 1,000, # local minima: 47

RNAxplorer repulsion scheme Boltzmann sampling (distance)



iterations: 20, # samples: 1,000, # local minima: 47

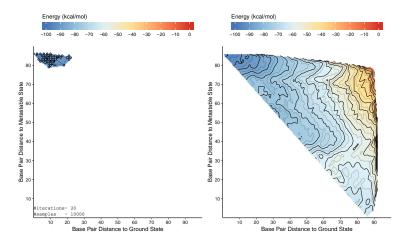
RNAxplorer repulsion scheme Boltzmann sampling (distance)



iterations: 20, # samples: 10,000, # local minima: 92

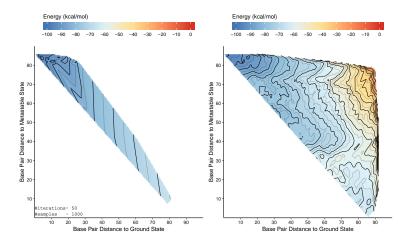
Example: $\mathbf{Q}\beta$ replicase template SV11

RNAxplorer repulsion scheme Boltzmann sampling (distance)



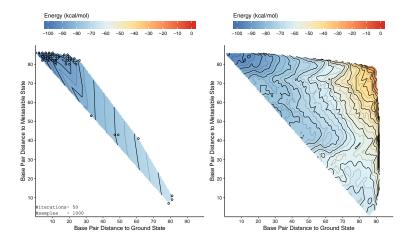
iterations: 20, # samples: 10,000, # local minima: 92

RNAxplorer repulsion scheme Boltzmann sampling (distance)



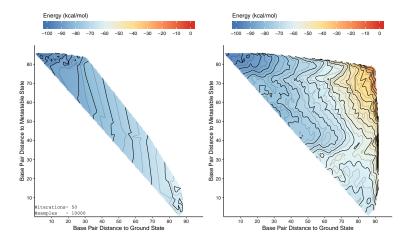
iterations: 50, # samples: 1,000, # local minima: 119

RNAxplorer repulsion scheme Boltzmann sampling (distance)



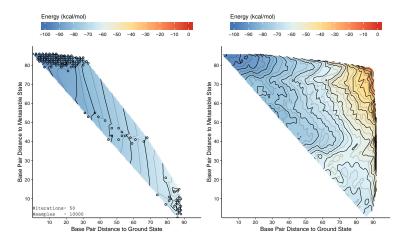
iterations: 50, # samples: 1,000, # local minima: 119

RNAxplorer repulsion scheme Boltzmann sampling (distance)



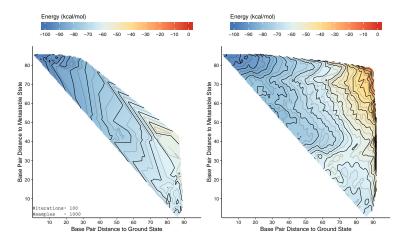
iterations: 50, # samples: 10,000, # local minima: 484

RNAxplorer repulsion scheme Boltzmann sampling (distance)



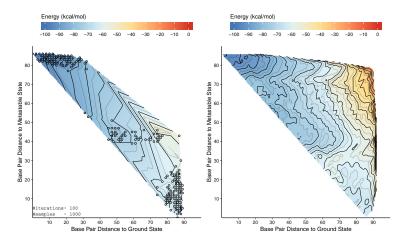
iterations: 50, # samples: 10,000, # local minima: 484

RNAxplorer repulsion scheme Boltzmann sampling (distance)



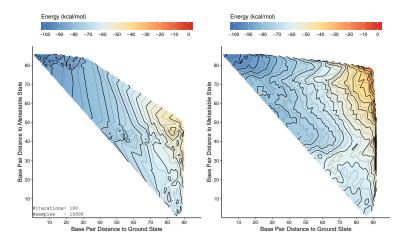
iterations: 100, # samples: 1,000, # local minima: 608

RNAxplorer repulsion scheme Boltzmann sampling (distance)



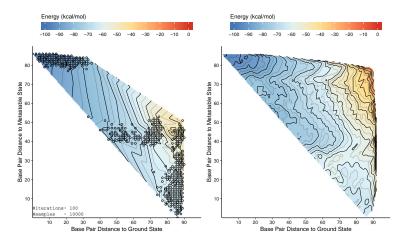
iterations: 100, # samples: 1,000, # local minima: 608

RNAxplorer repulsion scheme Boltzmann sampling (distance)



