Sampling RNA Secondary Structure Landscapes for Kinetics Simulations

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Paris, France, October 3, 2018

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

$$\begin{array}{lcl} \frac{dp_i(t)}{dt} & = & \displaystyle \sum_{j \neq i} p_j(t) r_{ji} - p_i(t) r_{ij} \\ \\ \frac{d}{dt} \vec{p}(t) & = & \mathbf{R} \vec{p}(t) \quad \text{with formal solution} \quad \vec{p}(t) = e^{t \cdot \mathbf{R}} \cdot \vec{p}(0) \end{array}$$

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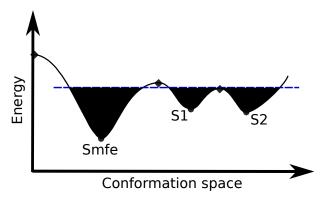
Still, vast numbers of trajectories or exhaustive enumeration of all states is required!

¹Flamm et al. 2001

²Isambert et al. 2001

³Wolfinger et al. 2004

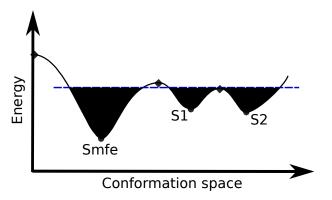
1. Exhaustive Enumeration⁴



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

⁴Wuchty et al. 1999

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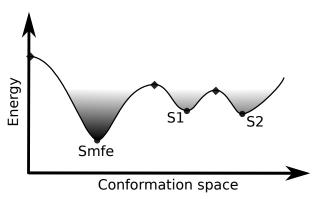


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Draw representative structure samples instead...

⁴Wuchty et al. 1999

2. Boltzmann Sampling⁵

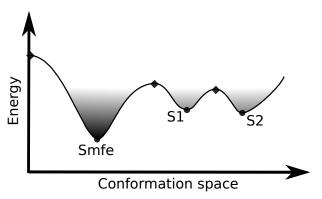


Boltzmann distribution:

•
$$p(s) \propto e^{-E(s)/RT}$$

⁵Ding et al. 2003

2. Boltzmann Sampling⁵

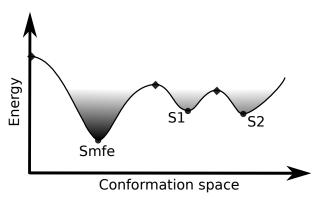


Boltzmann distribution:

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$$p(s) = e^{-E(s)/RT}/Q$$
 with $Q = \sum_{x \in \Omega} e^{-E(x)/RT}$

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2. Boltzmann Sampling⁵



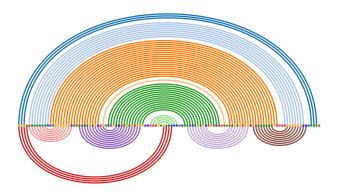
Boltzmann distribution:

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Sample highly redundant and dominated by low energy states!

⁵Ding et al. 2003

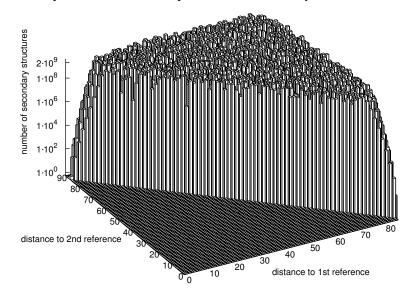
Example: $Q\beta$ replicase template SV11⁶



- artificial RNA sequence of 115 nt, $\approx 7 \cdot 10^{27}$ structures
- 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

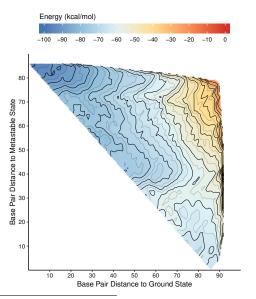
⁶Biebricher et al. 1992

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

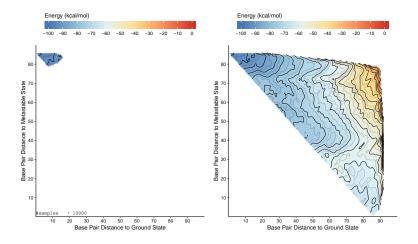


⁷Lorenz et al. 2009

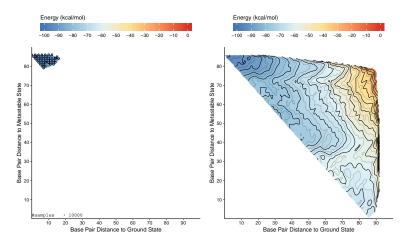
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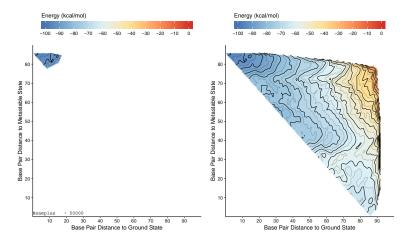
⁷Lorenz et al. 2009



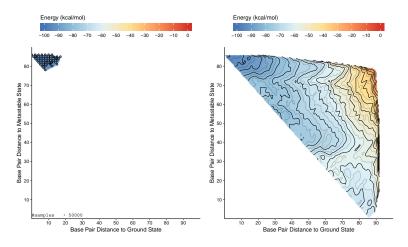
samples: 10,000, # local minima: 35



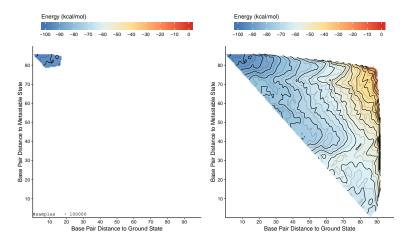
samples: 10,000, # local minima: 35



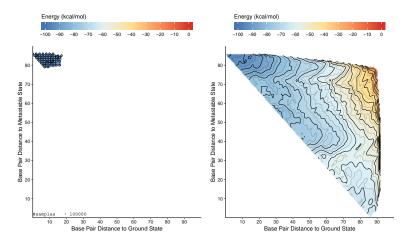
samples: 50,000 / # local minima: 49



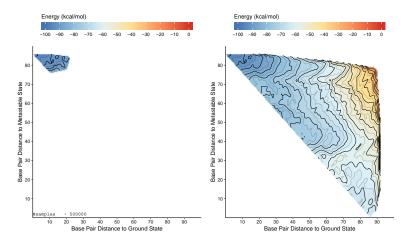
samples: 50,000 / # local minima: 49



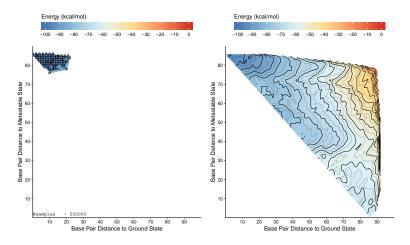
samples: 100,000 / # local minima: 58



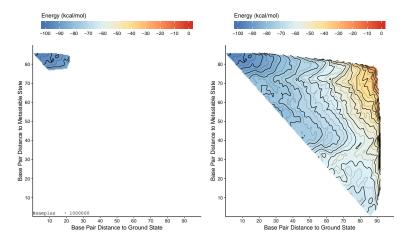
samples: 100,000 / # local minima: 58



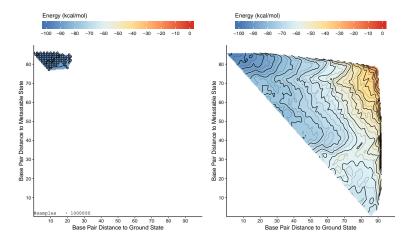
samples: 500,000 / # local minima: 101



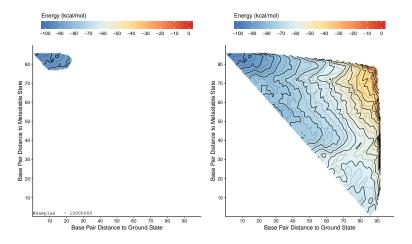
samples: 500,000 / # local minima: 101



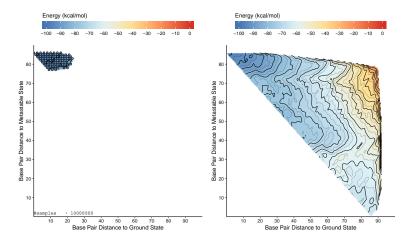
samples: 1,000,000 / # local minima: 132



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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 (RNAShapes 10)

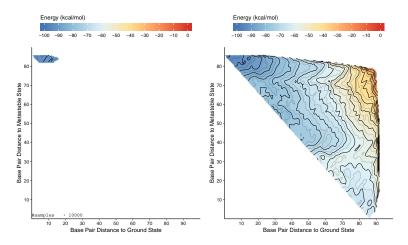
Unfortunately...

- # of local optimal structures still grow exponentially
- most approaches show rather high asymptotic time/memory complexities

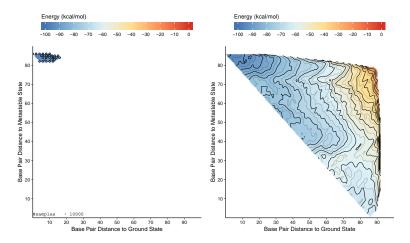
⁷Lorenz WA et al. 2011

⁸Michalik et al. 2017

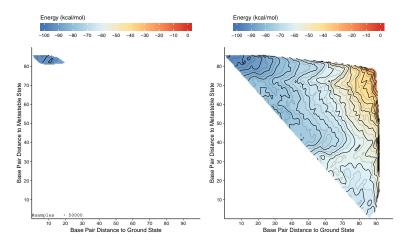
⁹Li et al. 2011



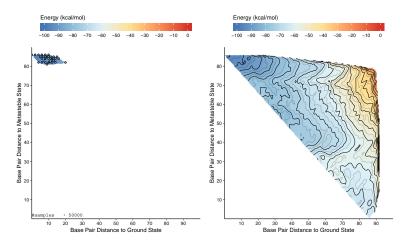
samples: 10,000, # local minima: 41



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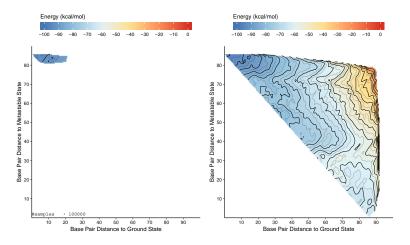


