

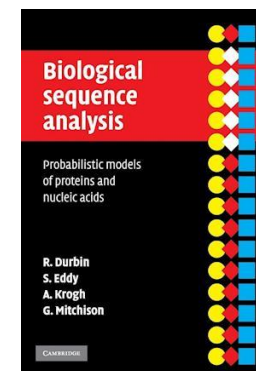
Sampling/searching in *simple*
generative models:
A ~~details-oriented~~ CS perspective

Yann Ponty

LIX, Ecole Polytechnique, France

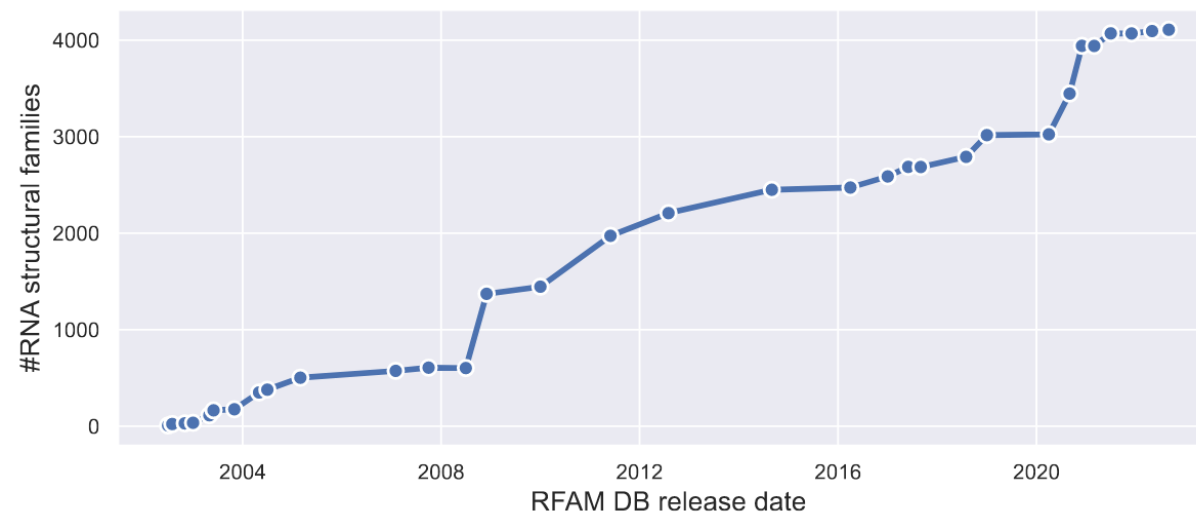
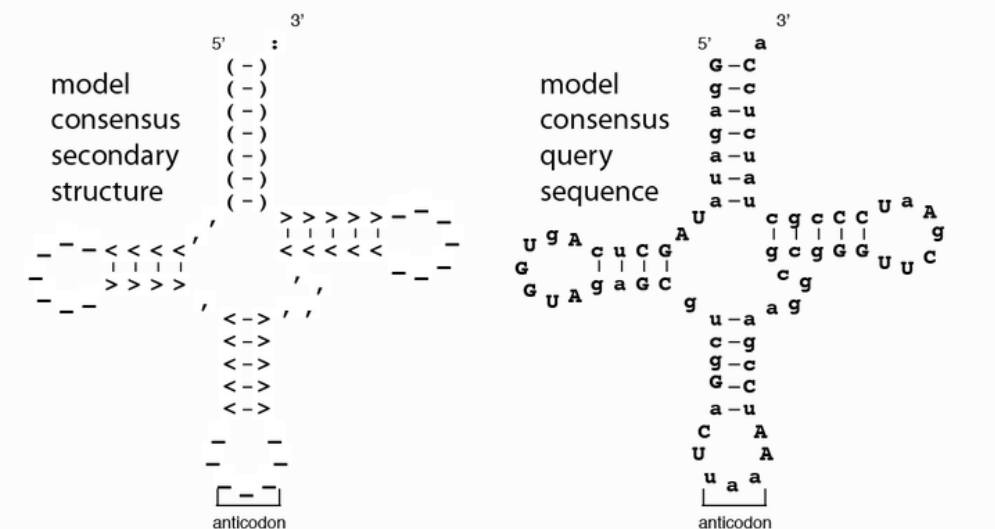
Generative models for RNA design/modeling

- 1998: Covariance Models (CMs)
- InfeRNA1 is the **workhorse** underlying RFAM [Nawrocki *et al* 2009]



```

(((((, ,<<<< . . . >>>>, <<<< >>>>, , , <<<< >>>>))))):
tRNA      1  GgagauUAGcucAgU. .GGU.AgAGCgucgGacUuaaAAuCcgaaggcgGgUUCgAaUCCcgcuauucCa
G:AG:U:U+G:: AGU GGU A ::C U GG:CUU AA:CC A ++C:CGGUUCGAAUCCCG::A:CU:CA
NC_013790.1 2130335 GcAGcUGGUAUAGucUgGUuAUUAcUUGGGCCUCCAAGCCUACAACCCGGGUUCGAAUCCCGCAGCUGCA
*****
  
```

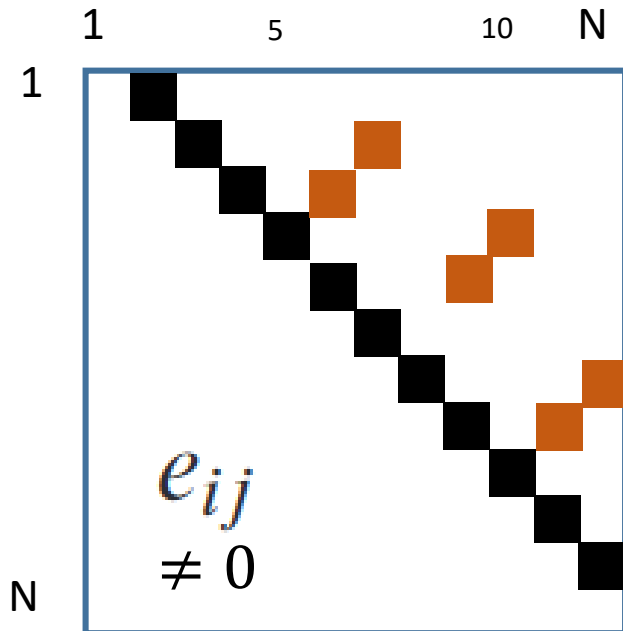


- CMs can be used to search novel ncRNAs, but also as **generative models**

Modern physics-inspired generative models

Potts model (DCA)

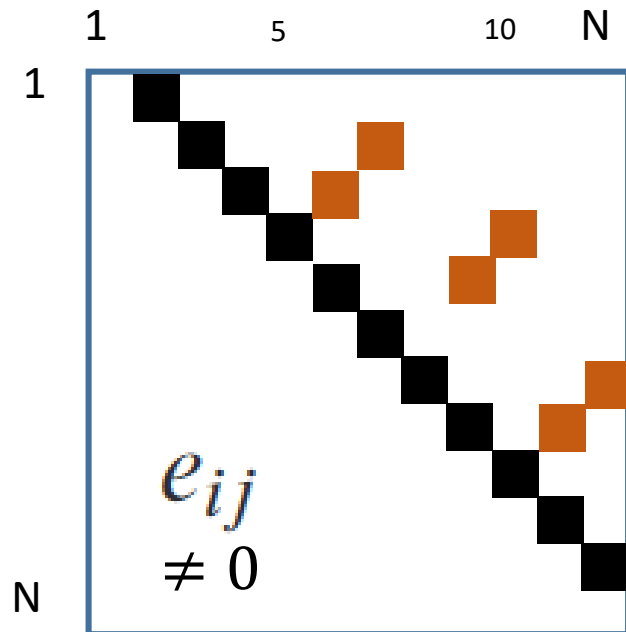
$$\mathbb{P}(\mathbf{w}) \propto \exp \left\{ \sum_{i=1}^N \sum_{j=i+1}^N e_{i,j}(w_i, w_j) + \sum_{i=1}^N h_i(w_i) \right\}$$



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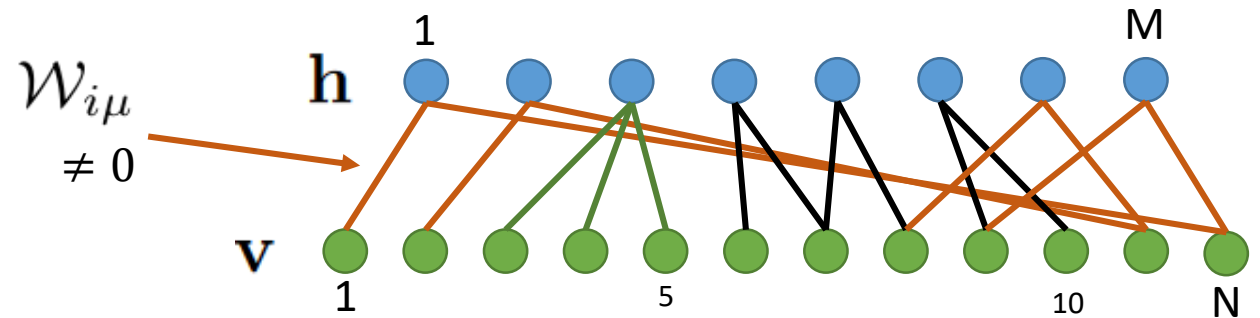
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Restricted Boltzmann Machines

$$\mathbb{P}(\mathbf{w}, \mathbf{h}) \propto \exp \left\{ \sum_{i=1}^N \mathcal{V}_i(w_i) + \sum_{\mu=1}^M \mathcal{U}_\mu(h_\mu) - \sum_{\mu=1}^M I_\mu(\mathbf{w}) h_\mu \right\}$$

$$I_\mu(\mathbf{w}) = \sum_{i=1}^N \mathcal{W}_{i\mu}(w_i)$$

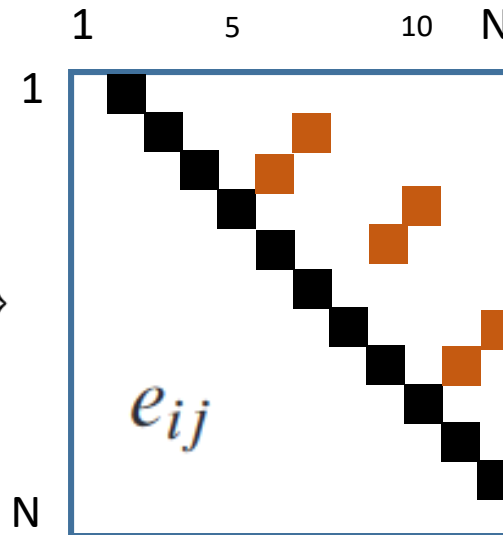


Generative models as (hyper)graphs

- CS perspective: Weighted CSP ([W]CSP), aka graphical models
- (Hyper)**Graph** model $G=(V,E)$: $V \rightarrow$ sequence positions | + Evaluation functions
 $E \rightarrow$ Informative pairs | $f_1, f_2 \dots : v \in V \cup V^2 \mapsto \mathbb{R}$

