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Tutte polynomials and random-cluster models in Bernoulli cell complexes

By

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Abstract

This paper studies Bernoulli cell complexes from the perspective of persistent homology, Tutte polynomials, and random-cluster models. Following the previous work [9], we first show the asymptotic order of the expected lifetime sum of the persistent homology for the Bernoulli cell complex process on the ℓ-cubical lattice. Then, an explicit formula of the expected lifetime sum using the Tutte polynomial is derived. Furthermore, we study a higher dimensional generalization of the random-cluster model derived from the Edwards-Sokal type coupling, and show some basic results such as the positive association and the relation to the Tutte polynomial.

§ 1. Introduction

Random graphs have been studied in many fields of science such as communication systems, neural networks, infectious diseases and so on. As a mathematical framework of random graphs, one of the most standard models is the Erdös-Rényi random graphs [5]. Given a complete graph $K_n = (V_n, E_n)$, the Erdös-Rényi random graph $G(n, p)$ is defined as a subgraph of K_n with the same vertex set V_n in such a way that each edge appears in probability p. Namely, this random graph models the connection between each pair of individuals (e.g., humans, neurons, etc) independently of the others with the same randomness parameter.

Recently, the concept of random topology has emerged for the study of higher dimensional generalizations of random graphs, and is used for studying multi-individuals

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interactions (e.g., [2]). In this area, the randomness is often added on the simplicial or cell complexes, and classical results on random graphs which can be expressed by 0- or 1-dimensional homology (components or cycles, respectively) are now being generalized using higher dimensional homology and also new phenomena have been found (e.g., [11, 13]).

In the previous work [9], the authors study the ℓ-Linial-Meshulam random process on the maximal simplicial complex with n vertices by using persistent homology [3]. The Linial-Meshulam random process is a natural generalization of the Erdös-Rényi random graph process based on maximal (complete) simplicial complexes. For the ℓ-Linial-Meshulam process, they obtain the asymptotic order of the expected lifetime sum of the persistent homology as n goes to infinity, which can be regarded as a generalization of Frieze's theorem [6].

In the present paper, we introduce a wider class of random cell complexes which includes the Bernoulli bond percolation on graphs as well as the Linial-Meshulam random complex. Given a cell complex X, the ℓ-Bernoulli cell complex process $\mathcal{X} = \{X(t) : t \in [0,1]\}$ on X is defined in such a way that we first assign a uniform random variable t_σ on $[0,1]$ for each ℓ-cell σ independently and construct a filtration by $X(t) = X^{\ell-1} \sqcup \{\sigma : t_\sigma \leq t\}$, where $X^{\ell-1}$ is the $(\ell-1)$-skeleton of X. Thus, by fixing t, we obtain a random complex $X(t)$ called the Bernoulli cell complex, which is a higher dimensional generalization of the Erdös-Rényi random graph on K_n and the Bernoulli bond percolation model on graphs.

Following the previous work, in this paper, we study the Bernoulli cellular models by using persistent homology and Tutte polynomials. First, as in the previous work, we derive the order of the expected lifetime sum on the ℓ-cubical lattice, which is the most natural generalization of bond percolation on a sublattice in $\mathbb{Z}^d$. Then, we modify the result by Steele [14] into our setting by introducing a generalized version of Tutte polynomial and obtain an explicit formula of the lifetime sum for arbitrary cell complexes. Furthermore, we also investigate a higher dimensional generalization of the random-cluster model [7] for the Bernoulli cell complex. The random-cluster model is known to be a variant of the Erdös-Rényi random graph in which the edge probabilities are modified respecting the global topology. This model has a strong connection to the Ising and Potts models in statistical mechanics. In this paper, we reconsider the Edwards-Sokal coupling [4] from the viewpoint of cohomology, and generalize it to connect between the ℓ-dimensional random-cluster model and the Potts model.

§ 2. Persistent homology

In this paper, $\mathbb{R}_{\geq 0}$ (resp. $\mathbb{Z}_{\geq 0}$) is the set of nonnegative reals (resp. integers). Let X be a cell complex. The set of ℓ-cells and the ℓ-skeleton of X are denoted by

$X_\ell = \{\sigma_i^\ell : i = 1, \dots, n_\ell\}$ and X^ℓ, respectively. For an ℓ-cell σ_i^ℓ, ℓ is called its dimension, and the dimension $\dim X$ of X is given by the maximum dimension of cells in X. All cell complexes studied in this paper are assumed to be finite in the sense that $\dim X < \infty$ and $|X_\ell| < \infty$. Homology and cohomology groups are considered in the cellular setting, and its coefficient ring is taken from a field K with characteristic zero, unless specified otherwise. We refer the reader to [8] for the details of cellular homology and cohomology theory, or refer to Appendix A for its brief exposition.

Let $\mathcal{X} = \{X(t) : t \in \mathbb{R}_{\geq 0}\}$ be a right continuous filtration[1] of a cell complex X. Namely, $X(t)$ is a subcomplex of X, $X(t) \subset X(t')$ for $t \leq t'$, and $X(t) = \bigcap_{t<t'} X(t')$. We assume that there exists a saturation time T such that $X(T) = X$. For each cell $\sigma \in X$, let $t_\sigma = \min\{t \in \mathbb{R}_{\geq 0} : \sigma \in X(t)\}$ denote the birth time of σ.

Let $K[\mathbb{R}_{\geq 0}]$ be a monoid ring. The elements in $K[\mathbb{R}_{\geq 0}]$ are expressed by linear combinations of (formal) monomials az^t, where $a \in K$, $t \in \mathbb{R}_{\geq 0}$, and z is an indeterminate. The product of two elements are given by the linear extension of $az^t \cdot bz^s = abz^{t+s}$.

