Finding Many Stable Molecular Arrangements

Conformational Searching with Genetic Algorithms

Evan Curtin

December 2, 2016

University of Illinois at Urbana-Champaign

Outline

1. Background Information
2. The Genetic Algorithm
3. Finding Low Energy Conformers of Dipeptides
4. Concluding Remarks

Primary Resource

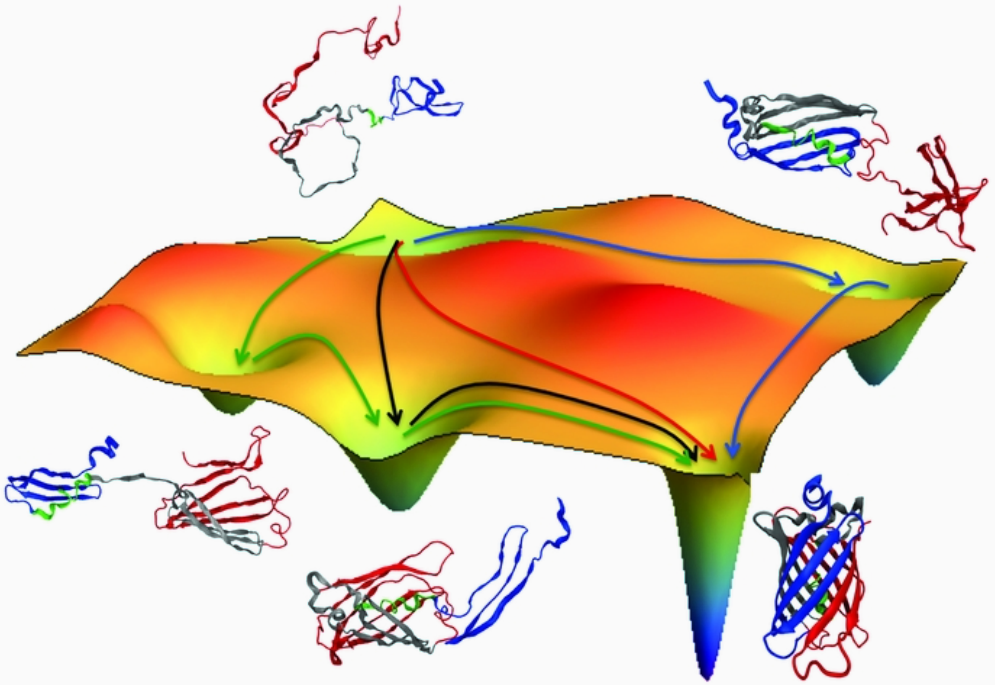
First-Principles Molecular Structure Search with a Genetic Algorithm
Supady, A.P^{1}; Blum, V.[1]; Baldauf, C. J.[1,2] Chem. Inf. Model. 2015, 55 (11), 23382348.

1. Fritz-Haber-Institut der Max-Planck-Gesellschaft, Berlin
2. Department of Mechanical Engineering & Materials Science, Duke University

Background Information

The Problem

- Protein folding is important



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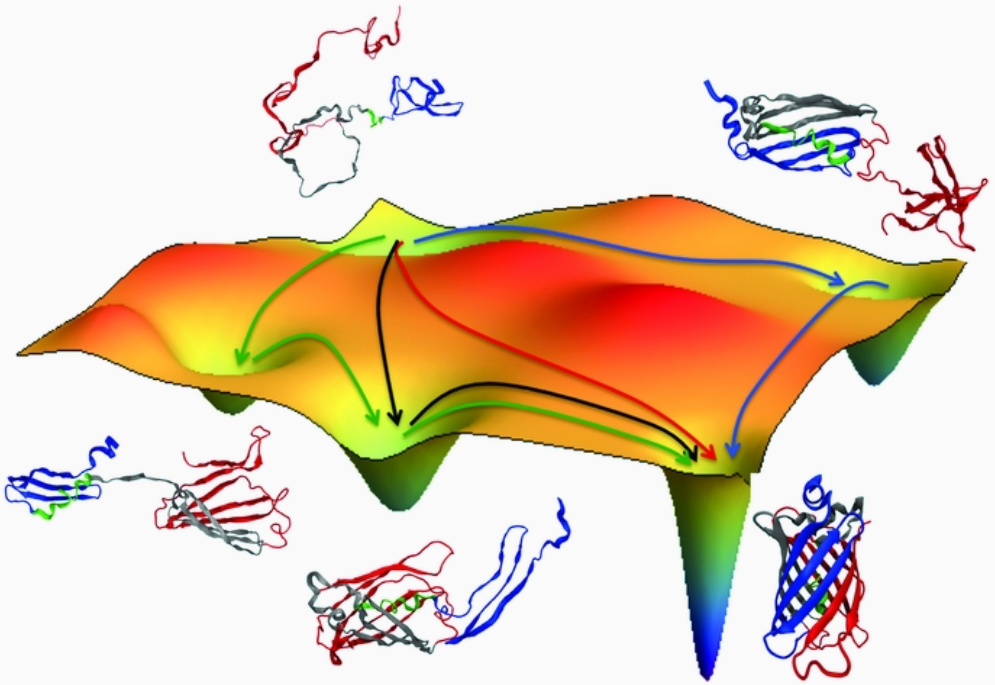

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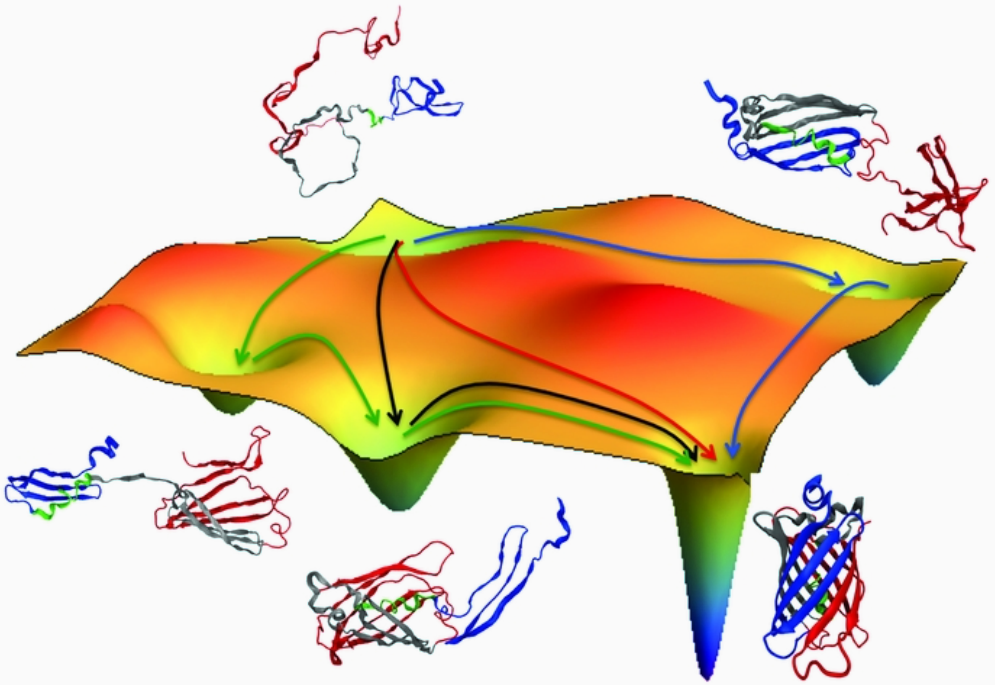

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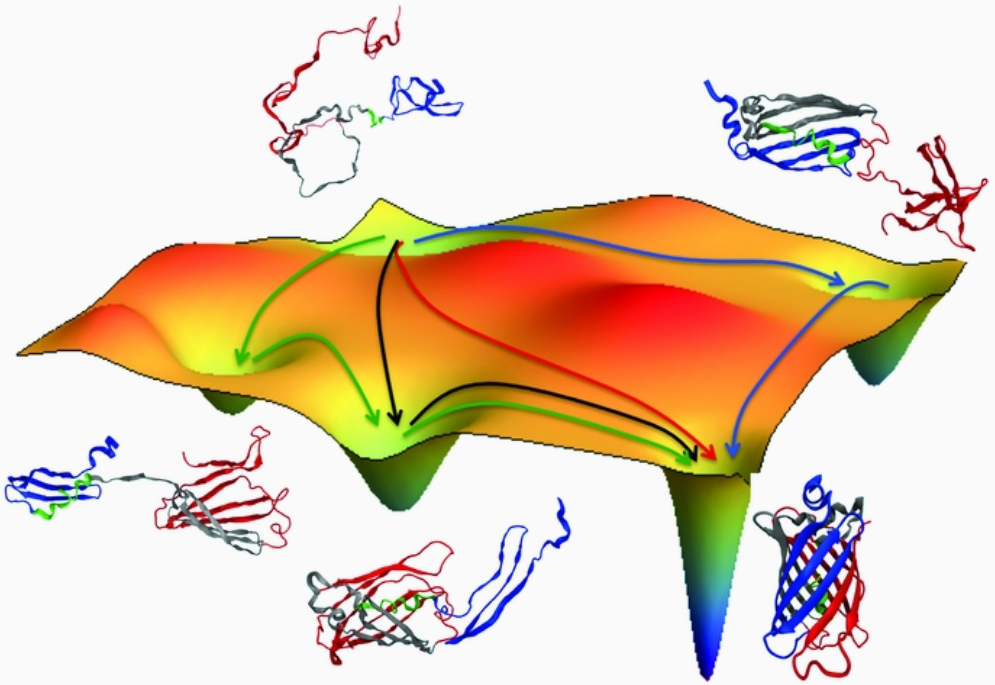
- Peptides are building blocks of protein
- Peptide conformations $\rightarrow$ protein folding
- How do we understand peptide conformations?