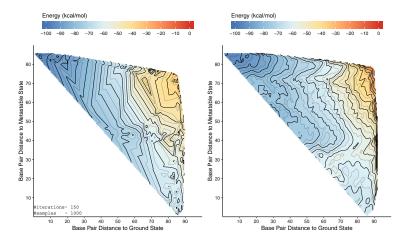
iterations: 100, # samples: 10,000, # local minima: 2,853

RNAxplorer repulsion scheme Boltzmann sampling (distance)



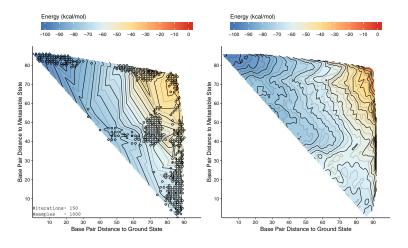
iterations: 100, # samples: 10,000, # local minima: 2,853

RNAxplorer repulsion scheme Boltzmann sampling (distance)



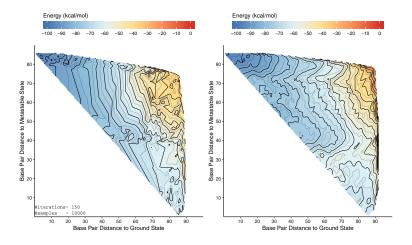
iterations: 150, # samples: 1,000, # local minima: 2,818

RNAxplorer repulsion scheme Boltzmann sampling (distance)



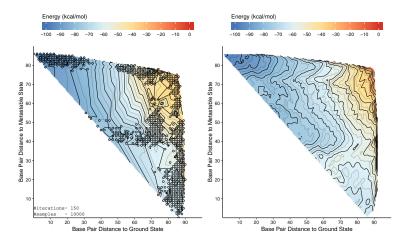
iterations: 150, # samples: 1,000, # local minima: 2,818

RNAxplorer repulsion scheme Boltzmann sampling (distance)



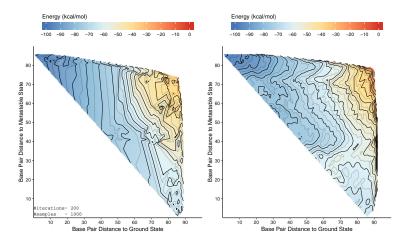
iterations: 150, # samples: 10,000, # local minima: 7,111

RNAxplorer repulsion scheme Boltzmann sampling (distance)



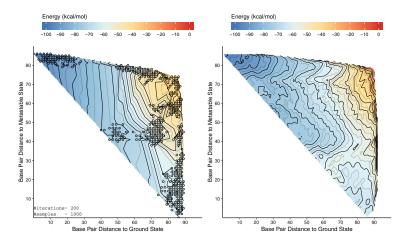
iterations: 150, # samples: 10,000, # local minima: 7,111

RNAxplorer repulsion scheme Boltzmann sampling (distance)



iterations: 200, # samples: 1,000, # local minima: 3,147

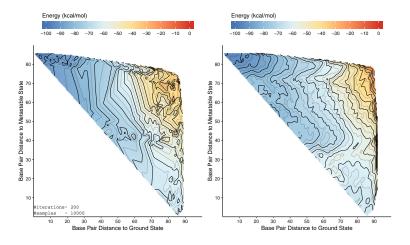
RNAxplorer repulsion scheme Boltzmann sampling (distance)



iterations: 200, # samples: 1,000, # local minima: 3,147

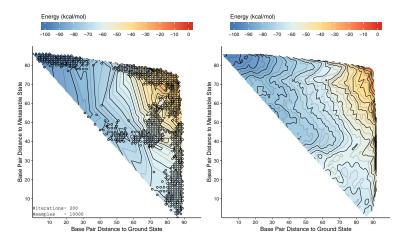
Example: $\mathbf{Q}\beta$ replicase template SV11

RNAxplorer repulsion scheme Boltzmann sampling (distance)



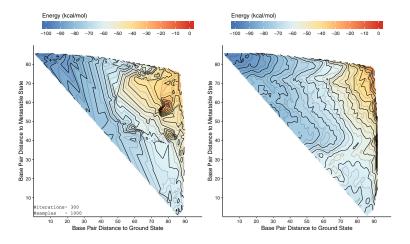
iterations: 200, # samples: 10,000, # local minima: 10,342

RNAxplorer repulsion scheme Boltzmann sampling (distance)



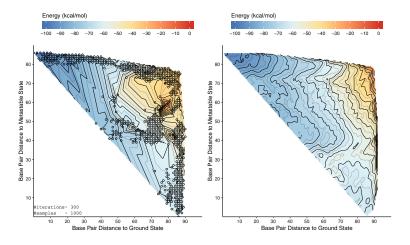
iterations: 200, # samples: 10,000, # local minima: 10,342

RNAxplorer repulsion scheme Boltzmann sampling (distance)



