We study classical dimers on two-dimensional quasiperiodic Ammann-Beenker (AB) tilings. Despite the lack of periodicity we prove that each infinite tiling admits ‘perfect matchings’ in which every vertex is touched by one dimer. We introduce an auxiliary ‘AB∗’ tiling obtained from the AB tiling by deleting all 8-fold coordinated vertices. The AB∗ tiling is again two-dimensional, infinite, and quasiperiodic. The AB∗ tiling has a single connected component, which admits perfect matchings. We find that in all perfect matchings, dimers on the AB∗ tiling lie along disjoint one-dimensional loops and ladders, separated by ‘membranes’, sets of edges where dimers are absent. As a result, the dimer partition function of the AB∗ tiling factorizes into the product of dimer partition functions along these structures. We compute the partition function and free energy per edge on the AB∗ tiling using an analytic transfer matrix approach. Returning to the AB tiling, we find that membranes in the AB∗ tiling become ‘pseudomembranes’, sets of edges which collectively host at most one dimer. This leads to a remarkable discrete scale-invariance in the matching problem. The structure suggests that the AB tiling should exhibit highly inhomogenous and slowly decaying connected dimer correlations. Using Monte Carlo simulations, we find evidence supporting this supposition in the form of connected dimer correlations consistent with power law behaviour. Within the set of perfect matchings we find quasiperiodic analogues to the staggered and columnar phases observed in periodic systems.
route to glassy quantum dynamics and slow thermalization [24–27].

Here we consider classical dimer models on bipartite graphs [1, 11, 25, 26]. A graph is a set of vertices connected by edges. It is bipartite if its vertices can be partitioned into two mutually exclusive sets such that there are no edges between vertices belonging to the same set (same bipartite ‘charge’). Dimers are placed on the edges such that each vertex connects to zero or one dimers (a hard-core constraint). This defines a dimer covering, or matching. An unmatched vertex not connected to a dimer is termed a monomer. A monomer-free configuration, if one exists, is called a perfect matching. Classical dimer models and their associated matching problems have attracted sustained interest from the physics, mathematics, and computer science communities over the last century owing to their ubiquity in problems of constraint satisfaction, optimization, and combinatorics [5, 45–47].

The perfect matchings of graphs admitting planar embeddings can be counted exactly using Pfaffian techniques [11, 29, 30]. However, while mathematically rigorous, these do not provide especially transparent physical insight, and are often computationally demanding. A more intuitive perspective is afforded by the height representation [25, 51], particularly when it is applied to periodic bipartite lattices that admit perfect matchings. On these lattices, the statistical mechanics of dimer configurations can be understood by mapping dimer coverings to configurations of an integer-valued ‘height’ field on edges of the dual lattice. The hard-core constraint becomes a zero-divergence condition on this field — i.e. a Gauss law — allowing it to be re-expressed as the lattice curl of a scalar (vector) height variable in 2D (3D). The height mapping is most useful when entropically favoured dimer coverings correspond to locally flat height configurations. This allows us to deduce dimer correlations using a coarse-grained free energy density for the height field, taking a local Gaussian form at long wavelengths. Monomers appear as vortex defects of the height field. In 2D, if the microscopic parameters correspond to the vorticity being irrelevant (as on the square and honeycomb lattices), the height model is in a rough phase, implying critical (power law) dimer correlations and logarithmic confinement of monomers (i.e. the free energy cost of a pair of test monomers in an otherwise-perfect matching diverges logarithmically with their separation). When the vorticity is relevant (as on the square lattice with interactions [53]), the height model is in its flat phase, with exponentially decaying connected correlations of dimers and linearly confined monomers. Since vortex defects are never relevant in 3D, dimer correlations are always algebraic, and monomers are deconfined, i.e. a test pair can be separated to arbitrary distance with finite free energy cost. However, these arguments rely on (i) the existence of perfect matchings; and (ii) the identification of locally flat height configurations with high-probability configurations. Neither is guaranteed for a generic bipartite graph.

Classical dimers have also been studied in settings with disorder, such as random regular graphs and Erdős–Rényi random graphs [52, 55], using approaches that are asymptotically exact in the thermodynamic limit [56, 57]. However, the absence of locality in these ensembles rules out any simple generalization of the notions of dimer correlations and monomer confinement.