For a filtration $\mathcal{X} = \{X(t)\}_{t\in\mathbb{R}_{\geq 0}}$, the *persistent homology* of $\mathcal{X}$ is defined as a graded module

$$H_\ell(\mathcal{X}) = \bigoplus_{t\in\mathbb{R}_{\geq 0}} H_\ell(X(t)) \tag{2.1}$$

over the monoid ring $K[\mathbb{R}_{\geq 0}]$ with the action

$$z^a \cdot ([c_t])_{t\in\mathbb{R}_{\geq 0}} = ([c'_t])_{t\in\mathbb{R}_{\geq 0}}, \quad c'_t = \begin{cases} c_{t-a} & \text{if } t \geq a, \\ 0 & \text{otherwise.} \end{cases}$$

The persistent homology characterizes the persistence of topological features during the filtration $\mathcal{X}$. In particular, since $\mathcal{X}$ is defined on a finite cell complex with a saturation time T, the structure theorem of the persistent homology holds:

Theorem 2.1 ([15])**.** *There uniquely exist indices $p, q \in \mathbb{Z}_{\geq 0}$ and $(b_i, d_i) \in \mathbb{R}^2_{\geq 0}$ for $i = 1, \dots, p$ with $b_i < d_i$ and $b_i \in \mathbb{R}_{\geq 0}$ for $i = p+1, \dots, p+q$ such that the following isomorphism holds:*

$$H_\ell(\mathcal{X}) \simeq \bigoplus_{i=1}^{p} \left((z^{b_i}) \Big/ (z^{d_i}) \right) \oplus \bigoplus_{i=p+1}^{p+q} (z^{b_i}), \tag{2.2}$$

where (z^a) expresses an ideal in $K[\mathbb{R}_{\geq 0}]$ generated by the monomial z^a. When p or q is zero, the corresponding direct sum is ignored.

[1] In this paper, the term "filtration" is used to mean an increasing sequence of cell complexes as usual in topology.

Here b_i and d_i are called the birth and death times, respectively, and they measure the events of appearance and disappearance of topological features in the filtration $\mathcal{X}$. Namely, it expresses that a homology generator is born at $H_\ell(X(b_i))$, persists during $H_\ell(X(t))$ for $b_i \leq t < d_i$, and dies at $H_\ell(X(d_i))$. The reduced persistent homology $\tilde{H}_\ell(\mathcal{X})$ is defined by using the reduced homology $\tilde{H}_\ell(X(t))$ in (2.1), which corresponds to remove the generator with maximum lifetime in $H_0(\mathcal{X})$.

The lifetime l_i of the birth-death pair (b_i, d_i) is defined by $l_i = d_i - b_i$. For $p+1 \leq i \leq p+q$, we assign the death time as the saturation time $d_i = T$. In this paper, we study the lifetime sum of the ℓ-th reduced persistent homology $\tilde{H}_\ell(\mathcal{X})$ given by $L_\ell = \sum_{i=1}^{p+q} l_i$ for $\ell \geq 1$ and $L_0 = \sum_{i=1}^{p+q-1} l_i$. Then, we can easily check the following

$$L_\ell = \int_{[0,T]} \tilde{\beta}_\ell(t) dt, \tag{2.3}$$

where $\tilde{\beta}_\ell(t) = \tilde{\beta}_\ell(X(t)) = \operatorname{rank} \tilde{H}_\ell(X(t))$ is the ℓ-th reduced betti number of $X(t)$.

§ 3. Bernoulli model for cell complexes

§ 3.1. Lifetime sum and generalization of Frieze's theorem

Let X be a cell complex. For $F \subset X_\ell$, we set a subcomplex of X by $X_F = X^{\ell-1} \sqcup F$. For $p \in [0,1]$, the *ℓ-Bernoulli cell complex on X* is defined as a random cell complex whose law is given by the probability measure P_p on $\Omega_\ell(X) = \{X_F : F \subset X_\ell\}$ such that $P_p(X_F) = p^{|F|}(1-p)^{|X_\ell \setminus F|}$. We often identify $\Omega_\ell(X)$ with $\{0,1\}^{X_\ell}$ as usual, and for an element $F \in \{0,1\}^{X_\ell}$, we use the notation

$$F(\sigma) = \begin{cases} 1 & \text{for } \sigma \in F, \\ 0 & \text{for } \sigma \notin F. \end{cases}$$

Note that, when X is given by the complete graph and $\ell = 1$, this model is nothing but the Erdös-Rényi random graph model [5].

We next introduce a random filtration of the Bernoulli cell complex model. Let $\{t_\sigma : \sigma \in X_\ell\}$ be i.i.d. random variables uniformly distributed on $[0,1]$. We regard t_σ as the birth time of the ℓ-cell σ. Let $\mathcal{X} = \{X^\ell(t)\}_{0 \leq t \leq 1}$ be an increasing stochastic process on cell complexes defined by

$$X^\ell(t) = X^{\ell-1} \sqcup \{\sigma \in X_\ell : t_\sigma \leq t\}.$$

The process starts from the $(\ell-1)$-skeleton $X^{\ell-1}$ at time 0 and ends up with the ℓ-skeleton X^ℓ at time 1, i.e.,

$$X^{\ell-1} = X^\ell(0) \subset X^\ell(t) \subset X^\ell(1) = X^\ell.$$

We call $\mathcal{X}$ the *ℓ-Bernoulli cell complex process on X*. We note that, by definition, $X^\ell(t)$ is equal in law to the ℓ-Bernoulli cell complex for each $t \in [0,1]$.

In the paper [9], the authors study the ℓ-Linial-Meshulam process ($\ell \geq 1$), which is nothing but the Bernoulli cell complex process on the maximal simplicial complex Δ_n with n-vertices, and show the asymptotic order of the expected lifetime sum of the $(\ell-1)$-st reduced persistent homology.

Theorem 3.1 ([9]). *Let $L_{\ell-1}$ be the lifetime sum of the $(\ell-1)$-st reduced persistent homology of the ℓ-Linial-Meshulam process ($\ell \geq 1$) on Δ_n. Then,*

$$\mathbb{E}[L_{\ell-1}] = \Theta(n^{\ell-1})$$

as $n \to \infty$.

