

Stochastic Enumeration Method for Counting NP-hard Problems

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Sequential Importance Sampling (SIS) Method

Sequential importance sampling (SIS) is importance sampling carried out in a sequential manner. To explain, consider the expected performance

$$\ell = \mathbb{E}_f[S(\boldsymbol{X})] = \int S(\boldsymbol{x}) f(\boldsymbol{x}) \, \mathrm{d}\boldsymbol{x} \,, \qquad (1)$$

where S is the sample performance and f is the probability density of X.

Let g be another probability density such that S f is *dominated* by g. That is, $g(\mathbf{x}) = 0 \implies S(\mathbf{x}) f(\mathbf{x}) = 0$. We have

$$\ell = \int S(\boldsymbol{x}) \, \frac{f(\boldsymbol{x})}{g(\boldsymbol{x})} \, g(\boldsymbol{x}) \, \mathrm{d}\boldsymbol{x} = \mathbb{E}_g \left[S(\boldsymbol{X}) \, \frac{f(\boldsymbol{X})}{g(\boldsymbol{X})} \right]. \quad (2)$$



Consequently, if X_1, \ldots, X_N is a *random sample* from g, that is, X_1, \ldots, X_N are iid random vectors with density g, then

$$\hat{\ell} = \frac{1}{N} \sum_{k=1}^{N} S(\boldsymbol{X}_k) \frac{f(\boldsymbol{X}_k)}{g(\boldsymbol{X}_k)}$$
(3)

is an unbiased estimator of ℓ . This estimator is called the *importance sampling estimator*. The ratio of densities,

$$W(\boldsymbol{x}) = \frac{f(\boldsymbol{x})}{g(\boldsymbol{x})} , \qquad (4)$$

is called the *likelihood ratio*.



Suppose that (a) X is decomposable, that is, it can be written as a vector $X = (X_1, ..., X_n)$, where each of the X_i may be multi-dimensional, and (b) it is easy to sample from g(x)sequentially. Specifically, suppose that g(x) is of the form

 $g(\boldsymbol{x}) = g_1(x_1) g_2(x_2 \mid x_1) \cdots g_n(x_n \mid x_1, \dots, x_{n-1}).$ (5)

To further simplify the notation, we abbreviate (x_1, \ldots, x_t) to $x_{1:t}$ for all t. In particular, $x_{1:n} = x$.



By the product rule of probability, the target pdf f(x) can also be written sequentially, that is,

$$f(\boldsymbol{x}) = f(x_1) f(x_2 | x_1) \cdots f(x_n | \boldsymbol{x}_{1:n-1}).$$
 (6)

We can write the likelihood ratio in product form as

$$W(\boldsymbol{x}) = \frac{f(x_1) f(x_2 \mid x_1) \cdots f(x_n \mid \boldsymbol{x}_{1:n-1})}{g_1(x_1) g_2(x_2 \mid x_1) \cdots g_n(x_n \mid \boldsymbol{x}_{1:n-1})}$$
(7)



If $w_t(\boldsymbol{x}_{1:t})$ denotes the likelihood ratio up to time t, recursively as

$$w_t(\boldsymbol{x}_{1:t}) = u_t w_{t-1}(\boldsymbol{x}_{1:t-1}), \quad t = 1, \dots, n$$
, (8)

with initial weight $w_0(\boldsymbol{x}_{1:0}) = 1$ and *incremental weights* $u_1 = f(x_1)/g_1(x_1)$ and

$$u_{t} = \frac{f(x_{t} \mid \boldsymbol{x}_{1:t-1})}{g_{t}(x_{t} \mid \boldsymbol{x}_{1:t-1})} = \frac{f(\boldsymbol{x}_{1:t})}{f(\boldsymbol{x}_{1:t-1}) g_{t}(x_{t} \mid \boldsymbol{x}_{1:t-1})}, \quad t = 2, \dots, n.$$
(9)



The final estimator is

$$\hat{\ell}_w = \frac{\sum_{k=1}^N S(\mathbf{X}_k) W_k}{\sum_{k=1}^N W_k} .$$
 (10)

Algorithm 0.1 (SIS Algorithm)

- 1. For each finite t = 1, ..., n, sample X_t from $g_t(x_t | \boldsymbol{x}_{1:t-1})$.
- 2. Compute $w_t = u_t w_{t-1}$, where $w_0 = 1$ and u_t is given above.
- 3. Repeat N times and estimate ℓ via $\hat{\ell}$ as above.