Recent work explored the problem of classical dimer models on Penrose tilings [58]. These are infinite tilings of the plane constructed from two types of tile. The tiles fit together without gaps or defects, in such a way that no patch can be tessellated periodically to reproduce the pattern [59, 61]. Despite lacking the discrete translational symmetries of crystal lattices, they nevertheless feature a great deal of order. For example, their Fourier transforms, which are tenfold rotationally symmetric, feature sharp Bragg peaks which can be labelled by a finite number of wave vectors. This latter condition defines the Penrose tiling to be quasiperiodic [61]. Penrose tilings came to prominence in the physics community with the discovery of quasicrystals, real materials whose atoms are arranged quasiperiodically [62]. Considering the edges and vertices of the tiles as those of a bipartite graph, Penrose tilings do not admit perfect matchings despite having no net imbalance in their bipartite charge [58]. Instead, they have a finite density of monomers in the thermodynamic limit. The maximum matchings on Penrose tilings, which contain the maximum number of dimers, have an unusually rich underlying structure, quite distinct from either periodic or random systems. In general maximum matchings, monomers can be thought of as moving via dimer re-arrangements. On Penrose tilings, monomers are always confined within regions bound by nested loops, or membranes. These membranes are comprised of edges which do not host a dimer in any maximum matching. Each such region has an excess of vertices belonging to one or the other bipartite charge, and hosts a corresponding number of monomers. Adjacent regions have monomers of the opposite bipartite charge. The properties of these membranes and the regions that they enclose follow directly from the dimer constraint and the underlying symmetry of the tiling, and can hence be precisely determined. Ref. 63 identified similar monomer-confining regions, separated either by membranes or perfectly matched regions, as components of the Dulmage–Mendelsohn decomposition of generic bipartite graphs [64, 67]. This was used to investigate phase transitions of such monomer-confining regions in ensembles of periodic lattices with random vertex dilution, such as those used to model vacancy disorder in quantum magnets.

While both Refs. [58] and [63] consider bipartite dimer models, the usual mapping to height models does not apply to quasiperiodic graphs, or graphs where vertices can have different co-ordination numbers. While a more general height mapping is possible in principle [68], the resulting height functions typically do not lead to analytically tractable coarse-grained continuum free energy...
FIG. 1. Clockwise: (a) A finite patch of the Ammann-Beenker (AB) tiling. Composed of copies of square and rhombus tiles, the (infinite) tiling covers the plane in an ordered fashion, yet never repeats periodically. (b) A maximum matching (dimer covering) of a patch of the AB tiling. The tiling can be perfectly matched in the thermodynamic limit; on finite patches, an $O(1)$ number of unmatched vertices (monomers) generally appear, which can be moved to the boundary. Thick black lines indicate links which comprise overlapping pseudomembranes, each of which collectively host one dimer. Yellow edges indicate a dimer on a pseudomembrane. (c) A patch of the $AB^*$ tiling, obtained from AB by removing all 8-connected vertices. (d) A maximum matching of a patch of the $AB^*$ tiling. Pseudomembranes become membranes, hosting zero dimers and leading to a decoupling of the partition function.

functionals. This is because there is no longer a simple relationship between the local configuration of the height field and the statistical weight of the global dimer covering. In any case, due to a sizeable density of monomers in the cases studied in Refs. 58 and 63, connected correlation functions of dimers are short-ranged and more or less unremarkable. In addition, monomer correlation functions are non-monotonic and strongly site-dependent, making it challenging to define a crisp notion of monomer confinement. These facts challenge the goal of a precise characterization of long-wavelength properties of dimer models in quasiperiodic environments.