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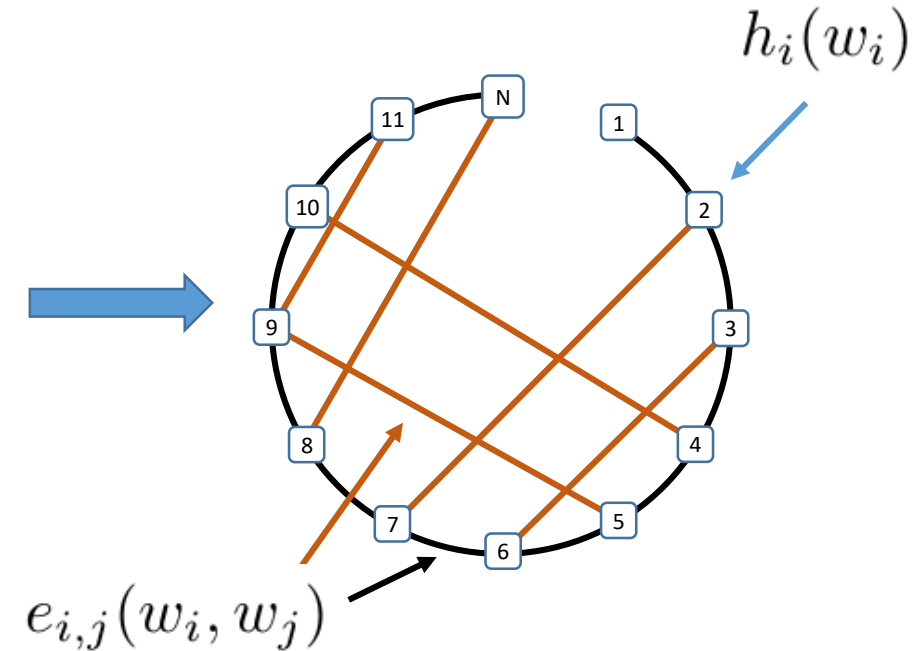
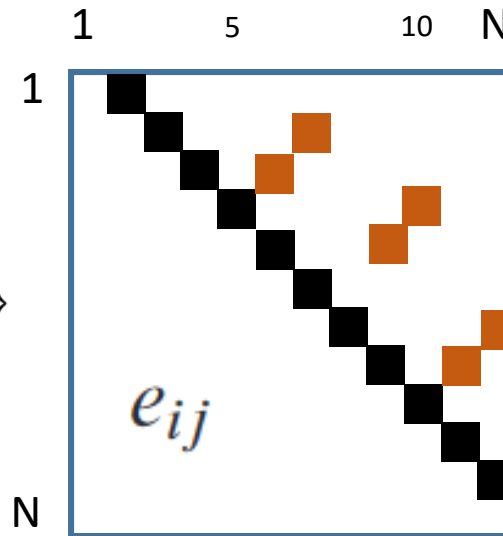


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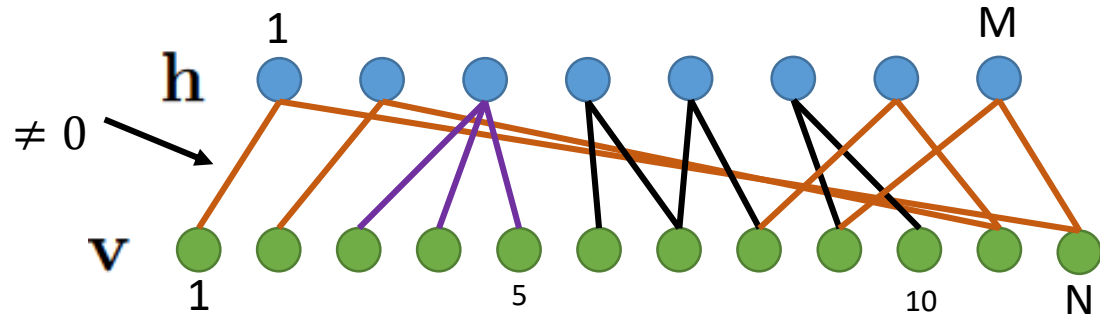


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Restricted Boltzmann Machine $\mathbb{P}(\mathbf{w}, \mathbf{h}) \propto \exp \left\{ \sum_{i=1}^N \mathcal{V}_i(w_i) + \sum_{\mu=1}^M \mathcal{U}_\mu(h_\mu) - \sum_{\mu=1}^M I_\mu(\mathbf{w}) h_\mu \right\}$

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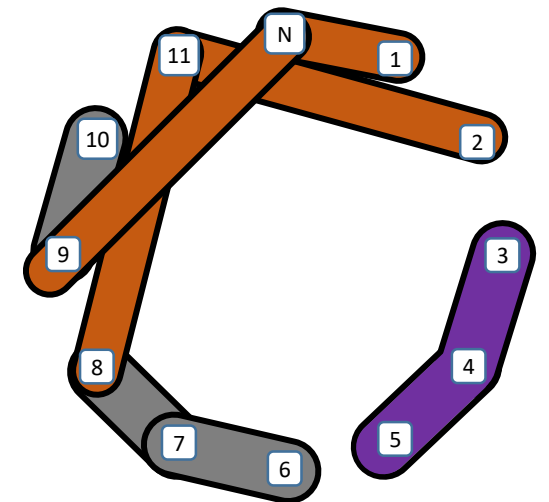
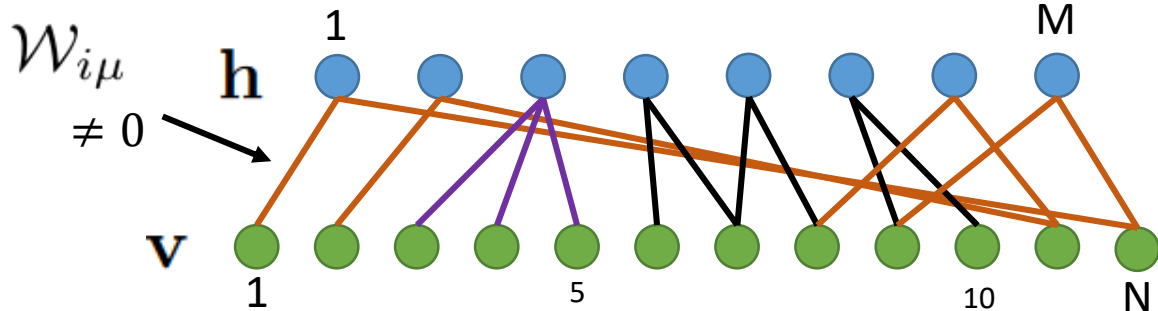


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Generative models: Algorithmic problems

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Algorithmic questions/problems (fixed \mathbf{h} for RBMs):

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- **Sampling:** Generate sequence from $\mathbb{P}(\mathbf{w}) \propto e^{-\beta \cdot E(\mathbf{w})}$
- **Searching:** Given large sequence (genome), find ML match

Generating from physics-inspired models

Ask a physicist

Ask a Computer Scientist



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Monte Carlo for the win!



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If you feel paranoid,
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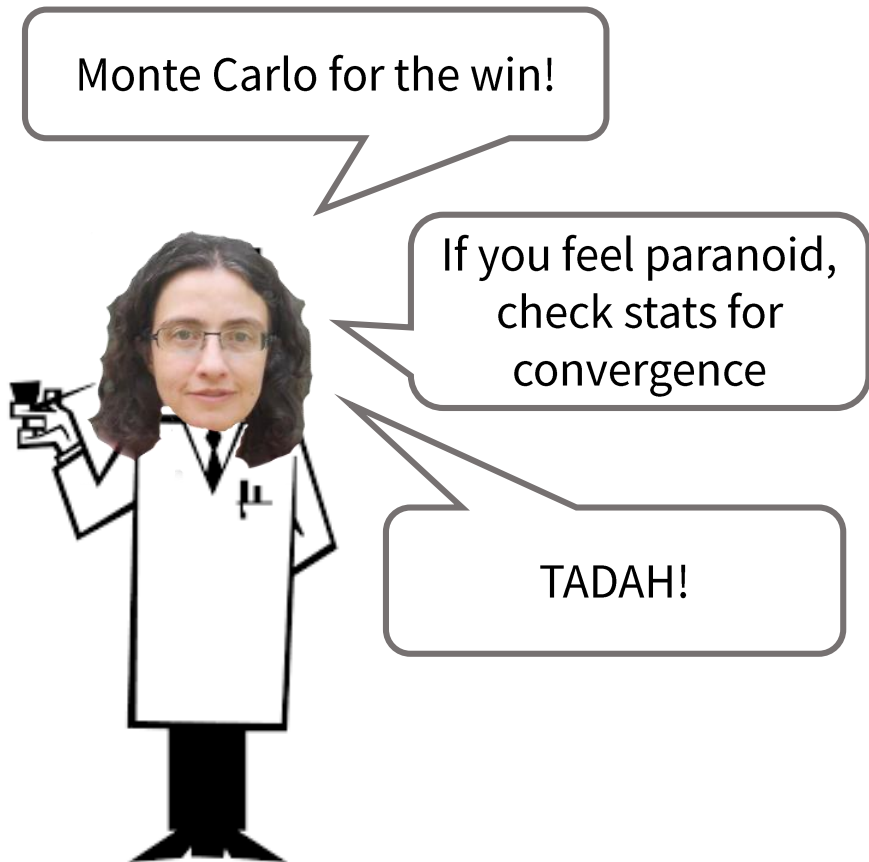
Ask a Computer Scientist

OPT generalizes SAT, MIS... \rightarrow decision NP-hard!
Partition function #P hard & APX!!
Markov Chain may be disconnected!!!
Mixing time could be exponential!!!!