OSLA is the state of the art procedure due to Rosenbluth and Rosenbluth (1959).

- Start from X₀ = (0,0). Set t = 1. Let d_t be the number of neighbors of X_{t-1} that have not yet been visited. If d_t > 0, choose X_t with probability 1/d_t from its neighbors. If d_t = 0 stop generating the path.
- 2. Stop if t = n. Otherwise increase t by 1 and go to step 2.

Note that the procedure either generates a SAW x of fixed length n or the path gets value zero. The SIS pdf g(x) is

$$g(\boldsymbol{x}) = \frac{1}{d_1} \frac{1}{d_2} \cdots \frac{1}{d_n} = \frac{1}{|\widehat{\mathscr{X}^*}|}, \ (|\widehat{\mathscr{X}^*}| = d_1 \dots d_n) \ . \tag{11}$$







- 1. Generate independently M paths X_1, \ldots, X_M via the OSLA procedure.
- 2. For each SAW X_k compute the corresponding $[\mathscr{X}^*]$ as above. For the other parts (which do not reach the value n) set $w(X_k) = 0$.
- 3. Return

$$\widetilde{|\mathscr{X}^*|} = \frac{1}{M} \sum_{i=k}^{M} \widehat{|\mathscr{X}^*|} .$$
 (12)

OSLA Looses Trajectories

A SAW (with arrows) trapped after 15 iterations. The corresponding ν values (based on short lines without arrows) are

$$\nu_1 = 4, \ \nu_2 = 3, \ \nu_3 = 3, \ \nu_4 = 3, \ \nu_5 = 3, \ \nu_6 = 3, \ \nu_7 = 2, \ \nu_8 = 3,$$

 $\nu_9 = 3, \ \nu_{10} = 3, \ \nu_{11} = 2, \ \nu_{12} = 3, \ \nu_{13} = 2, \ \nu_{14} = 1, \ \nu_{15} = 0.$





As for another situation where OSLA can be readily trapped consider a directed graph below with source s and sink t.





The exception is the OSLA algorithm of Rasmussen for counting the permanent. Rasmussen proofs that if the a_{ij} entries of the permanent matrix A are Bernoulli outcomes each generated randomly with probability p = 1/2 then OSLA estimator is FPRAS.

This is quite a remarkable result!



We next extend OSLA to k-step-look ahead and in particular to n-step-look ahead, called nSLA. Here n denotes the size of the problem, such as the number of variables (literals) in SAT and the number of edges in a network. We assume that all n variables x_1, \ldots, x_n are binary, that is $x \in \{0, 1\}$. The n-SLA (based an oracle) is very similar to OSLA.

Its major advantage versus OSLA: it never

looses a trajectory.



Our main strategy (slogan) is as follows: Use fast polynomial decision making oracles to solve #P-sharp problems.

In particular use

- Breadth first search (BFS) or Dijkstra's decision making algorithms for counting the number of paths in a network.
- Hungarian decision making algorithm for counting the number of perfect matchings (permanent) in a bipartite graph.
- DPLL decision making algorithm for counting the number of valid assignments in 2-SAT.



The goal is to count the number of paths $|\mathscr{X}^*|$ in a dodecahedron graph, say from node 1 to node 20 using BFS





To see how nSLA works consider a tree with the set of paths $\{000, 001, 100, 110, 111\}.$





The sub-trees $\{000, 001\}$ (in bold) generated by *n*SLA using the oracle.





Figure below presents the dynamics of the SE Algorithm for the first 3 iterations in a model with n variables using $N^{(e)} = 1$. The accumulated weights are $\nu_1 = 2, \nu_2 = 2, \nu_3 = 1$.



Drawback of *n***SLA Method**

Although *n*SLA never looses trajectories its main drawback is that the generated trajectories are not uniformly distributed. As results its estimators are heavily biased. To see this consider a graph with n = 4 variables and $|\mathscr{X}^*| = 5$. This is a 2-SAT model with clauses $C_1 \wedge C_2 \wedge, \ldots, \wedge C_n$, where $C_i = x_i \vee \bar{x}_{i+1} \ge 1$.



Extension of *n***SLA - the SE Method**

Straightforward calculation yield that for this particular case $(|\mathscr{X}^*| = 5)$ variance reduction obtained from using $N^{(e)} = 2$ instead of $N^{(e)} = 1$ is about 150 times.

To overcome the drawback of high variance of nSLA we modify it as:

Instead of a single trajectory we ran in parallel multiple ones.