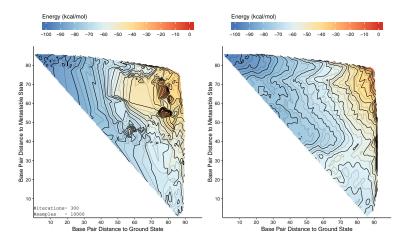
iterations: 300, # samples: 1,000, # local minima: 4,820

RNAxplorer repulsion scheme Boltzmann sampling (distance)



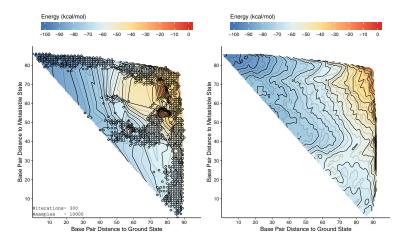
iterations: 300, # samples: 1,000, # local minima: 4,820

RNAxplorer repulsion scheme Boltzmann sampling (distance)



iterations: 300, # samples: 10,000, # local minima: 12,486

RNAxplorer repulsion scheme Boltzmann sampling (distance)



iterations: 300, # samples: 10,000, # local minima: 12,486

Conclusion

What's been done:

- Unsupervised directed repellent scheme
- Efficient Boltzmann sampling from distorted energy landscape $O(n^3) + O(k \cdot n \log n)$ for k samples per iteration
- · Good approximation for even extreme cases

Next steps:

- · Removal of too similar and shallow local minima
- Restrict guiding potential to structure domains
- Computation of effective transition rates
- Comparison of kinetics prediction against other programs
- Make RNAxplorer accessible
- Release non-redundant sampling for RNAsubopt

Thanks to

- Gregor Entzian
- Andrea Tanzer
- Yann Ponty
- · Juraj Michalik
- Ivo L Hofacker
- TBI team

Thank You for your attention!

This work was funded in parts by the Austrian/French project 'RNAlands', FWF-I-1804-N28 and ANR-14-CE34-0011



Thanks to

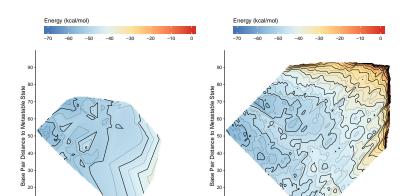
- Gregor Entzian
- Andrea Tanzer
- Yann Ponty
- · Juraj Michalik
- Ivo L Hofacker
- TBI team

Thank You for your attention!

This work was funded in parts by the Austrian/French project 'RNAlands', FWF-I-1804-N28 and ANR-14-CE34-0011



Example: 5UTR of MS2 coat protein mRNARNAxplorer repulsion scheme Boltzmann sampling



10

90

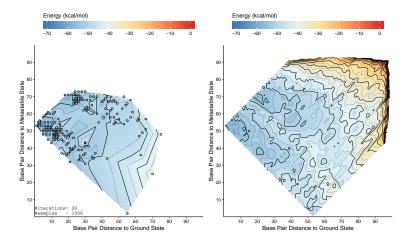
Base Pair Distance to Ground State

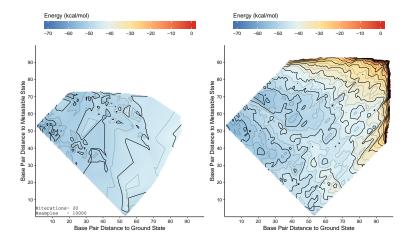
90

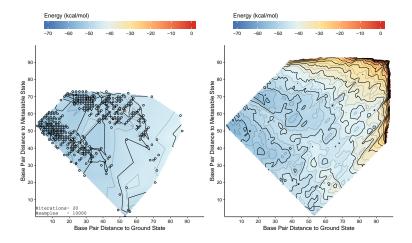
Base Pair Distance to Ground State

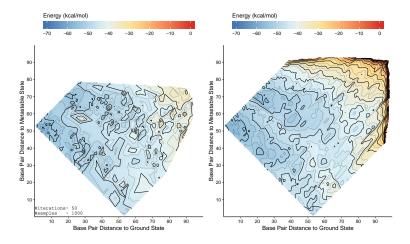
Example: 5UTR of MS2 coat protein mRNA

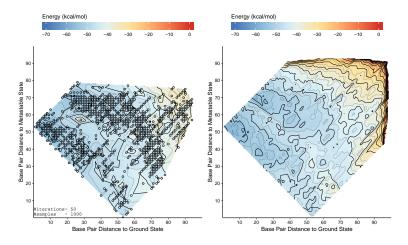
RNAxplorer repulsion scheme Boltzmann sampling