In this work, we meet this challenge in the setting of a distinct quasiperiodic dimer problem for which we can make a series of exact, and asymptotic, statements. Specifically, we study classical dimers on the Ammann-
FIG. 2. The $e_j$-dependence of the connected dimer correlations, $C(e_0, e_j)$ (Eq. (33)). The source edge $e_0$, indicated by the green triangle, connects an $8_2$-unit to a nearby ladder. The resulting correlations are typical of slowly decaying examples, and resemble a power law. (See Sec. VI)

Beenker (AB) tiling, shown in Fig. 1. This tiling has been the topic of much recent attention, with investigations involving its magnetism [69–71], superconductivity [72], critical eigenstates [73] and protected Majorana modes [74]. Like the Penrose tilings, AB tilings exhibit discrete scale invariance: deflations (vertex decimations followed by rescaling lengths by the irrational silver ratio) map an AB tiling to another AB tiling. We prove that these tilings host a perfect matching in the thermodynamic limit, in contrast to the Penrose tilings investigated in Ref. [58]. Our proof makes use of the discrete scale invariance characteristic of quasicrystals: we find that at any given coarse-graining scale, special vertices that are left invariant by double deflations retain strong dimer-dimer correlations at the next scale. This suggests that certain regions associated with these vertices retain mutual dimer correlations. The preserved vertices have edge-co-ordination eight and we refer to them as ‘8-vertices’.

The success of this iterative construction of dimer coverings motivates us to consider an auxiliary problem on a related graph that we dub the AB* tiling, Fig. 1c. This is obtained from the AB tiling by removing all the 8-vertices. The AB* tiling is also perfectly matched and does not host monomers, and we show that it decomposes into perfectly matched one-dimensional regions that we call ladders, separated by membranes. These membranes, like those in Refs. [58] and [53] are comprised of edges between different ladders and do not host a dimer in any maximum matching. However, unlike the monomer-confining regions of Refs. [58] and [53], they separate perfectly matched regions. This structure allows us to exactly compute the partition function of the dimer model on the AB* tiling. We show that membranes in the AB* tiling can be decomposed into non-intersecting but overlapping pseudomembranes in the full AB tiling when the 8-vertices are reintroduced: the edges belonging to every pseudomembrane now collectively host exactly one dimer.

Each 8-vertex is surrounded by at least one pseudomembrane. Loosely speaking, a double deflation maps this 8-vertex and its surrounding pseudomembrane-bounded region into a single vertex at the next scale. Intuitively, since each pseudomembrane is pierced by exactly one dimer, this procedure preserves the dimer constraint at each successive scale. This remarkable property provides a heuristic picture of how power law connected correlations emerge. It also suggests that the AB tiling is an intriguing example of a deterministic lattice-level (rather than continuum) coarse-graining of a constrained system that faithfully imposes the constraint at each successive decimation scale.

We show that the discrete scale invariance exhibited by perfect matchings leaves its imprint in connected dimer correlations, as exhibited in Fig. 2. Investigating dimer correlations numerically we show that, while they are strongly anisotropic and site-dependent, the asymptotic behaviour of connected correlations of dimers are consistent with power law scaling. This is particularly striking given the absence of the continuum height description which mandates power law correlations in periodic bipartite lattices [47, 51]. We also investigate the phase diagram of dimer models on both the AB tiling and AB* tiling in the presence of a classical aligning interaction resembling the Rokhsar-Kivelson potential term, as a step on the road towards a study of quasiperiodic quantum dimer models.

The remainder of this paper is organized as follows. We introduce the necessary background on dimer covers and AB tilings in Sec. II. In Sec. III we prove that perfect matchings exist for AB tilings in the thermodynamic limit. The construction leads to the introduction of the auxiliary AB* tiling, which we also prove to be perfectly matched. In Sec. IV_A we prove the existence of membranes in the AB* tiling; in Sec. IV_B we demonstrate how these become pseudomembranes in the AB tiling. In Sec. V we present an exact calculation of the partition function and free energy of the classical dimer model on the AB* tiling. Turning to numerical results, we consider

We emphasize the deterministic nature, since real-space decimations can have an especially simple structure in random systems.
the full AB tiling, where, after outlining our choice of samples and boundary conditions in Sec. VIA, we identify connected correlations consistent with power laws in Sec. VIB. In Sec. VIC we include a classical aligning interaction to both the AB tiling and AB\textsuperscript{*} tiling. We provide concluding remarks in Sec. VII.

