Part 1

#### Advancing AND/OR Abstraction Sampling

#### Part 2

#### K\*-Based Computational Protein Design using AND/OR Search

Bobak Pezeshki's PhD Final Defense

(Advised by Prof. Rina Dechter and Prof. Alexander Ihler)







**Bobak Pezeshki**, Kalev Kask, Alex Ihler, and Rina Dechter. "Value-Based Abstraction Functions for Abstraction Sampling". *Proceedings of the 40th Conference on Uncertainty in Artificial Intelligence (UAI 2024).*



KALEV KASK, BOBAK PEZESHKI, FILJOR BROKA, ALEX IHLER, RINA DECHTER

### **Outline**

- **General Background**
- **Abstraction Sampling**
	- **General Scheme**
	- **AND/OR Abstraction Sampling**
		- **AOAS Algorithm**
		- **Analysis of its Properties**
	- **Abstraction Function Schemes**
		- **Context-based Abstraction Functions**
		- **Value-based Abstraction Functions**
		- **Completely Random Abstractions**
- **Empirical Evaluation**
- **Conclusion**

#### **Main Contributions**

#### **Abstraction Sampling**

- 
- **AND/OR Abstraction Sampling**
	- **AOAS Algorithm**
	- **Analysis of its Properties**
- **Abstraction Function Schemes**
	-
	- **Value-based Abstraction Functions**
	- **Completely Random Abstractions**

#### **Empirical Evaluation**

**Conclusion and Future Work**

# **Background**

#### **Graphical Models – Overview**



#### **Graphical Models – Formal Definition**

$$
\mathcal{M} = \{ \mathbf{X}_1, X_2, \dots, X_N \} \quad \leftarrow \text{Variables}
$$
\n
$$
\mathbf{D} = \{ D_{X_1}, D_{X_2}, \dots, D_{X_N} \} \leftarrow \text{Domain}
$$
\n
$$
\mathbf{F} = \{ f_{\alpha_1}, f_{\alpha_2}, \dots, f_{\alpha_N} \} \quad \leftarrow \text{Factors}
$$

**A combination operator** ⊗ **defines a global function.**

$$
p(A, B, C) \propto f_{AB}(A, B) \times f_{BC}(B, C)
$$
  
ex. 
$$
\otimes
$$
 = multiplication



 $f_{AB}(A,B),\quad f_{BC}(B,C)$ 

Example:  $A \mid B \mid f(A,B)$ 

 $A \in \{0, 1\}$ 

 $B \in \{0, 1\}$ 

 $C \in \{0, 1\}$ 

 $0 0 2$ 

 $0 \mid 1 \mid 4$ 

1 0 3

 $1 \mid 1 \mid 1$ 

Primal graph

#### **Tasks**



• **NP-hard:** exponentially many terms

Systematic Search



- Enumerate states
- Every stone turned
- No stone turned more than once

 $\overline{\mathbf{c}}$ 

 $\mathbf D$ 

A

 $\left( \mathsf{B}\right)$ 

Systematic Search



- Enumerate states
- Every stone turned
- No stone turned more than once

 $\overline{\mathbf{c}}$ 

 $\Omega$ 

A

 $\left( \mathsf{B}\right)$ 





 $A$ :  $Z \sim 90$  $B:$  $C:$  $\overline{\bigcirc}$  $\boxed{1}$  $\boxed{\mathbf{0}}$  $\overline{\mathbf{1}}$  $\boxed{1}$  $\boxed{0}$  $\overline{\bigcirc}$  $\overline{\mathbf{1}}$ D:  $\overline{0}$  $\mathbf{1}$  $\mathbf 0$  $\overline{\mathbf{0}}$  $|1|$  $w = 45$  $2*(45) = 90$ 

Importance Sampling

[Liu, 2001]

 $\left( \mathsf{B}\right)$ 

- Enumerate states
- Every stone turned
- No stone turned more than once

• Monte Carlo sampling method

 $\overline{\mathbf{c}}$ 

<sup>D</sup>

Systematic Search





Importance Sampling

- Enumerate states
- Every stone turned
- No stone turned more than once

• Monte Carlo sampling method

[J. Liu, Monte-Carlo strategies in scientific computing, Springer-Verlag, New York, 2001]