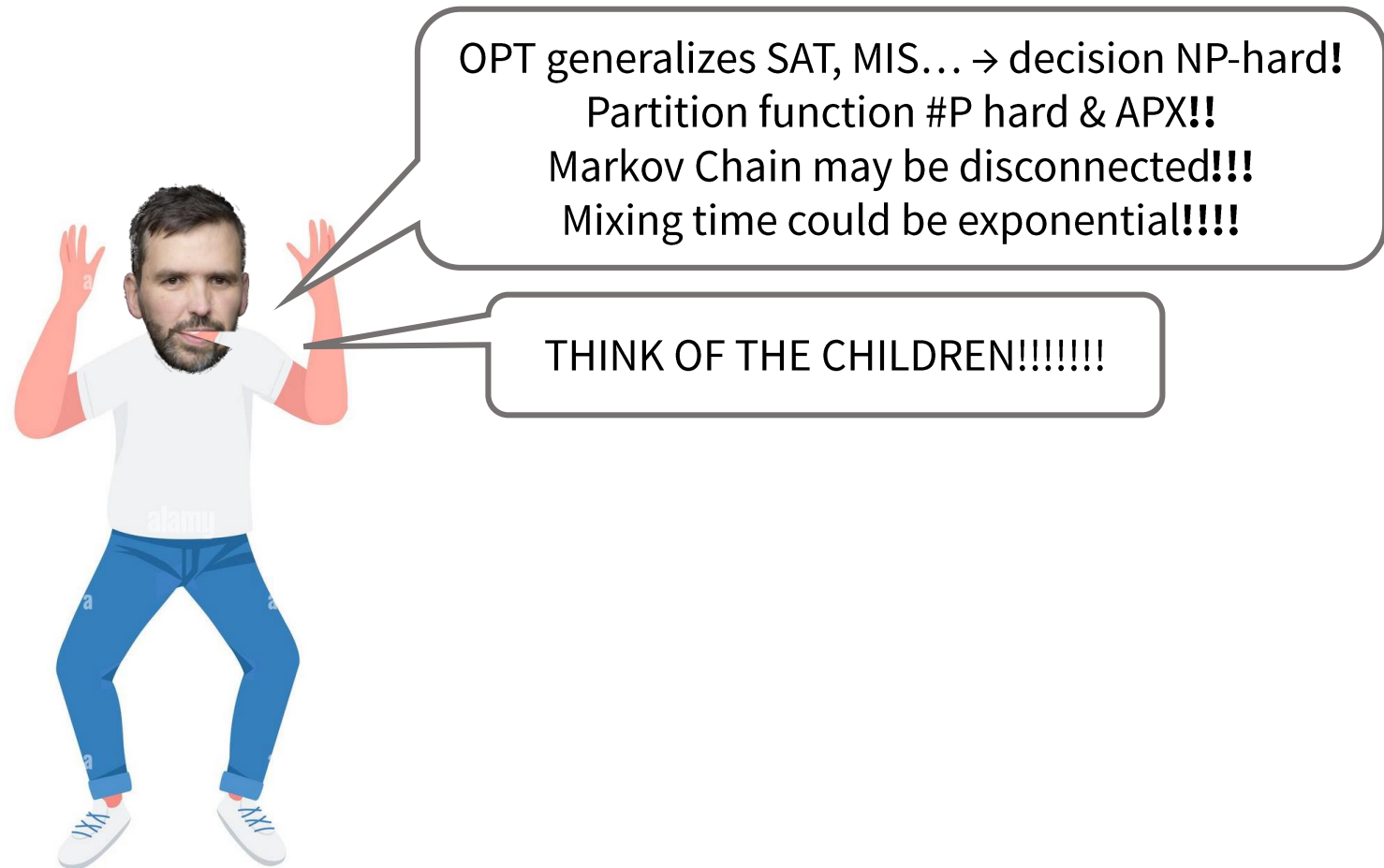


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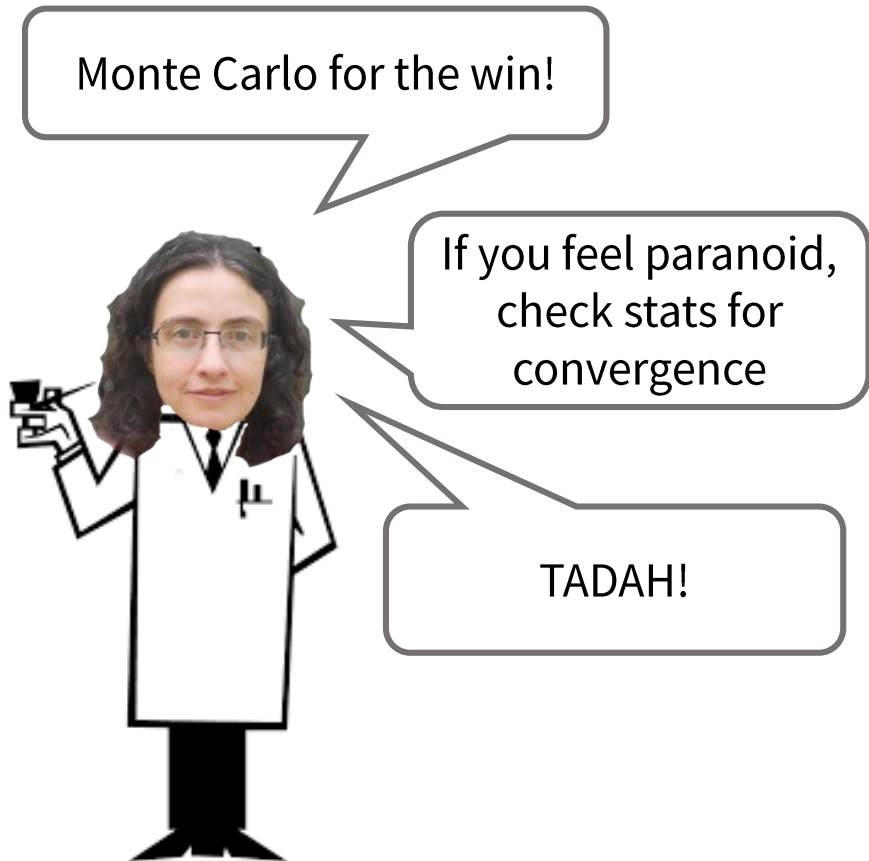


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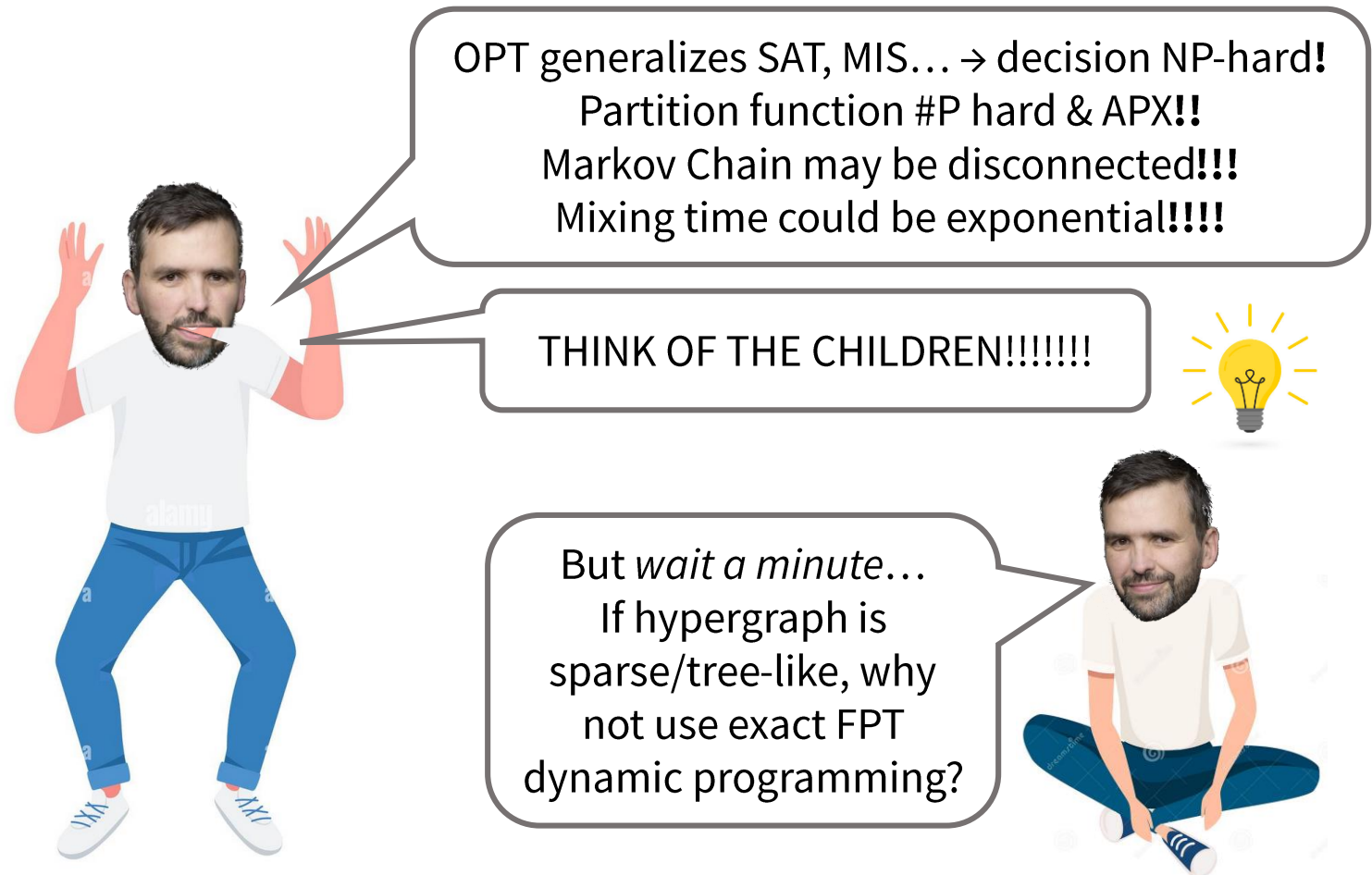


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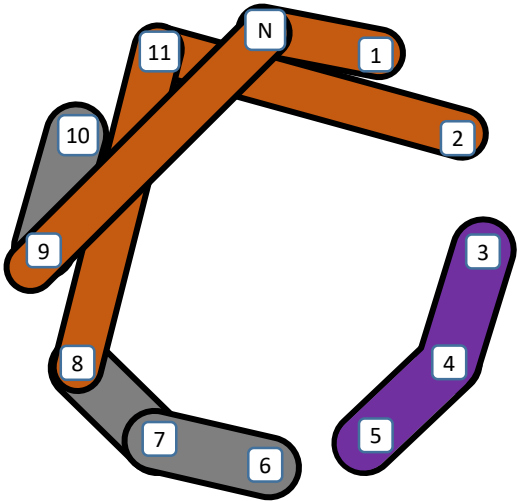


Ask a Computer Scientist



Computing the partition function

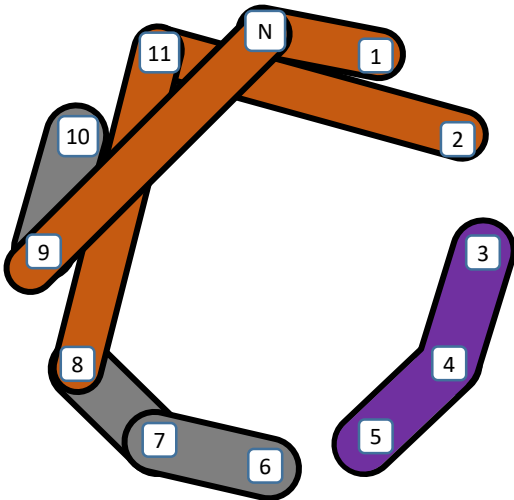
Goal: Compute PF $\mathcal{Z} = \sum_{\mathbf{w} \in \Sigma^N} e^{-\beta \cdot E(\mathbf{w})}$



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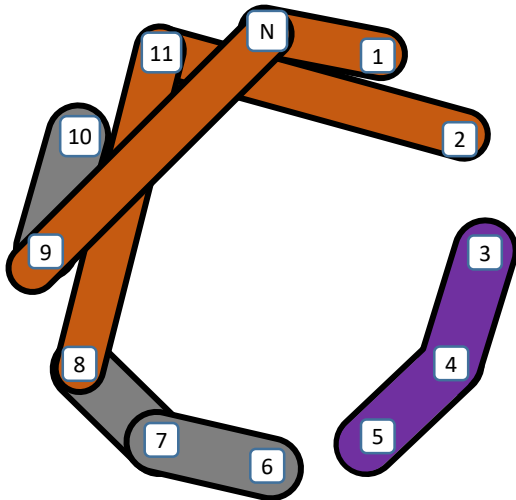
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- Brute force $\mathcal{O}(|\Sigma|^N)$