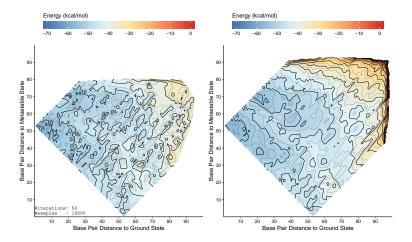


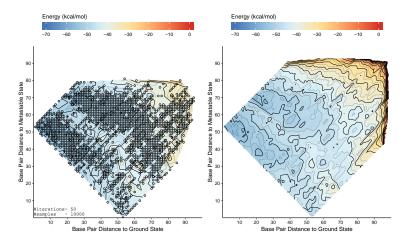


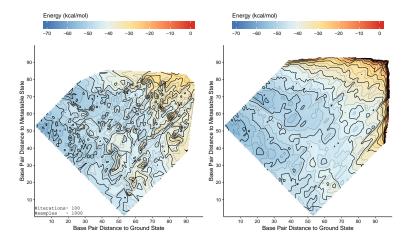


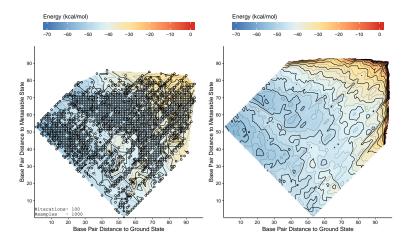


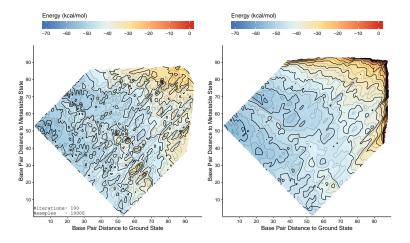


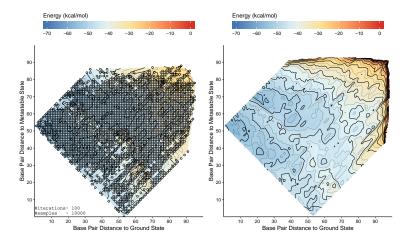


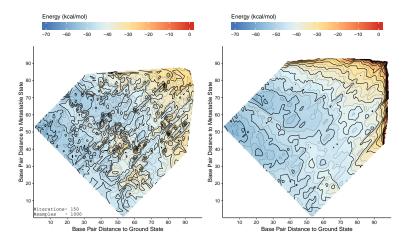


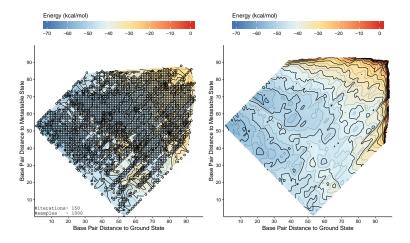


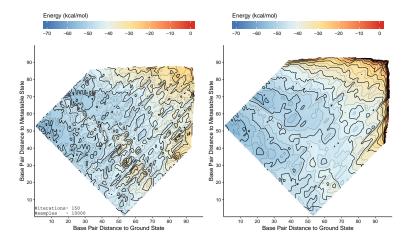


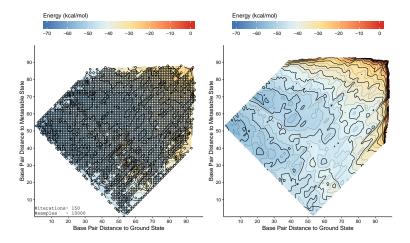


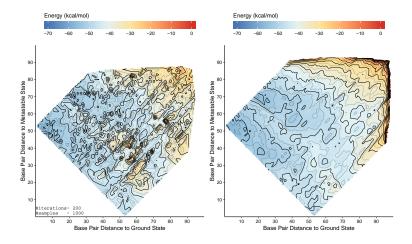


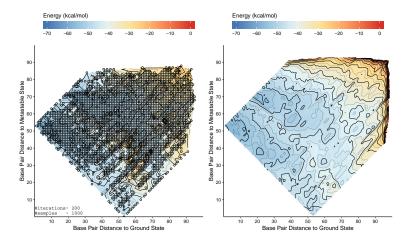


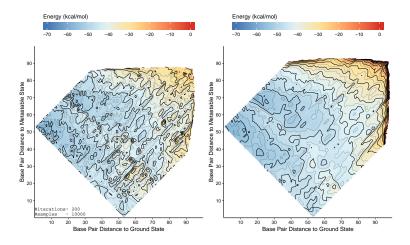


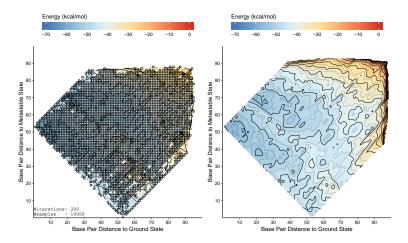