One of the key steps to obtain this order is the following formula of the lifetime sum relating to the weight of spanning acycles. We recall [9] that a subset $S \subset X_k$ is called a *k-spanning acycle* of X if $\tilde{H}_k(X_S;\mathbb{Z}) = 0$ and $|\tilde{H}_{k-1}(X_S;\mathbb{Z})| < \infty$, and denote the set of k-spanning acycles by $\mathcal{S}^k$. The weight of S is given by $\mathrm{wt}(S) = \sum_{\sigma\in S} t_\sigma$.

Theorem 3.2 ([9]). *Let $\mathcal{X} = \{X(t)\}_{t\in\mathbb{R}_{\geq 0}}$ be a filtration of a cell complex X satisfying*

$$\tilde{\beta}_{\ell-1}(X^\ell) = \tilde{\beta}_{\ell-2}(X^{\ell-1}) = 0.$$

Then, the lifetime sum of the $(\ell-1)$-st reduced persistent homology of $\mathcal{X}$ is expressed as

$$L_{\ell-1} = \min_{S\in\mathcal{S}^\ell} \mathrm{wt}(S) - \max_{S\in\mathcal{S}^{\ell-1}} \mathrm{wt}(X_{\ell-1} \setminus S).$$

Here, we remark that the original formula is derived for simplicial complexes, and all the proofs to derive the above formula for cell complexes are similarly performed as in the original discussion. We also note from Theorem 3.2 that L_0 is the same as the weight of the minimum spanning tree. Hence, Theorem 3.1 can be regarded as a higher dimensional generalization of Frieze's theorem [6], known as $\mathbb{E}[L_0] \to \zeta(3)$ as the number of vertices tends to ∞, where $\zeta(s)$ is Riemann's zeta function.

§ 3.2. Bernoulli cell complex on the ℓ-cubical lattice

Let I be a closed interval in $\mathbb{R}$ of the form $I = [a, a+1]$ or $I = [a, a]$ for some $a \in \mathbb{Z}$. We call these intervals elementary intervals. Elementary intervals of the form $[a, a+1]$ (resp. $[a, a]$) are called nondegenerate (resp. degenerate). A cell

$$Q = I_1 \times \cdots \times I_\ell \subset \mathbb{R}^\ell$$

consisting of elementary intervals I_k, $k = 1, \dots, \ell$, is called an elementary cube in $\mathbb{R}^\ell$. The dimension $\dim Q$ of Q is given by the number of nondegenerate intervals. For more details on cubical settings, we refer the reader to [10].

For $\boldsymbol{n} = (n_0, \dots, n_\ell)$ with $n_k \in \mathbb{N}$, let $\widetilde{\mathrm{CL}}(\boldsymbol{n})$ be the cell complex consisting of all the elementary cubes Q in $[0, n_0] \times \cdots \times [0, n_\ell] \subset \mathbb{R}^{\ell+1}$. We define the *$\ell$-cubical lattice* $\mathrm{CL}(\boldsymbol{n})$ in $\mathbb{R}^{\ell+1}$ as the ℓ-skeleton of $\widetilde{\mathrm{CL}}(\boldsymbol{n})$. For $\boldsymbol{n} = (n, \dots, n)$ with the same entry n, we simply denote them by $\widetilde{\mathrm{CL}}(n)$ and $\mathrm{CL}(n)$, respectively.

When $\ell = 1$, the 1-Bernoulli cell complex model on $\mathrm{CL}(n)$ in $\mathbb{R}^2$ is the Bernoulli bond percolation model on a sublattice in $\mathbb{Z}^2$. In this section, we prove the following theorem.

Theorem 3.3. *Let $L_{\ell-1}$ be the expected lifetime sum of the ℓ-Bernoulli cell complex process on the ℓ-cubical lattice $\mathrm{CL}(n)$ in $\mathbb{R}^{\ell+1}$. Then,*

$$\mathbb{E}[L_{\ell-1}] = \Theta(n^{\ell+1})$$

as $n \to \infty$.

This theorem shows that the asymptotic order of the expected lifetime sum is equal to that of the number of vertices in $\mathrm{CL}(n)$.

Before proving the theorem, we give some basic properties of $\mathrm{CL}(\boldsymbol{n})$ and ℓ-spanning acycles on it.

Lemma 3.4. *Let $\tilde{X} = \widetilde{\mathrm{CL}}(\boldsymbol{n})$. Then, for $k \in \{0, 1, \dots, \ell+1\}$,*

$$|\tilde{X}_k| = \sum_{p=k}^{\ell+1} \binom{p}{k} S_p(\boldsymbol{n}), \tag{3.1}$$

where $S_p(\boldsymbol{n})$ is the elementary symmetric polynomial in $\boldsymbol{n}$ of degree p.

Proof. Let $\tilde{X} = \widetilde{\mathrm{CL}}(\boldsymbol{n})$. We can see that

$$|\tilde{X}_k| = \sum_{\substack{I \subset [\ell] \\ |I| = k}} \left(\prod_{i \in I} n_i \right) \left(\prod_{j \in [\ell] \setminus I} (n_j + 1) \right)$$

for $k = 0, 1, 2, \dots, \ell+1$, where $[\ell] = \{0, \dots, \ell\}$. It is also easy to see that

$$G(z, \boldsymbol{n}) := \sum_{k=0}^{\ell+1} |\tilde{X}_k| z^k = \prod_{i=0}^{\ell} (n_i z + n_i + 1).$$

By expanding the right-hand side, we have

$$G(z, \boldsymbol{n}) = \sum_{p=0}^{\ell+1} S_p(\boldsymbol{n})(1+z)^p = \sum_{k=0}^{\ell+1} z^k \sum_{p=k}^{\ell+1} \binom{p}{k} S_p(\boldsymbol{n}),$$

and this completes the proof. □

We remark that, since $X = \mathrm{CL}(\boldsymbol{n})$ is the ℓ-skeleton of $\tilde{X} = \widetilde{\mathrm{CL}}(\boldsymbol{n})$, $|X_k| = |\tilde{X}_k|$ for $k \in \{0, \dots, \ell\}$.