samples: 50,000, # local minima: 61



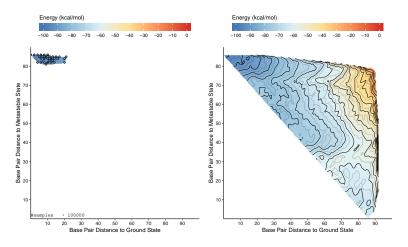
samples: 50,000, # local minima: 61

RNAlocopt Boltzmann sampling



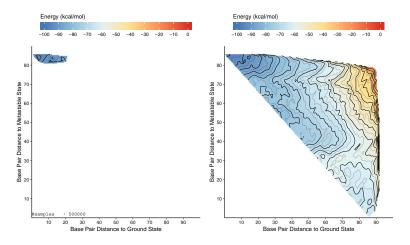
samples: 100,000, # local minima: 72

RNAlocopt Boltzmann sampling



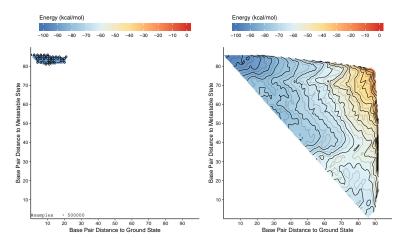
samples: 100,000, # local minima: 72

RNAlocopt Boltzmann sampling

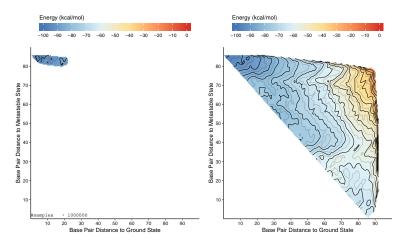


samples: 500,000, # local minima: 107

RNAlocopt Boltzmann sampling

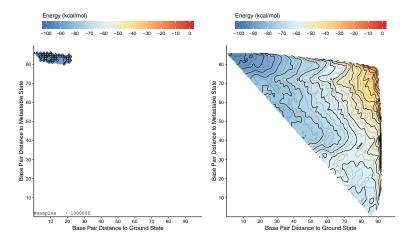


samples: 500,000, # local minima: 107



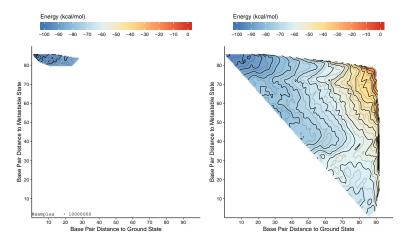
samples: 1,000,000, # local minima: 130

RNAlocopt Boltzmann sampling



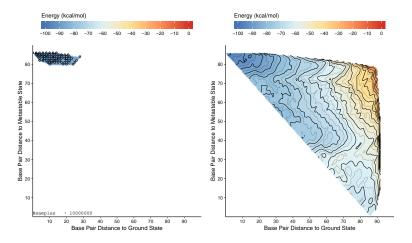
samples: 1,000,000, # local minima: 130

RNAlocopt Boltzmann sampling



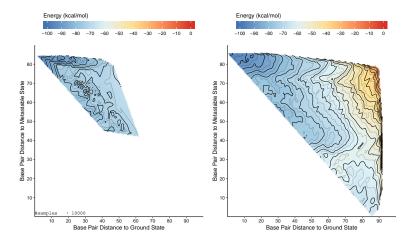
samples: 10,000,000, # local minima: 272

RNAlocopt Boltzmann sampling



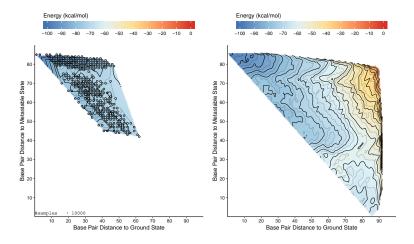
samples: 10,000,000, # local minima: 272

RNANR non-redundant Boltzmann sampling



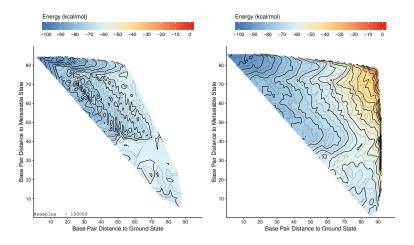
samples: 10,000, # local minima: 10,000

RNANR non-redundant Boltzmann sampling



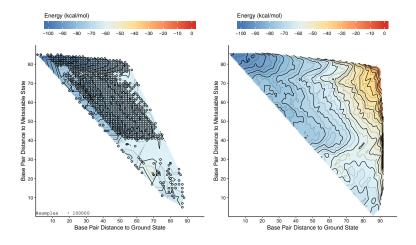
samples: 10,000, # local minima: 10,000

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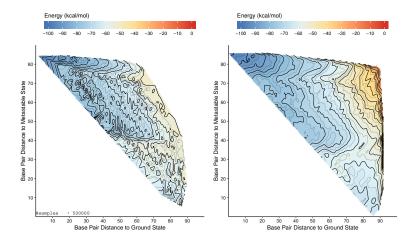
samples: 100,000, # local minima: 100,000

RNANR non-redundant Boltzmann sampling



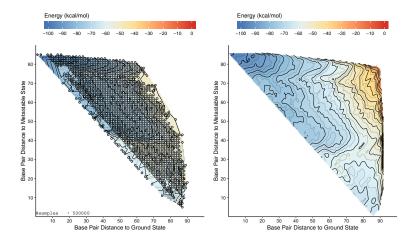
samples: 100,000, # local minima: 100,000

RNANR non-redundant Boltzmann sampling



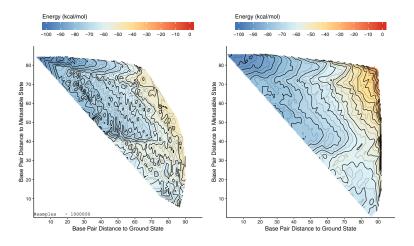
samples: 500,000, # local minima: 500,000

RNANR non-redundant Boltzmann sampling



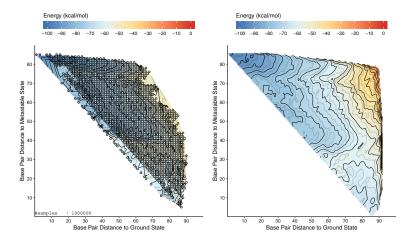
samples: 500,000, # local minima: 500,000

RNANR non-redundant Boltzmann sampling



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

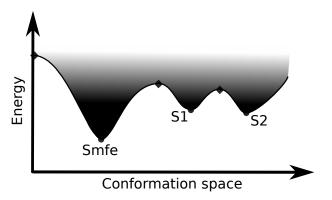
RNANR non-redundant Boltzmann sampling



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

Sampling Strategies

4. Elevated Temperature Boltzmann Sampling

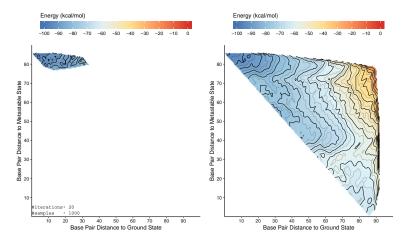


RNAlocmin¹¹:

- reminder: $p(s) = e^{-E(s)/RT} / \sum_{x \in \Omega} e^{-E(x)/RT}$
- iteratively draw samples at different $T = \xi \cdot T_0, \, \xi > 1$
- $T \to \infty$: uniform distribution

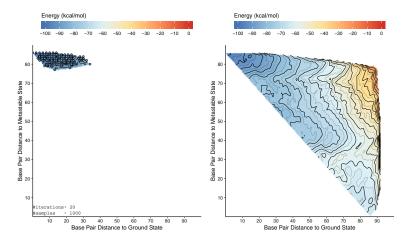
¹¹Kucharik et al. 2014

RNAlocmin temperature elevation scheme Boltzmann sampling



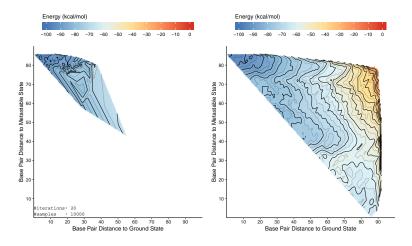
iterations: 20, # samples: 1,000, # local minima: 528

RNAlocmin temperature elevation scheme Boltzmann sampling



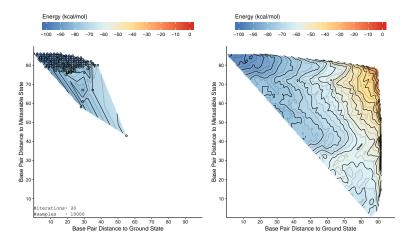
iterations: 20, # samples: 1,000, # local minima: 528

RNAlocmin temperature elevation scheme Boltzmann sampling



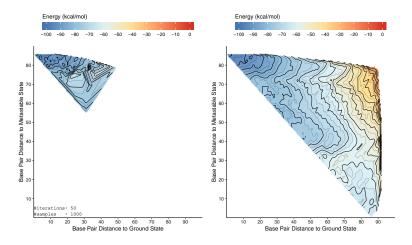
iterations: 20, # samples: 10,000, # local minima: 2,283

RNAlocmin temperature elevation scheme Boltzmann sampling



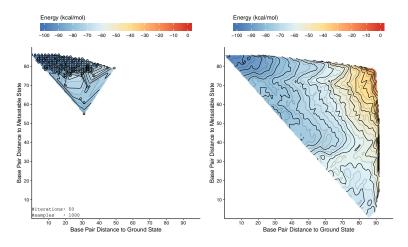
iterations: 20, # samples: 10,000, # local minima: 2,283

RNAlocmin temperature elevation scheme Boltzmann sampling



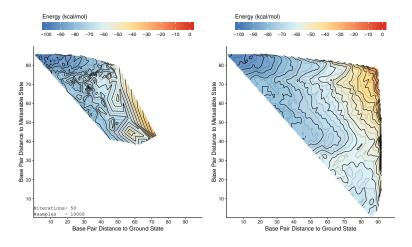
iterations: 50, # samples: 1,000, # local minima: 2,669

RNAlocmin temperature elevation scheme Boltzmann sampling



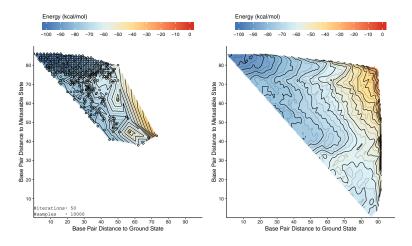
iterations: 50, # samples: 1,000, # local minima: 2,669