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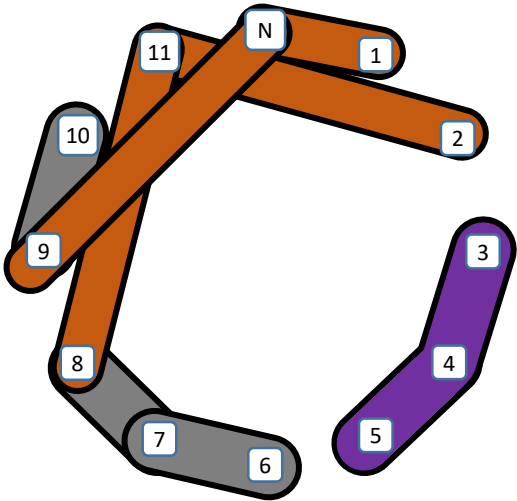
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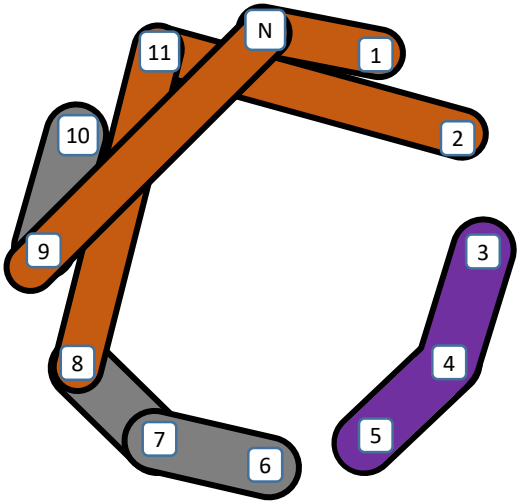
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$$\mathcal{Z}(i_1 \cdots i_k) = \sum_{w_{i_1} \in \Sigma} \mathcal{Z}(i_2 \cdots i_k | w_{i_1})$$

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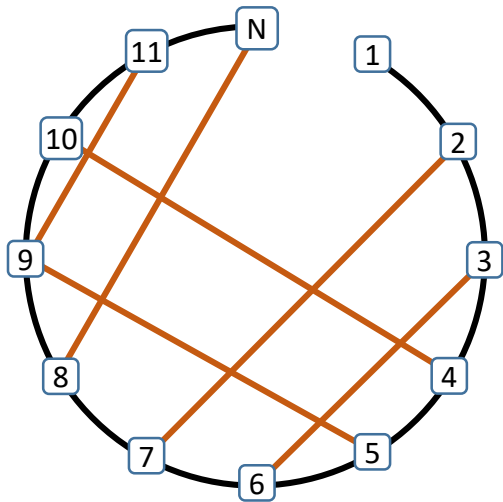
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- Complexity dominated by **largest card. hyperedge**

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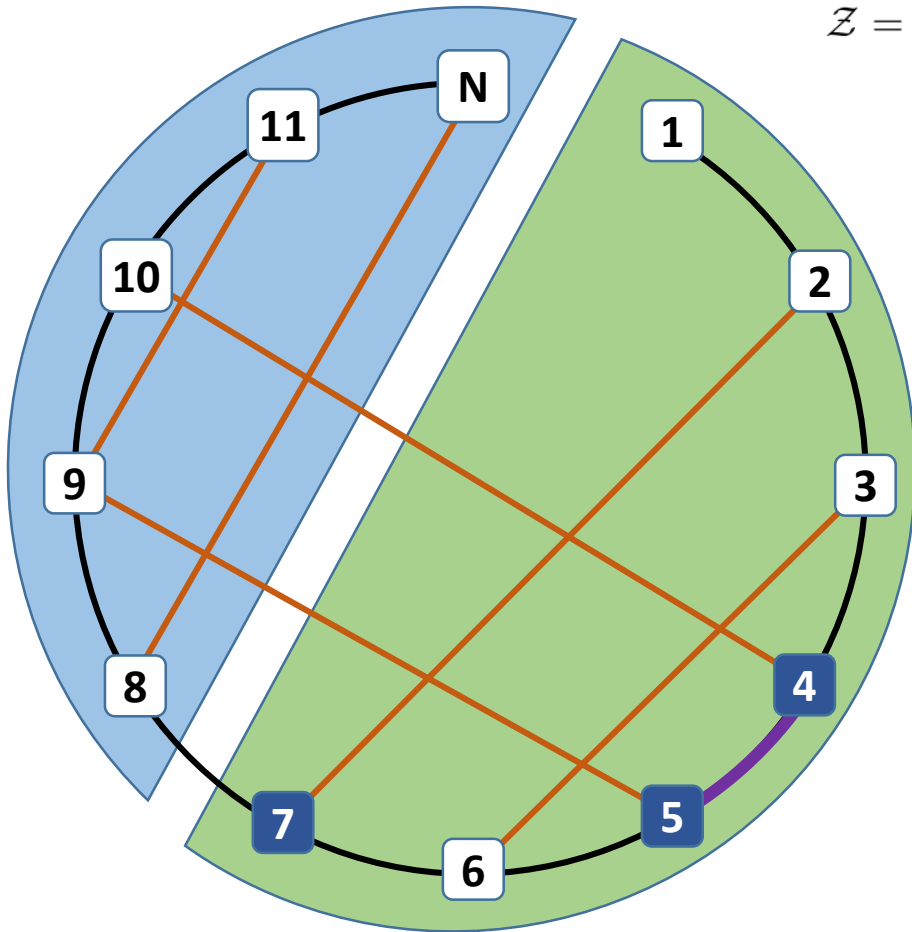
- Cycles can be *broken* through **variable elimination**

Divide and conquer-ing the partition function

Rem: Given values for **separator** {4,5,7}, **Left** and **Right** contributions become independent

$$\mathcal{Z} = \sum_{w_4, w_5, w_7 \in \Sigma^3} \mathcal{Z}(1 \cdots 7 \mid w_4, w_5, w_7) \times \mathcal{Z}(8 \cdots N \mid w_4, w_5, w_7) \times e^{-\beta \left(h(w_4) + h(w_5) + h(w_7) + e_{4,5}(w_4, w_5) \right)}$$

Work sequentially through **Right**



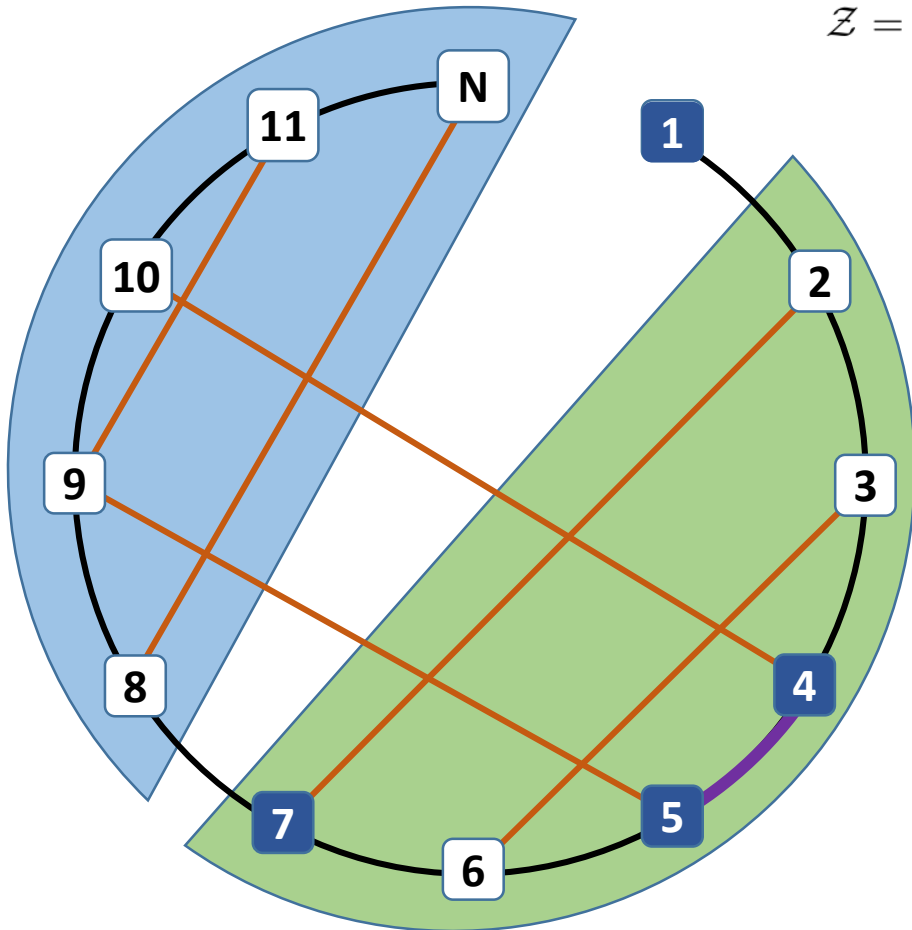
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Work sequentially through **Right**

$$\mathcal{Z}(\mathbf{1} \cdots 7 \mid w_4, w_5, w_7) = \sum_{w_1 \in \Sigma} \mathcal{Z}(2 \cdots 7 \mid w_1, w_4, w_5, w_7) \times e^{-\beta \cdot h(w_1)}$$



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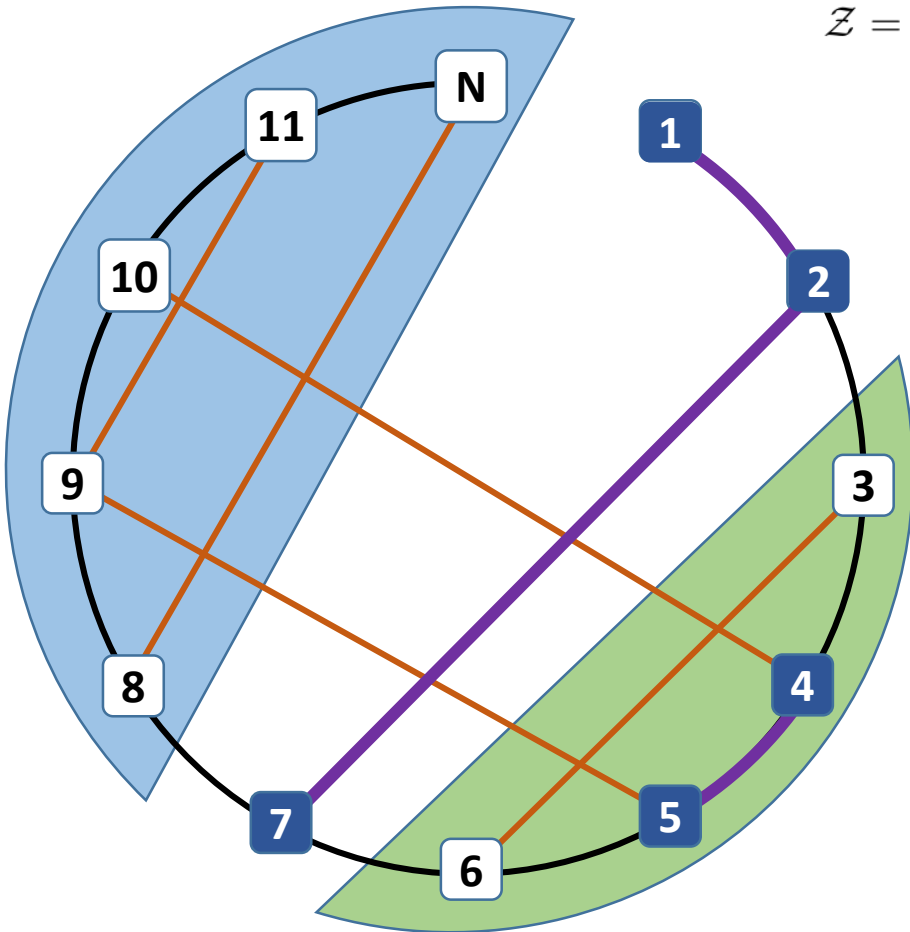
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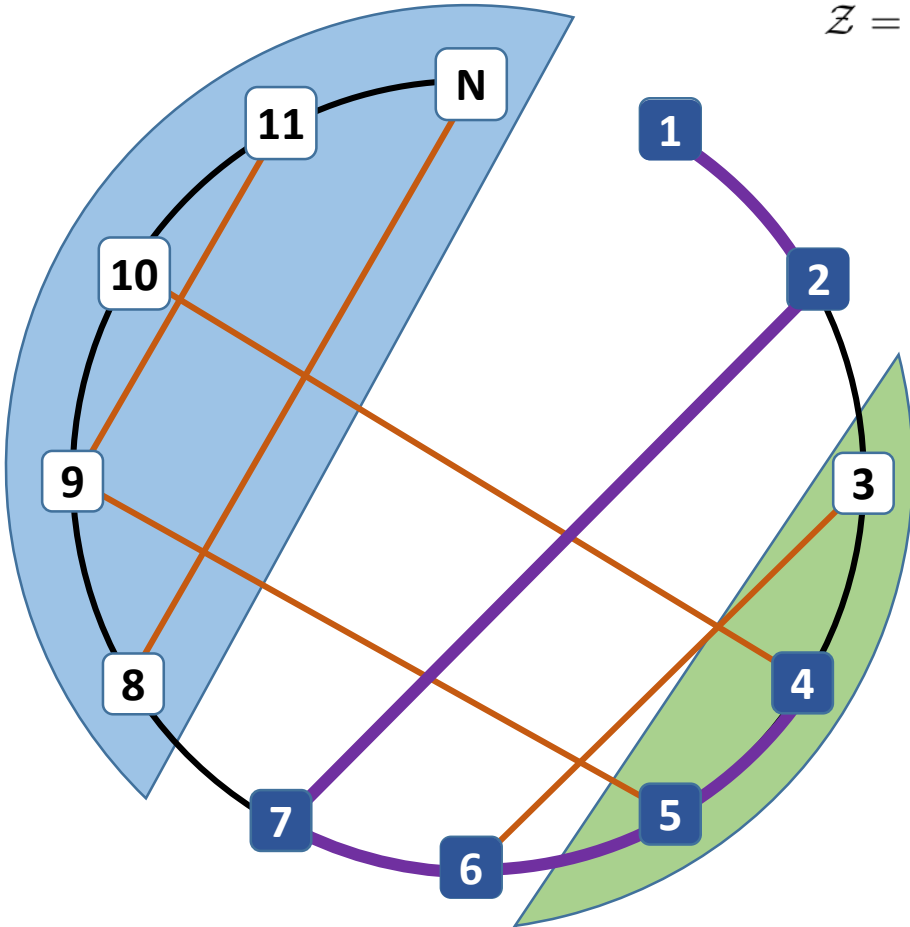
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$$\mathcal{Z}(3 \cdots \mathbf{6} \mid w_2, w_4, w_5, w_7) \rightarrow \mathcal{Z}(\mathbf{3} \cdots 5 \mid w_2, w_4, w_5, w_6)$$