Proposition 3.5. *For $\boldsymbol{n} = (n_0, \dots, n_\ell)$, the number of ℓ-cells in ℓ-spanning acycles is $N(\boldsymbol{n}) = \ell S_{\ell+1}(\boldsymbol{n}) + S_\ell(\boldsymbol{n})$.*

Proof. Let $\tilde{X} = \widetilde{\mathrm{CL}}(\boldsymbol{n})$, $X = \mathrm{CL}(\boldsymbol{n})$ and $F \subset X_\ell$. The Euler characteristics of $\tilde{X}$ and X_F are given by $\chi(\tilde{X}) = 1$ and $\chi(X_F) = 1 + (-1)^{\ell-1}\tilde{\beta}_{\ell-1}(X_F) + (-1)^\ell \tilde{\beta}_\ell(X_F)$, respectively, since $\tilde{X}$ is contractible and the $(\ell-1)$-skeleton of X_F is homotopy equivalent to the wedge sum of $(\ell-1)$-spheres. By applying the Euler-Poincaré formula to $\tilde{X}$ and X_F and taking the difference, we easily see that $\tilde{\beta}_\ell(X_F)$ and $\tilde{\beta}_{\ell-1}(X_F)$ are related as

$$\tilde{\beta}_\ell(X_F) = \tilde{\beta}_{\ell-1}(X_F) + |F| - (|\tilde{X}_\ell| - |\tilde{X}_{\ell+1}|). \tag{3.2}$$

Since $\tilde{\beta}_\ell(X_F) = \tilde{\beta}_{\ell-1}(X_F) = 0$ for $F \in \mathcal{S}^\ell$, (3.1) and (3.2) lead to $N(\boldsymbol{n}) = |F| = |\tilde{X}_\ell| - |\tilde{X}_{\ell+1}| = \ell S_{\ell+1}(\boldsymbol{n}) + S_\ell(\boldsymbol{n})$ for $F \in \mathcal{S}^\ell$. □

Proof of Theorem 3.3. From (3.1) the inequality $\tilde{\beta}_{\ell-1}(t) \le |X_{\ell-1}| = \binom{\ell+1}{2} n^{\ell+1} + O(n^\ell)$ holds, which together with (2.3) implies $\mathbb{E}[L_{\ell-1}] \le \binom{\ell+1}{2} n^{\ell+1} + O(n^\ell)$. For lower bound, we note that the assumption in Theorem 3.2 is satisfied on $\mathrm{CL}(n)$, and we have $L_{\ell-1} = \min_{S \in \mathcal{S}^\ell} \mathrm{wt}(S)$. Let $0 \le t_{\sigma_1} < \cdots < t_{\sigma_m} \le 1$ be the reordering of the ℓ-cells with respect to the birth times, where $m = |X_\ell| = (\ell+1)n^\ell(n+1)$ from (3.1). Hence, Theorem 3.2, Proposition 3.5, and the expectation of the ordered statistics lead to

$$\mathbb{E}[L_{\ell-1}] \ge \mathbb{E}[t_{\sigma_1} + \cdots + t_{\sigma_{N(n)}}] = \sum_{k=1}^{N(n)} \frac{k}{m+1} = \frac{\ell^2}{2(\ell+1)} n^{\ell+1} + O(n^\ell).$$

This concludes the proof. □

§ 4. Tutte polynomial and expected lifetime sum

This section derives an explicit formula for the expected lifetime sum in the Bernoulli cell complex process using the Tutte polynomial. In this paper, we define the *ℓ-Tutte polynomial* of a cell complex X as

$$T_\ell(X; x, y) = \sum_{F \subset X_\ell} (x-1)^{\tilde{\beta}_{\ell-1}(X_F)} (y-1)^{\tilde{\beta}_\ell(X_F)}. \tag{4.1}$$

This definition is essentially the same as [12], and its contraction-deletion reduction is also studied in [1]. We also note that $T_\ell(X; 1, 1) = |\mathcal{S}^\ell|$ counts the number of ℓ-spanning acycles.

First of all, as used in (3.2), we have

$$\tilde{\beta}_\ell(X_F) = \tilde{\beta}_{\ell-1}(X_F) + |F| - \rho(X),$$

where $\rho(X)$ is independent of the choice of $F \subset X_\ell$ and expressed as

$$\rho(X) = (-1)^\ell \left(\sum_{k=0}^{\ell-2} (-1)^k \tilde{\beta}_k(X) - \sum_{k=0}^{\ell-1} (-1)^k |X_k| + 1 \right).$$

Then, the ℓ-Tutte polynomial can be represented as an expectation with respect to the Bernoulli measure:

$$\begin{aligned} T_\ell(X; x, y) &= \sum_{F \subset X_\ell} (x-1)^{\tilde{\beta}_{\ell-1}(X_F)} (y-1)^{\tilde{\beta}_\ell(X_F)} \\ &= \sum_{F \subset X_\ell} (x-1)^{\tilde{\beta}_{\ell-1}(X_F)} (y-1)^{\tilde{\beta}_{\ell-1}(X_F) + |F| - \rho(X)} \\ &= y^{|X_\ell|} (y-1)^{-\rho(X)} \sum_{F \subset X_\ell} \left(1 - \frac{1}{y}\right)^{|F|} \left(\frac{1}{y}\right)^{|X_\ell \setminus F|} \{(x-1)(y-1)\}^{\tilde{\beta}_{\ell-1}(X_F)} \\ &= y^{|X_\ell|} (y-1)^{-\rho(X)} \mathbb{E}\left[\{(x-1)(y-1)\}^{\tilde{\beta}_{\ell-1}(X_F)} \right]. \end{aligned}$$

Here the law of X_F is given by the Bernoulli cell complex model with probability $1 - \frac{1}{y}$.