RNAlocmin temperature elevation scheme Boltzmann sampling



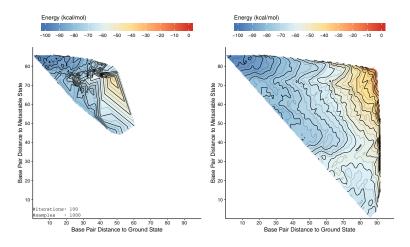
iterations: 50, # samples: 10,000, # local minima: 14,092

RNAlocmin temperature elevation scheme Boltzmann sampling



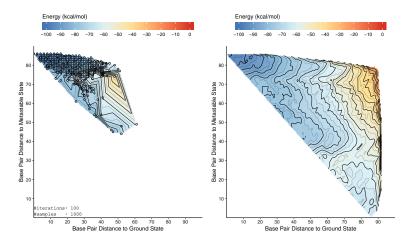
iterations: 50, # samples: 10,000, # local minima: 14,092

RNAlocmin temperature elevation scheme Boltzmann sampling



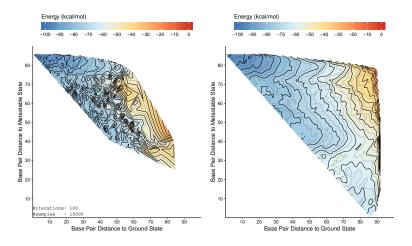
iterations: 100, # samples: 1,000, # local minima: 6,422

RNAlocmin temperature elevation scheme Boltzmann sampling



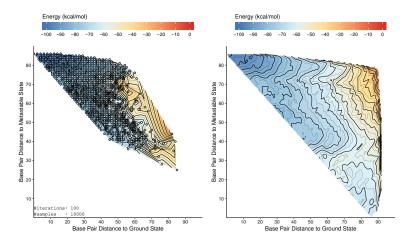
iterations: 100, # samples: 1,000, # local minima: 6,422

RNAlocmin temperature elevation scheme Boltzmann sampling



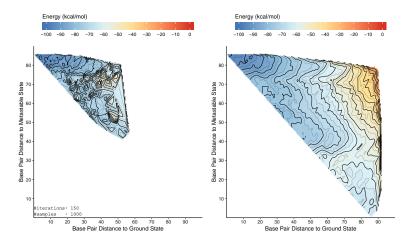
iterations: 100, # samples: 10,000, # local minima: 51,470

RNAlocmin temperature elevation scheme Boltzmann sampling



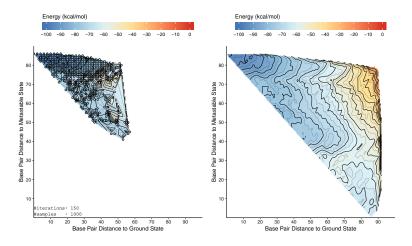
iterations: 100, # samples: 10,000, # local minima: 51,470

RNAlocmin temperature elevation scheme Boltzmann sampling



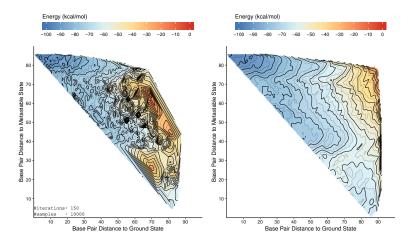
iterations: 150, # samples: 1,000, # local minima: 12,741

RNAlocmin temperature elevation scheme Boltzmann sampling



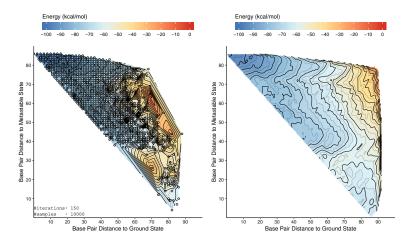
iterations: 150, # samples: 1,000, # local minima: 12,741

RNAlocmin temperature elevation scheme Boltzmann sampling



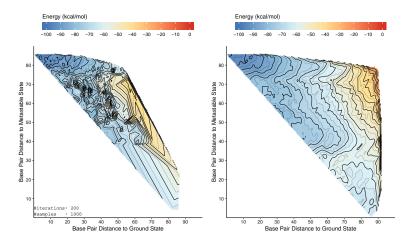
iterations: 150, # samples: 10,000, # local minima: 97,756

RNAlocmin temperature elevation scheme Boltzmann sampling



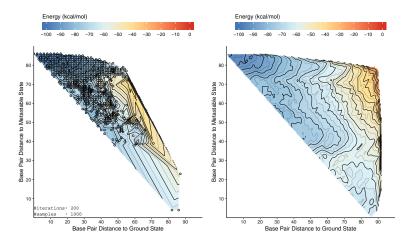
iterations: 150, # samples: 10,000, # local minima: 97,756

RNAlocmin temperature elevation scheme Boltzmann sampling



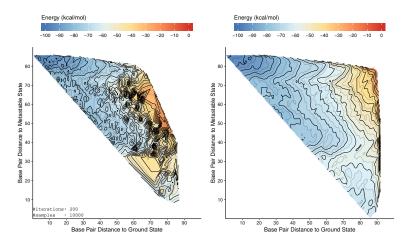
iterations: 200, # samples: 1,000, # local minima: 18,221

RNAlocmin temperature elevation scheme Boltzmann sampling



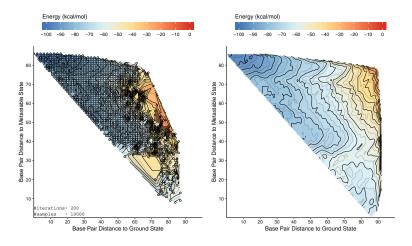
iterations: 200, # samples: 1,000, # local minima: 18,221

RNAlocmin temperature elevation scheme Boltzmann sampling



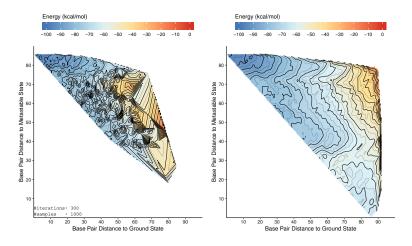
iterations: 200, # samples: 10,000, # local minima: 145,391

RNAlocmin temperature elevation scheme Boltzmann sampling



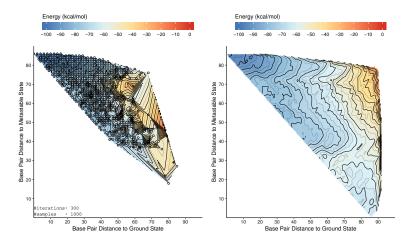
iterations: 200, # samples: 10,000, # local minima: 145,391

RNAlocmin temperature elevation scheme Boltzmann sampling



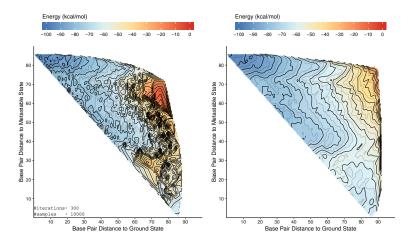
iterations: 300, # samples: 1,000, # local minima: 32,569

RNAlocmin temperature elevation scheme Boltzmann sampling



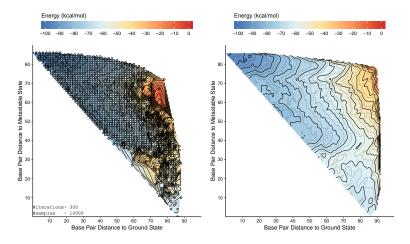
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RNAlocmin temperature elevation scheme Boltzmann sampling



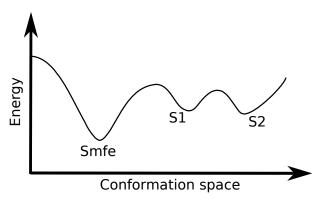
iterations: 300, # samples: 10,000, # local minima: 260,994

RNAlocmin temperature elevation scheme Boltzmann sampling



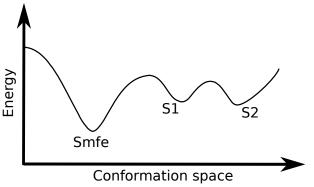
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5. Sampling with Guiding Potentials (RNAxplorer)¹²



¹²Entzian et al. (manuscript in preparation)

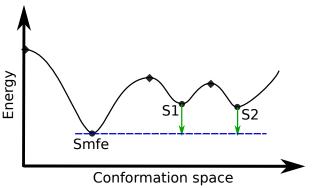
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• $p(s) = e^{-E(s)/RT} / \sum_{x \in \Omega} e^{-E(x)/RT}$

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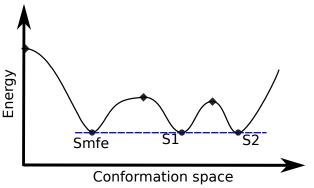
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- $E(s_{mfe}) = [E(s_1) + \hat{E}(s_1)] = [E(s_2) + \hat{E}(s_2)]$

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¹²Entzian et al. (manuscript in preparation)

5. Sampling with Guiding Potentials (RNAxplorer)¹²

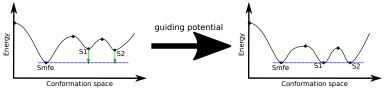


Guiding potential needs to allow for efficiently:

- computing partition function Q
- sampling from distorted energy ensemble

¹²Entzian et al. (manuscript in preparation)

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

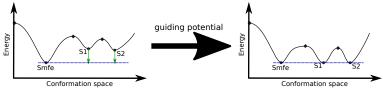
$$E(s_{mfe}) = [E(s_1) + \hat{E}(s_1)] = [E(s_2) + \hat{E}(s_2)]$$

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

¹²Entzian et al. (manuscript in preparation)

¹³Lorenz et al. 2016

5. Sampling with Guiding Potentials (RNAxplorer)¹²



Guiding potential needs to allow for efficiently:

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Make use of soft constraints feature of ViennaRNA Package 13

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

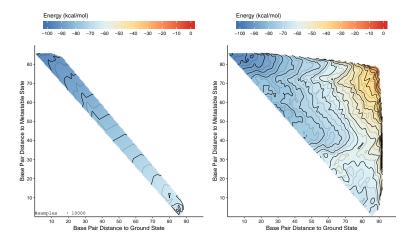
$$\hat{E}(s) = d_{BP}(s, s_1) \cdot w_1 + d_{BP}(s, s_2) \cdot w_2$$

How to choose reference structures S_x ?