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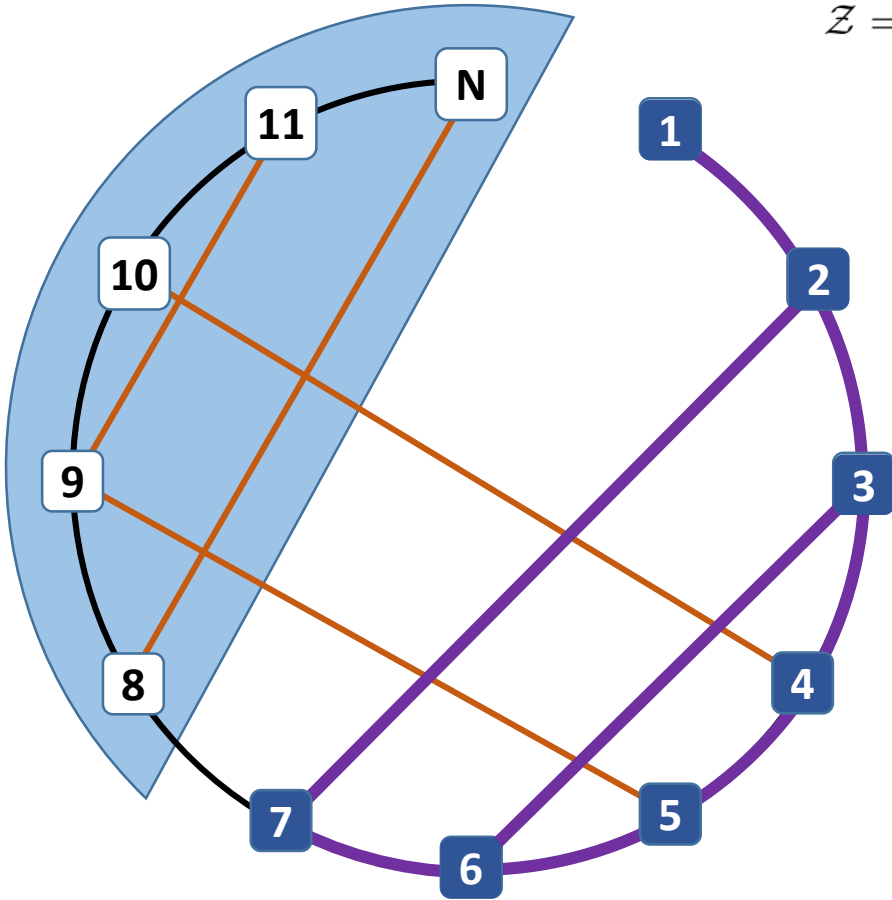
Work sequentially through **Right**

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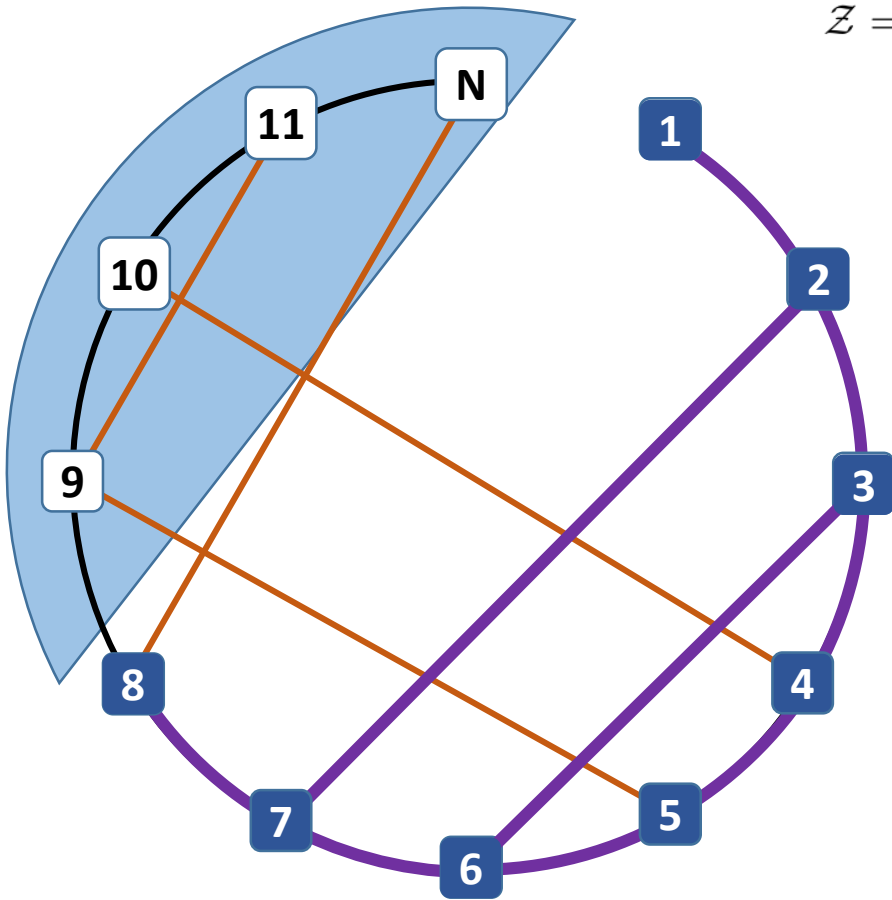
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Work sequentially through **Left**



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Work sequentially through **Right**

$$\mathcal{Z}(1 \cdots 7 \mid w_4, w_5, w_7) = \sum_{w_1 \in \Sigma} \mathcal{Z}(2 \cdots 7 \mid w_1, w_4, w_5, w_7) \times e^{-\beta \cdot h(w_1)}$$

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$$\mathcal{Z}(3 \cdots 6 \mid w_2, w_4, w_5, w_7) \rightarrow \mathcal{Z}(3 \cdots 5 \mid w_2, w_4, w_5, w_6)$$

Work sequentially through **Left**

$$\mathcal{Z}(8 \cdots N \mid w_4, w_5, w_7) = \sum_{w_8 \in \Sigma} \mathcal{Z}(9 \cdots N \mid w_4, w_5, w_8) \times e^{-\beta (h(w_8) + e(w_7, w_8))}$$

Divide and conquer-ing the partition function

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Work sequentially through **Right**

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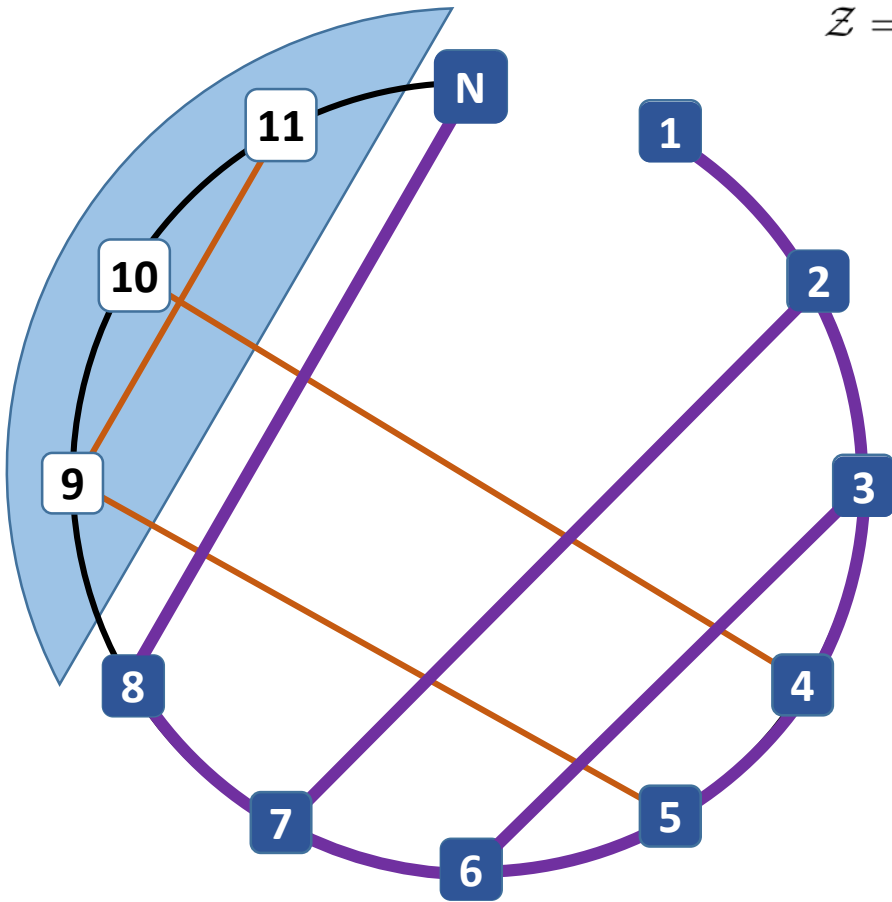
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Work sequentially through **Left**