For a Bernoulli cell complex process $\mathcal{X} = \{X(t)\}_{0 \le t \le 1}$ of X, we consider the Laplace transform of $\beta_{\ell-1}(X(t))$ defined by

$$\phi(\lambda, t) = \mathbb{E}\left[e^{\lambda \tilde{\beta}_{\ell-1}(X(t))} \right]. \tag{4.2}$$

Then, by setting $e^\lambda = (x-1)(y-1)$ and $t = 1 - \frac{1}{y}$, we immediately obtain from (4.1) that

$$\phi(\lambda, t) = y^{-|X_\ell|} (y-1)^{\rho(X)} T_\ell \left(X; 1 + \frac{1-t}{t} e^\lambda, \frac{1}{1-t} \right). \tag{4.3}$$

From these expressions (4.2) and (4.3), by taking logarithmic derivative at $\lambda = 0$, we have

$$\frac{\partial}{\partial \lambda} \log \phi(\lambda, t) \Big|_{\lambda=0} = \mathbb{E}[\tilde{\beta}_{\ell-1}(X_t)] = \frac{1-t}{t} \cdot \frac{\partial_x T_\ell \left(X; \frac{1}{t}, \frac{1}{1-t} \right)}{T_\ell \left(X; \frac{1}{t}, \frac{1}{1-t} \right)}.$$

Thus, from (2.3), this leads to following formula.

Theorem 4.1. *Let $L_{\ell-1}$ be the lifetime sum of the $(\ell-1)$-st reduced persistent homology of the ℓ-Bernoulli complex process on X. Then,*

$$\mathbb{E}[L_{\ell-1}] = \int_0^1 \frac{1-t}{t} \cdot \frac{\partial_x T_\ell \left(X; \frac{1}{t}, \frac{1}{1-t} \right)}{T_\ell \left(X; \frac{1}{t}, \frac{1}{1-t} \right)} dt. \tag{4.4}$$

This can be regarded as a formula for minimum spanning acycle taking Theorem 3.2 into account. In this context, the above formula for $\ell = 1$ is derived in [14].

Example 4.2. Let Δ_n^2 be the 2-skeleton of the maximal simplicial complex with n vertices. Let us write $L_1(n)$ for the lifetime sum of the 1st reduced persistent homology of the 2-Linial-Meshulam process on Δ_n^2. For $n = 4, 5$, the Tutte polynomials (4.1) and the expected lifetime sum (4.4) are obtained as follows.

$$T_2(\Delta_4^2; x, y) = (x-1)^3 + 4(x-1)^2 + 6(x-1) + 4 + (y-1) = x^3 + x^2 + x + y$$

$$\mathbb{E}[L_1(4)] = \int_0^1 (1-t)^2(3+2t+t^2)dt = \frac{6}{5}$$

$$T_2(\Delta_5^2; x, y) = 6x + 15x^2 + 15x^3 + 10x^4 + 4x^5 + x^6 + 6y + 20xy + 15x^2y + 5x^3y + 11y^2 + 10xy^2 + 6y^3 + y^4$$

$$\mathbb{E}[L_1(5)] = \int_0^1 (1-t)^3(1+t)(6+2t+4t^2-4t^3-t^4-8t^5+6t^6)dt = \frac{1817}{924} = 1.96645\ldots$$

Similarly, we can compute $\mathbb{E}[L_1(6)] = \frac{5337295}{1939938} = 2.75127\ldots$.

§ 5. The ℓ-random-cluster model

The ℓ-Bernoulli cell complex is regarded as the product measure of those defined on ℓ-cells with the same probability p. In the context of the Erdös-Rényi random graph, there is a variant known as the random-cluster model [7] which differs from the product measure by respecting the topology of the connectedness. For $p \in [0, 1]$ and $q > 0$, the random-cluster measure $\phi_{p,q}$ on $\Omega_1(X)$ is defined by

$$\phi_{p,q}(X_F) = \frac{1}{Z_{\mathrm{RC}}} p^{|F|}(1-p)^{|X_1 \setminus F|} q^{\beta_0(X_F)}, \tag{5.1}$$

where Z_{RC} is the normalizing constant (or partition function). By definition, the Erdös-Rényi random graph corresponds to the model with $q = 1$.

When q is an integer with $q \geq 2$, the random-cluster model is known to be related to the so-called Ising and Potts models arising in the statistical mechanics. In this model, we consider an assignment $s \in S = \{0, 1, \ldots, q-1\}^{X_0}$ of a value $s_x \in \{0, 1, \ldots, q-1\}$ to each vertex $x \in X_0$. For $s \in S$ and $e = |xy| \in X_1$, let us write $\delta_e(s) = \delta_{s_x, s_y}$, where $\delta_{a,b}$ is the Kronecker delta. Then, the probability law of the Potts model (the Ising model for $q = 2$) is given by

$$\pi_{\alpha,q}(s) = \frac{1}{Z_{\mathrm{P}}} e^{-\alpha H(s)}, \quad s \in S, \tag{5.2}$$

where Z_{P} is the normalizing constant and the Hamiltonian is given by

$$H(s) = -\sum_{e \in X_1} \delta_e(s).$$

Then, it is known in [4] that the random-cluster model and the Potts model can be coupled with a coupling measure μ on $S \times \Omega_1(X)$ defined by

$$\mu(s, X_F) = \frac{1}{Z_{\mathrm{ES}}} \prod_{e \in X_1} \{(1-p)\delta_{F(e),0} + p\delta_{F(e),1}\delta_e(s)\} \tag{5.3}$$

so that the random-cluster model and Potts model are obtained as the marginals of s and X_F, respectively.

In the rest of this section, we modify the coupling (5.3) so that the higher dimensional generalizations of the random-cluster model and the Potts model based on the Bernoulli cell complex model are derived as the marginals. The key for the higher dimensional generalization is to regard $s \in S$ as a 0-cochain in $C^0(X; \mathbb{Z}_q)$ and $\delta_e(s)$ as a local obstruction of s along the edge e. We also note that the coupling (5.3) can also be written as

$$\mu(s, X_F) = \frac{1}{Z_{\mathrm{ES}}}(1-p)^{|X_1 \setminus F|} p^{|F|} \prod_{e \in F} \delta_e(s).$$

Then, $\prod_{e \in F} \delta_e(s) = 1$ if and only if $\partial^0 s|_{X_F} = 0$, i.e., $s \in Z^0(X_F; \mathbb{Z}_q)$. Here ∂^0 and $Z^0(X_F; \mathbb{Z}_q)$ express the 0-coboundary map of the cochain complex $C_*(X; \mathbb{Z}_q)$ and the cocycle group of X_F.