¹²Entzian et al. (manuscript in preparation)

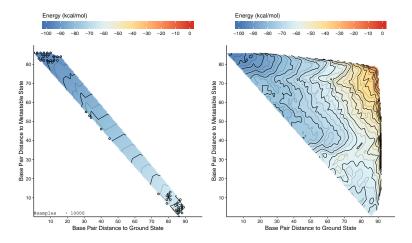
¹³Lorenz et al. 2016

RNAxplorer attraction scheme Boltzmann sampling



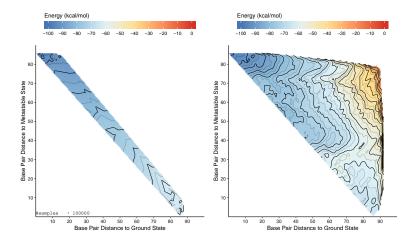
references: 2, # samples: 10,000, # local minima: 86

RNAxplorer attraction scheme Boltzmann sampling



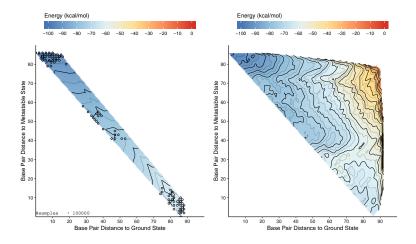
references: 2, # samples: 10,000, # local minima: 86

RNAxplorer attraction scheme Boltzmann sampling



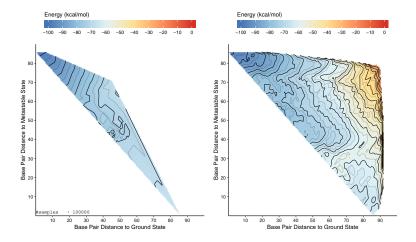
references: 2, # samples: 100,000, # local minima: 167

RNAxplorer attraction scheme Boltzmann sampling



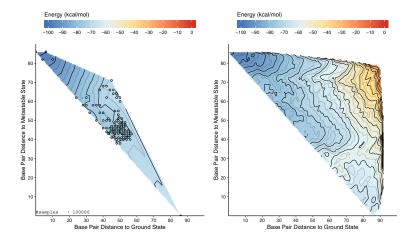
references: 2, # samples: 100,000, # local minima: 167

RNAxplorer attraction scheme Boltzmann sampling



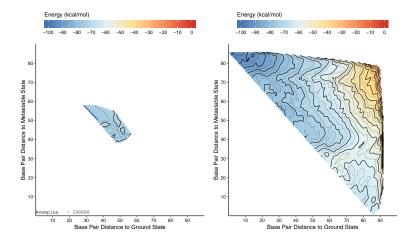
references: 3, # samples: 100,000, # local minima: 182

RNAxplorer attraction scheme Boltzmann sampling



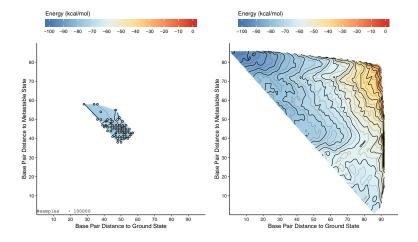
references: 3, # samples: 100,000, # local minima: 182

RNAxplorer attraction scheme Boltzmann sampling

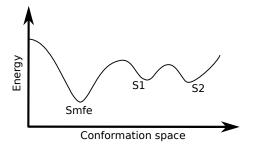


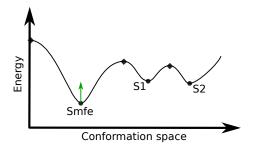
references: 4, # samples: 100,000, # local minima: 143

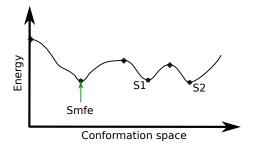
RNAxplorer attraction scheme Boltzmann sampling

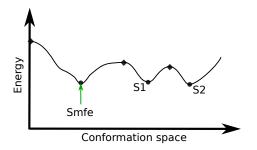


references: 4, # samples: 100, 000, # local minima: 143





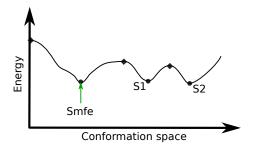




- draw samples and determine corresponding local minima
- add most over-represented local minimum s_m to list L
- assign $\hat{E}(s)$ according to structures in L, e.g.

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

5b. Sampling with (repellent) Guiding Potentials

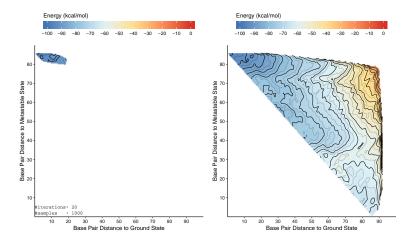


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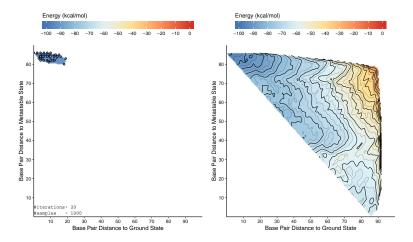
Choose moderate weighting factors, e.g. $w(s_m) = \gamma RT$

RNAxplorer repulsion scheme Boltzmann sampling



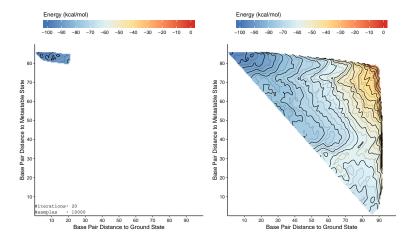
iterations: 20, # samples: 1,000, # local minima: 52

RNAxplorer repulsion scheme Boltzmann sampling



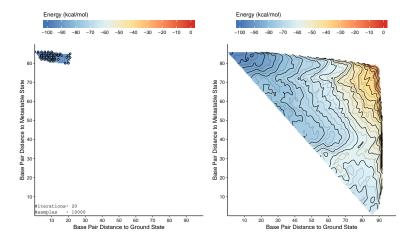
iterations: 20, # samples: 1,000, # local minima: 52

RNAxplorer repulsion scheme Boltzmann sampling



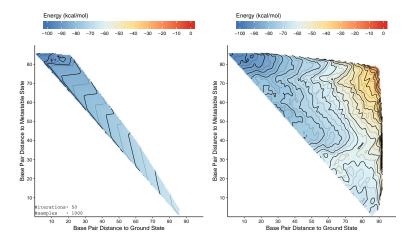
iterations: 20, # samples: 10,000, # local minima: 97

RNAxplorer repulsion scheme Boltzmann sampling



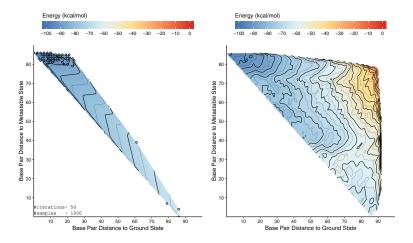
iterations: 20, # samples: 10,000, # local minima: 97

RNAxplorer repulsion scheme Boltzmann sampling



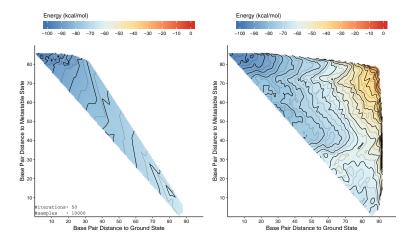
iterations: 50, # samples: 1,000, # local minima: 133

RNAxplorer repulsion scheme Boltzmann sampling



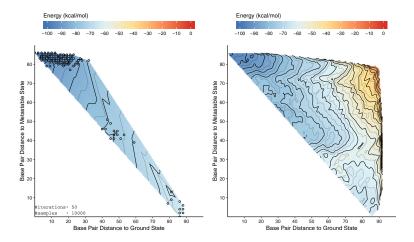
iterations: 50, # samples: 1,000, # local minima: 133

RNAxplorer repulsion scheme Boltzmann sampling



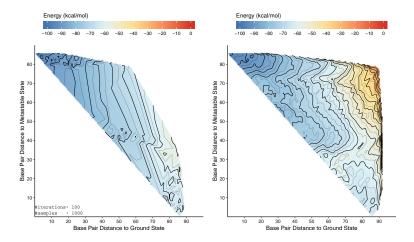
iterations: 50, # samples: 10,000, # local minima: 320

RNAxplorer repulsion scheme Boltzmann sampling



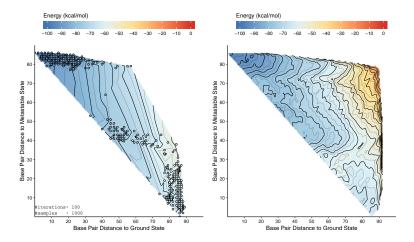
iterations: 50, # samples: 10,000, # local minima: 320

RNAxplorer repulsion scheme Boltzmann sampling



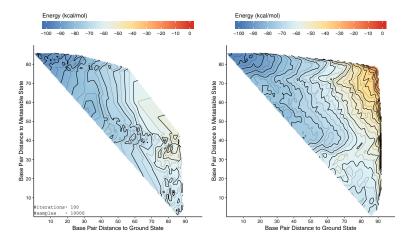
iterations: 100, # samples: 1,000, # local minima: 765

RNAxplorer repulsion scheme Boltzmann sampling



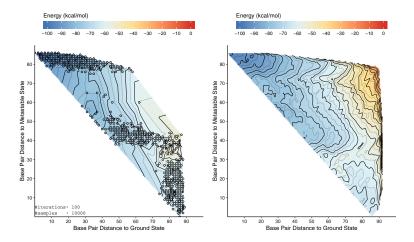
iterations: 100, # samples: 1,000, # local minima: 765

RNAxplorer repulsion scheme Boltzmann sampling



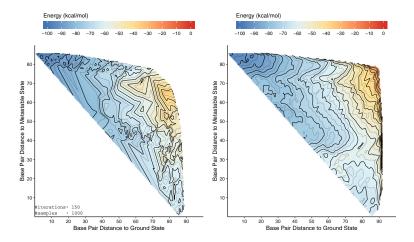
iterations: 100, # samples: 10,000, # local minima: 2,549

RNAxplorer repulsion scheme Boltzmann sampling



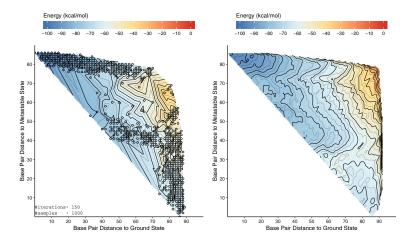
iterations: 100, # samples: 10,000, # local minima: 2,549