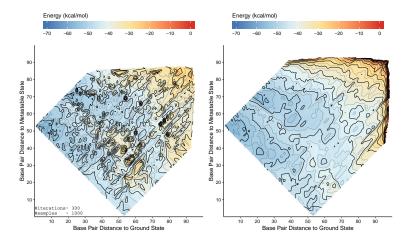


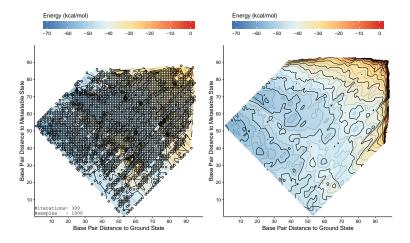


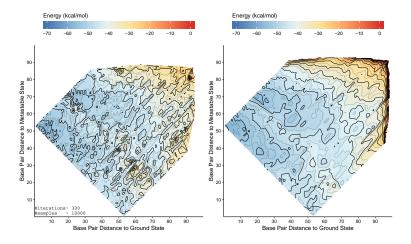


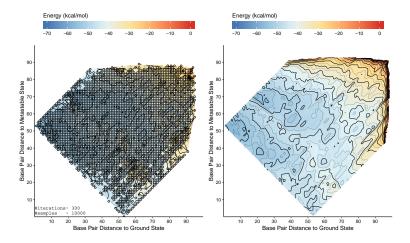


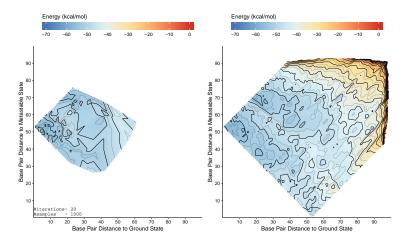


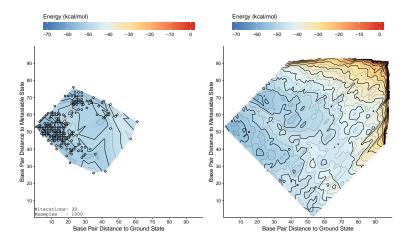


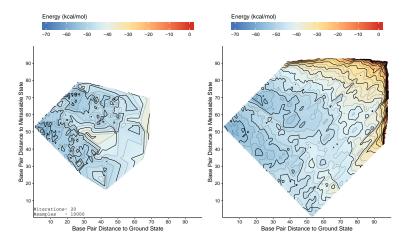


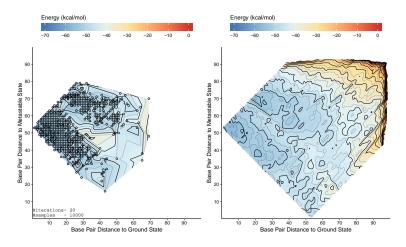


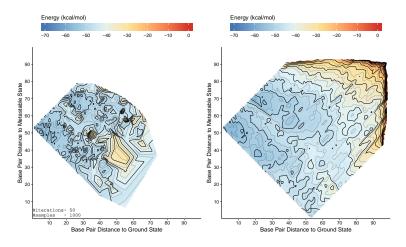


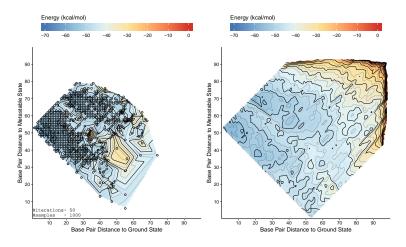


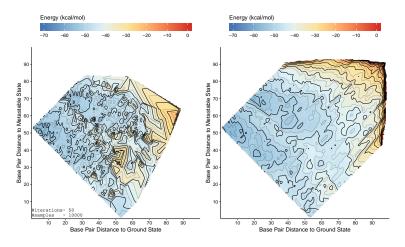


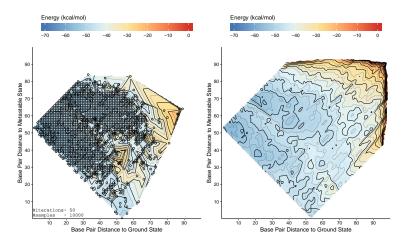


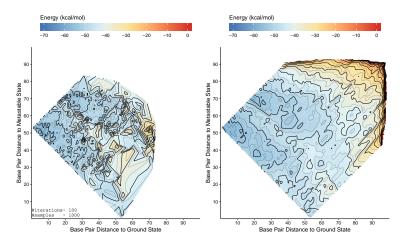


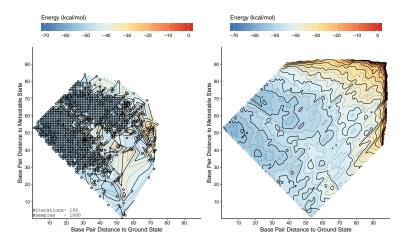