From this observation, we now generalize the coupling so that the marginals naturally define a random-cluster model and a Potts model on a cell complex X. In the following derivation, we assume $\mathbb{Z}_q = \{0, 1, \ldots, q-1\}$ to be a finite field with the order q and use it for the coefficient ring of cohomology. Let

$$\cdots \longrightarrow C^{\ell-1}(X; \mathbb{Z}_q) \xrightarrow{\partial^{\ell-1}} C^{\ell}(X; \mathbb{Z}_q) \xrightarrow{\partial^{\ell}} \cdots$$

be the cellular cochain complex and $H^k(X; \mathbb{Z}_q)$ be its cohomology. We note that $H^k(X; \mathbb{Z}_q) \simeq \mathrm{Hom}_{\mathbb{Z}_q}(H_k(X; \mathbb{Z}_q), \mathbb{Z}_q)$, and especially, $\dim H_k(X; \mathbb{Z}_q) = \dim H^k(X; \mathbb{Z}_q)$. We denote this dimension by $\beta_k(X; \mathbb{Z}_q)$ and call it the k-th Betti number with $\mathbb{Z}_q$ coefficient.

We define a coupling μ on $C^{\ell-1}(X; \mathbb{Z}_q) \times \Omega_\ell(X)$ by

$$\mu(s, X_F) \propto \prod_{\sigma \in X_\ell} \left\{(1-p)\delta_{F(\sigma),0} + p\delta_{F(\sigma),1}\delta_\sigma(s)\right\}, \tag{5.4}$$

where

$$\delta_\sigma(s) = \begin{cases} 1 & \text{if } \partial^{\ell-1} s(\sigma) = 0, \\ 0 & \text{otherwise.} \end{cases}$$

We note that, when $\ell = 1$, this is the same as the original definition of δ_σ.

The first marginal becomes

$$\begin{aligned}\sum_{X_F \in \Omega_\ell(X)} \mu(s, X_F) &\propto \sum_{X_F \in \Omega_\ell(X)} \prod_{\sigma \in X_\ell} \left\{(1-p)\delta_{F(\sigma),0} + p\delta_{F(\sigma),1}\delta_\sigma(s)\right\} \\ &= \prod_{\sigma \in X_\ell} \{(1-p) + p\delta_\sigma(s)\}.\end{aligned}$$

By setting $p = 1 - e^{-\alpha}$, we have

$$\begin{aligned}\sum_{X_F \in \Omega_\ell(X)} \mu(s, X_F) &\propto \prod_{\sigma \in X_\ell} \{e^{-\alpha} + (1 - e^{-\alpha})\delta_\sigma(s)\} \\ &= e^{-\alpha|X_\ell|} \prod_{\sigma \in X_\ell} \{1 + (e^\alpha - 1)\delta_\sigma(s)\} \\ &= e^{-\alpha|X_\ell|} e^{-\alpha H(s)},\end{aligned}$$

where $H(s) = -\sum_{\sigma \in X_\ell} \delta_\sigma(s)$. For $\ell = 1$, this recovers the q-Potts model (5.2).

The second marginal becomes

$$\begin{aligned}\sum_{s \in C^{\ell-1}(X;\mathbb{Z}_q)} \mu(s, X_F) &\propto \sum_{s \in C^{\ell-1}(X;\mathbb{Z}_q)} \prod_{\sigma \in X_\ell} \left\{(1-p)\delta_{F(\sigma),0} + p\delta_{F(\sigma),1}\delta_\sigma(s)\right\} \\ &= (1-p)^{|X_\ell \setminus F|} p^{|F|} \sum_{s \in C^{\ell-1}(X;\mathbb{Z}_q)} \prod_{\sigma \in F} \delta_\sigma(s).\end{aligned} \tag{5.5}$$

Note that $\prod_{\sigma \in F} \delta_\sigma(s) = 1$ if and only if $s \in Z^{\ell-1}(X_F; \mathbb{Z}_q)$. Hence, we have

$$\sum_{s \in C^{\ell-1}(X)} \mu(s, X_F) \propto (1-p)^{|X_\ell \setminus F|} p^{|F|} q^{\dim Z^{\ell-1}(X_F;\mathbb{Z}_q)}. \tag{5.6}$$

For $\ell = 1$, since $\beta_0(X_F) = \beta_0(X_F; \mathbb{Z}_q) = \dim Z^0(X_F; \mathbb{Z}_q)$, this recovers the random-cluster model (5.1).

The second marginal (5.6) is defined on the space $\Omega_\ell(X)$ in which each element X_F has the same $(\ell-1)$-skeleton $X^{\ell-1}$. This leads to $B^{\ell-1}(X_F; \mathbb{Z}_q) = B^{\ell-1}(X; \mathbb{Z}_q)$, and in particular, $\dim B^{\ell-1}(X_F; \mathbb{Z}_q)$ is independent of the choice of F. Therefore, by appropriately changing the normalizing constant, the second marginal has the following formulation

$$\mu_{p,q}(Y) = \frac{1}{Z_{p,q}} p^{|Y_\ell|} (1-p)^{|X_\ell \setminus Y_\ell|} q^{\beta_{\ell-1}(Y;\mathbb{Z}_q)}, \qquad Y \in \Omega_\ell(X).$$

In the derivation above, we assume that q is a prime number, and $\beta_{\ell-1}(Y; \mathbb{Z}_q)$ is dependent on the choice of q for $\ell > 1$. In what follows, we study a slightly generalized probability measure

$$\mu_{p,q}(Y) = \frac{1}{Z_{p,q}} p^{|Y_\ell|} (1-p)^{|X_\ell \setminus Y_\ell|} q^{\beta_{\ell-1}(Y)}, \qquad Y \in \Omega_\ell(X)$$

for $p \in [0,1]$ and $q > 0$. Here, we also allow to take the coefficient of the Betti number $\beta_{\ell-1}(Y) = \beta_{\ell-1}(Y;K)$ in some fixed field K, which is not necessary to be $\mathbb{Z}_q$. We call this probability measure the *ℓ-random-cluster measure* on a cell complex X with K coefficient.