This will improve dramatically the non- uniformity issue. Our strategy is similar to the one proposed by Albert Einstein:

Everything should be made as simple as possible, but not simpler



SE in action. The sub-trees $\{100, 000, 001\}$ (in bold) of the original tree generated with $N^{(e)} = 2$.





To see how SE improves *n*SLA consider again the 2-SAT model with clauses $C_1 \wedge C_2 \wedge, \ldots, \wedge C_n$, where $C_i = x_i \vee \bar{x}_{i+1} \ge 1$. Figure below presents a graph with n = 4 variables and $|\mathscr{X}^*| = 5$.



Extension of *n***SLA: the SE Method**

The table below corresponds to the above figure for n = 99 and $|\mathscr{X}^*| = 100$. It shows how bad SE works for $N^{(e)} = 1$, (which is nSLA) and how SE improves for $N^{(e)} > 1$. Here $N^{(e)}$ denotes the number of multiple trajectories and RE-relative error.

$(N^{(e)},\ M)$	$ \widetilde{\mathscr{X}^*} $	RE
$(N^{(e)} = 1, M = 500)$	11.110	0.296
$(N^{(e)} = 10, M = 50)$	69.854	0.175
$(N^{(e)} = 50, M = 10)$	100.11	0.032



Performance of SE Algorithm for the 3-SAT 75×325 model with $N_t^{(e)} = 20$ and M = 100

Run N ₀	Iterations	$ \widetilde{\mathscr{X}^*} $	RE of $ \widetilde{\mathscr{X}^*} $	CPU
1	75	2359.780	0.045	2.74
2	75	2389.660	0.058	2.77
3	75	2082.430	0.078	2.79
4	75	2157.850	0.044	2.85
5	75	2338.100	0.035	2.88
Average	75	2247.077	0.040	2.83



Performance of SE for SAT 300×1080 model with $N_t^{(e)} = 300$, M = 300 and r = 1 with exact solution $|\mathscr{X}^*| = 3.297E + 24$.

	Run N ₀	Iterations	$ \widetilde{\mathscr{X}^*} $	RE of $ \widetilde{\mathscr{X}^*} $	CPU	
	1	300	3.30E+24	2.61E-03	2010.6	
	2	300	3.46E+24	5.10E-02	2271.8	
	3	300	3.40E+24	3.22E-02	2036.8	
	4	300	3.42E+24	4.00E-02	2275.8	
	5	300	3.39E+24	2.83E-02	2022.4	
	Average	300	3.36E+24	2.21E-02	2134.1	
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Comparison of the efficiencies of SE and standard splitting. It follows that SE is about 50 times faster than splitting.

Instance	Time	SE	SE RE	Split	Split RE
20x80	1 sec	15.0158	5.51E-03	14.97	3.96E-02
75x325	137 sec	2248.8	9.31E-03	2264.3	6.55E-02
75x270	122 sec	1.34E+06	1.49E-02	1.37E+06	3.68E-02
300x1080	1600 sec	3.32E+24	3.17E-02	3.27E+24	2.39E-01



The goal is to count the number of paths $|\mathscr{X}^*|$ in a dodecahedron graph from node 1 to node 20. Using full enumeration, we obtained $|\mathscr{X}^*| = 1338$.





Performance of the SE Algorithm for the dodecahedron graph with $N_t^{(e)} = 5$ and M = 20. Based on 100 runs, we found that RE = 0.0121.

Run N ₀	Iterations	$ \widetilde{\mathscr{X}}^* $	CPU
1	15	1567.3	3.467
2	17	1644.8	3.252
3	15	1220.3	2.956
4	15	1364.4	2.992
5	17	1567.4	3.134



Counting the Number of Perfect Matchings

(Permanent)

Consider the adjacency matrix A with |V| = 20, |E| = 78 and the number of perfect matchings (permanent) $|\mathscr{X}^*| = 255, 112$, obtained using full enumeration.





(Permanent)

Performance of the SE Algorithm for the matrix A. The relative error is near 0.0275.

Run N ₀	Iterations	$ \widetilde{\mathscr{X}^*} $	CPU
1	10	2.59E+05	1.911
2	10	2.48E+05	1.882
3	10	2.67E+05	1.889
4	10	2.44E+05	1.887
5	10	2.53E+05	1.889



We hope that following Albert Einstein's suggestion we made everything as simple as possible, but not simpler.

Thank You !!!