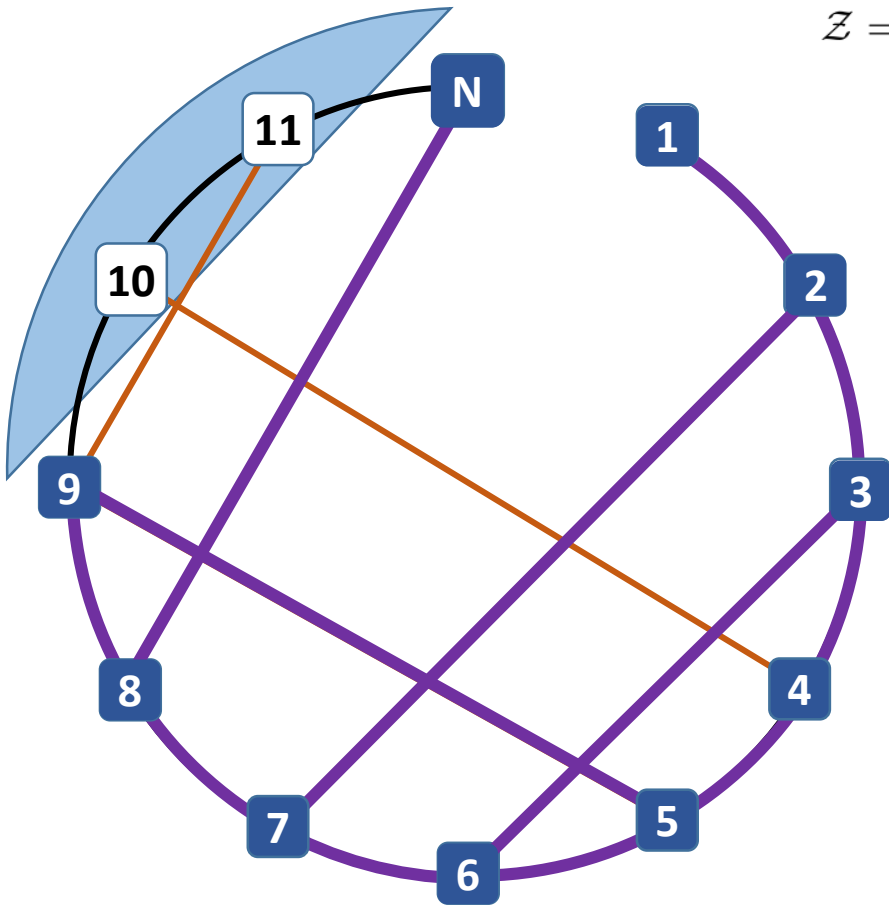
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Divide and conquer-ing the partition function

Rem: Given values for **separator** {4,5,7}, **Left** and **Right** contributions become independent



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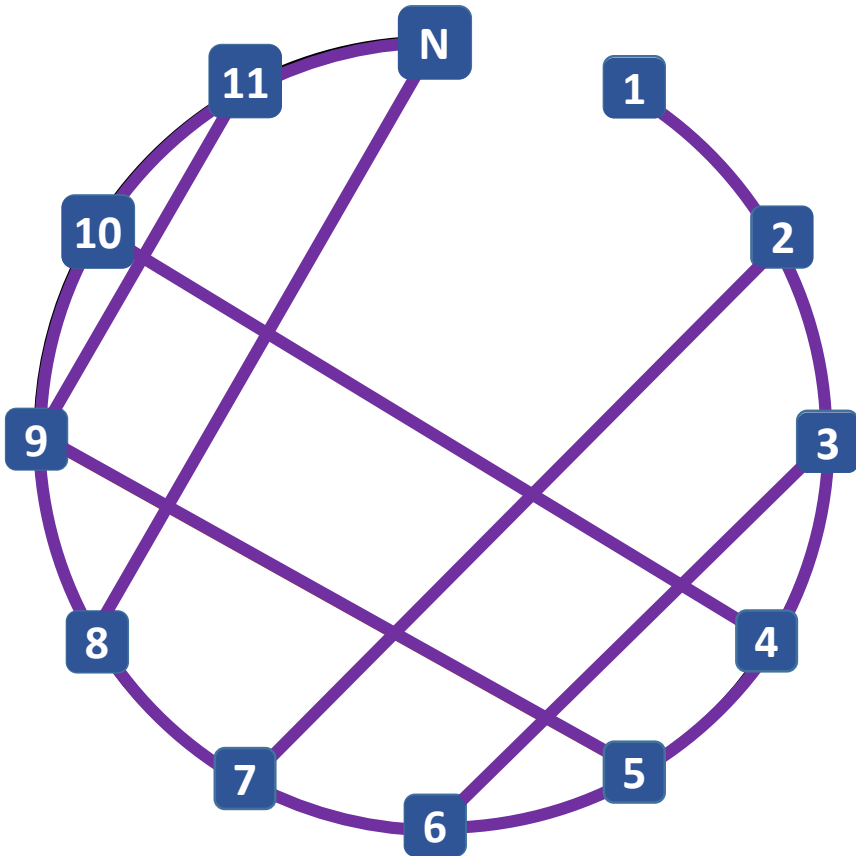
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Tree decomposition (TD)

Definition :

A **tree decomposition** for $G = (V, E)$ is a tree T of bags $B_1, B_2, \dots, B_i \subseteq V$, such that :

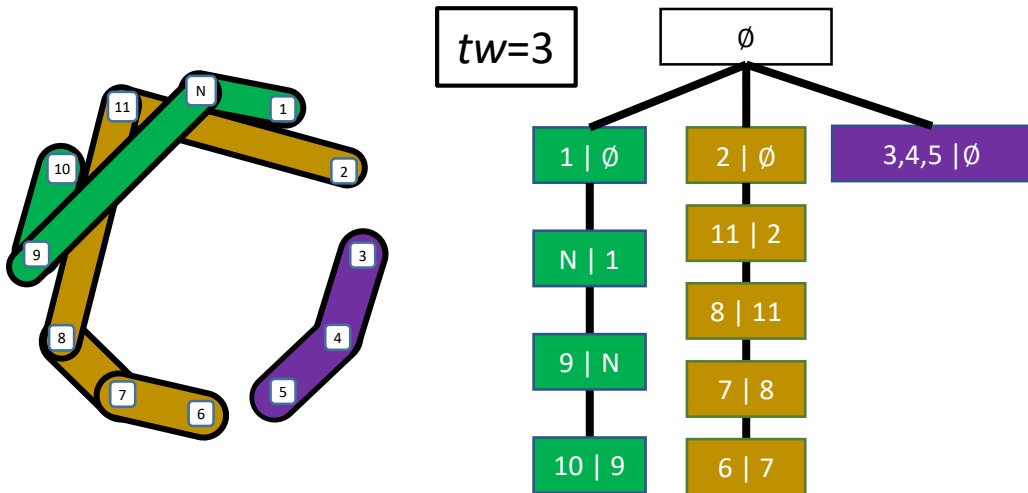
- Each vertex $v \in V$ is *represented* in some bag/node B of T ($v \in B$)
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- Consistency: For all $v \in V$, the bags featuring v are connected in T

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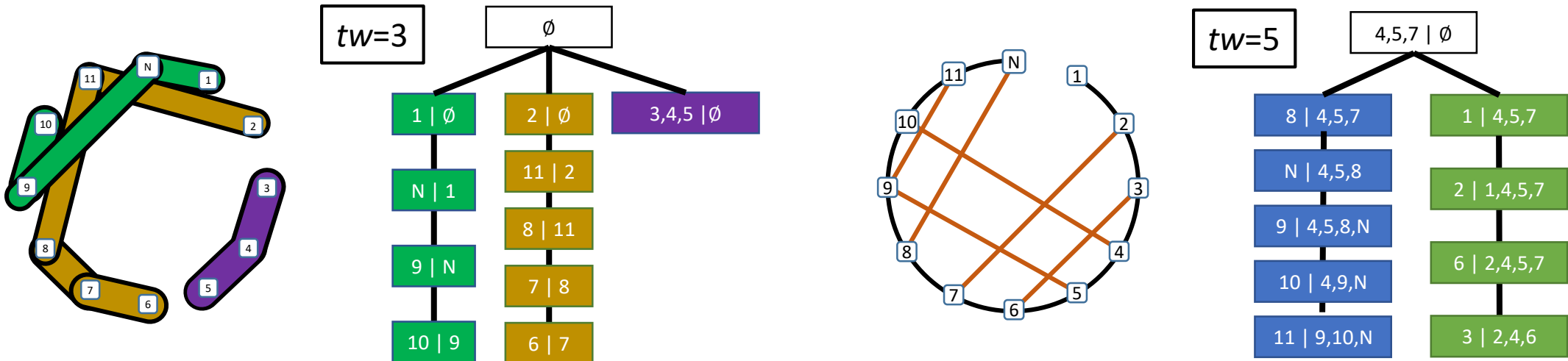


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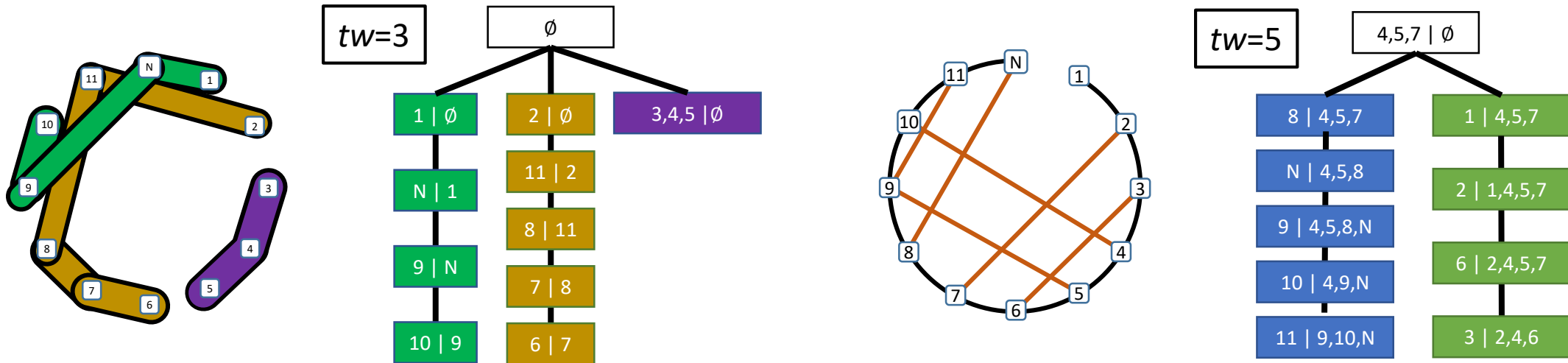


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Tree width tw of a tree decomposition = Size (#indices) of largest bag

Partition function computed in $\mathcal{O}(N |\Sigma|^{tw})$ time using dyn. prog.