II. BACKGROUND

A. Dimer models and graph theory

In this section we introduce the necessary terminology to discuss dimer coverings on graphs. The graphs of interest in this paper have two important properties. First, they are bipartite, meaning the vertices can be partitioned into two mutually exclusive subsets, \( \mathcal{U} \) and \( \mathcal{V} \), so that every vertex in \( \mathcal{U} \) (\( \mathcal{V} \)) only has edges to vertices in \( \mathcal{V} \) (\( \mathcal{U} \)). If two vertices belong to the same subset, we will say they have equal (bipartite) charge; otherwise, they are oppositely charged. Second, the graphs admit planar embeddings. We keep the geometry of the tiling, although strictly speaking only the graph topology is relevant to the matching problem.

A matching of a graph is a subset of edges such that no vertex is incident with more than one edge in the subset \[75\]. A matching is equivalent to a dimer configuration, as edges in the matching can be covered by dimers, with no vertex touching more than one dimer. A vertex connected to an edge in the matching is said to be matched; an unmatched vertex is called a monomer. A perfect matching is a matching with every vertex matched or, equivalently, a monomer-free dimer covering. Not every graph admits a perfect matching — a simple counterexample is any graph with an odd number of vertices. A maximum matching is a matching with the maximum number of dimers (minimum number of monomers): Fig. 3a-b shows examples of maximum and perfect matchings. If a graph admits a perfect matching, then any maximum matching is necessarily perfect. Usually a graph will have multiple maximum or perfect matchings. From a statistical mechanics perspective, our interest is in understanding the complete space of such matchings. Of particular interest is the partition function \( Z \), which is a sum over all possible dimer configurations \( \mathcal{C} \) weighted according to the details of the configuration and the model under consideration, \( w(\mathcal{C}) \):

\[
Z = \sum_\mathcal{C} w(\mathcal{C}).
\]  

(1)

For example, we may be interested in penalising monomers, or favouring certain alignments of dimers. In Sec. V we consider the partition function of an equally weighted sum over perfectly matched configurations of the AB\textsuperscript{*} tiling, i.e. \( w(\mathcal{C}) = 1 \) only if \( \mathcal{C} \) is a perfect matching, otherwise \( w(\mathcal{C}) = 0 \). Monomer-monomer, dimer-dimer, and monomer-dimer correlations are then typically the observables of interest, although their analytic computation is usually a formidable task. Detailed discussions on classical dimer coverings and their application to physics can be found in e.g. Refs. 68, 76, and 77.

Much of the recent interest in dimers originated with the quantum dimer model introduced on the square lattice by Rokhsar and Kivelson \[2\]. Defining a plaquette to be the four edges of a single square tile, the Rokhsar-Kivelson Hamiltonian is defined to be

\[
\hat{H}_{\text{RK}} = \sum_\square -t \left( |\square\rangle \langle \square| + |\square| \langle \square| \right) \\
+ V \left( |\square\rangle \langle \square| + |\square| \langle \square| \right)
\]  

(2)

where the sum is taken over all plaquettes \( \square \). The notation indicates that the objects of interest are flippable plaquettes: plaquettes which host a pair of parallel dimers.
Such a configuration can always be ‘flipped’ to the other pair of dimers without changing the rest of the graph. The kinetic term $t$ takes advantage of this local move to introduce a natural form of local quantum dynamics, quantum ‘resonances’ between the two perfectly matched configurations of the plaquette. These resonances give resonating valence bond states their name [7]. In this paper we will instead exclusively consider the classical problem with $t = 0$. The $V$ terms, which are essentially classical, favour (disfavour) alignment of dimers on plaquettes for $V < 0$ ($V > 0$). We return to these in Sec. VI C. The square plaquette notation remains relevant in our case since all the tiles we consider have four edges.

An alternating path is a connected subset of edges along which edges are alternately covered and uncovered by dimers. Starting from any matching, switching which edges are covered/uncovered in a closed alternating path (alternating cycle) results in another matching with the same number of dimers (see Fig. 3). All alternating cycles are of even length (on a bipartite graph this statement is trivial since all cycles are of even length). This process of switching covered and uncovered edges is known as augmenting the path. The simplest such augmentation, of the smallest alternating cycle, is the flip of a flippable plaquette.