 $\overline{\mathbf{c}}$ 

<sup>D</sup>

 $\left( \mathsf{B}\right)$ 

#### **AND/OR Search Space**



**Compact search space taking advantage of conditional independencies**



### **Guiding Pseudo-Tree**



**Pseudo-Trees capture conditional independencies and guide the construction of the search space.**





g(A=0, B=1, C=2, D=1) =  $1 \times ((2) \times (1 \times 2)) = 4$ 





Stochastically select a value to assign the variable according to a proposal distribution, p.





Update importance weight according to  $w(n) = w/p(n)$ 







Stochastically assign value to variable according to proposal and update weights accordingly



Repeat until every variable is assigned a value (a *solution tree* is sampled) <sup>A</sup>





An estimate can be produced considering the cost associated with the sampled solution tree upweighted by the assigned importance weights.







### **Stratified [Importance] Sampling**

*[Knuth, 1975], [Chen, 1992], [Rizzo, 2007]*

Main idea: partially enumerate and partially sample search space

Steps:

- Subdivide space into set strata
- Enumerate strata choosing reweighted samples from each to form a probe
- Average estimates from sampled probes



### **Stratified [Importance] Sampling**

*[Knuth, 1975], [Chen, 1992], [Rizzo, 2007]*

Main idea: partially enumerate and partially sample search space

Steps:

- Subdivide space into set strata
- Enumerate strata choosing reweighted samples from each to form a probe
- Average estimates from sampled probes



#### **Interpolating Between Sampling and Search**



#### Importance Sampling



#### **Interpolating Between Sampling and Search**



**We can draw samples of multiple configurations to more closely resemble search.**



#### Sampling Search

#### **Interpolating Between Sampling and Search**

 $\mathbf{C}$  $\mathbf{B}$ D)

**We can draw samples of multiple configurations to more closely resemble search.**



## **Abstraction Sampling**



**A sampling scheme that enables the interpolating between sampling and search by performing abstractions level-by-level.**



#### **Original Work Set A Foundation…**

#### Main Questions 1:

- How to adapt to the more compact AND/OR spaces?
	- $\Box$  Should valid samples consist of only solution subtrees?
	- How to abstract across different branches of the AND/OR tree?

#### **Scalable AND/OR Abstraction Sampling (algorithm: AOAS)**

#### **AOAS**



**New AND/OR abstraction sampling scheme that allows for flexible abstractions while still ensuring formation of valid probes.**

#### Key Points:

- Allows for flexible abstractions
- Expands along a depth first traversal of the guiding pseudo tree
- $\Box$  Immediately performs recursive pruning of branches that cannot be part of valid configurations



#### **Proposal Distribution**

**A heuristic function h is used to estimate the value of unexplored subtrees.**

$$
p(n) \leftarrow \frac{w(n) \cdot g(n) \cdot h(n) \cdot r(n)}{\sum_{m \in A_i} w(m) \cdot g(m) \cdot h(m) \cdot r(m)}
$$

- $\Box$  *w(n)* captures the estimated weight of subtrees absorbed by the *n*'s ancestors during abstraction
- *g(n)* is the path cost from the root to *n*
- $\Box$  *h(n)* is the estimated mass of the subtree *n* roots
- *r(n)* is the estimated ancestor branching mass of *n*



B

 $r(n)$ 

 $n$ "

 $w(n)$ 

N

 $h(n)$ 

 $g(n)$ 

#### **Properties (Unbiasedness)**

- □ Proof-Strategy
	- Key observation: at each step in the algorithm, either
		- The probe is expanded
		- An abstraction occurs
		- **Pruning occurs**



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- □ Proof-Strategy
	- Key observation: at each step in the algorithm, either
		- The probe is expanded
		- An abstraction occurs
		- **Pruning occurs**
	- Main Idea:
		- Construct an estimator that equals
			- the exact Z value for the unexpanded probe *(base case)*
			- the value of AOAS's estimator for the final probe
			- needs to include consideration of different branchings in the tree
			- can be computed by analyzing the frontier nodes of a single variable
		- Show that, at each step, the expectation of the estimator remains unchanged