[Boedlander 1992]

+ **Computing** an **optimal** (min tw) TD \rightarrow NP-hard, but **Fixed Parameter Tractable** for tw

Meta algorithm – Partition function

Input. Trained generative model M

- Convert M to (hyper)graph instance G
- Run external algorithm to get (approx.) optimal TD, having treewidth tw , for G
- Precompute partition function (bottom-up dyn. prog.) through:

$$\mathcal{Z}(B \mid \mathbf{v}) = \sum_{w \in \Sigma} e^{-\beta \sum_{f \in F(B)} f(\mathbf{v} \cup \{w\})} \prod_{B' \in \text{children}(B)} \mathcal{Z}(B' \mid \mathbf{v} \cup \{w\})$$

\mathbf{v} : Assignments to variables shared with parent; $F(B)$: Functions assigned to bag

Output. Return $\mathcal{Z}(\text{root})$ **Complexity:** $\mathcal{O}(N |\Sigma|^{tw})$ + Tree decomposer ($\mathcal{O}(N)$, exp. on tw)

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+ **OPT:** Max. probability/min. energy sequence **for free**

InfraRed – A practical implementation

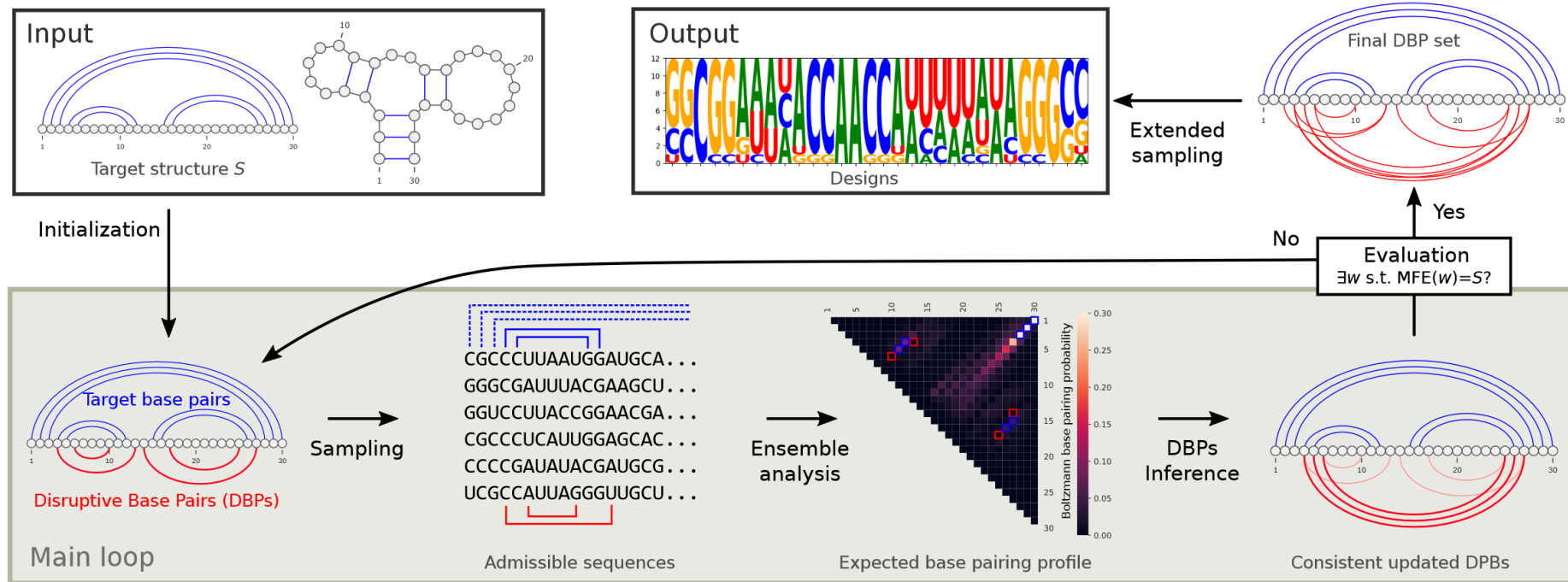
<https://gitlab.inria.fr/amibio/InfraRed/>

```
1 def single_target_design_model(target):
2     n, bps = len(target), rna.parse(target)
3     model = ir.Model(n, 4)
4     model.add_constraints(rna.BPComp(i, j) for (i, j) in bps)
5     model.add_functions([rna.GCCont(i) for i in range(n)], 'gc')
6     model.add_functions([rna.BPEnergy(i, j, (i-1, j+1) not in bps)
7         for (i,j) in bps], 'energy')
8     model.set_feature_weight(-1.5, 'energy')
9     return model
```

- Python/C++ declarative framework (constraints and pseudo-energies)
- Runs tree decomp.; Reports part. fun.; Samples Boltzmann distr.; Optimal sequence
- **Bonus:** Autolearns weights to target expected features (ΔG , GC%...)
- Use-cases:
 - RNA multiple design - RNARedPrint [Hammer *et al*, RECOMB 2018; BMC Bioinfo 2019]
 - RNA inverse folding - RNAPond [Yao *et al*, RECOMB 2021]

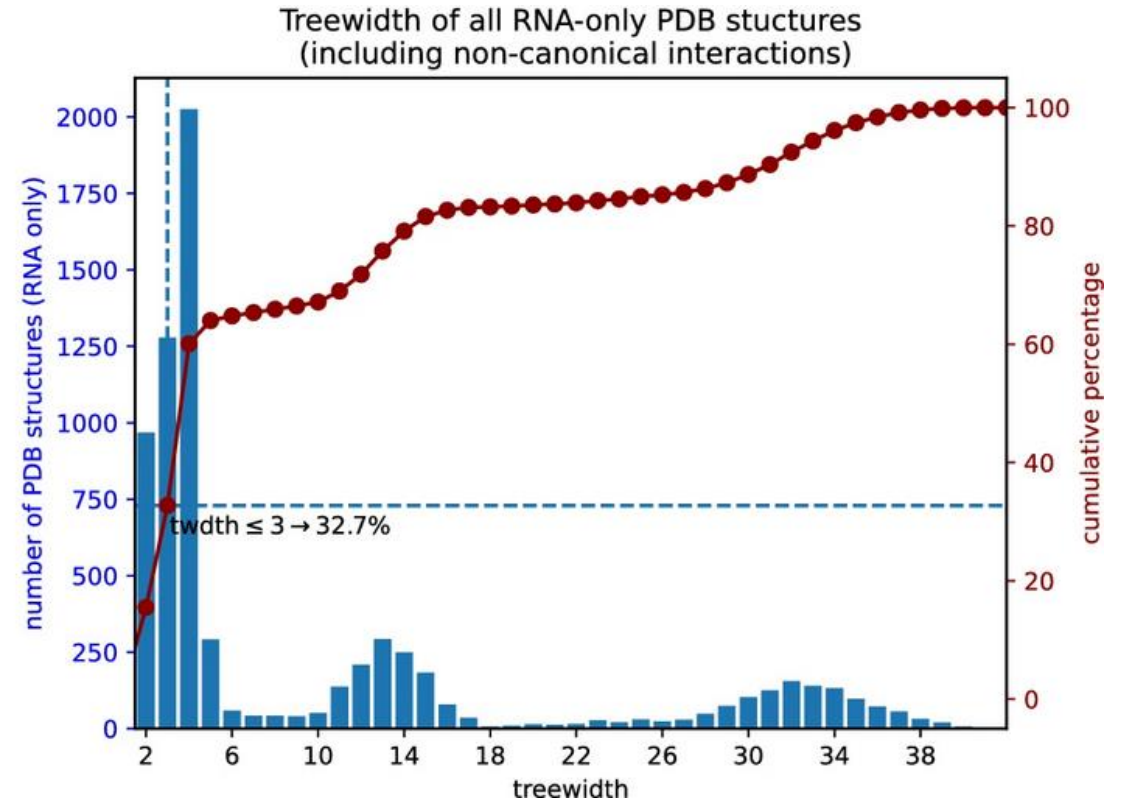
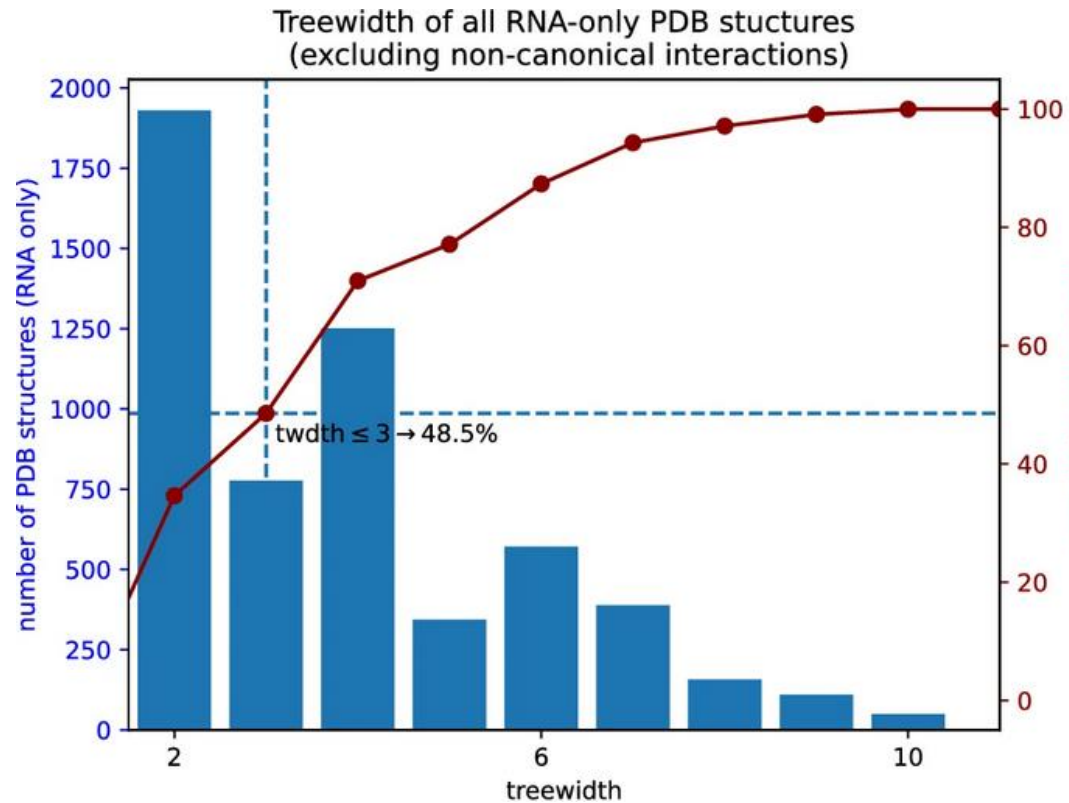
RNAPoND – Positive and Negative Design

[Yao et al, RECOMB 2021]



- Obeys positive constraints but learns disruptive BPs and **Cancels** them
- Naïve infrared ($tw < 10$) implementation competitive with state of the art

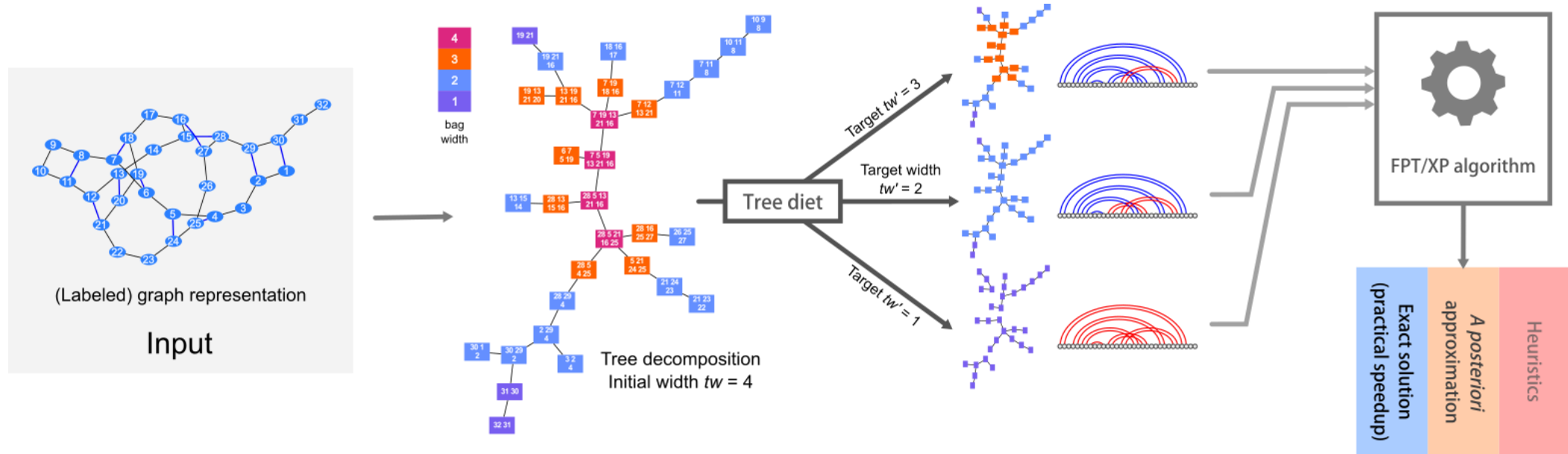
Treewidths of actual RNAs (PDB)



Treewidth of generative models???