RNAxplorer repulsion scheme Boltzmann sampling



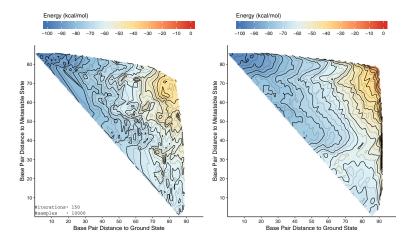
iterations: 150, # samples: 1,000, # local minima: 3,781

RNAxplorer repulsion scheme Boltzmann sampling



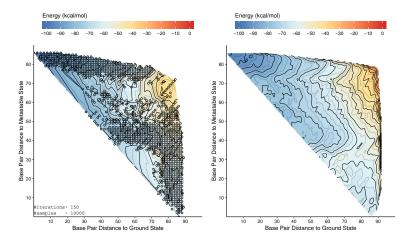
iterations: 150, # samples: 1,000, # local minima: 3,781

RNAxplorer repulsion scheme Boltzmann sampling



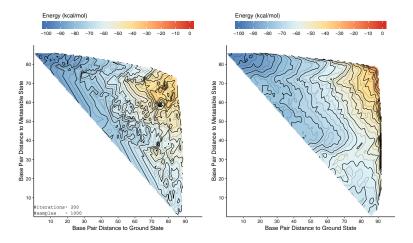
iterations: 150, # samples: 10,000, # local minima: 15,041

RNAxplorer repulsion scheme Boltzmann sampling



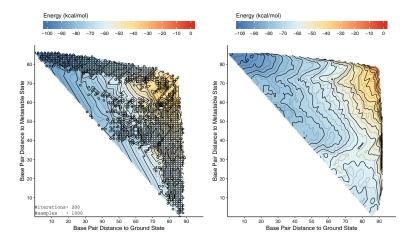
iterations: 150, # samples: 10,000, # local minima: 15,041

RNAxplorer repulsion scheme Boltzmann sampling



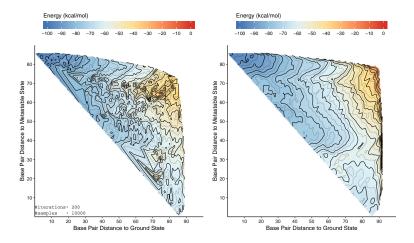
iterations: 200, # samples: 1,000, # local minima: 13,066

RNAxplorer repulsion scheme Boltzmann sampling



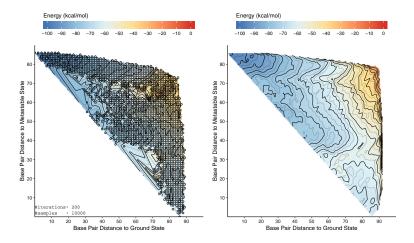
iterations: 200, # samples: 1,000, # local minima: 13,066

RNAxplorer repulsion scheme Boltzmann sampling



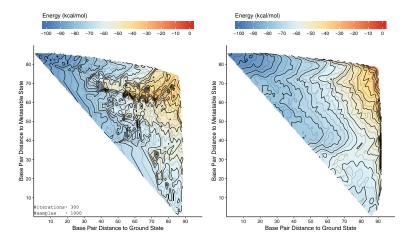
iterations: 200, # samples: 10,000, # local minima: 57,296

RNAxplorer repulsion scheme Boltzmann sampling



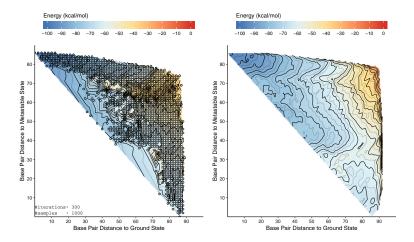
iterations: 200, # samples: 10,000, # local minima: 57,296

RNAxplorer repulsion scheme Boltzmann sampling



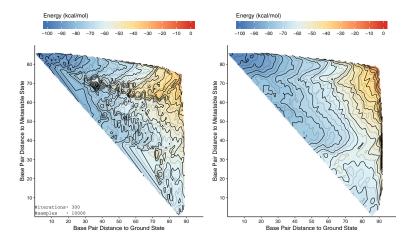
iterations: 300, # samples: 1,000, # local minima: 61,952

RNAxplorer repulsion scheme Boltzmann sampling



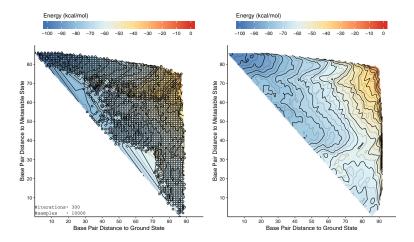
iterations: 300, # samples: 1,000, # local minima: 61,952

RNAxplorer repulsion scheme Boltzmann sampling



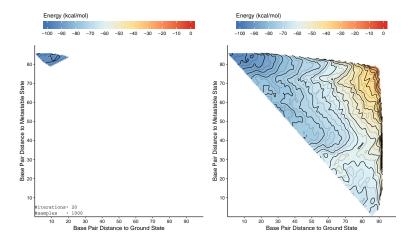
iterations: 300, # samples: 10,000, # local minima: 309,669

RNAxplorer repulsion scheme Boltzmann sampling



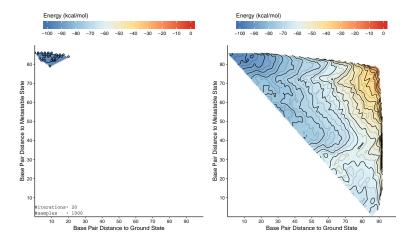
iterations: 300, # samples: 10,000, # local minima: 309,669

RNAxplorer repulsion scheme Boltzmann sampling (distance)



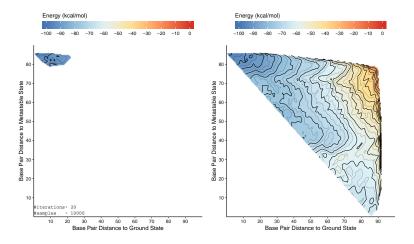
iterations: 20, # samples: 1,000, # local minima: 47

RNAxplorer repulsion scheme Boltzmann sampling (distance)



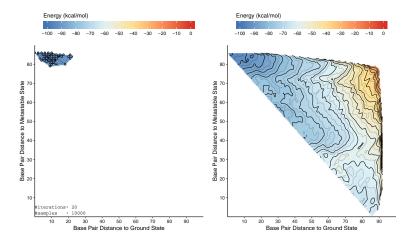
iterations: 20, # samples: 1,000, # local minima: 47

RNAxplorer repulsion scheme Boltzmann sampling (distance)



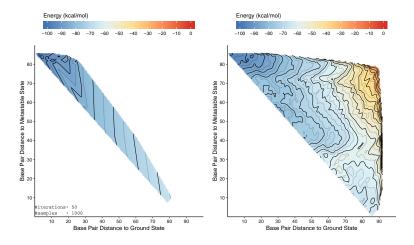
iterations: 20, # samples: 10,000, # local minima: 92

RNAxplorer repulsion scheme Boltzmann sampling (distance)



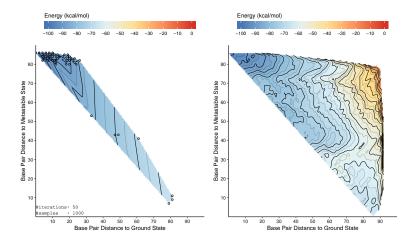
iterations: 20, # samples: 10,000, # local minima: 92

RNAxplorer repulsion scheme Boltzmann sampling (distance)



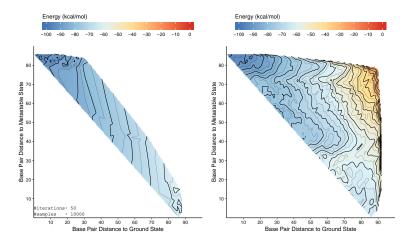
iterations: 50, # samples: 1,000, # local minima: 119

RNAxplorer repulsion scheme Boltzmann sampling (distance)



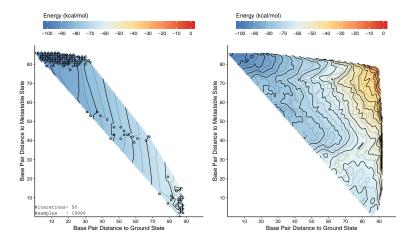
iterations: 50, # samples: 1,000, # local minima: 119

RNAxplorer repulsion scheme Boltzmann sampling (distance)



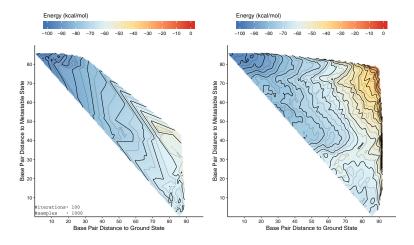
iterations: 50, # samples: 10,000, # local minima: 484

RNAxplorer repulsion scheme Boltzmann sampling (distance)



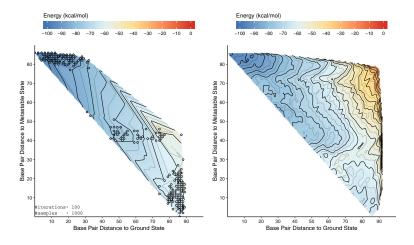
iterations: 50, # samples: 10,000, # local minima: 484

RNAxplorer repulsion scheme Boltzmann sampling (distance)



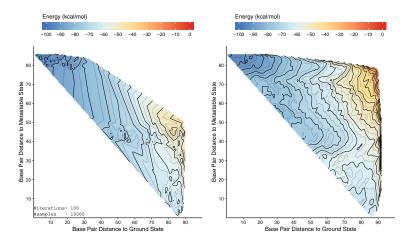
iterations: 100, # samples: 1,000, # local minima: 608

RNAxplorer repulsion scheme Boltzmann sampling (distance)



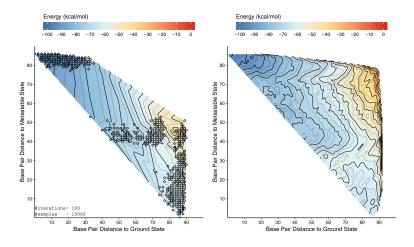
iterations: 100, # samples: 1,000, # local minima: 608

RNAxplorer repulsion scheme Boltzmann sampling (distance)