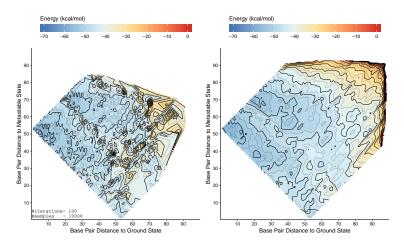


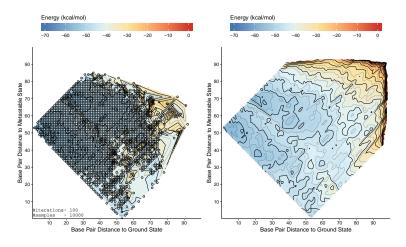


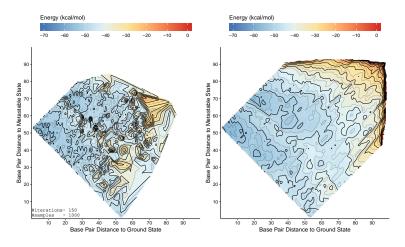


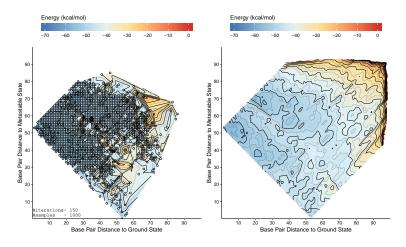


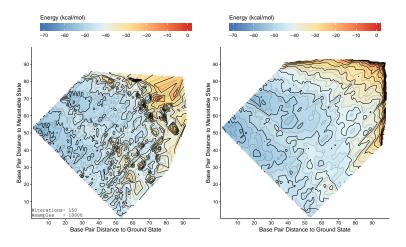


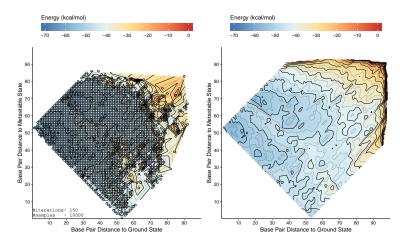


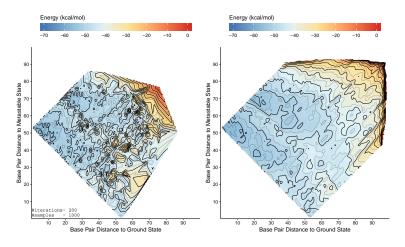


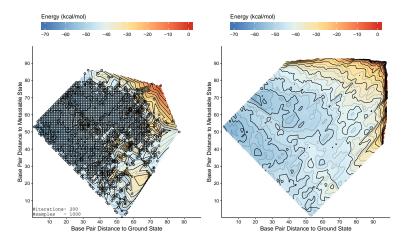


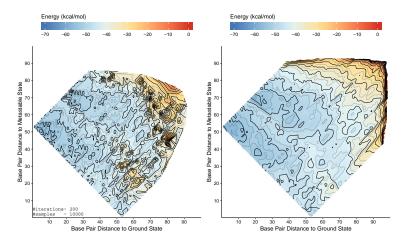


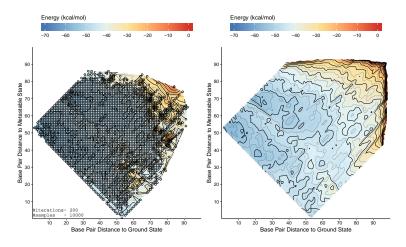


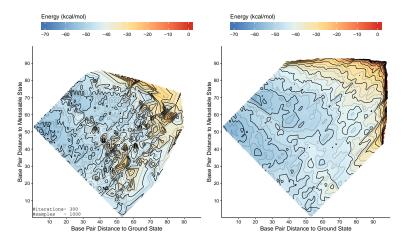


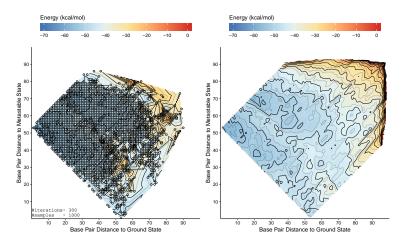


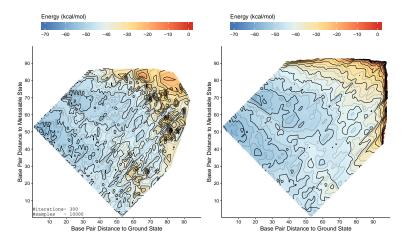


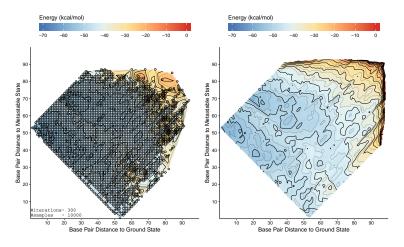