Augmenting an odd-length alternating path changes the number of dimers on the matching. At the most basic level, two monomers can be created by removing one dimer. On a bipartite graph, these monomers have opposite charge, and so the process has a physical analogy in the excitation of a particle-antiparticle or defect pair above the vacuum state (viewed as one where all monomers are paired into neutral dimers). These monomers are then able to ‘move’ through the dimer vacuum: taking an even-length alternating path with one end terminating on one of the monomers, augmenting the path results in the monomer being translated to the opposite end of the path, while conserving the monomer's charge (see Fig. 3). Given a maximum matching, all other maximum matchings can be generated by combinations of two basic ‘moves’: (i) augmenting alternating cycles; and (ii) transporting monomers along alternating paths of even length.

By reversing the above logic, starting from a non-perfect matching, if an odd-length alternating path can be found with end points terminating on two monomers (an augmenting path), then this path can be augmented to annihilate the two monomers in favour of a dimer (see Fig. 3). If augmenting paths can be sequentially found between all remaining monomers of a matching, so that no monomer appears in more than one path, then the augmentation of these paths results in a perfect matching. We will use these facts to prove the AB tiling can be perfectly matched.

Efficient algorithms exist to determine the maximum matching of finite graphs [78, 79]. However, showing that an infinite graph (the relevant case in the thermodynamic limit) admits a perfect matching is in general non-trivial. Quasiperiodic Penrose tilings cannot be perfectly matched: though the infinite tiling is charge neutral, monomers are confined within regions with an excess of one or the other type of the bipartite charge. Such confinement emerges as a direct consequence of the quasiperiodic geometry: monomers cannot cross monomer membranes to annihilate those of the opposite charge. Monomer membranes are closed loops of edges which cannot be covered by dimers in any maximum matching; equivalently, no augmenting paths exist between monomers on opposite sides of a membrane. In Sec. IV we will demonstrate that similar membrane structures exist on the AB tiling, but in this case they do not frustrate the perfect matching.

### B. Ammann-Beenker tilings

Although we will use the language of graph theory in our discussion of AB, the mathematical theory of quasicrystals has traditionally been developed in the language of tilings. A tiling is a filling of space with congruent shapes without overlaps or gaps [61]. For clarity we will use tiling to refer to an infinite tiling of the plane; finite sections of a tiling we refer to as patches. Simple tilings can be formed by periodic repetition of a single tile, such as a square or hexagon. Conventional crystals can be seen as regular tilings of space by an atomic unit cell; the underlying symmetries can be deduced from diffraction experiments, and yield the 230 crystallographic space groups [80]. However, the only rotational symmetries compatible with such periodic long-range order (in 2D or 3D) are 2-, 3-, 4-, and 6-fold. When diffraction experiments on AlMn-alloys revealed structures compatible with 5-fold rotational symmetry [81], crystallographic theory had to be extended to include quasicrystals — alloys with long-range atomic order but no translation symmetry. Quasicrystals can feature finite patches of 5-, 8-, 10- or 12-fold rotational symmetry [82–84].

Quasiperiodic tilings are a class of planar tilings without translation symmetry, capable of accounting for the symmetries observed in quasicrystals which are forbidden in periodic tilings [60, 61, 85]. They are distinguished from the more general set of aperiodic tilings by the fact that their diffraction patterns can be indexed by a finite number of wavevectors [61]. The most famous family of quasiperiodic tilings is due to Penrose [59]. Penrose tilings have local patches of 5-fold symmetry (and can have at most one true 5-fold rotational centre). The Ammann-Beenker tilings [60, 85] similarly have 8-fold symmetry, and together with the decagonal (10-fold) and dodecagonal (12-fold) tilings, they make up the ‘Penrose-like’ tilings [87]. The remarkable fact that the four symmetries displayed by these tilings account for the symmetries of all physical quasicrystals (i.e. those observable in experiment) was explained by Levitov based on
arguments of energetic stability \[SS\]. The Penrose-like tilings have therefore seen extensive study in connection to physics.

Classical dimers on Penrose tilings were studied in previous work \[SS\]; here we focus on the Ammann-Beenker (AB) tiling, a patch of which is shown in Fig. 1. The AB tiling is constructed from copies of two inequivalent tiles: a square, and a rhombus with angles \(\pi/4\) and \(3\pi/4\). Both tiles have edges of unit length. No shifted copy of this tiling can be exactly overlaid with the original. Many mathematical properties of AB tilings are well understood and can be found in e.g. \[61\]. Here we briefly mention those relevant to the following discussion.

