

# SUPPLEMENT B TO “BAYESIAN COMPLEMENTARY CLUSTERING, MCMC AND ANGLO-SAXON PLACENAMES”: COMPUTATIONAL COMPLEXITY OF THE MODEL

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We provide some results and references coming from the complexity theory literature regarding the intractability of the model described in Section 3.6 of Zanella (2014).

We consider the full conditional distribution  $\pi(\rho|\mathbf{x}, \sigma, \mathbf{p}^{(e)}, \lambda)$  arising from the model described in Section 3.6 of Zanella (2014). As in Zanella (2014), we will denote  $\pi(\rho | \mathbf{x}, \sigma, \mathbf{p}^{(e)}, \lambda)$  by  $\hat{\pi}(\rho)$ .

In Section 3.6.1 of Zanella (2014) we described  $\hat{\pi}(\rho)$  in terms of a hypergraph construction. There we show that every partition  $\rho$  that is admissible for our model can be interpreted as a partial matching. In such a way the sample space of  $\hat{\pi}(\rho)$  can be seen as the space of partial matchings contained in  $G$ , where  $G = (V, E)$  is the complete  $k$ -partite hypergraph induced by  $k$  sets  $V_1, \dots, V_k$  (see Section 3.6.1 of Zanella (2014) for more details and definitions of those terms). Moreover  $\hat{\pi}(\rho)$  is proportional to the weight of the matching  $\rho$ , defined as  $\prod_{e \in \rho} w(e)$ , where  $w(e)$  is the weight of the hyperedge  $e = \{x_1, \dots, x_s\} \in E$  defined in (3.7) of Zanella (2014)

**1. Computational complexity of  $\hat{\pi}(\rho)$ .** We consider the complexity of the following tasks: finding the normalizing constant of  $\hat{\pi}(\rho)$ , finding the mode  $\rho_{max} = \arg \max_{\rho \in \mathcal{P}_n} \hat{\pi}(\rho)$  and sampling from  $\hat{\pi}(\rho)$ .

We will distinguish between the two-color case ( $k = 2$ ) and the multi-color case ( $k \geq 3$ ) because they present substantially different complexity issues. Motivated by the corresponding literature in the theory of algorithms we often refer to those as two-dimensional and  $k$ -dimensional case.

1.1. *Finding the normalizing constant.* The normalizing constant of  $\hat{\pi}(\rho)$  is the sum of the weights of all the matchings  $\rho$  contained in  $G$ , that is the total weight of  $G$ . The problem of computing the total weight of a  $k$ -partite hypergraph is an  $\#P$ -hard counting problem (Valiant, 1979), even in the easiest version where  $k = 2$  and the edge weights can only be 0 or

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1 (i.e. counting the number of partial matchings in a bipartite graph). The  $\#P$ -hard complexity class for counting problems is analogous to the  $NP$ -hard complexity class for decision problems. A counting problem  $y$  is said to be  $\#P$ -hard if and only if every problem in  $\#P$  (i.e. every polynomially checkable counting problem) is Cook-reducible to  $y$  (see [Valiant \(1979\)](#) for definitions of these terms).

1.2. *Finding the posterior mode.* Finding  $\rho_{max} = \operatorname{argmax}_{\rho} \hat{\pi}(\rho)$  can be reduced to a  $k$ -dimensional optimal assignment problem as follows.

PROBLEM 1. (*k-dimensional optimal assignment problem*)

*Instance:*  $k$  sets  $I_1, \dots, I_k$  of size  $n$  and a cost function  $C : I_1 \times \dots \times I_k \rightarrow \mathbb{R}$ .  
*Problem:* find an assignment  $A$ , i.e. a subset  $A \subseteq I_1 \times \dots \times I_k$  containing each point of  $I_1, \dots, I_k$  exactly once, that minimizes  $\sum_{(i_1, \dots, i_k) \in A} C(i_1, \dots, i_k)$ .

First note that  $\rho_{max} = \operatorname{argmax}_{\rho} \sum_{e \in \rho} \log(w(e))$ , where  $\rho$  belongs to the set of matchings of  $G = (V, E)$ . Suppose now that  $V$  is made of  $n_1, \dots, n_k$  vertices of colors  $1, \dots, k$  respectively. For each color  $i$  add  $n - n_i$  auxiliary points that do not contribute to the weight of any edge. Each partial matching  $\rho$  of  $G$  can then be seen as a complete matching  $\tilde{\rho}$  (i.e. a matching connecting all the vertices in  $V$ ) in the augmented version of  $G$  such that  $\rho$  and  $\tilde{\rho}$  have the same weight. Expressing  $\tilde{\rho}$  as an assignment  $A$  we obtain Problem 1.