In this section, we show two basic properties on $\mu_{p,q}$. Both of them are independent of the choice of K.

Theorem 5.1. *Let X be a cell complex. For $p \in (0,1)$ and $q \geq 1$, the ℓ-random-cluster measure $\mu_{p,q}$ on X is positively associated, i.e.,*

$$\mu_{p,q}(fg) \geq \mu_{p,q}(f)\mu_{p,q}(g)$$

for any increasing functions $f, g : \Omega_\ell(X) \to \mathbb{R}$.

For $\ell = 1$, the positive association plays a key role to study phase transitions of the 1-random-cluster model of infinite graphs. We generalized the random-cluster model for higher dimension so that topological nature of this model became clearer. Here we give a proof of the theorem by emphasizing with a topological viewpoint.

To prove the theorem, we need the following lemma.

Lemma 5.2. *For topological spaces A and B,*

$$\beta_k(A \cap B) + \beta_k(A \cup B) \geq \beta_k(A) + \beta_k(B).$$

Proof. Let us consider the Mayer-Vietoris sequence:

$$\cdots \longrightarrow H_k(A \cap B) \xrightarrow{i} H_k(A) \oplus H_k(B) \xrightarrow{j} H_k(A \cup B) \xrightarrow{\delta} H_{k-1}(A \cap B) \longrightarrow \cdots$$

This exact sequence leads to the following relations:

$$\begin{aligned}
\beta_k(A \cap B) &= \operatorname{rank} i + \dim \ker i, \\
\beta_k(A \cup B) &= \operatorname{rank} \delta + \dim \ker \delta, \\
\beta_k(A) + \beta_k(B) &= \operatorname{rank} j + \dim \ker j.
\end{aligned}$$

Then, it follows from $\operatorname{im} i = \ker j$, and $\operatorname{im} j = \ker \delta$ that

$$\beta_k(A \cap B) + \beta_k(A \cup B) - \beta_k(A) - \beta_k(B) = \dim \ker i + \operatorname{rank} \delta \geq 0.$$

This completes the proof. □

Proof of Theorem 5.1. Since $\mu_{p,q}$ is strictly positive for $p \in (0,1)$, it is sufficient to prove that the measure $\mu_{p,q}$ has the so-called FKG lattice property [7]. Here, the FKG lattice property is expressed as

$$\mu_{p,q}(Y \cup Y')\mu_{p,q}(Y \cap Y') \geq \mu_{p,q}(Y)\mu_{p,q}(Y')$$

for $Y, Y' \in \Omega_\ell(X)$. If $q \geq 1$, this is equivalent to show

$$\beta_{\ell-1}(Y \cup Y') + \beta_{\ell-1}(Y \cap Y') \geq \beta_{\ell-1}(Y) + \beta_{\ell-1}(Y'),$$

which is proved from Lemma 5.2. □

Next, we show a relation between the normalizing constant and the ℓ-Tutte polynomial. Here, for the consistency to the known result for $\ell = 1$, we use the non-reduced ℓ-Tutte polynomial

$$T_\ell(X; x, y) = \sum_{F \subset X_\ell} (x-1)^{\beta_{\ell-1}(X_F)} (y-1)^{\beta_\ell(X_F)}. \tag{5.7}$$

Theorem 5.3. *Let X be a cell complex. Then, the normalizing constant $Z_{p,q}$ of the ℓ-random-cluster model on X is expressed as*

$$Z_{p,q} = \left(\frac{p}{1-p}\right)^{\beta_{\ell-1}(X)} p^{r(X)} (1-p)^{\beta_\ell(X^\ell)} T_\ell\left(X; 1 + \frac{q(1-p)}{p}, \frac{1}{1-p}\right),$$

where $T(X; x, y)$ is the ℓ-Tutte polynomial (5.7) *and $r(X) = \operatorname{rank} \partial_\ell$.*

Proof. Since $\beta_\ell(Y) = |Y_\ell| - r(Y)$ and $\beta_{\ell-1}(Y) = \dim \ker \partial_{\ell-1} - r(Y)$, we have

$$|Y_\ell| = \beta_\ell(Y) - \beta_{\ell-1}(Y) + \dim \ker \partial_{\ell-1}$$

for every $Y \in \Omega_\ell$. Therefore,

$$\begin{aligned}
&\sum_{Y \in \Omega_\ell} p^{|Y_\ell|} (1-p)^{|X_\ell \setminus Y_\ell|} q^{\beta_{\ell-1}(Y)} \\
&= p^{\dim \ker \partial_{\ell-1}} (1-p)^{|X_\ell| - \dim \ker \partial_{\ell-1}} \sum_{Y \in \Omega_\ell} \left(\frac{q(1-p)}{p}\right)^{\beta_{\ell-1}(Y)} \left(\frac{p}{1-p}\right)^{\beta_\ell(Y)} \\
&= \left(\frac{p}{1-p}\right)^{\beta_{\ell-1}(X)} p^{r(X)} (1-p)^{\beta_\ell(X^\ell)} T_\ell\left(X; 1 + \frac{q(1-p)}{p}, \frac{1}{1-p}\right).
\end{aligned}$$

□

As is the case of the 1-random-cluster model on graphs, the situation is more subtle for $q < 1$. Here we just remark that as $p \to 0$ and $q/p \to 0$

$$\mu_{p,q}(Y) \to \frac{1}{|\mathcal{S}^\ell|} \mathbf{1}(Y \in \mathcal{S}^\ell),$$

that is, the ℓ-random-cluster measure converges to the uniform ℓ-spanning acycle measure.