#### **Properties (Unbiasedness)**

#### Illuminating characteristics

- Works for any valid importance sampling proposal distribution
- Generalizes to BF expansion of the pseudo-tree
- Generalizes to algorithms that allow non-solution trees as samples



#### **Properties (Complexity)**




## **Properties (Complexity)**



R

M

| 0

 $|0|$ 

 $\boxed{0}$ 

 $|0|$  $|1|$ 

 $\vert 1 \vert$ 

 $\vert$ 1

 $|1|$ 



## **Properties (Complexity)**





### **Other Properties (see Thesis)**

Conditions for exact AOAS estimates Proposal-based conditions Abstraction-based conditions

## **Original Work Set A Foundation…**

Main Questions 2:

 $\Box$  How to construct powerful abstraction functions?

### **Abstraction Function Schemes**

### **What did the previous abstraction schemes capture?**



### **Context-Based Schemes:**

RelCB and RandCB only estimate similarity of this piece and based only on graph structure

### **Value-Based Abstraction Functions - Intuition**



- Use relevant quantities to assign a values to nodes
- Use those values to guide abstractions

### **Value-Based Abstraction Functions - Classes**



Potential Candidates:

HB:  $\mu(n) = h(n)$ 

```
HRB: \mu(n) = h(n) r(n)
```
QB:  $\mu(n) = w(n) g(n) h(n) r(n)$ 

### **Value-Based Abstraction Functions - Classes**



Potential Candidates:

HB:  $\mu(n) = h(n)$ 

HRB: 
$$
\mu(n) = h(n) r(n)
$$

 $QE:  $\mu(n) = w(n) g(n) h(n) r(n)$$ 

*(best performing)*

### **Value-Based Abstraction Functions - Partitioning Intuition**

- **□** Simple and fast
- $\Box$  Group similar nodes together Minimize with-in variance of abstract states
- $\Box$  Form abstract states of roughly equal mass *[Rizzo, 2007]*



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### **Purely Random Abstractions**



# **Empirical Evaluation**

- Performance of Abstraction Sampling comparing against existing schemes?
- Does sampling over the AND/OR space provide benefits?
- What abstraction functions empower Abstraction Sampling most?

## **Setup**

- $\Box$  Problems (480+)
	- DBN, Grids, Linkage-Type4, Pedigree, Promedas
- **Abstraction Sampling Algorithms** 
	- **Q** Sampling Schemes:
		- ORAS, proper-restricted-AOAS (pAOAS), **AOAS**
	- **Q** Abstraction Functions:
		- Context-Based, Value-Based, and Purely Random abstractions
		- Varying granularities
	- **Heuristic:** 
		- Weighted Mini-Bucket Elimination (wMBE) [Liu, Ihler, 2012]
- $\Box$  Competing Algorithms ■ IS, DIS [WMB-IS, IJGP-SS] [Liu, Fisher III, Ihler, 2015]
- **Q** Questions
- [Lou, Dechter, Ihler, 2019]
- Quality of estimates, Scalability of Abstraction Functions

### **Plots**

#### grid80x80.f10.wrap

Graph Type: MARKOV, N: 6400, cliques: 19200, K(min): 2, K(max): 2, K(avg): 2.0, Scope Size (max): 2, Fxn Size (max): 4



**#p**: number of probes

**#n/p**: number of nodes per probe

**est. error**:  $log_{10}Z$  error w.r.t. the reference value

## **Aggregation Tables**

**Bmk**: benchmark name

- **Sz**: difficulty of subset of problems {small, LARGE}
- **Graph Scheme**: Abstraction Sampling search scheme
- **Abs**: granularity of abstraction function
- **n\***: number of problems solved
- **log(err)**: average log<sub>10</sub> Z error
- **error distr.**: count of problems solved within an error threshold
- **#probes**: average number of probes