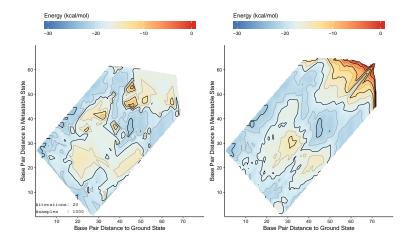


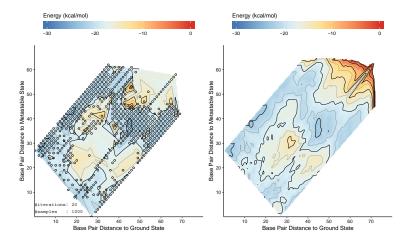


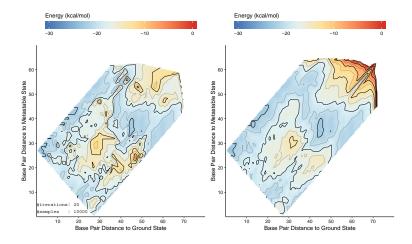


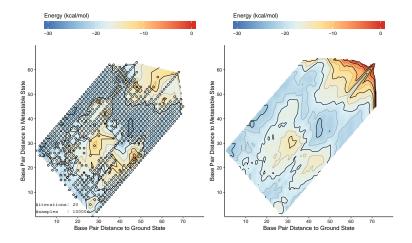


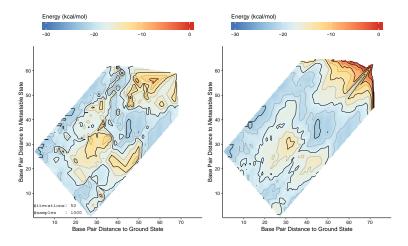


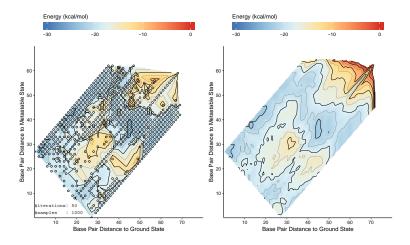


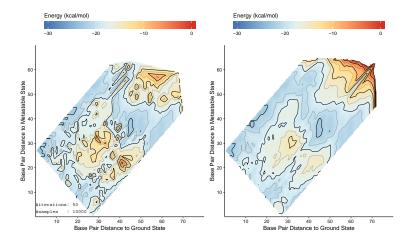


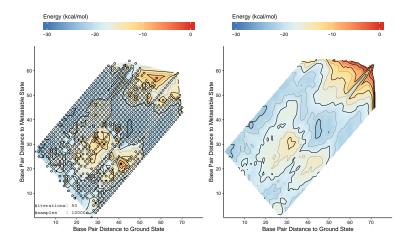


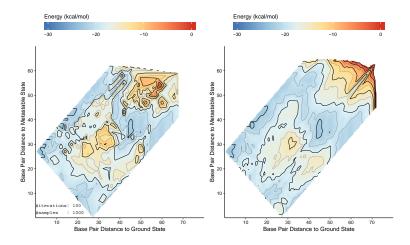


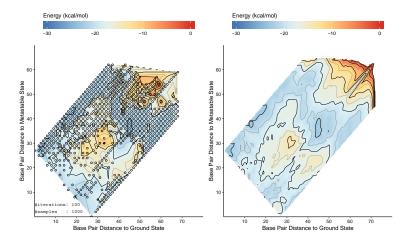


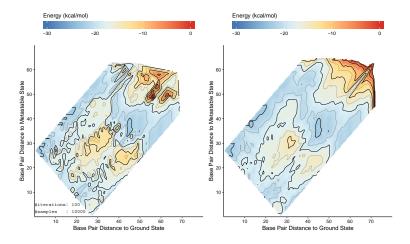


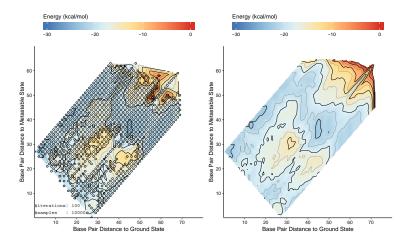


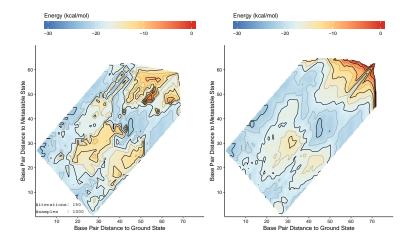


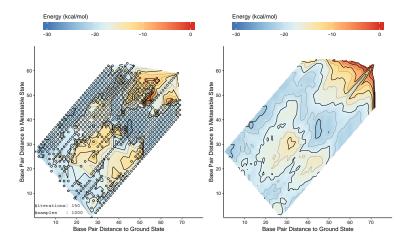