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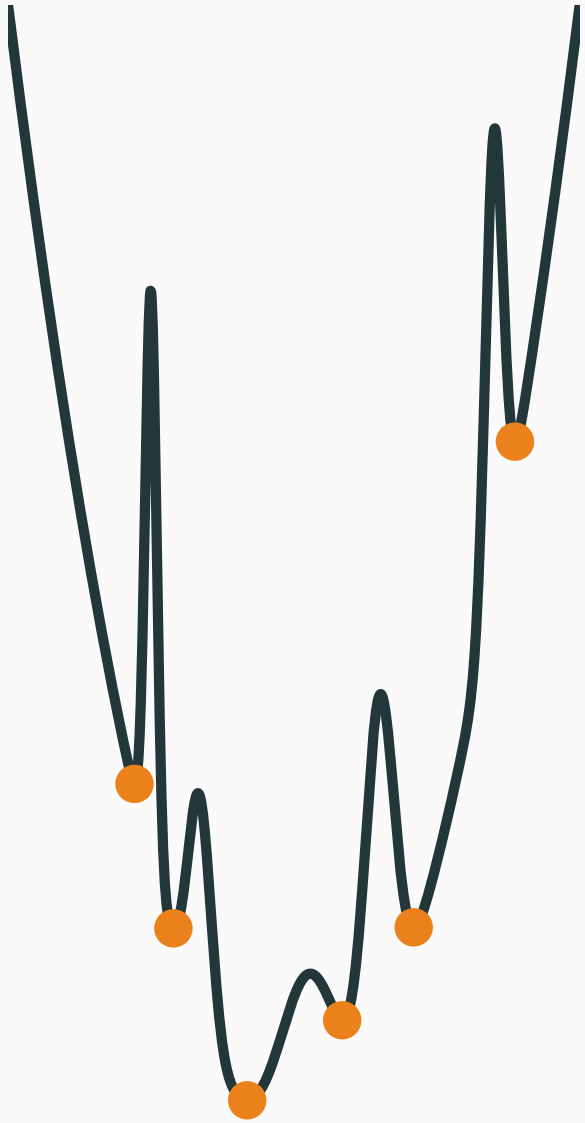

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Possible Solutions

- Many techniques are well established

Method	Implented in
grid-based	CEASAR, **Open Babel, Confab,** MacroModel, MOE
rule-based	**ALFA, CONFECT,** CORINA, ROTATE, **COSMOS**, OMEGA
population-based	**Balloon, Cyndi**
basin-hopping	**ASE, GMIN, TINKER SCAN**

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5. Parallel

The Genetic Algorithm

Outline

- At least 23 years

  Judson, R. S.; Jaeger, E. P.; Treasurywala, A. M.; Peterson, M. L. J. Comput. Chem. 1993, 14 (11), 14071414.

- Flexible ligand docking (Most cited: 7428)

  Morris, G. et al. J. Comput. Chem. 1998, 19 (14), 16391662.

- Precombustion CO_2 adsorbing MOFs (October 14^{th})

  Chung, Y. G.; Gomez-Gualdron, D. A.; Li, P.; Leperi, K. T.; Deria, P.; Zhang, H.; Vermeulen, N. A.; Stoddart, J. F.; You, F.; Hupp, J. T.; Farha, O. K.; Snurr, R. Q. Sci. Adv. 2016, 2 (10)

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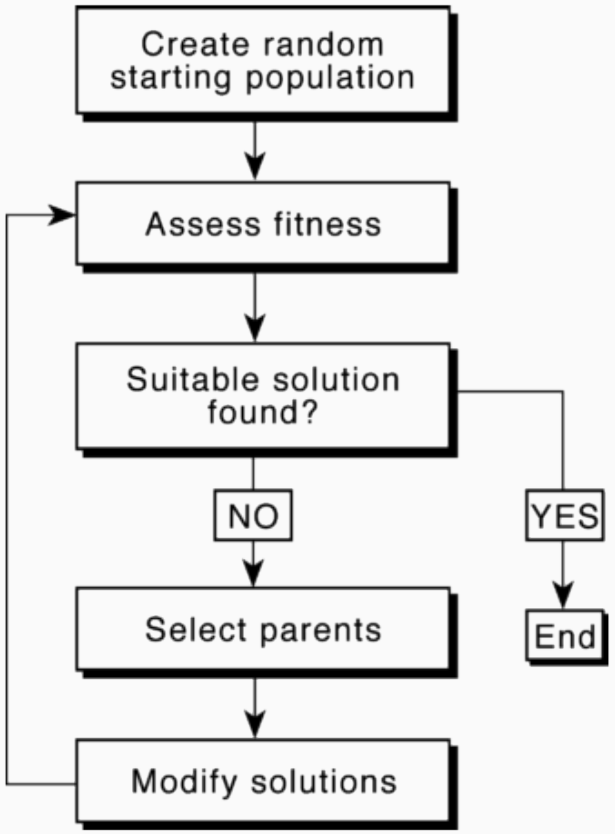
- Inspired by biological evolution



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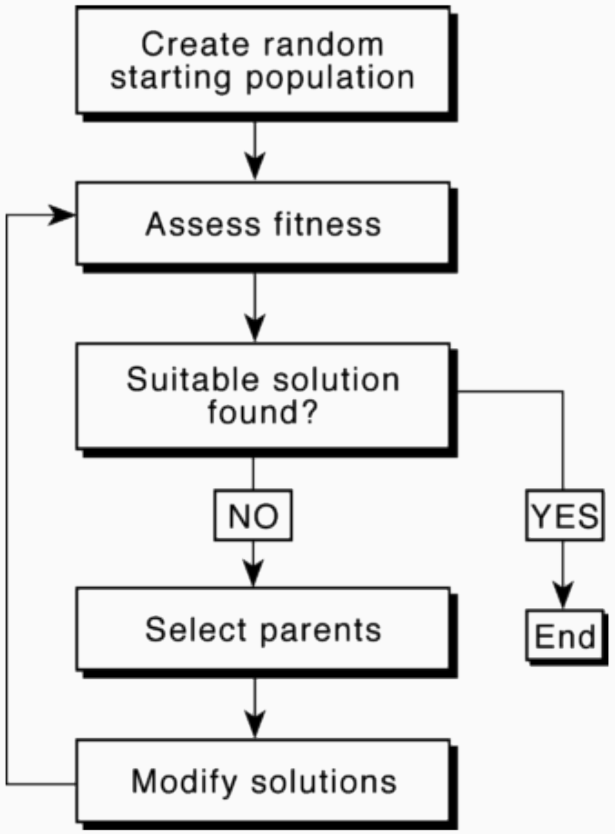

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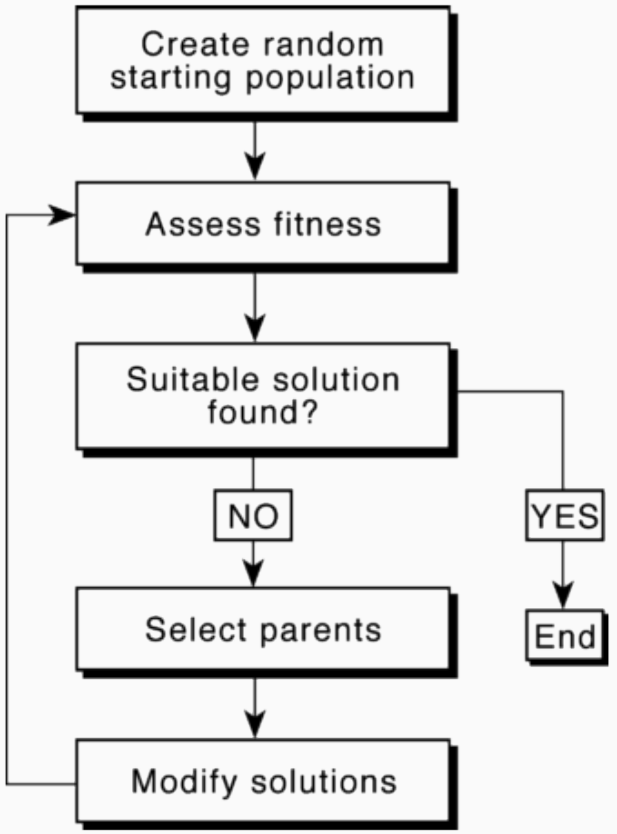