§ 6. Discussion

In this paper, we studied the ℓ-Bernoulli cell complexes from the perspective of persistent homology, Tutte polynomials, and the random-cluster model. From the positive association property on the ℓ-random-cluster model, it would become an interesting research area to study infinite cell complex models (e.g., the ℓ-cubical lattice), thermodynamic limits, and phase transitions.

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§ Appendix A. Cellular homology and cohomology

Let $X = \{\sigma_i^\ell : i = 1, \dots, n_\ell, \ell = 1, \dots, d\}$ be a d-dimensional cell complex. The cellular chain complex of X is defined by the horizontal sequence of the diagram

(A.1)
$$\begin{array}{ccccccccc} & & & & H_{\ell-1}(X^{\ell-1}) & & & & \\ & & & \overset{d_\ell}{\nearrow} & & \overset{j_{\ell-1}}{\searrow} & & & \\ \cdots & \longrightarrow & H_\ell(X^\ell, X^{\ell-1}) & & \xrightarrow{\partial_\ell = j_{\ell-1}\circ d_\ell} & & H_{\ell-1}(X^{\ell-1}, X^{\ell-2}) & \longrightarrow & \cdots \end{array}$$

where the homology is in the sense of singular homology with a field K coefficient (arbitrary characteristics), d_ℓ is the connecting morphism and $j_{\ell-1}$ is induced by the quotient chain map of the singular chain groups. Since $d_{\ell-1} \circ j_{\ell-1}$ is the composition of consecutive maps in the exact sequence of the pair $(X^{\ell-1}, X^{\ell-2})$, we have $\partial_{\ell-1} \circ \partial_\ell = 0$, showing that the horizontal sequence becomes a chain complex. Then, the cellular homology is defined by $H_\ell^{\mathrm{cell}}(X) = \ker \partial_\ell / \operatorname{im} \partial_{\ell+1}$.

Because of the isomorphism $H_\ell(X) \simeq H_\ell^{\mathrm{cell}}(X)$, we use the same symbol $H_\ell(X)$ even for the cellular homology. We also denote the cellular chain complex defined by the horizontal sequence in (A.1) by

(A.2)
$$\cdots \xrightarrow{\partial_{\ell+1}} C_\ell(X) \xrightarrow{\partial_\ell} C_{\ell-1}(X) \xrightarrow{\partial_{\ell-1}} \cdots$$

as usual. The reduced homology $\tilde{H}_\ell(X)$ is defined by $H_0(X) \simeq K \oplus \tilde{H}_0(X)$ and $H_\ell(X) = \tilde{H}_\ell(X)$ for $\ell > 0$. The betti number (or the reduced betti number, resp.) is given by $\beta(X) = \operatorname{rank} H_\ell(X)$ (or $\tilde{\beta}(X) = \operatorname{rank} \tilde{H}_\ell(X)$, resp.).

We recall that $H_\ell(X^\ell, X^{\ell-1})$ is generated by the set X_ℓ of ℓ-cells, i.e.,

$$H_\ell(X^\ell, X^{\ell-1}) \simeq \operatorname{Span}_K X_\ell.$$

Thus, we obtain a matrix representation $(M_{i,j})_{1 \le i \le n_{\ell-1}, 1 \le j \le n_\ell}$ of ∂_ℓ using the bases X_ℓ and $X_{\ell-1}$. Here, $M_{i,j}$ is given by the degree of the map

$$S^{\ell-1}_{\sigma_j^\ell} \to X^{\ell-1} \to S^{\ell-1}_{\sigma_i^{\ell-1}},$$

where the first map is the attaching map of the ℓ-cell σ_j^ℓ and the latter map is the quotient map collapsing $X^{\ell-1} \setminus \sigma_i^{\ell-1}$ to a point.

Let us consider examples of cell complexes $X = \{e^0, e^1\}$ and $Y = \{e_1^0, e_2^0, e_1^1, e_2^1\}$ shown in Figure 1. Then, the chain complexes of X and Y are given by

$$0 \longrightarrow K \xrightarrow{0} K \longrightarrow 0,$$

$$0 \longrightarrow K^2 \xrightarrow{\begin{pmatrix} 1 & 1 \\ -1 & -1 \end{pmatrix}} K^2 \longrightarrow 0,$$

respectively. Hence, we have

$$H_\ell(X) \simeq H_\ell(Y) \simeq \begin{cases} K, \ell = 0, 1 \\ 0, \ \ell \neq 0, 1 \end{cases}.$$

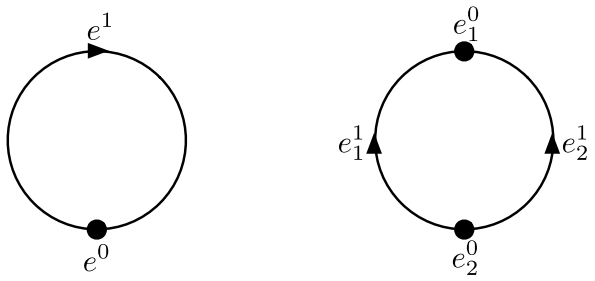

Figure 1. 1-dimensional cell complexes X (left) and Y (right).

By taking the dual $(\bullet)^* = \mathrm{Hom}_K(\bullet, K)$ of (A.2), we obtain a cochain complex

$$\cdots \xleftarrow{\partial^\ell} C^\ell(X) \xleftarrow{\partial^{\ell-1}} C^{\ell-1}(X) \xleftarrow{\partial^{\ell-2}} \cdots, \tag{A.3}$$

where $C^\ell(X) = C_\ell(X)^*$ and $\partial^{\ell-1} = \partial_\ell^*$. Then, the cellular cohomology is defined by $H^\ell(X) = \ker \partial^\ell / \operatorname{im} \partial^{\ell-1}$. It is known that $H^\ell(X) \simeq \mathrm{Hom}_K(H_\ell(X), K)$.