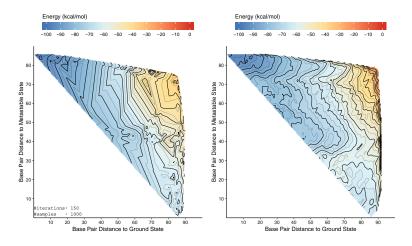
iterations: 100, # samples: 10,000, # local minima: 2,853

RNAxplorer repulsion scheme Boltzmann sampling (distance)



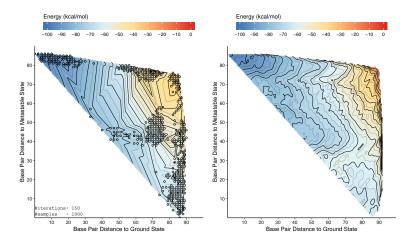
iterations: 100, # samples: 10,000, # local minima: 2,853

RNAxplorer repulsion scheme Boltzmann sampling (distance)



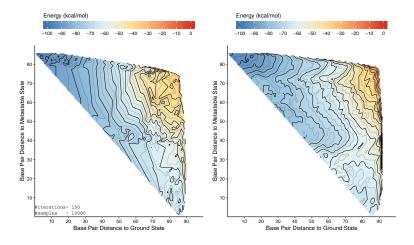
iterations: 150, # samples: 1,000, # local minima: 2,818

RNAxplorer repulsion scheme Boltzmann sampling (distance)



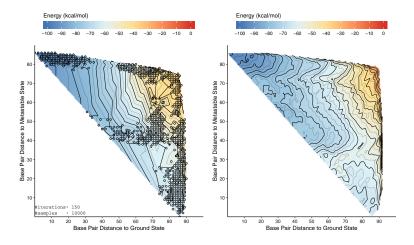
iterations: 150, # samples: 1,000, # local minima: 2,818

RNAxplorer repulsion scheme Boltzmann sampling (distance)



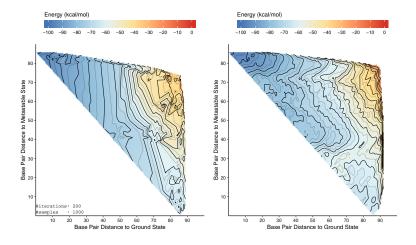
iterations: 150, # samples: 10,000, # local minima: 7,111

RNAxplorer repulsion scheme Boltzmann sampling (distance)



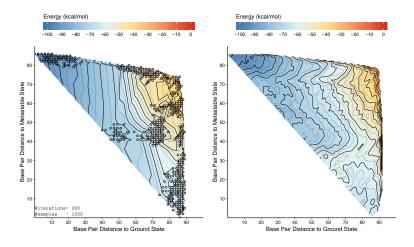
iterations: 150, # samples: 10,000, # local minima: 7,111

RNAxplorer repulsion scheme Boltzmann sampling (distance)



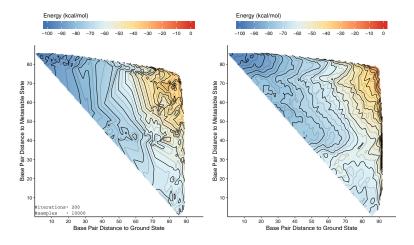
iterations: 200, # samples: 1,000, # local minima: 3,147

RNAxplorer repulsion scheme Boltzmann sampling (distance)



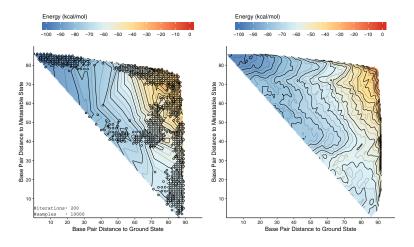
iterations: 200, # samples: 1,000, # local minima: 3,147

RNAxplorer repulsion scheme Boltzmann sampling (distance)



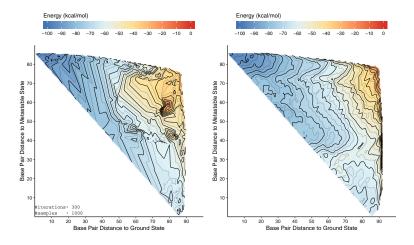
iterations: 200, # samples: 10,000, # local minima: 10,342

RNAxplorer repulsion scheme Boltzmann sampling (distance)



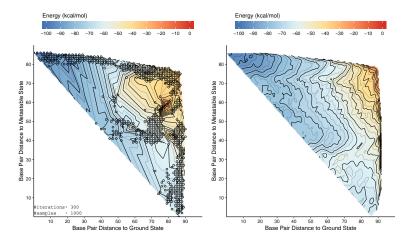
iterations: 200, # samples: 10,000, # local minima: 10,342

RNAxplorer repulsion scheme Boltzmann sampling (distance)



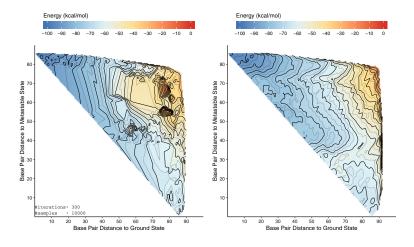
iterations: 300, # samples: 1,000, # local minima: 4,820

RNAxplorer repulsion scheme Boltzmann sampling (distance)



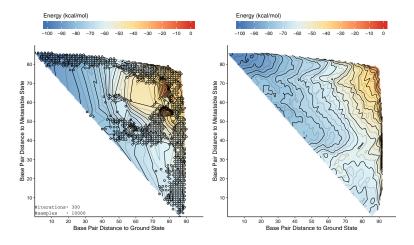
iterations: 300, # samples: 1,000, # local minima: 4,820

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

Sampling Quality

Goal:

- (reliatively) low number of representative structures
- capture a diverse, yet important set of states

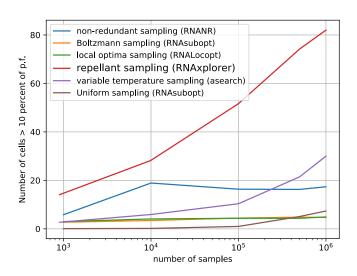
Use 2D projections and compare samples against RNA2Dfold¹⁴

- count number of samples per disance-class
- compute deviation of distance-class MFEs or Q, e.g. L1-norm
- distance-class coverage, e.g. $|\mathcal{C}(\delta)|$ with $\mathcal{C}(\delta) = \{\mathcal{C}|Q_{\mathcal{C}}^{\mathrm{sampled}} \geq \delta \cdot Q_{\mathcal{C}}^{\mathrm{real}}\}$

¹⁴Lorenz et al. 2009, computes MFE and Q in $\mathcal{O}(n^7)$

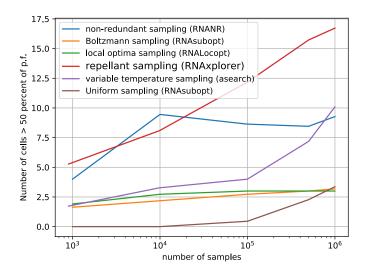
Sampling Quality - Partition Function Coverage

- SV11 example
- δ = 0.1



Sampling Quality - Partition Function Coverage

- SV11 example
- $\delta = 0.5$



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



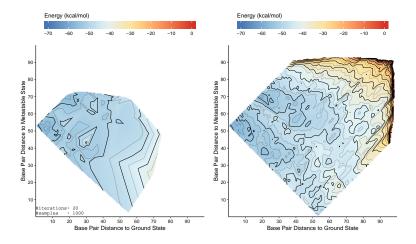
Thanks to

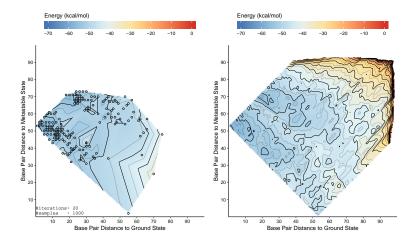
- Gregor Entzian
- Andrea Tanzer
- Yann Ponty
- Juraj Michalik
- Ivo L Hofacker
- TBI team

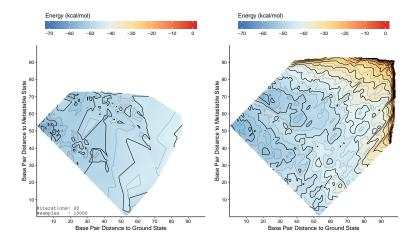
Thank You for your attention!

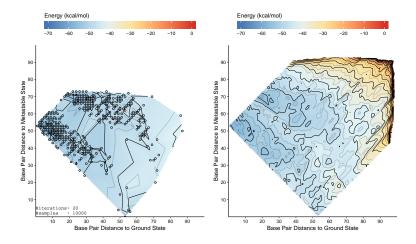
This work was funded in parts by the Austrian/French project 'RNAlands', FWF-I-1804-N28 and ANR-14-CE34-0011