For  $k = 2$  this problem is efficiently solvable, in  $O(n^3)$  steps, using the Hungarian Algorithm ([Kuhn, 1955](#)), which is based on concepts from Optimal Transportation Theory ([Villani, 2009](#)). In contrast for  $k \geq 3$  this is an  $NP$ -hard optimization problem. Even more, unless  $P=NP$ , there is no deterministic polynomial-time approximation algorithm for a general cost function (i.e. the problem is not in  $APX$ ). The same holds even if the cost function  $C$  is decomposable as  $C(x_1, \dots, x_k) = \sum_{i \neq j} d(x_i, x_j)$ . Some polynomial time approximation algorithms exist if  $d$  satisfies the triangle inequality, but this is not our case (see, for example, [Crama and Spieksma \(1992\)](#) and [Bandelt, Crama and Spieksma, 1994](#)). [Balas and Saltzman \(1991\)](#) propose an heuristic algorithm for a general cost function  $C$ , but no constant of approximation is provided and only the case  $k = 3$  is considered.

Finally [De la Vega et al. \(2003\)](#) propose a polynomial time approximation scheme to partition  $n$  points of  $\mathbb{R}^d$  in  $m$  clusters that minimize the sum of the intra-clusters squared Euclidean distances. This problem is similar to ours but unfortunately the running time of their algorithm is polynomial in  $n$  but exponential in  $m$  and in our context it seems reasonable to suppose  $m$  to be of the same order of  $n$  in magnitude.

In conclusion the literature does not appear to provide a generic bounded-complexity method to obtain (or approximate)  $\rho_{max}$ . We might therefore resort to heuristics suited to our particular case.

1.3. *Approximate sampling.* In Statistical Physics a monomer-dimer system is a collection of  $n$  sites covered by molecules occupying one site, monomers, or two sites, dimers. It can be described with the following model.

MODEL 1. (*monomer-dimer system*)

*Instance:* A finite undirected graph  $G = (V, E)$  with non negative edge weights  $w : E \rightarrow [0, \infty)$  such that  $w(e) > 0$  for at least one  $e \in E$ .

*State space:* the set of partial matchings  $\rho \subseteq E$ .

*Probability distribution:*  $\hat{\pi}(\rho) \propto \prod_{e \in \rho} w(e)$ .

Although monomer-dimer system are usually considered in lattice frameworks, the two-dimensional version of our model can be interpreted as a monomer-dimer system (see Section 3.6.1 of Zanella, 2014). Jerrum and Sinclair (1996) propose a Metropolis-Hastings (MH) random walk algorithm to obtain approximate samples from monomer-dimer systems distributions in polynomial time. Using a canonical paths argument they prove that for any starting state  $\rho$  the mixing time of their Markov Chain satisfy

$$(1.1) \quad \tau_{\rho}(\epsilon) \leq 4(\#E)(\#V)w'^2 (\log(\#E)\#E + \log(\epsilon^{-1})),$$

where  $w' = \max\{1, \max_{e \in E} w(e)\}$ . Huber and Law (2012) consider the same Markov Chain starting from the mode  $\rho_{max}$  (which can be found in  $O(\#V)^3$  by the Hungarian algorithm) and improve slightly the bound (1.1) to

$$(1.2) \quad \tau_{\rho_{max}}(\epsilon) \leq 4(\#E)(\#V)w'^2 (\log(2)\#E + \log(\epsilon^{-1})).$$

REMARK 1. *The bounds (1.1) and (1.2) seem to be very conservative in practice. For example in the framework of Section 4.1.2 of Zanella (2014) the bound in (1.2) is of order  $10^9$  (depending weakly on  $\epsilon$ ). Convergence diagnostic methods, though, suggest that order  $10^5$  steps are enough to approximate  $\hat{\pi}$ .*

Can we approximately sample from  $\hat{\pi}(\rho)$  in polynomial time for  $k \geq 3$  too? This is equivalent to approximately count matchings in hypergraphs in polynomial time (see Chapter 3 of Jerrum (2003) for the relationship between approximate sampling and approximate counting). Unfortunately, as far as we are aware, there are not many results in this field. Karpinski, Rucinski and Szymanska (2012) try to extend the methods of Jerrum and Sinclair

(1996) to a hypergraph setting but they managed to do it only for a specific class of sparse hypergraphs, that do not include our case. They also prove a negative result: unless  $\text{NP}=\text{RP}$  ( $\text{RP}$  is the analogous of  $\text{P}$  but for randomized decision algorithms), there cannot be any FPRAS (Fully Polynomial Random Approximation Scheme, see for example [Jerrum, 2003](#)) to obtain approximate samples from the  $k$ -dimensional version of the monomer-dimer system for  $k \geq 6$  (see Proposition 3 of [Karpinski, Rucinski and Szymanska, 2012](#)). Strictly speaking, this still does not imply that such a scheme cannot exist for our problem, because our problem is constrained by additional conditions (e.g. our hypergraph is  $k$ -partite).

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