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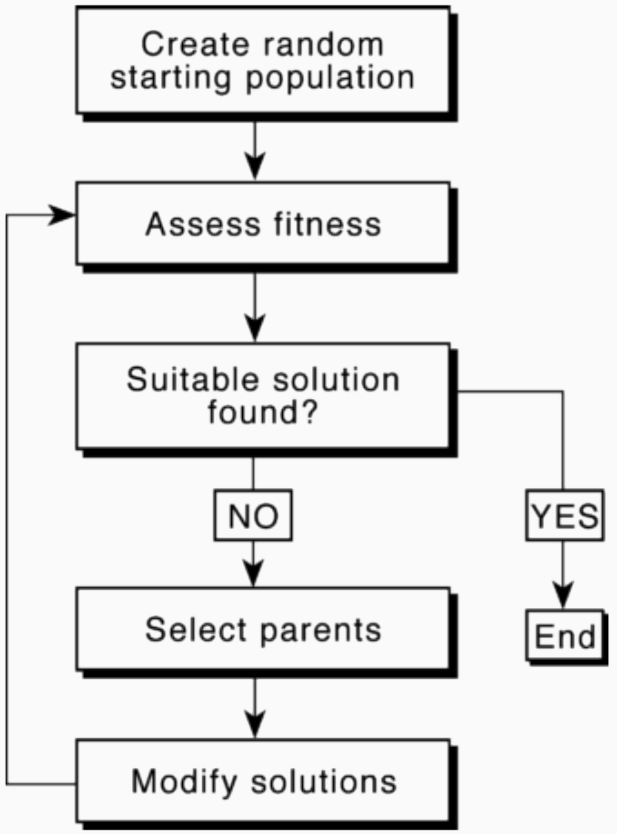

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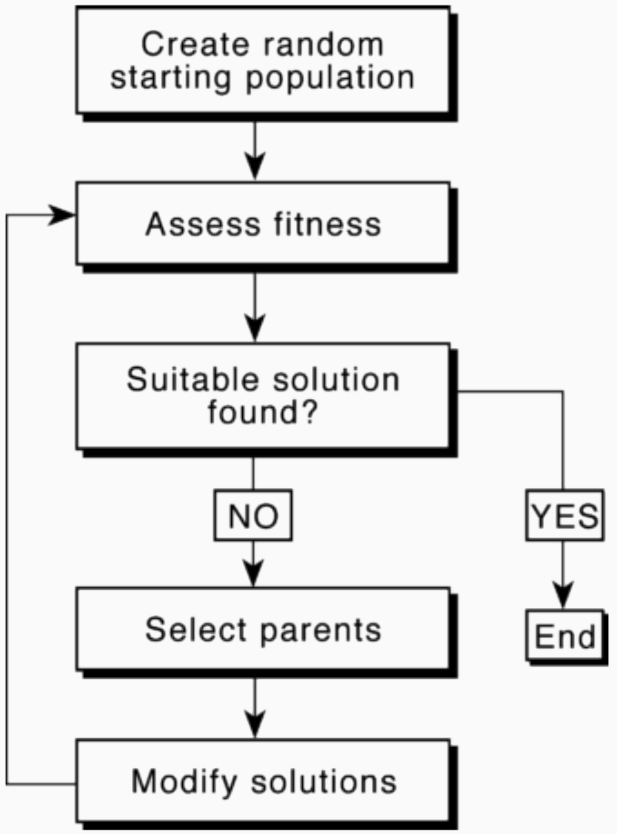

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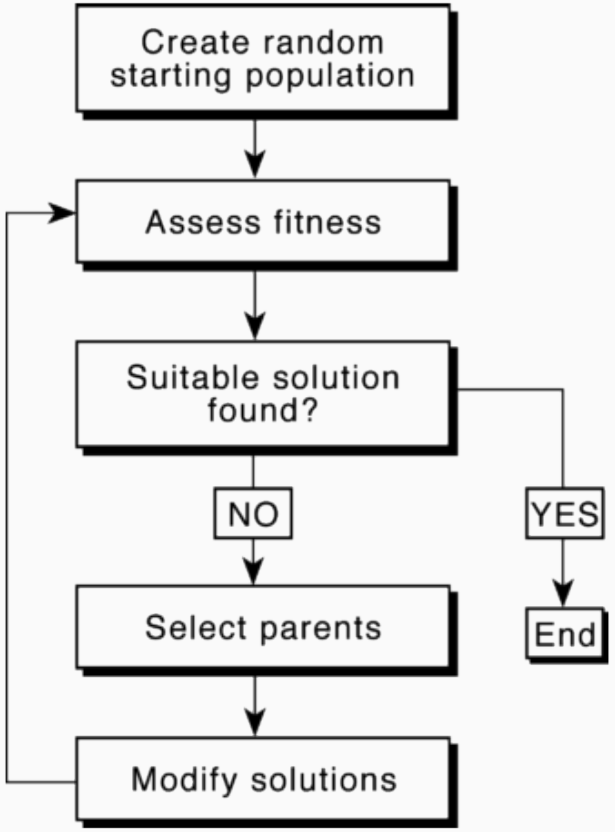

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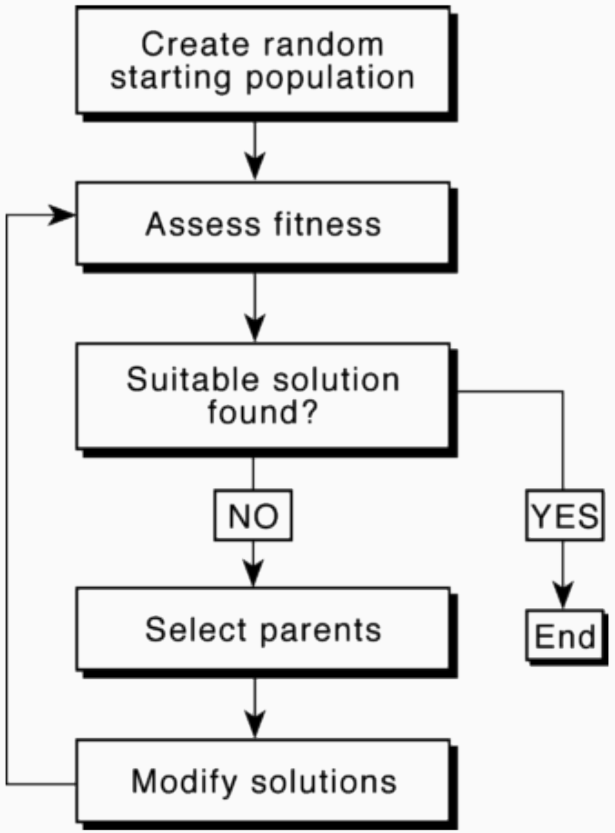

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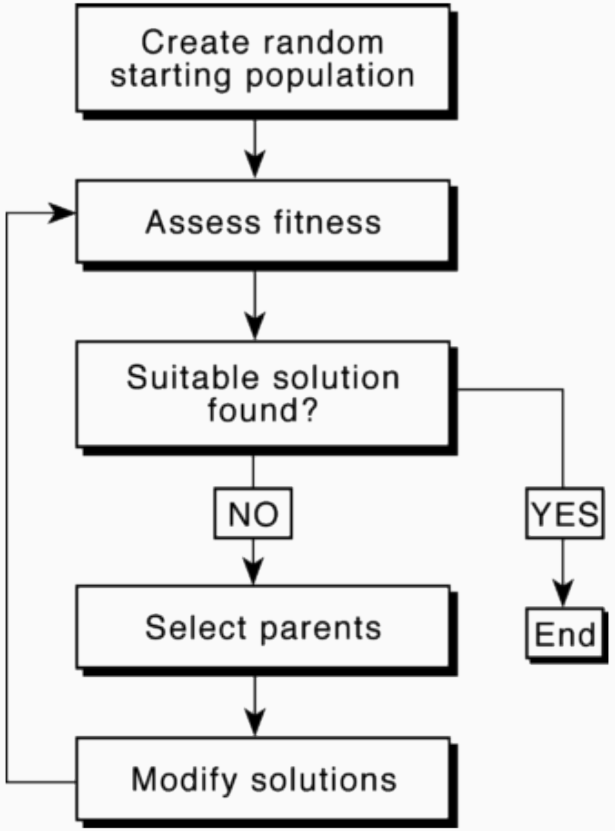

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The Many Representations of a Molecule

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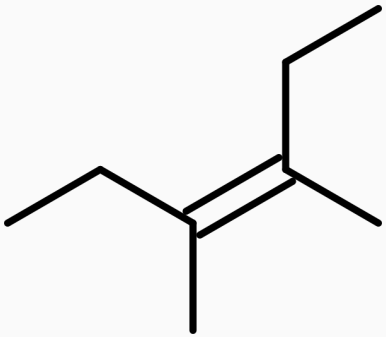

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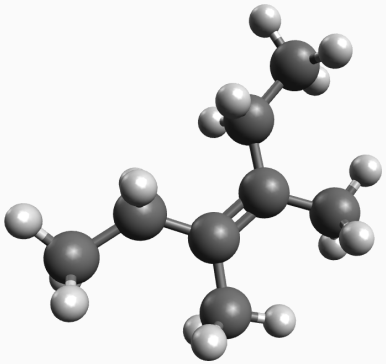

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SMILES

CCC(C)=C(C)CC

InChI

1S/C8H16/c1-5-7(3)8(4)6-2/h5-6H2,1-4H3/b8-7-

Cartesian Coords

	x	y	z
C	0.90	-0.25	0.02
C	2.35	0.15	-0.17
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Internal Coords