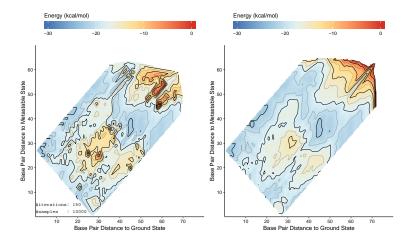


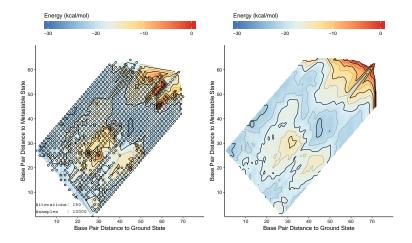


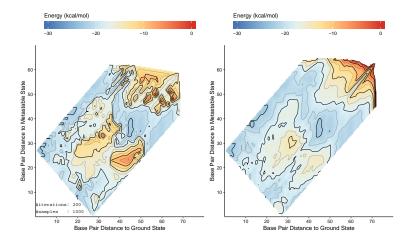


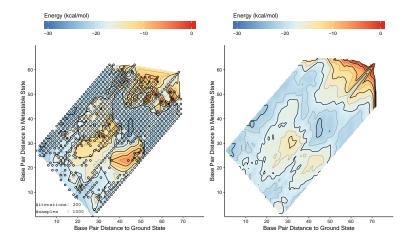


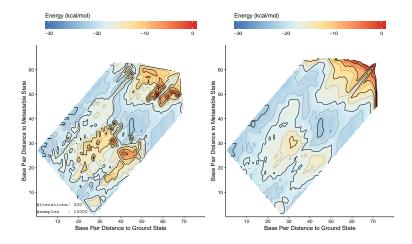


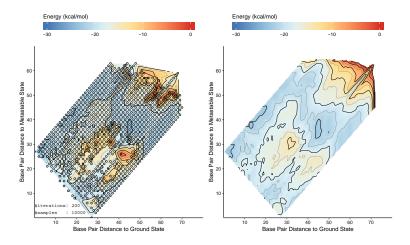


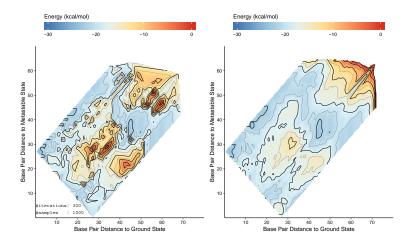


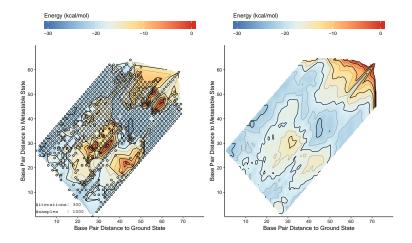


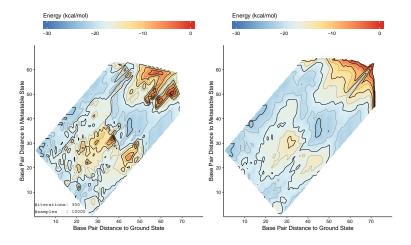


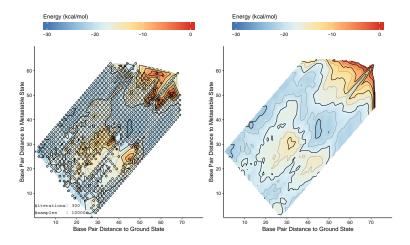




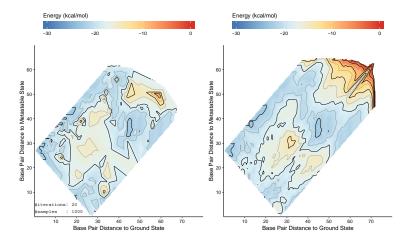








RNAxplorer repulsion scheme Boltzmann sampling (distance)



RNAxplorer repulsion scheme Boltzmann sampling (distance)