**#nodes/probe**: average number of nodes per probe



 $[$ [Lou et al., 2019]















### **Comparison of Abstraction Granularity**



### **Comparison of Abstraction Granularity**



### **Comparison of Abstraction Granularity**



## **AS Comparison Chart**



### **Value-Based Abstraction Functions - Best Scheme**

### Score >  $1.0 \Rightarrow$  better than context-based



# **Conclusion**

*AND/OR Abstraction Sampling via AOAS is an efficient effective stratified sampling method for solving summation tasks and can be empowered by use of several of the newly proposed abstraction functions.*

# **End Part 1**

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# **K\*-Based Computational Protein**

### Bobak Pezeshki, Radio Varmesco, Atex Illet and Rina Dechter. AND VOR Branch fand. Boemd for componition and rendering *TPM 2022 Best Paper Award*

**Bobak Pezeshki**, Radu Marinescu, Alex Ihler, and Rina Dechter. "Boosting AND/OR-Based Computational Protein Design: Dynamic Heuristics and Generalizable UFO". *Proceedings of the 39th Conference on Uncertainty in Artificial Intelligence (UAI 2023).*


#### **Special thanks to…**



THOMAS SCHIEX

#### **Special thanks to…**



## **Outline**

- **Background: Computational Protein Design (CPD)**
- **K\*MAP using AND/OR Search**
	- **Problem Formulation**
	- **AOBB-K\* (using wMBE-K\*)**
	- **Scalability Improvements**
- **Empirical Evaluation**
- **Conclusion and Future Work**

#### **Contributions**

**Background: Computational Protein Design (CPD)**

#### **K\*MAP using AND/OR Search**

- **Problem Formulation**
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- **Scalability Improvements**

#### **Empirical Evaluation**

**Conclusion and Future Work**

# **Background**

## **Computational Protein Design (CPD)**

[Re]design proteins to perform desired biological functions.

CPD often manifests as an optimization problem:

*Ex. find the optimal composition that maximizes binding between* 

*subunits.*





## **Computational Protein Design**



**Primary Protein Structure** Sequence of a chain of amino acids

**Secondary Protein Structure** Local folding of the polypeptide chain into helices or sheets

**Tertiary Protein Structure** three-dimensional folding pattern of a protein due to side chain interactions

**Quaternary Protein Structure** protein consisting of more than one amino acid chain

## **Computational Protein Design**

Cannot be made by the human body



## **Computational Protein Design**

Amino Acid Rotamers: Select conformational isomers of an amino acid





Peter Carlsson, Konrad F. Koehler, and Lennart Nilsson Molecular Endocrinology 19(8):1960–1977. https://doi.org/10.1210/me.2004-0203

#### **Proteins are Dynamic Structures**

A protein's structural state is probabilistic

Proteins continuously transition between various energetically favorable conformation.



#### **Partition Function**

Partition Function (Z) Normalizes the Likelihood of the Protein In A Particular Conformational State

$$
Z(r) = \sum_{c \in C(r)} \exp\{-E(c)/RT\}
$$



r = amino acid assignments to the residues

C(r) = possible rotamer conformations given a.a. sequence r

 $E(c)$  = energy given conformation c

 $R =$  universal gas constant (for unit conversion between kJ and K)

T = absolute temperature (Kelvin)

#### K<sup>\*</sup> Objective [Ojewole et al., 2018, Hill, 1987, Mc-Quarrie, 2000]

#### K\* approximate Ka, the affinity equilibrium constant

$$
K^*(r) = \frac{Z_{complex}(r)}{Z_{subunit 1}(r) Z_{subunit 2}(r)}
$$

Note that K\* not only considers the "goodness" of the bonded state (PL),

but also weighs it relative to the "goodness" of the unbound (dissociate) states



## **K\* Objective**

$$
K^*MAP = \max_R K^*(r)
$$



ie. Find the sequence with the greatest  $K^* \sim Ka$ 





- A\*-like algorithm for designing proteins to improve binding
- Our objective: solve the same problem with algorithms that offer something more
	- New heuristic
	- Capture independences
	- Sampling