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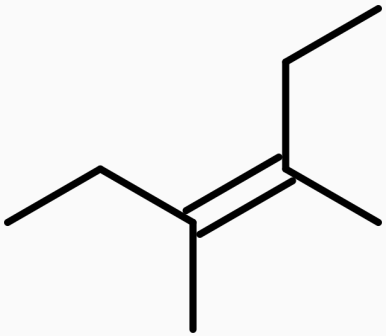

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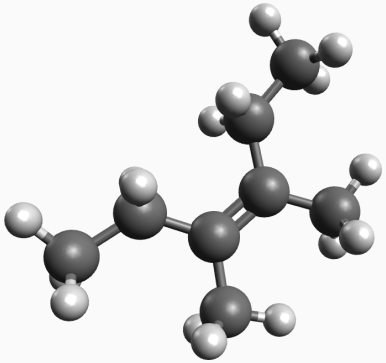

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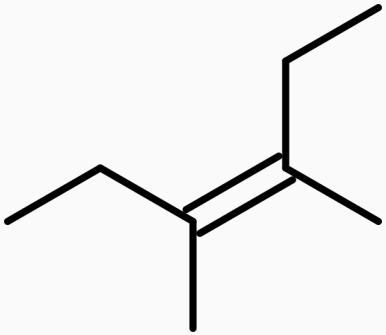

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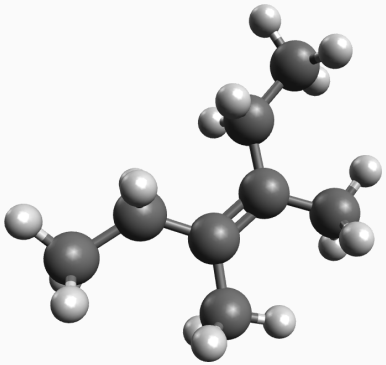

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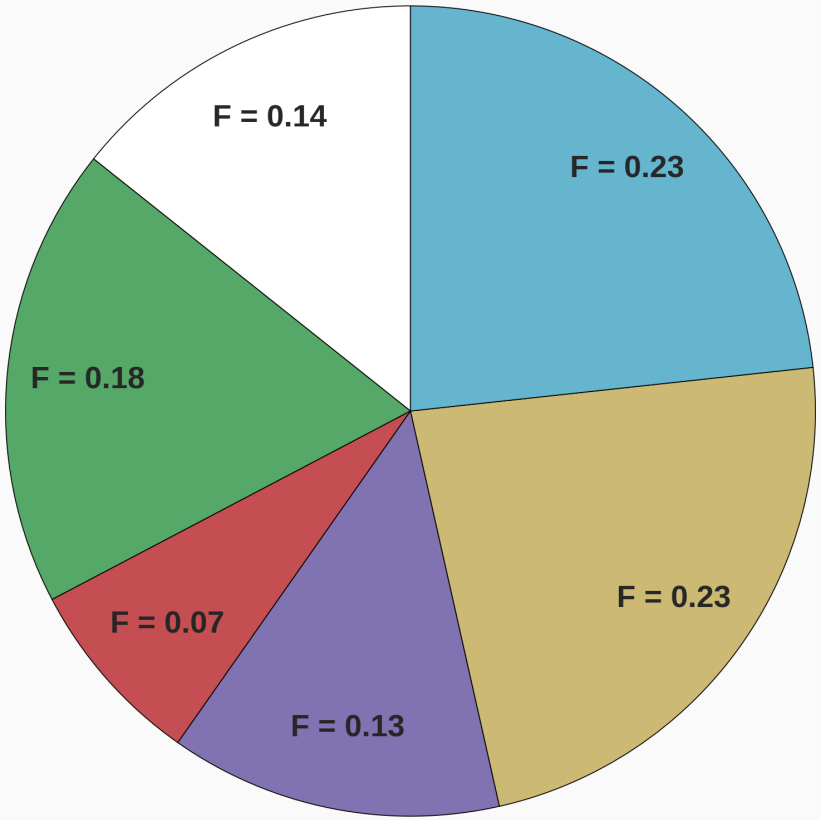

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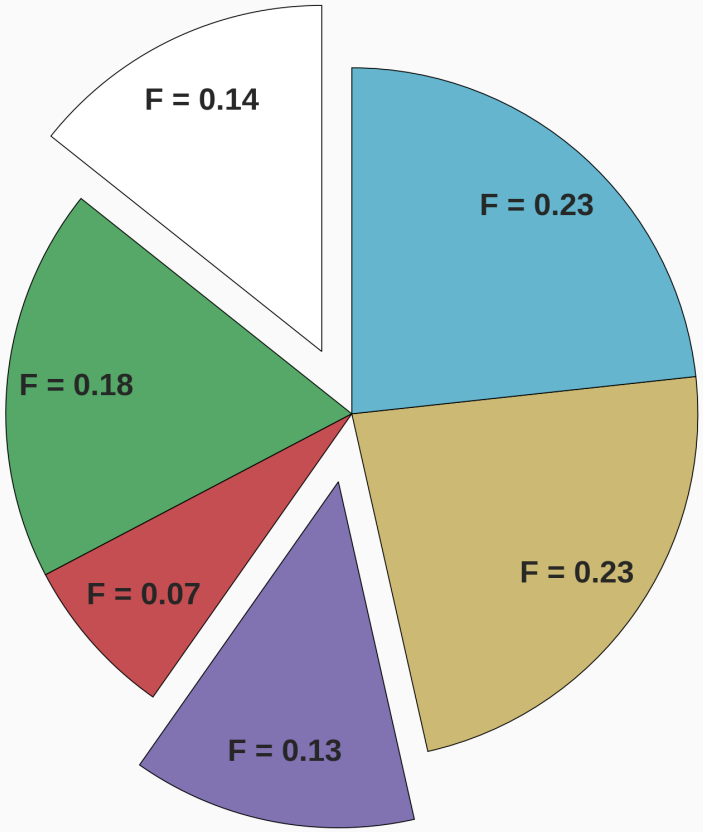
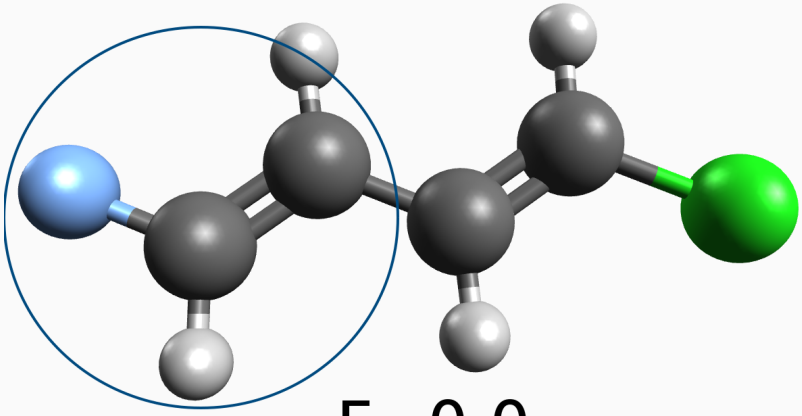


The Next Generation



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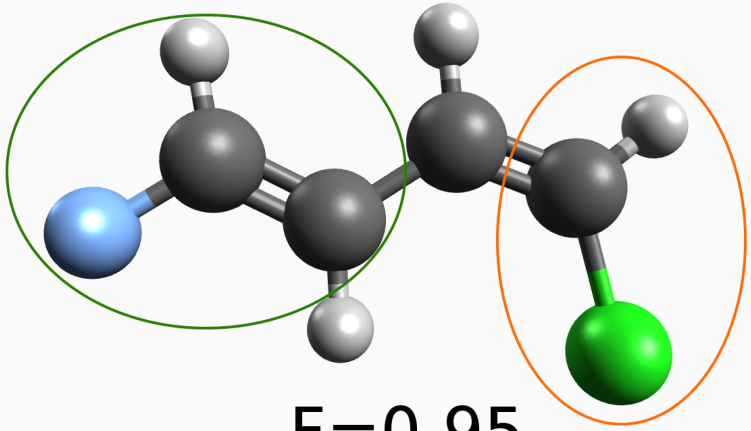

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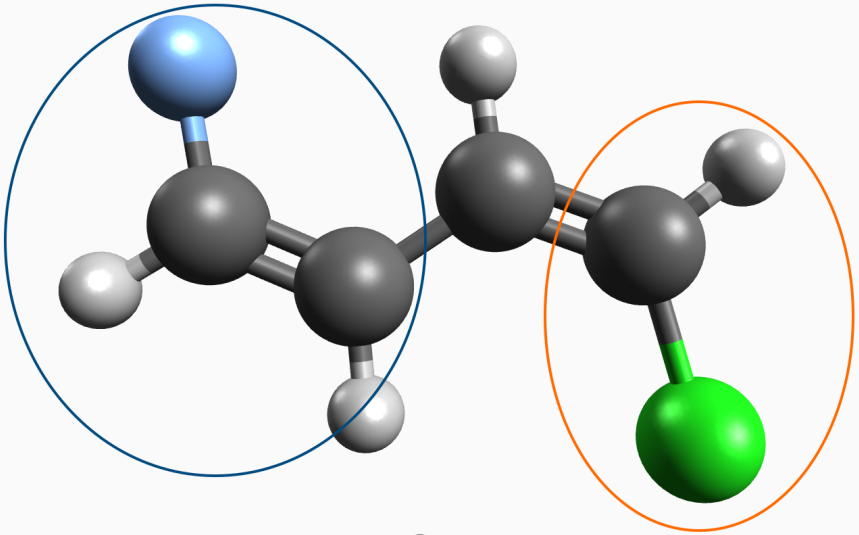