Formally, one should really refer to Ammann-Beenker tilings (plural), the uncountable set of equivalence classes of LI (locally indistinguishable or locally isomorphic) tilings. Two tilings are LI if any finite patch of one can be found in the other. In this way, all AB tilings 'look the same' from a local perspective, distinguished only in their global structure. In fact, every finite patch recurs with positive frequency, in all tilings, a property that accounts for the long-range order of the quasiperiodic tilings. This structure can be compared to that of the periodic tilings, where the long-range order arises from the repeated unit cell. Results that we discuss in the following sections apply in generality to the entire set of AB tilings.

Any AB tiling \(\mathcal{T}\) can be generated by several methods \[60\], \[61\], \[89\]. Square and rhombus tiles can have their edges decorated by matching rules which force the tiles to fit together quasiperiodically; an AB tiling can be created as a slice through a higher dimensional periodic lattice (the cut-and-project technique); or the tilings can be generated via an inflation procedure.

This inflation method allows us to discuss the scale symmetry of the tilings, and is our primary workhorse in this paper. Starting from a finite seed patch \(\mathcal{T}_0\) (e.g. a single square tile) an inflation rule \(\sigma\) is repeatedly applied to grow the patch as \(\mathcal{T}_n = \sigma^n(\mathcal{T}_0)\), with the number of tiles growing exponentially under inflation. \(\sigma\) consists of two steps: decomposition, where every tile is divided into smaller tiles as shown in Fig. 4, followed by rescaling, where the decomposed tiling is scaled so that the new tiling is formed from exact copies of the original tiles. The inflation of the square tile breaks the square rotation symmetry down to a single mirror symmetry. Therefore we must keep track of the orientation of the square, as captured by the triangular motif shown. When this information is not pertinent to the discussion, we will generally leave the markings absent in future figures. The scaling factor is the silver ratio \(\delta_S\), defined by

\[
\delta_S^2 = 2\delta_S + 1
\]

and equal to

\[
\delta_S = 1 + \sqrt{2}.
\]

Note that it is the length (rather than area) of the tile edges that scales by \(\delta_S\) under decomposition: this can be seen geometrically in Fig. 1 with each edge divided into a rhombus edge and the square diagonal. The area of each tile scales by \(\delta_S^2\) under decomposition. In the following, if we say one tiling is larger than another by some power of the silver ratio, we are always referring to the respective lengths of their tile edges. The Penrose tiling instead has as its scale factor the golden ratio \(\varphi = \frac{1+\sqrt{5}}{2}\).

Patches of arbitrarily large size can be generated by the inflation process; the tiling \(\mathcal{T}\) is recovered after an infinite number of inflations. The inverse of the inflation rule, \(\sigma^{-1}\), deflation, is also uniquely specified on a tiling, consisting of composition — reconstruction of the larger tiles from smaller tiles — and rescaling by the inverse of the silver ratio. Acting with \(\sigma\) or \(\sigma^{-1}\) on \(\mathcal{T}\) returns another tiling in the same LI class.

Every possible configuration of tiles around a vertex in AB is identical to one of the seven vertex configurations shown in Fig. 5 (up to rotations). The 5-vertices (5A and 5B) yield two distinct results upon inflation depending on the orientation of the adjacent square plaquettes. All other vertices can be uniquely identified by their coordination number (valence, in graph theory nomenclature). Under \(\sigma\), each vertex configuration is mapped to a different configuration, e.g. 4 \(\rightarrow\) 6, with the exception of the 8-vertex, which inflates to another 8-vertex. These inflations are also shown in Fig. 5.

The scale symmetry of the Ammann-Beenker tilings arises from this inflation structure, and specifically from the invertibility of \(\sigma\). One expression of this symmetry is that all 8-vertices of \(\mathcal{T}\) are positioned at the vertices of the tiling obtained by twice-composing \(\mathcal{T}\) i.e. the twice-deflated tiling \(\mathcal{T}_{-2} \equiv \sigma^{-2}(\mathcal{T})\) with lengths rescaled by \(\delta_S^2\). This follows from noticing that every vertex is mapped to an 8-vertex under two inflations, as can be checked from the vertex inflations in Fig. 5. By the inverse, deflating twice maps the 8-vertices of \(\mathcal{T}\) to the vertices of \(\mathcal{T}_{-2}\). This scale symmetry is more clearly shown in Fig. 6 which shows a patch of \(\mathcal{T}\) overlaid with the scaled \(\mathcal{T}_{-2}\). The 8-vertices of \(\mathcal{T}\) are coloured by their bipartite charge,
FIG. 5. The seven vertex configurations, and their action under inflation (Fig. 4). All vertices map to 8-vertices under at most two inflations.