## **Task Difficulty**

$$
K^*(r) = \frac{Z_{complex}(r)}{Z_{subunit 1}(r) Z_{subunit 2}(r)}
$$



# **Marginal MAP (MMAP)**

State-of-the-art search and sampling algorithms

State-of-the-art Marginal MAP (MMAP) algorithms [Marinescu, Lee, Dechter, Ihler, 2018] Learning Depth-First AND/OR Search [Marinescu, Dechter, Ihler, 2018] Stochastic Best-First AND/OR Search [Marinescu, Dechter, Ihler, 2018] Recursive Best-First AND/OR Search [Marinescu, Dechter, Ihler, Kishimoto, Botea, 2018]

State-of-the-art sampling algorithms

Dynamic Importance Sampling [Liu, Dechter, Ihler, 2017]

Abstraction Sampling [Kask, Pezeshki, Broka, Ihler, Dechter, 2020]

# **K\*MAP using AND/OR Search**

# **Problem Formulation**

#### **Two Formulations**





 $\mathcal{C}_{n}$ 3

 $\bigcirc$ 



 $\circledR$ 

⊛

G9)

**F2**

 $\mathbb{C}$ 

 $\mathcal{C}$  2

**F1**

#### **Two Formulations**





**F1**

**F2**



Due to interactions when dissociated







 $\mathsf{P}$ 



#### **Problem Formulation: Assumptions**

**Select Residues:** Model using only a subset of the residues.

**Discrete Rotamers:** Use discrete side-chain conformations.

**Fixed Backbone:** Fix the position of the residues in space.

#### **Problem Formulation: Variables and Domains**

```
R = \{ R_i \mid i \in \{1, 2, ..., N\} \}
```
- Residues considered for mutation
	- ie. variables we maximize over
- Domain = possible amino acids



#### **Problem Formulation: Variables and Domains**

$$
C_X = \{ C_{X(i)} \mid i \in \{1, 2, ..., N\} \}
$$

- Side-chain rotamers of the residues
	- Two for each  $R_i$ , one capturing the rotamers of the bound and the other for the unbound states
- Domain = discretized amino acid rotamers

 $X \in \{Bound, Dissocial\}$ 



#### **Problem Formulation: Functions**

 **Interaction energies** between amino acid side chain rotamers

 **Constraints enforcing consistent assignments** between corresponding residue and conformation variables



# $K^*MAP$   $V \in \{Bound, Dissociate\}$

let... 
$$
Z_{\gamma}(\boldsymbol{r}) = \sum_{\boldsymbol{C}_{\gamma}} \prod_{\mathscr{C}_{\gamma}} \mathscr{C}_{\gamma(i)}(r_i, c_{\gamma(i)}) \cdot \prod_{\boldsymbol{E}_{\gamma}} e^{-\frac{E_{\gamma(ij)}(c_{\gamma(i)}, c_{\gamma(j)})}{\mathscr{R}T}}
$$

$$
\text{objective:} \qquad K^*(R) = \frac{Z_B(R)}{Z_U(R)}
$$

$$
\text{Task:} \qquad K^*\text{MAP} = \max_{\boldsymbol{R}} K^*(\boldsymbol{r})
$$

# **AOBB-K\***

*Based on AOBB-MMAP [Marinescu, Dechter, Ihler, 2014]*

#### **AOBB-K\***

- **Branch-and-bound** over **AND/OR** search space
- Uses **wMBE-based heuristics** to guide search and prune suboptimal paths
- Uses **encodes determinism** and uses Mini SAT to **prune inconsistent paths**
- Enforces **biologically-relevant stability constraints**
- **Exact**



## **wMBE Heuristic for MMAP**

Mini-bucket elimination [Dechter & Rish 2001]



- Weighted Mini-bucket [Liu & Ihler, 2012]
	- Holder's inequality



$$
\sum_{x}^{w} f(x) \triangleq \left[\sum_{x} f(x)^{\frac{1}{w}}\right]^{w} \qquad w = \sum_{r} w_{r}
$$

$$
\sum_{E} [\psi(A, E)\psi(C, E)] \leq [\sum_{E} \psi(A, E)][\sum_{E} \psi(C, E)]
$$