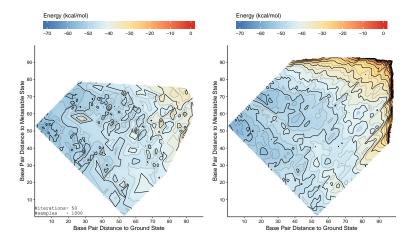


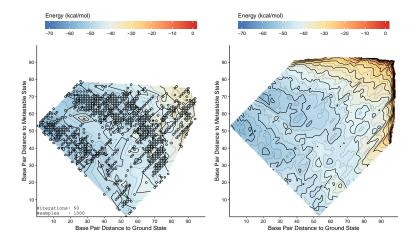


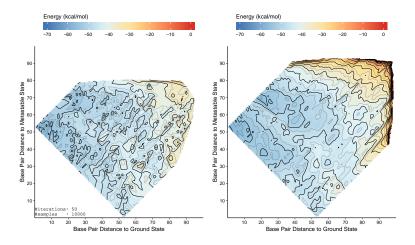


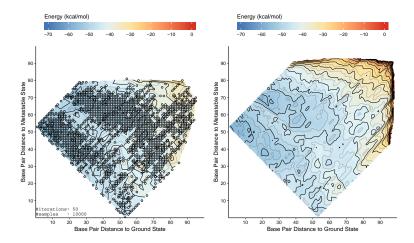


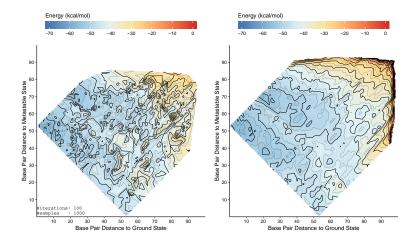


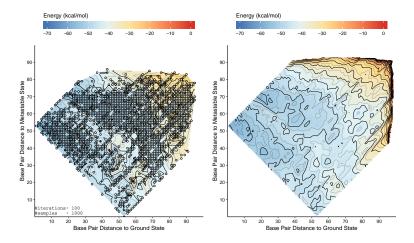


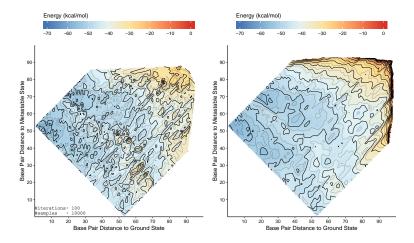


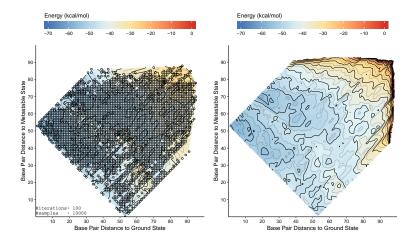


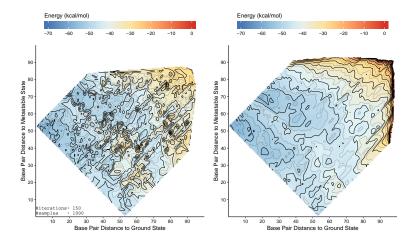


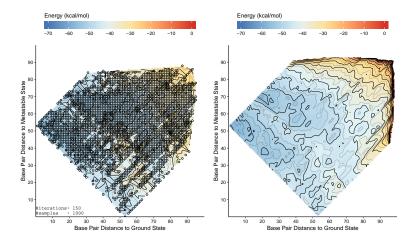


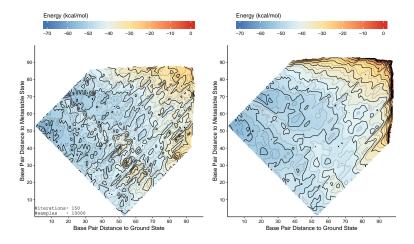


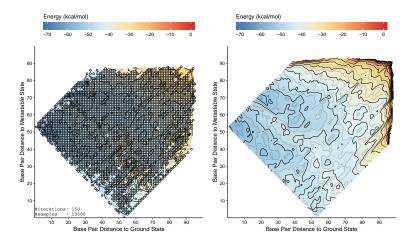


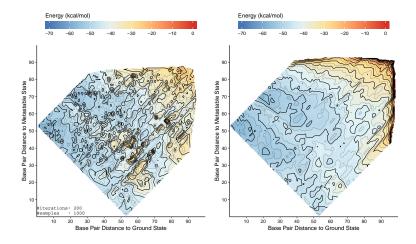


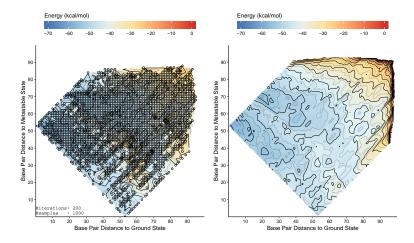


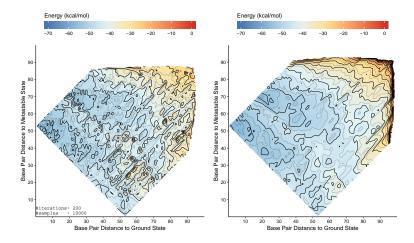


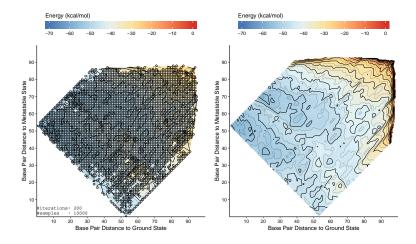


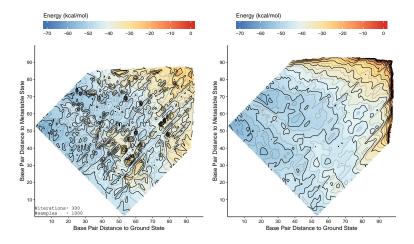


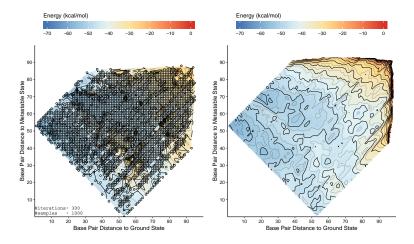


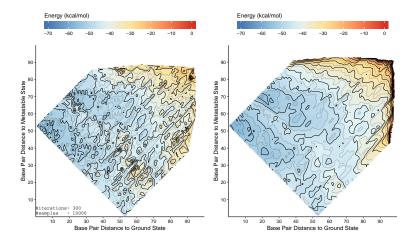


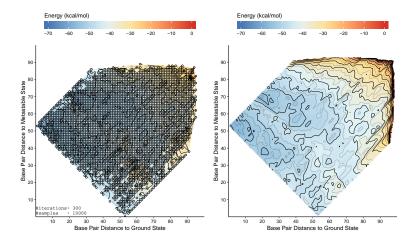


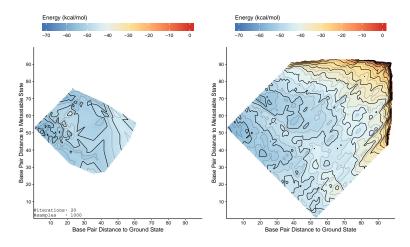


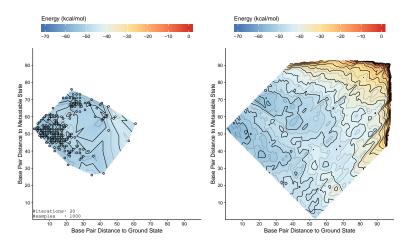


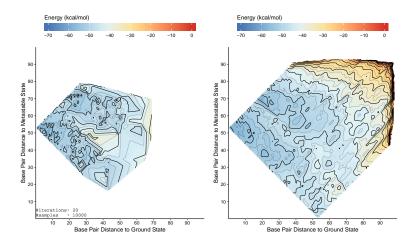


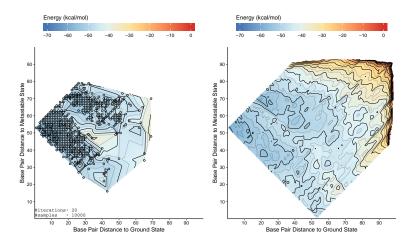


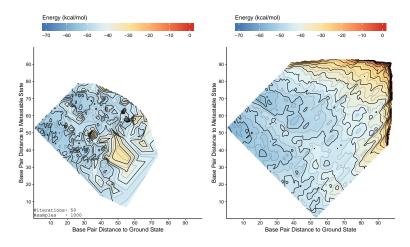


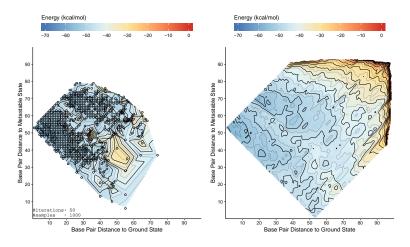


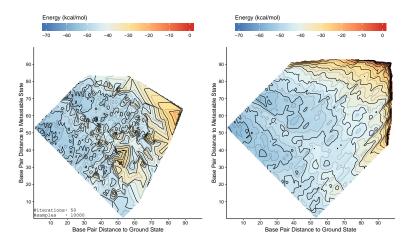


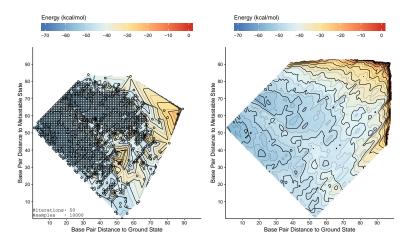


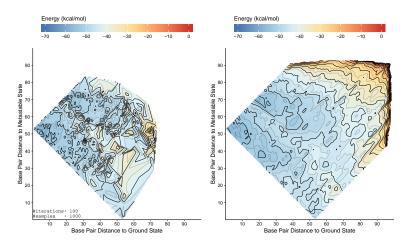


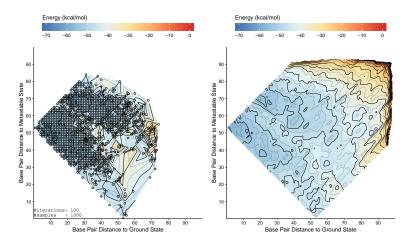


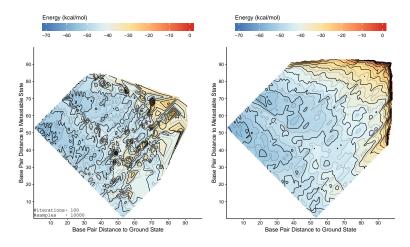


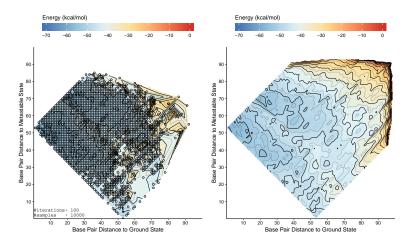


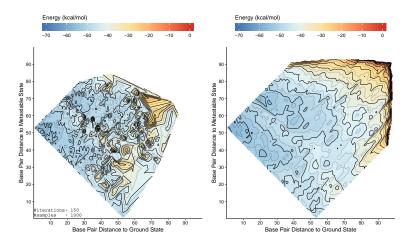


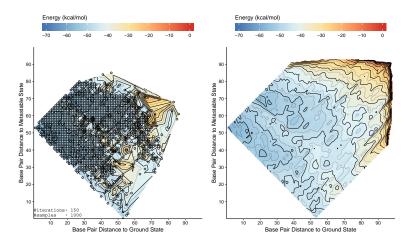