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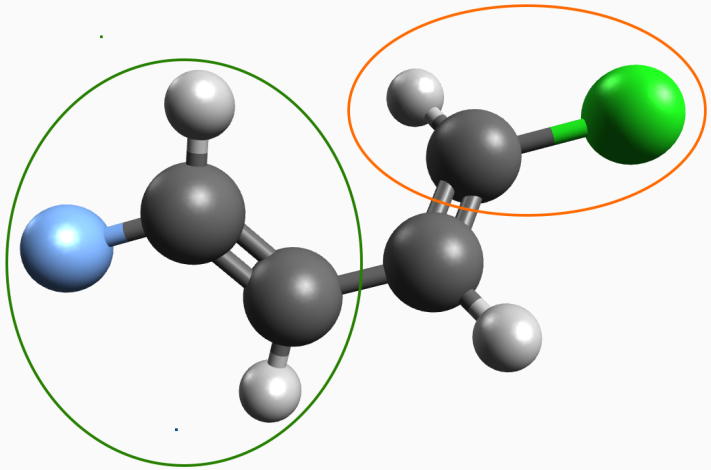

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The Whole Algorithm

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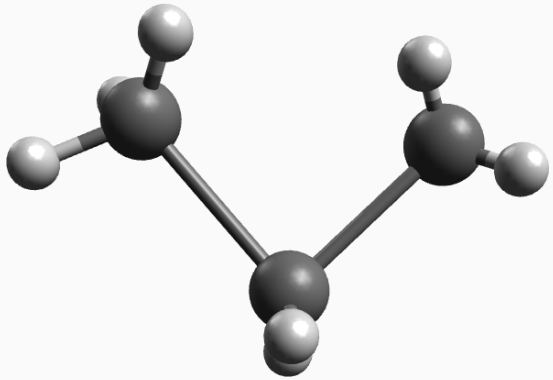

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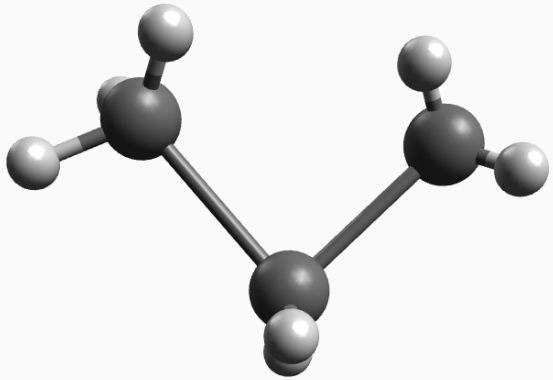

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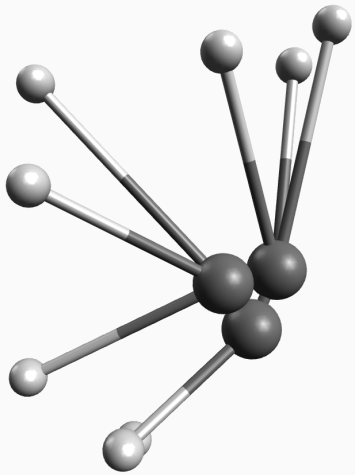

utter nonsense

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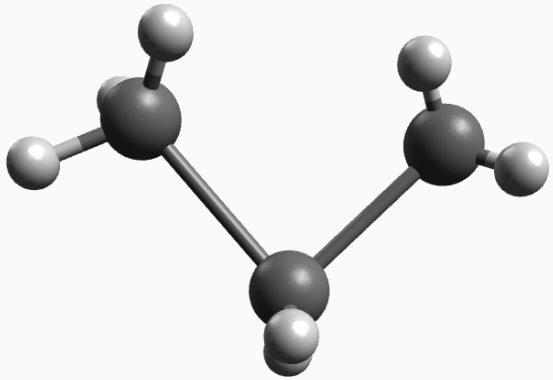

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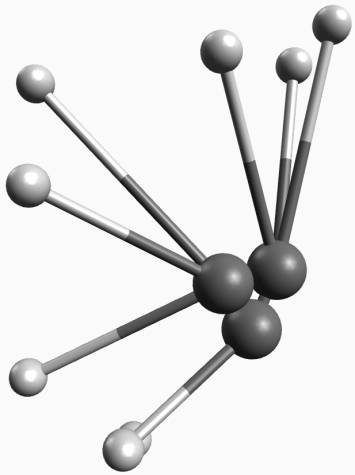

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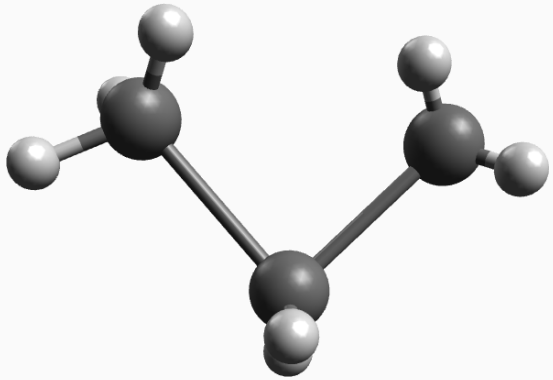
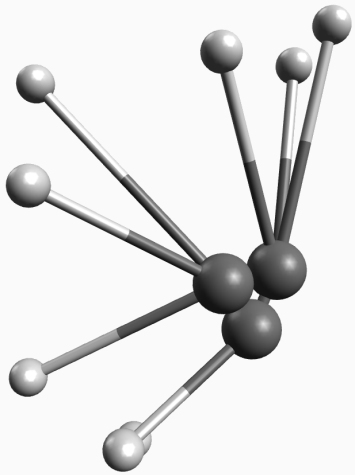
2. Optimize
3. Select Parents



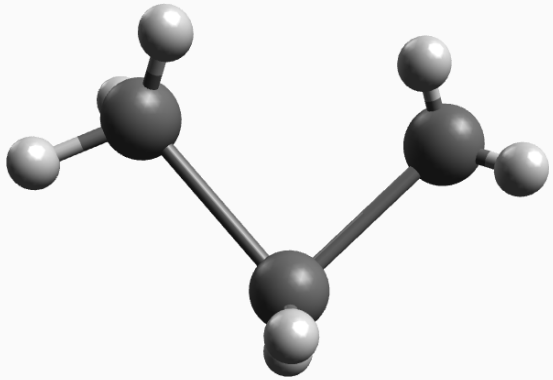
sensible



utter nonsense

The Whole Algorithm

1. Generate N random, sensible geometries
2. Optimize
3. Select Parents
4. Crossover & Mutate



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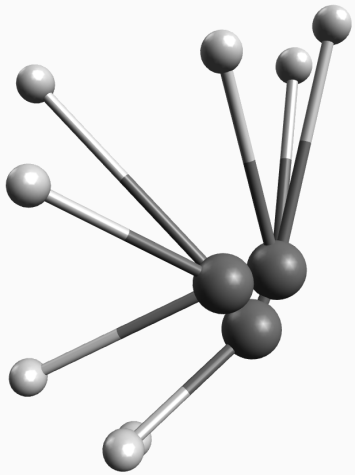

utter nonsense

The Whole Algorithm

1. Generate N random, sensible geometries
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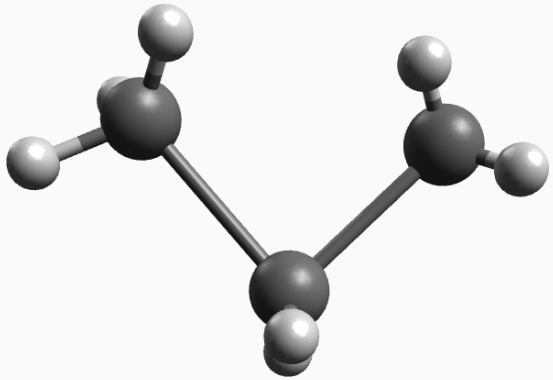
3. Select Parents
4. Crossover & Mutate
5. Add Children to population



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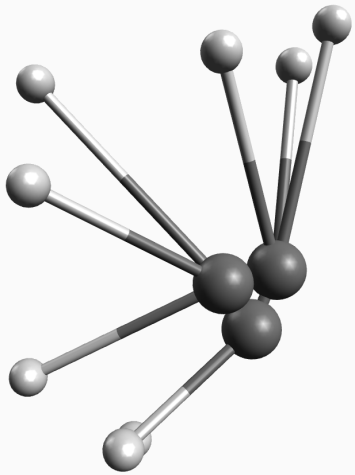
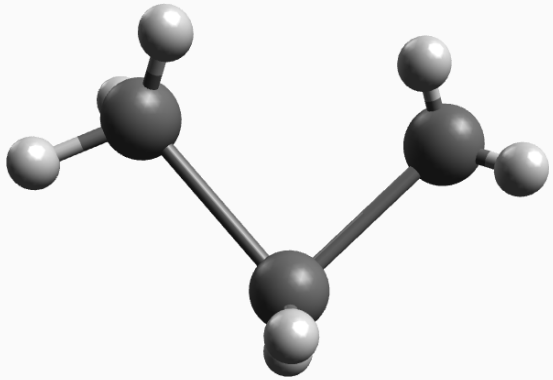


utter nonsense

The Whole Algorithm

1. Generate N random, sensible geometries
2. Optimize
3. Select Parents
4. Crossover & Mutate
5. Add Children to population
6. Remove the unfit