#### **AOBB-K\***

**Branch-and-bound** over **AND/OR** search space

Uses **wMBE-based heuristics** to guide search and prune suboptimal paths

#### Uses **encodes determinism and uses of property** in the property of the property of the paths of the paths of the paths **Performed well on small problems, Exact** but did not scale well



# **Scalability Improvements**

#### List of improvements tested…

- Numerical stability fixes (part of the boosted **AOBB-K\*-b** variant)
- Search the wild-type sequence first (part of the boosted **AOBB-K\*-b** variant)
- Improve heuristic lower-estimates (part of the boosted **AOBB-K\*-b** variant)
- Weighted heuristic search
- Dynamic heuristic recomputation
- Infuse artificial determinism to leverage CP

#### Underflow-Threshold Optimization (UFO)

General idea:

- During search we can use constraint processing schemes to identify inconsistent paths early on
- Problems may have "near-constraints" (i.e., very small function values) that prevent solutions that contain them in practice
- Treat "near-constraints" as constraints by underflowing their value to zero

#### Underflow-Threshold Optimization (UFO)

#### Algorithm Sketch:

- Set a time limit
- Use binary search to find the greatest constant  $\tau \in [0, v_{max}]$  such that
	- If we replace all function values  $v < \tau$  with *0, there still exists a consistent path (ie. path* with non-zero cost)
	- *CPD: wild-type remains consistent*
- Relax threshold:  $\tau := \tau \cdot \delta$ ,  $\delta \in (0, 1]$
- Replace any function value v < *τ with 0.*

# **Empirical Evaluation**

- Does formulating the K\*MAP task as a graphical model show potential?
- Which AOBB-K<sup>\*</sup> scheme is best performing?
- How does performance compare to state-of-the-art BBK\*?

## **Setup**

 $\Box$  Real protein benchmarks obtained by the Donald Lab at Duke University

- Contained instances for redesigning 1-3 residues
- These were expanded to also consider redesign of 4-5 residues
- Algorithms tested
	- $\Box$  AOBB-K\*
	- $\Box$  AOBB-K\*-ω
	- AOBB-K\*-b
	- AOBB-K\*-b-DH
	- AOBB-K\*-b-UFO
	- $\Box$  BBK\*

[Ojewole et al., 2018]
# **Setup**

 $\Box$  Real protein benchmarks obtained by the Donald Lab at Duke University

- Contained instances for redesigning 1-3 residues
- These were expanded to also consider redesign of 4-5 residues
- Algorithms tested
	- AOBB-K\*
	- $AOBB-K*-\omega$
	- AOBB-K\*-b
	- AOBB-K\*-b-DH
	- AOBB-K\*-b-UFO
	- $\Box$  BBK\*
		- [Ojewole et al., 2018]

### Redesign of 5 Residues



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### Redesign of 5 Residues



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# **Conclusion**

*This simplified K\*MAP task formulated as a graphical model allows existing graphical model algorithms to be adapted to the task and shows potential against current state of the art algorithms.* 

# **End Part 2**

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# **Special Thank You's**

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# Professor Rina Dechter



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*Thank you for investing in me and always helping me to understand complex concepts, both technically and intuitively…*

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RADU MARINESCU



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*Thank you for paving the way for our lunches, walks, and talks (research, philosophical, and otherwise). I look forward to many more to come.*



NICHOLAS COHEN ANNIE RAICHEV



*Thank you for being the burst of energy in our group. You give the best presentations, and your cats are the cutest. #Barcelona 2024*

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– **<sup>118</sup>** Bobak Pezeshki, PhD Final Defense, UCI 2024 **118**

# **My Family**





# **My Family**





# **…and friends**

– **<sup>120</sup>** Bobak Pezeshki, PhD Final Defense, UCI 2024 **120**

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- *Counseling Staff that helped guide me through this process*