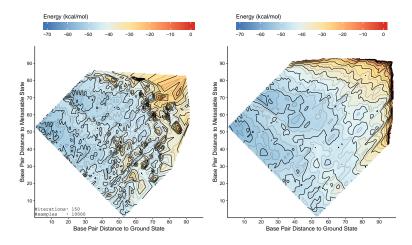


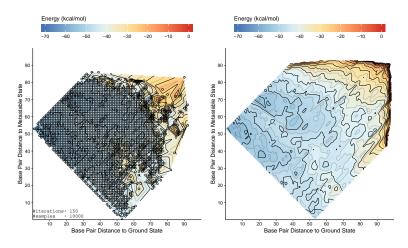


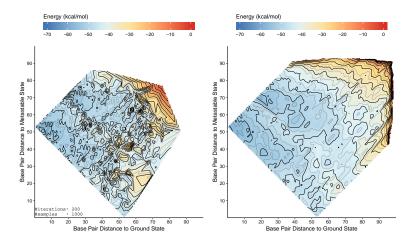


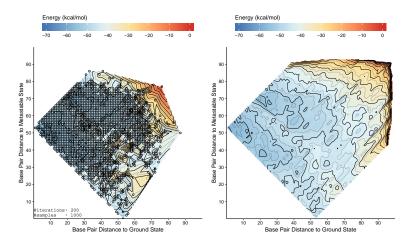


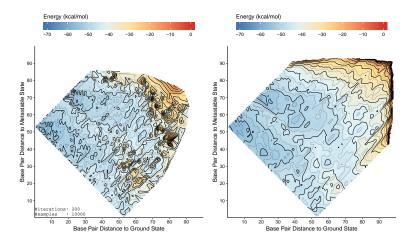


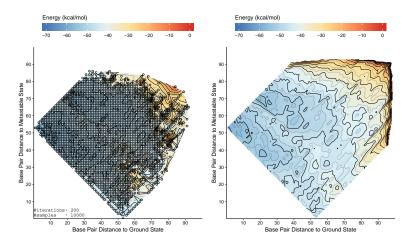


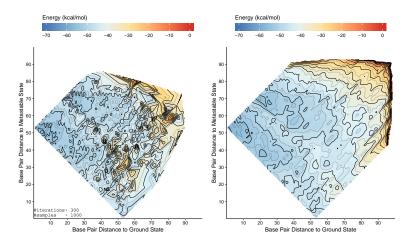


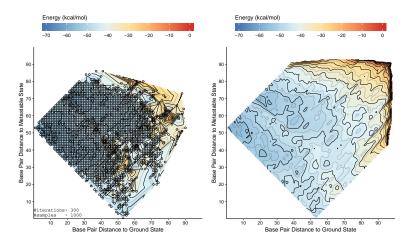


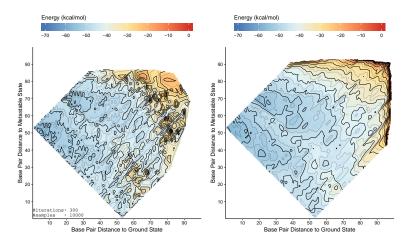


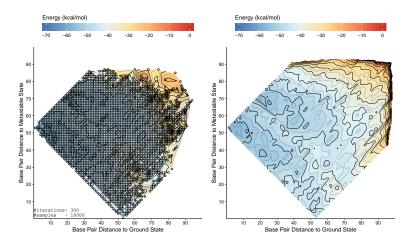


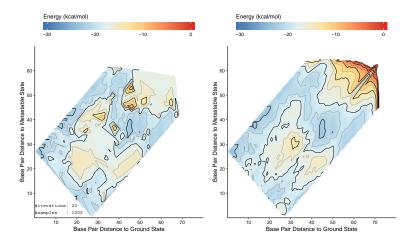


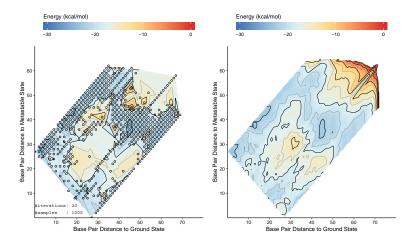


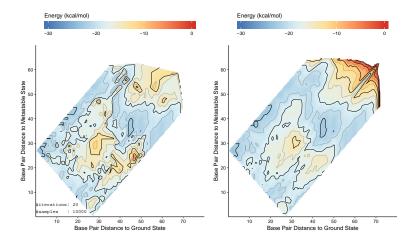


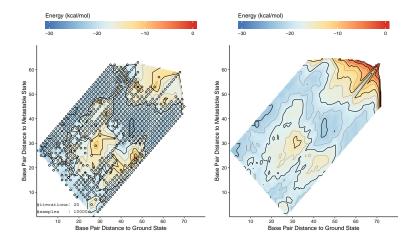


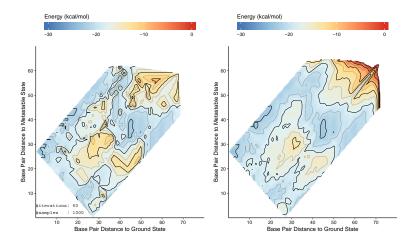


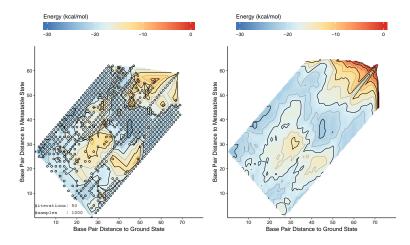


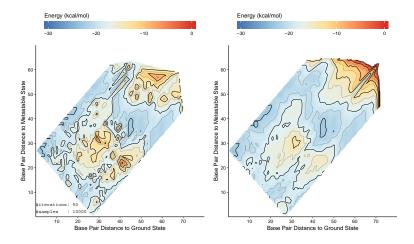


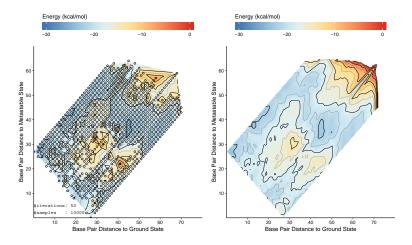


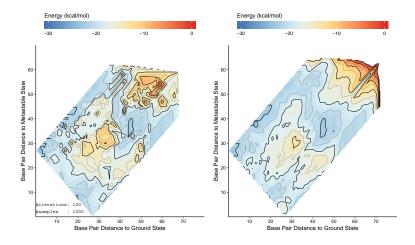


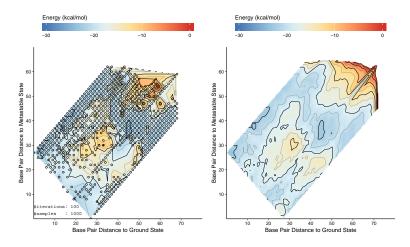


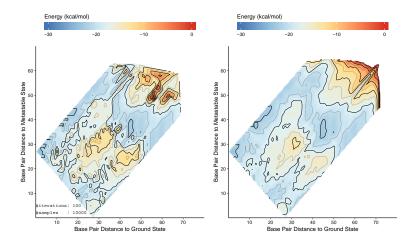


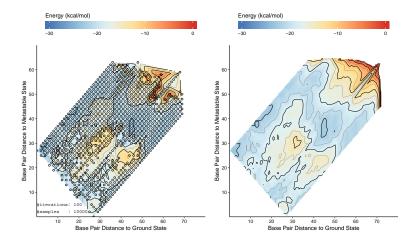


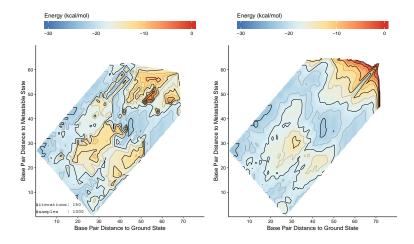


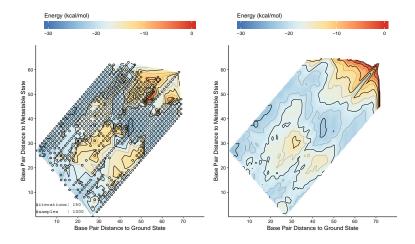


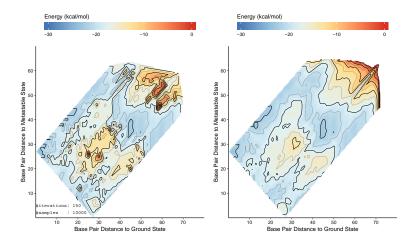


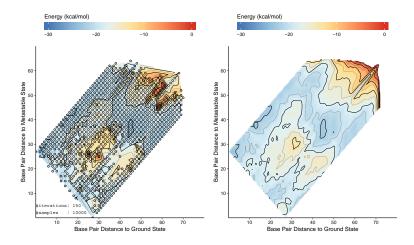


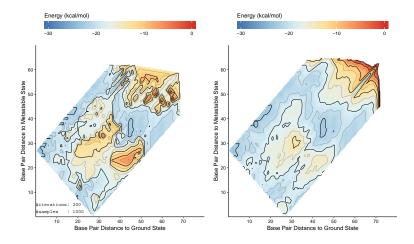


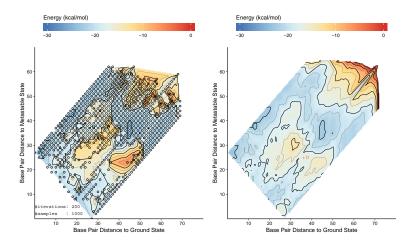


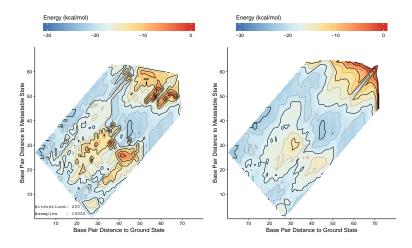


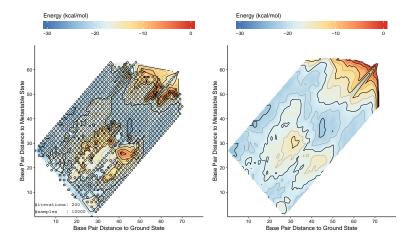


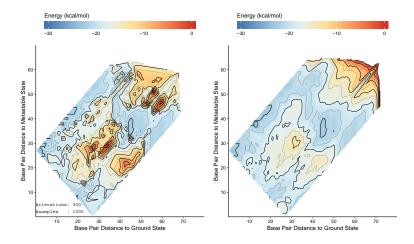


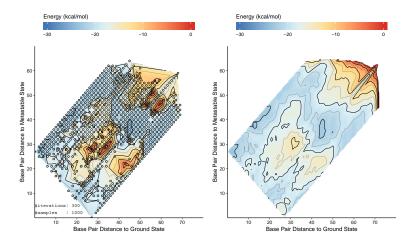




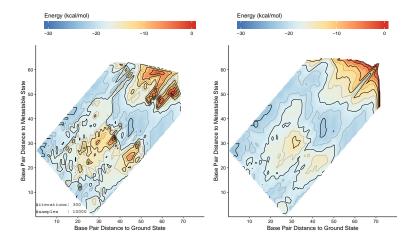








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