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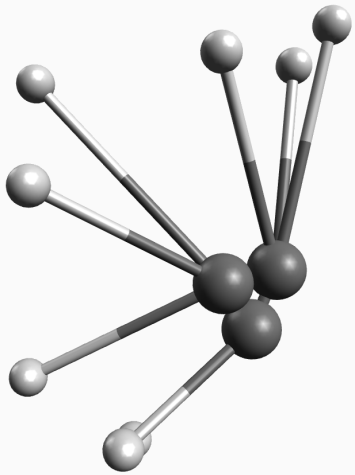
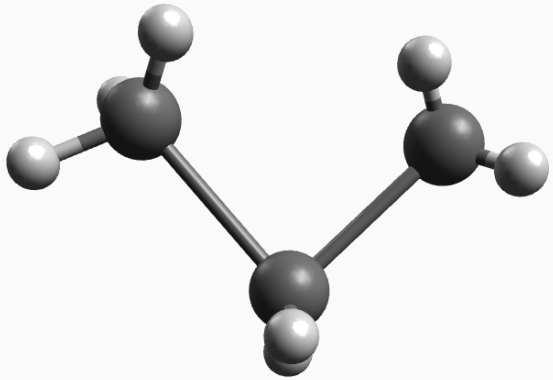


utter nonsense

The Whole Algorithm

1. Generate N random, sensible geometries
2. Optimize
3. Select Parents
4. Crossover & Mutate
5. Add Children to population
6. Remove the unfit
7. If converged:
    - Done!



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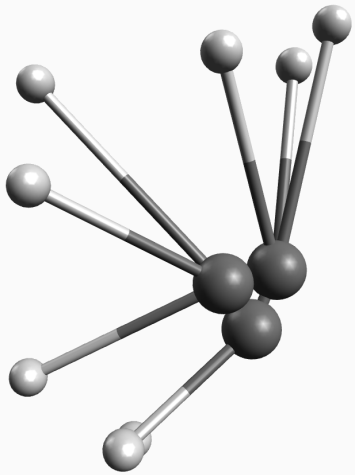
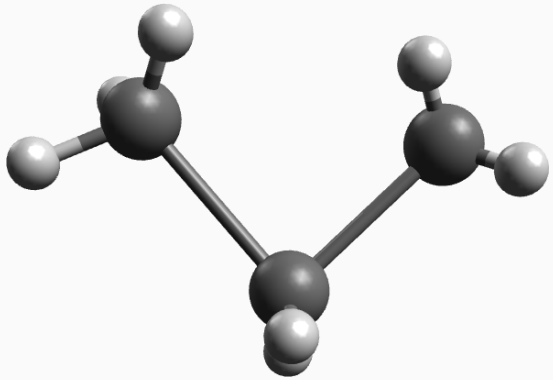


utter nonsense

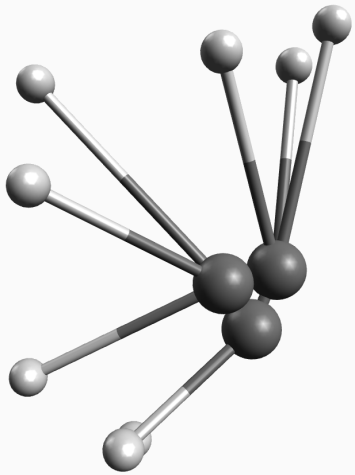
The Whole Algorithm

1. Generate N random, sensible geometries
2. Optimize
3. Select Parents
4. Crossover & Mutate
5. Add Children to population
6. Remove the unfit
7. If converged:
   - Done!

   Otherwise:
   - Go to 2



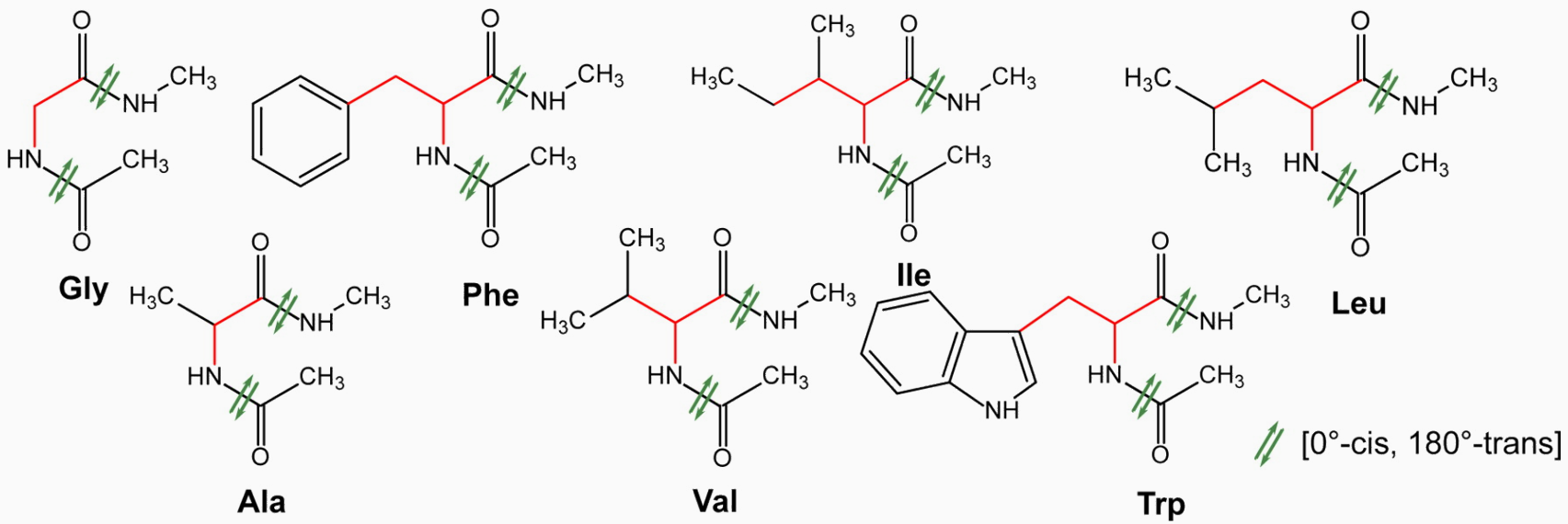
sensible



utter nonsense

Finding Low Energy Conformers of Dipeptides

"Dipeptide" Structures



Red = Rotatable bonds

⇌ = Cis/Trans Bonds

"We use the term dipeptide for amino acids with an acetylated N terminus and an amino-methylated C terminus"

Combinatorics

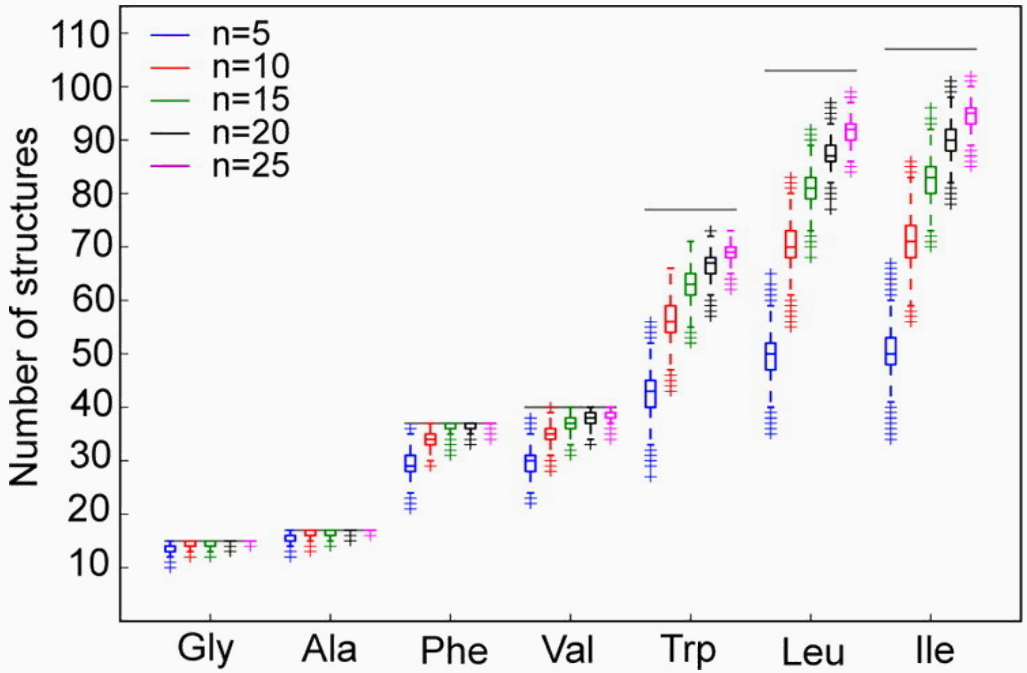
- GA beats other methods if space is large
- Space gets large **fast**

Molecule	N	# Rotatable + # Cis/Trans Bonds	# Conformers
Gly	19	2 + 2	15
Ala	22	2 + 2	28
Phe	32	4 + 2	64
Val	28	3 + 2	60
Trp	36	4 + 2	141
Leu	31	4 + 2	183
Ile	31	4 + 2	176

Supady, A.; Blum, V.; Baldauf, C. J. Chem. Inf. Model. 2015, 55 (11), 23382348.