# **END**

# **Ancestor Branching Mass**



# **AND/OR Schemes**



**"proper" abstractions ensure that every AND/OR probe includes a valid configuration.**



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# **Scalability Issues**



**Properness restricts the scope of abstractions leading to serious scalability issues.**



 $\leftarrow$  OR Abstraction Sampling

8 nodes; 2 solutions

### Proper AND/OR Abstraction Sampling



# **Properties**

#### **Complexity**



*O(n•m)* where *n* is the number of variables, and *m* is the number of abstract states per variable

#### **AOAS is and Unbiased Estimator of the Partition Function**

THEOREM 2 (unbiasedness). Given a graphical model  $\mathcal{M} =$  $(X, D, \Phi)$ , algorithm AOAS provides an unbiased estimate for the partition function of  $M$ .

# **Context-Based Abstractions – Defining Context**

**Set of pseudo tree ancestors whose assignment causes conditional independence of a variable's subtree with all other variables**



# **Context-based Abstractions - Intuition**

**We know from search that we can merge nodes that root identical subtrees.**

[Dechter and Mateescu, 2006]



### **similar Relaxed Context-Based Abstractions – Intuition**

**What if we abstract nodes that root intentical subtrees...** 



# **Relaxed Context-Based Abstractions**

Relaxed Context-Based Abstractions (RelCB)

- Use subset of *most recent* context variables
- Granularity parameter limits number context variables
- Randomized Context-Based Abstractions (RandCB)
	- Use full context, but randomly hash into a bounded number of abstract states
	- Granularity parameter limits number of abstract states

# AOAS **vs. DIS** [Lou, Dechter, Ihler, 2019]

**Problem**: benchmark name

**Size**: difficulty of subset of problems

**Total**: total number of instances

∈**Bnds**: number of times AOAS's estimate fell within DIS's 95% probabilistic bounds

**AOAS**≥ : number times AOAS's\* estimates were comparable to or better than DIS's\*\*

**AOAS>**: number times AOAS's\* estimates were strictly better than DIS's



\* for this table, AOAS refers to AOAS RandCB-256

 $*$ comparable means falling within  $\pm 0.1$  or  $\pm 0.5$  of DIS's estimate, for small and large problems respectively

# **Marginal MAP (MMAP)**

$$
MMAP(M, X_{MAP}) = \max_{X_{MAP}} \sum_{X/X_{MAP}} \prod_{\alpha} f_{\alpha}(X_{\alpha})
$$

► Max-Inference\n
$$
f(\mathbf{x}^*) = \max_{\mathbf{x}} \prod_{\alpha} f_{\alpha}(\mathbf{x}_{\alpha})
$$
\n>Sum-Inference\n
$$
Z = \sum_{\mathbf{x}_M} \prod_{\mathbf{x}_\alpha} f_{\alpha}(\mathbf{x}_{\alpha})
$$
\nMixed-Inference\n
$$
f(\mathbf{x}_M^*) = \max_{\mathbf{x}_M} \sum_{\mathbf{x}_S} \prod_{\alpha} f_{\alpha}(\mathbf{x}_{\alpha})
$$

• NP-hard: exponentially many terms

#### *MMAP*





### Example: decision making

Sum over random variables (random effects, etc.)

Max over decision variables (specify action policies)

# **GMEC Objective**

### Lower Energy  $\rightarrow$  More Stable  $\rightarrow$  Structure More Likely To Exist

Def. Global Minimum-Energy Conformation (GMEC):

• conformation that minimizes the energy of the complex

$$
GMEC(r) = \min_{c \in C(r)} E(c)
$$



r = amino acid assignments to the residues

C(r) = possible rotamer conformations given a.a. sequence r

 $E(c)$  = energy given conformation c

# **GMEC Objective**

$$
GMEC \; MAP = \min_{R} GMEC(r) \left[ \frac{1}{2} \left( \frac{1}{2} \right)^{1/2} \right]
$$



ie. Find the sequence with the lowest GMEC

• ie. Find sequence that has the most stable conformation

# **Proteins are Dynamic Structures**



Sowmya, Gopichandran & Vaishnavi, A. & Jigisha, A. & Kangueane, Pandjassarame. (2011). Protein-protein complexes.