TreeDiet – Simplifying tree decompositions

[Marchand et al, BMC Bioinfo 2022]



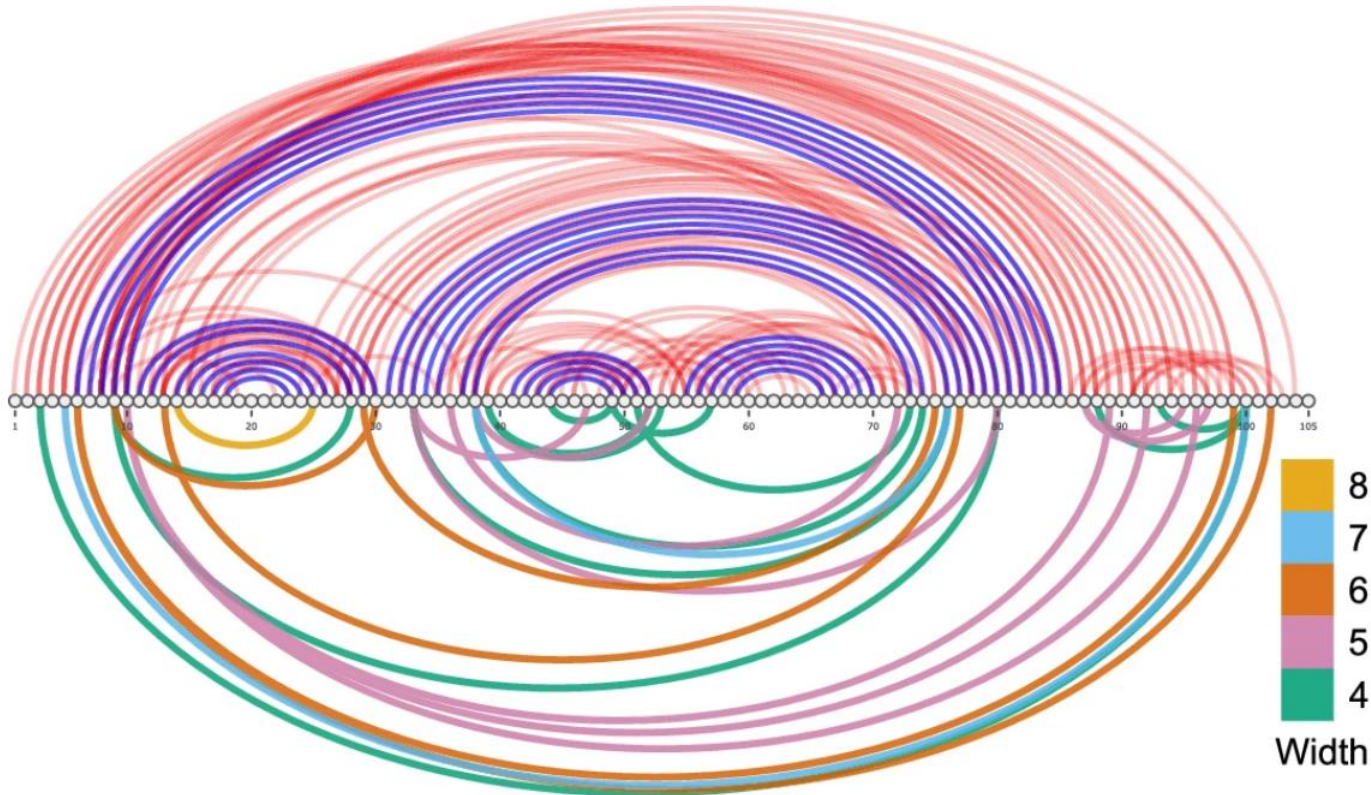
Goal: Remove few (weighted) edges from treewidth tw input graph, to reach $tw' < tw$

Theory: FPT on tw ; **Practice:** No reasonable tractable algorithm known

Idea: Start from tree decomposition, rephrase as **coloring** on tree (*practically* FPT on tw)

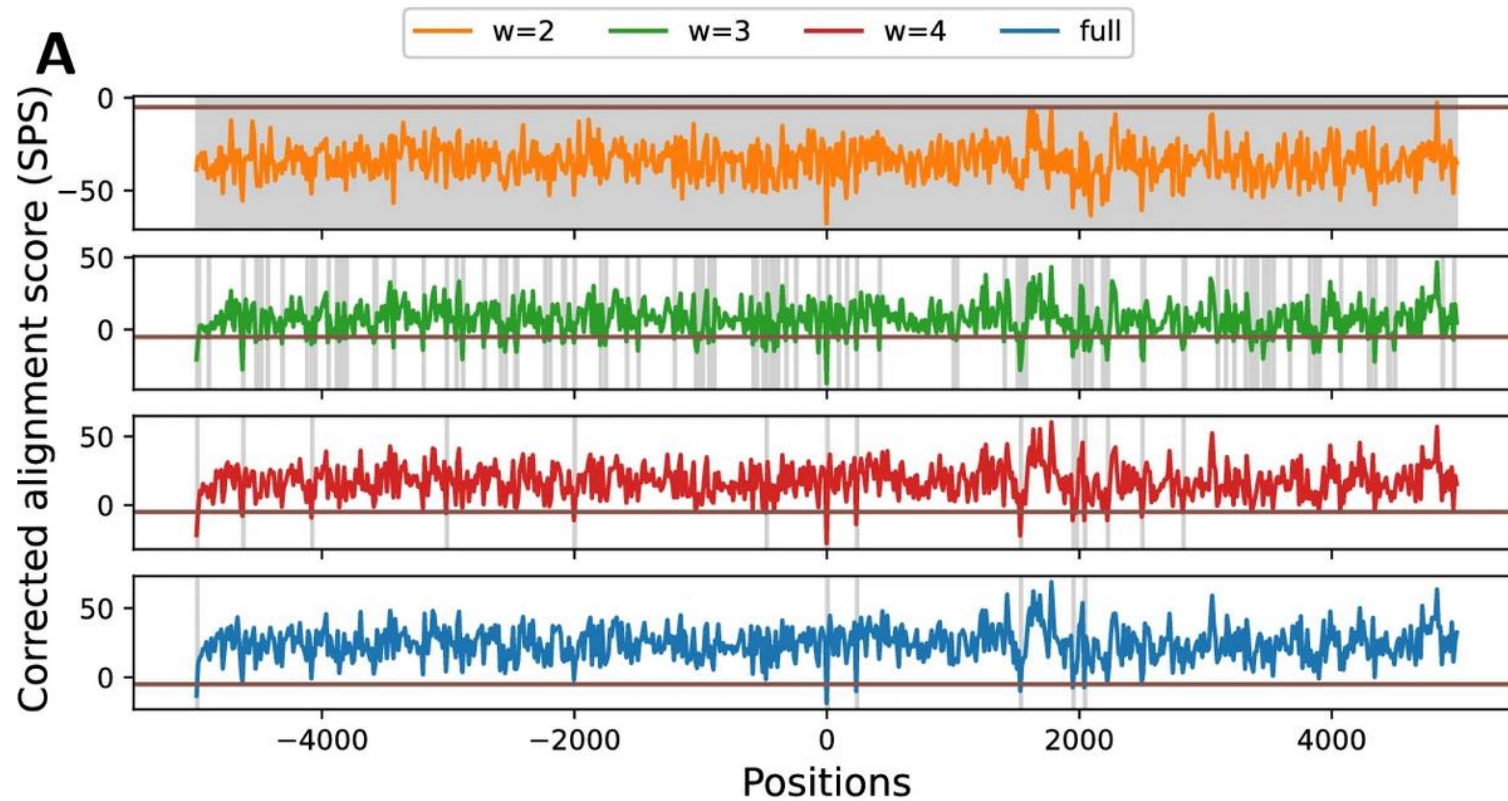
Correct induced error through **rejection sampling**, subopts or progressive filtering (search)

Treewidth can be reduced w/o much information loss



tw'	#Preserved BPs	
	EteRNA22	EteRNA77
9	—	183
8	—	182
7	—	180
6	465	176
5	460	168
4	456	157
3	445	144
2	418	121
1	320	86

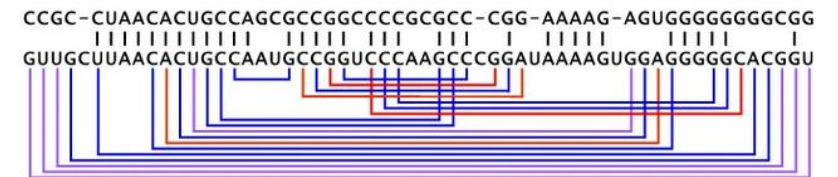
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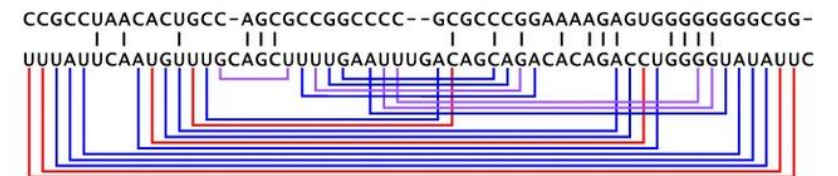
B – Twister Ribozyme (4OJI)



C – Best hit ($c = -18.7$)



D – Second best hit ($c = -9.9$)



Conclusion

*To a hammer, everything is a nail
Build it and they will come*

- Avenues to apply parameterized complexity to bio* generative models
- Purely declarative, exact sampling
- Low complexity post precomputation

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Additional assets:

[Saule *et al*, WABI 2011]

- Derivatives/moments/correlations exactly computable (same complexity)
- Genomic search for occurrences of gen model ($\Sigma \rightarrow [1, M]$, XP comp.)

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Limitation (possibly):

- Assumes that $tw \ll N$
- Sparseness in generative models: structure prediction vs design

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Acknowledgements



Sebastian Will



Sarah Berkemer



Hua-Ting Yao



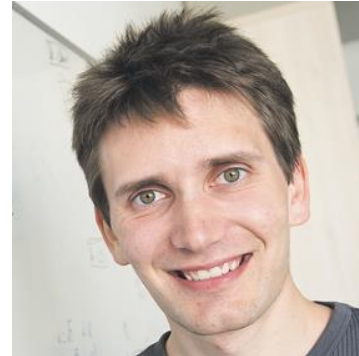
Stefan Hammer



Alain Denise



Bertrand Marchand



Laurent Bulteau



Philippe Rinaudo

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