Coverage

- Smaller systems are reliably sampled
- As # of conformers increases, miss more and more
- Is there a pattern to what is missed?

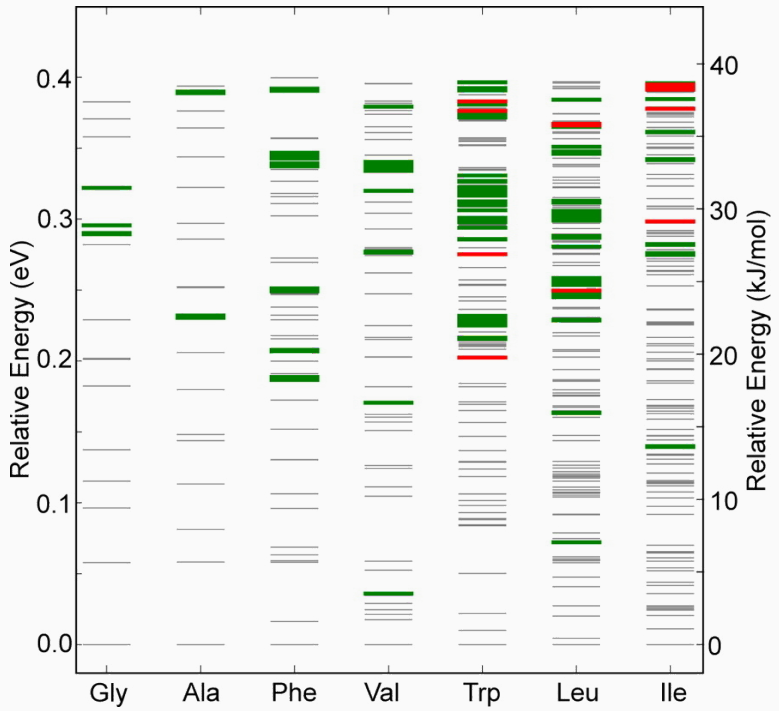


Proportion of conformers found with increasing runs of the GA

1) Supady, A.; Blum, V.; Baldauf, C. J. Chem. Inf. Model. 2015, 55 (11), 23382348.
2) Ropo, M.; Schneider, M.; Baldauf, C.; Blum, V. Sci. Data 2016, 3, 160009.

Coverage

- Most misses are very high energy



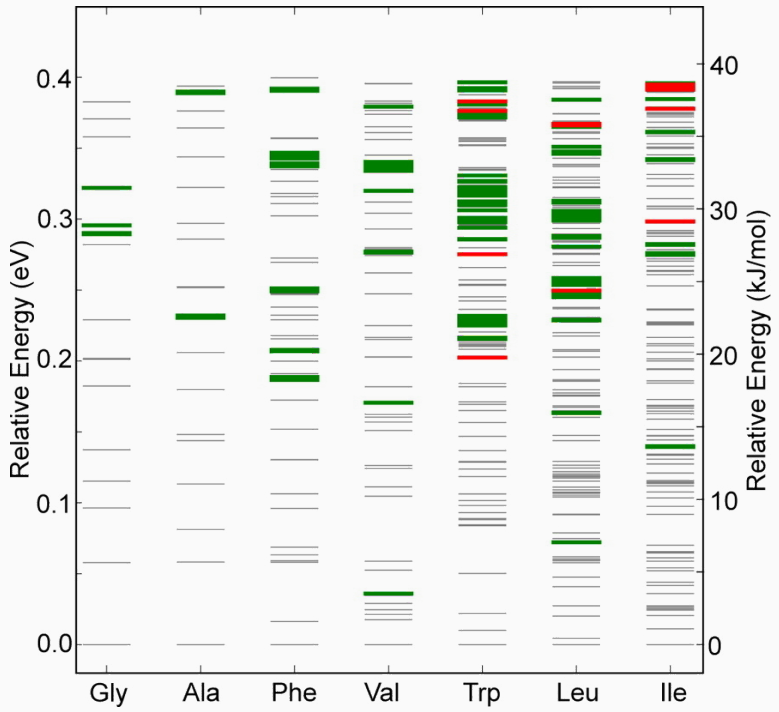
— Missed by the GA

— New Found by GA

— In Reference & GA

Coverage

- Most misses are very high energy
- Algorithm favors low energy areas of the space



— Missed by the GA

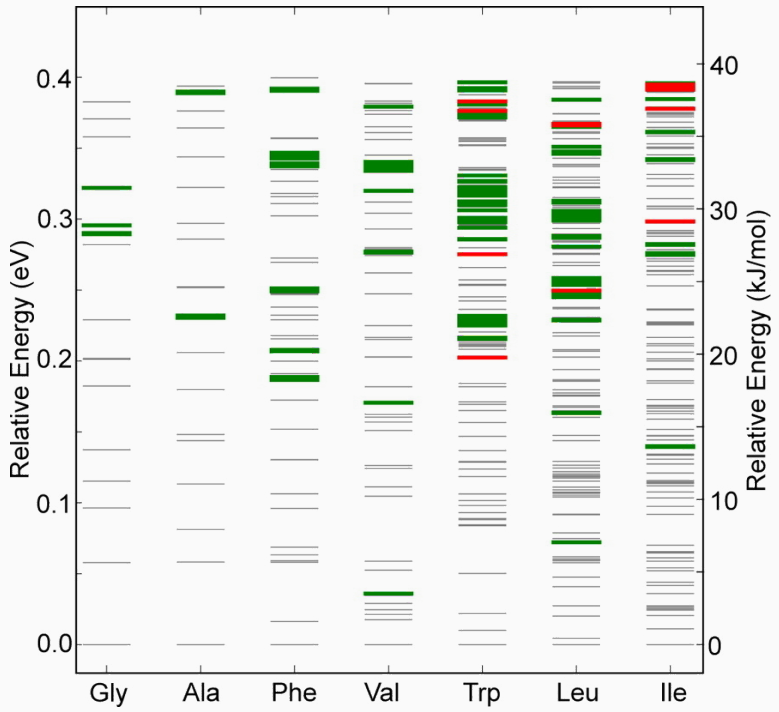
— New Found by GA

— In Reference & GA

Supady, A.; Blum, V.; Baldauf, C. J. Chem. Inf. Model. 2015, 55 (11), 23382348.

Coverage

- Most misses are very high energy
- Algorithm favors low energy areas of the space
- Features low in energy are favored and recombined



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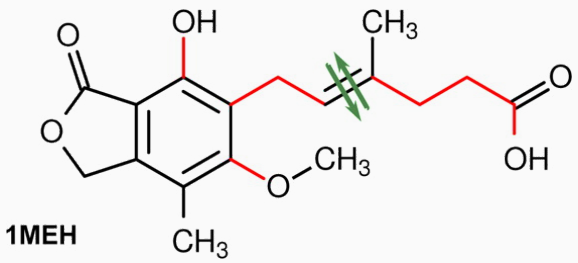
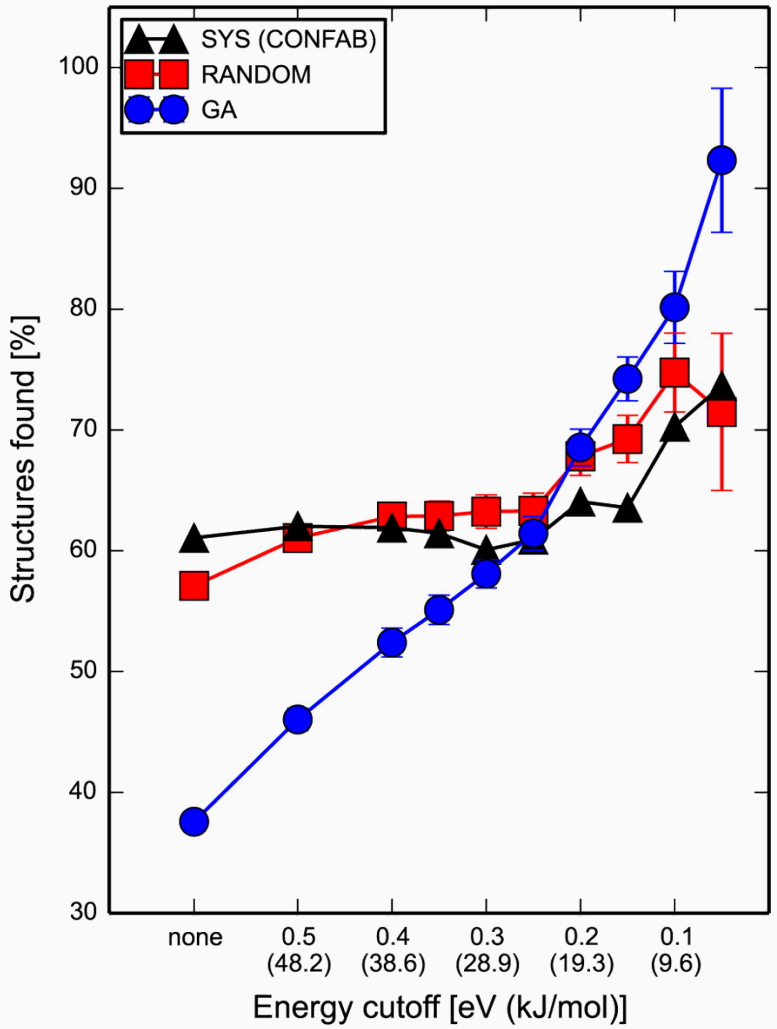
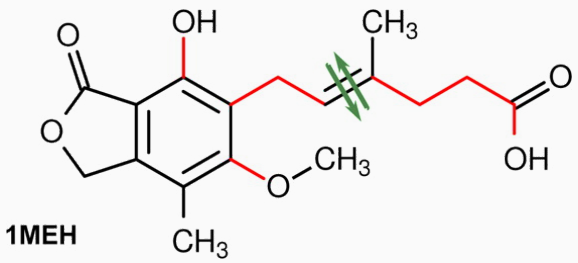
Energy Cutoff