# **GMEC Objective**



• **NP-hard:** exponentially many terms

# **Problem Formulation: Functions**

$$
E_X^{sb} = \{ E_{X(i)}^{sb}(R_i, C_i) | i \in \{1, 2, ..., N\} \}
$$

• Energy of interactions between residues and their surrounding backbone

 $X \in \{Bound, Dissocial\}$ 



Ε

## **Problem Formulation: Functions**

$$
E_X^{pw} = \left\{ E_{X(i,j)}^{pw}(R_i, C_i, R_j, C_j) \middle| \forall i, j \text{ st. } R_i \text{ and } R_j \text{ interact} \right\}
$$

• Energy of interactions between pairs of residues that interact

 $X \in \{Bound, Dissocial\}$ 



 $X \in \{Bound, Dissocial\}$ 

## **K\*MAP**



$$
K^*(\mathbf{r}) = \frac{Z_{Bound}(\mathbf{r})}{Z_{Dissocial}(\mathbf{r})} = \frac{Z_{complex}(\mathbf{r})}{Z_{subunit 1}(\mathbf{r}) Z_{subunit 2}(\mathbf{r})}
$$

$$
K^*MAP = \max_{\mathbf{R}} K^*(\mathbf{r})
$$

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# **Problem Formulation: Subunit-Stability Constraints**

 $K^*(r) = \frac{Z_{complex}}{Z_{z}}$  $Z_{\textit{subunit}~1}(r) \, Z_{\textit{subunit}~2}$ 

### Do not want dissociate subunits to be too unstable

 $Z_{\text{subunit}~i}(r) > Z_{\text{subunit}~i}(r^{wt})^* \exp\{-5/RT\}$ Likelihood of naturally occurring version Constant factor to threshold with

i = index of dissociate subunit

r = amino acid sequence assignments

D = indicating dissociate subunit

- $r<sup>wt</sup>$  = naturally occurring in nature amino acid sequence (wild type)
- **R** = universal gas constant (for unit conversion between kJ and K)

**T** = absolute temperature (Kelvin)

# **Problem Formulation: Pseudo Tree Overview for K\*MAP**



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## ω-**Weighted Search**



## Boosted Variants of AOBB-K\* / wMBE-K\*



### Dynamic Heuristics



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# **Conclusion**

- $\Box$  Graphical Model formulation for K\*MAP task
- $\Box$  wMBE-K\*, wMBE-based heuristic for bounding K\*
- $\Box$  AOBB-K<sup>\*</sup>, MMAP-like AND/OR search algorithms for K<sup>\*</sup>MAP
- $\Box$  Multiple improvements to improve scalability
	- □ Weighted Search
	- **Tuning of AOBB-K\*** and wMBE-K\*
	- **Dynamic Heuristics**
	- **Q** UFO
		- Also as an independent scheme
- $\Box$  Strong performance in comparison to state-of-the-art BBK\*

# **Future Work**

- Test structures that have conditional independences between their residues
- Extend other well-known approximate anytime methods
- More compact sparse representation
- Improve heuristic function
	- □ Use sampling / search for lower bound?
	- Incorporate pruning constraint
- k-Best Solutions





















#### **Bobak Pezeshki, PhD Final Defense, UCI 2024**



#### Cochrane 1977

This theorem leads to the following rules of conduct. In a given stratum, take a larger sample if

Ž.

- 1. The stratum is larger.
- 2. The stratum is more variable internally.
- 3. Sampling is cheaper in the stratum.

# **AOBB-K\*MAP K\* Pruning Condition**



## **AOBB-K\*MAP Subunit Stability Pruning Condition**

key observation: for any node in corresponding to subunit X, the progressively improving  $ub(z_x)$  can be computed via the expression:  $ub(Z_x) = gh)$   $ub_x(n) \cdot r_x(n) + Sum_x(n)$ MMAP summation term  $(n \in SUM)$ ancestor branching<br>factor which can be computed using information from n, par(n), and sib<sub>x</sub>(n)

## **AOBB-K\*MAP Subunit Stability Pruning Condition**



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