Mycophenolic Acid

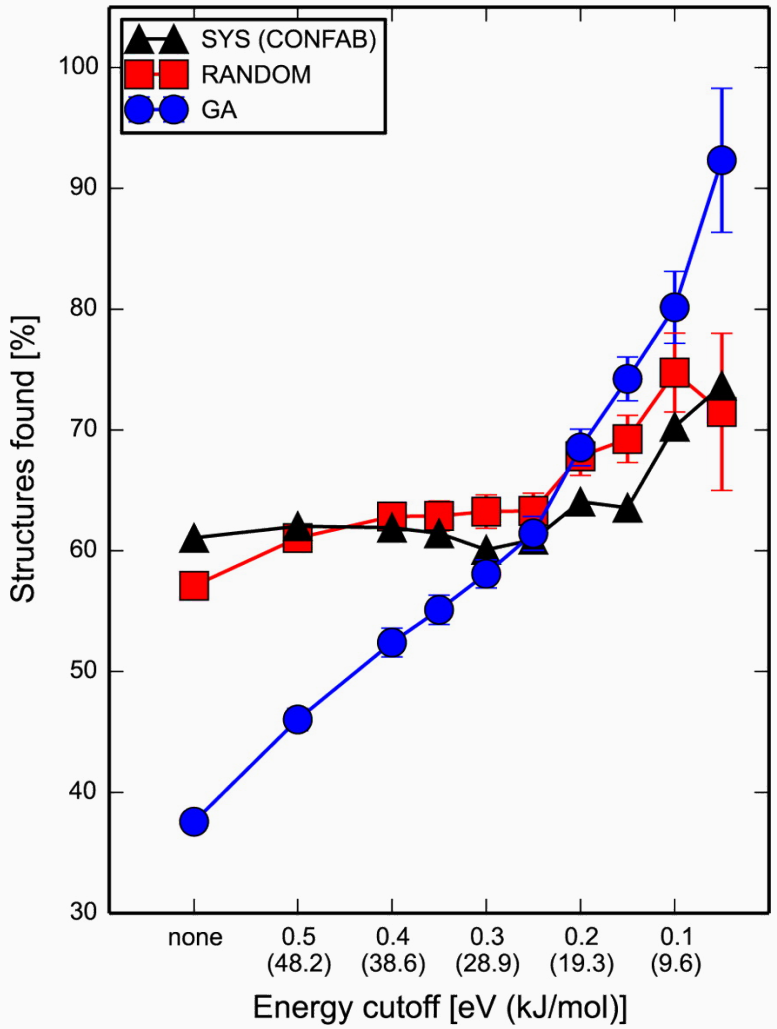


Energy Cutoff

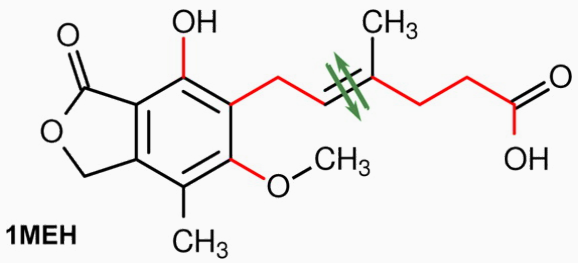


Mycophenolic Acid

- GA is more sensitive to energy cutoff

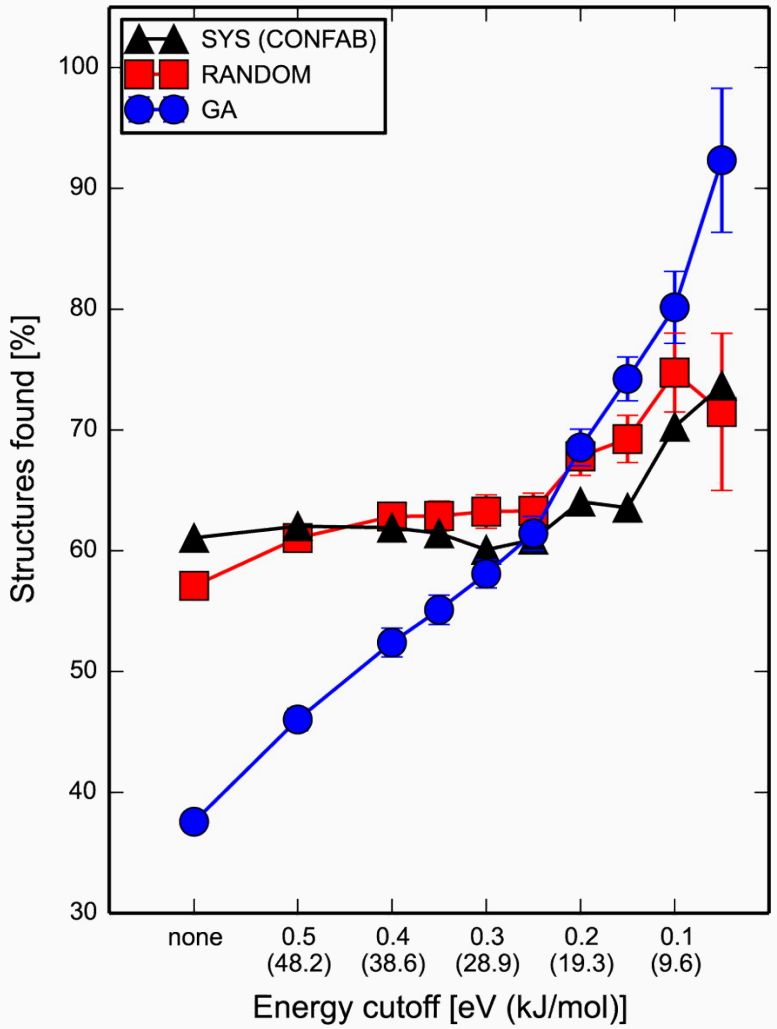


Energy Cutoff



Mycophenolic Acid

- GA is more sensitive to energy cutoff
- For finding low energy ensemble, GA outperforms purely stochastic/deterministic method



Supady, A.; Blum, V.; Baldauf, C. J. Chem. Inf. Model. 2015, 55 (11), 23382348.

Concluding Remarks

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Review

- Conformational searching is expensive

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- The Genetic Algorithm is a guided global search

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Review

- Conformational searching is expensive
- The Genetic Algorithm is a guided global search
- It shines when asked to find many low energy solutions
- GA can be used with any electronic structure package
- This one is available under the GNU Lesser General Public License: `https://github.com/adrianasupady/fafoom`

Questions?

Backup slide

- Geometry optimization step makes the algorithm more Lamarckian (Jean Baptiste Larmarck, [1744-1829])

Genetic Algorithm Parameters

Geometry Optimization: DFT PBE + VdW, *tier1* basis in FHI-aims[1].
Convergence at 0.005 eV /Å

	parameter	value
molecule	SMILES	CC(=O)N[C@H](C(=O)NC)[C@H](CC)C
	distance_cutoff_1	1.2 Å
	distance_cutoff_2	2.0 Å
	rmsd_cutoff_uniq	0.2 Å
	chiral	true
run settings	max_iter	10
	iter_limit_conv	10
	energy_diff_conv	0.001 eV
GA settings	popsize	5
	energy_var	0.001 eV
	selection	roulette wheel
	fitness_sum_limit	1.2
	prob_for_crossing	0.95
	cross_trial	20
	prob_for_mut_cistrans	0.5
	prob_for_mut_rot	0.5
	max_mutations_cistrans	1
	max_mutations_torsions	2
	mut_trial	100

GA Parameters for Isoleucine Dipeptide[2]

(1) Blum, V. et.'ál., M. Comput. Phys. Commun. 2009, 180 (11), 21752196.
(2) Supady, A.; Blum, V.; Baldauf, C. J. Chem. Inf. Model. 2015, 55 (11), 23382348.