FIG. 6. The scale symmetry of the AB tiling: the 8-vertices of an AB tiling are positioned to sit at the vertices of another locally indistinguishable AB tiling, with lengths increased by a factor of $\delta_S^2$, where $\delta_S = 1 + \sqrt{2}$ is the silver ratio. 8-vertices are coloured by their bipartite charge. We will rely on this symmetry in the rest of the paper. Anticipating this 8-vertex $\leftrightarrow$ vertex mapping, we introduce $\sigma^2$ inflation tiles, shown in Fig. 7. Compared to the basic inflation tiles (Fig. 4), the $\sigma^2$ tiles have the property that their vertices become 8-vertices in the inflated tiling.

This scale hierarchy continues: under $\sigma^2$, the 8-vertices of $T$ inflate to 8-vertices, and these twice-inflated 8-vertices are positioned to sit at the vertices of a tiling with lengths scaled by $\delta_S^4$. With this in mind, it is convenient to define an ordering to the 8-vertices. An 8-vertex is order-zero if it maps to a $T_-, 5_A-$, or 6-vertex under a single deflation; order-one if it deflates to an order-zero 8-vertex; and so on. This flow of vertices under (in/de)flation is represented in Fig. 8. We denote an order-$n$ 8-vertex an $8_n$-vertex. An $8_n$-vertex is therefore the $n^{th}$ inflation of an order-0 8-vertex, $8_0$. We find that $8_n$-vertices of $T$ sit at the vertices of an AB tiling, $T$ to $T$, with lengths scaled by a factor of $\delta_S^{2n+2}$. Since all vertices of $T$ are mapped to order-$n$ or higher 8-vertices under $\sigma^{2n+2}$, 8-vertices of order-$n$ and higher can also be viewed as those vertices of $T$ that are preserved under $n + 2$ deflations. We will denote the $n$-times deflated tiling of $T$ as $T_{-n}$.

To conclude this section, we discuss the 8-fold symmetry that defines the Ammann-Beenker tilings. First, as mentioned previously, the Bragg spectrum (Fourier transform of the lattice) has a discrete 8-fold rotational symmetry ($D_8$ in Schönhflies notation) [90]. Second, an 8-fold rotation of an AB tiling returns another AB tiling in the same LI class. Third, and most importantly to us, the symmetry shows up in the structure of tiles surrounding an 8-vertex. Every vertex configuration has a set of tiles which always appears around the vertex wherever it is
where the tiling covers the infinite plane and boundary effects can be ignored. Taking the thermodynamic limit is a delicate procedure in quasiperiodic systems since one must necessarily work with open boundary conditions and bound their contribution as the system size increases.

For a first pass at the problem, and to underscore its nontrivial nature, we note that the matching problem on finite patches of the AB tiling depends strongly on the exact patch considered. Trivially, a patch with a net imbalance of bipartite charge never admits a perfect matching. Less trivially, it is also possible to find charge-neutral patches with unpaired monomers. An example is the patch generated by inflating the basis square four times: exactly two monomers remain in the maximum matching, with opposite charges. In contrast to the Penrose case, where the presence of membranes leads to a monomer density that approaches $\sim 10\%$, the observed number of unpaired monomers on AB remains of order unity as the tiling is grown. This suggests that monomers on AB are artefacts of finite tilings, representing defects that ‘migrate in’ from the boundary, rather than a finite bulk monomer density persisting in the thermodynamic limit.

We have verified these statements using standard graph-theoretic methods \cite{78, 79} to compute maximum matchings on a large sample of patches generated via inflation. We will prove these statements regarding finite patches, and that the planar tilings can be perfectly matched. The strategy of our proof is as follows. Consider the perfect matching problem on an AB tiling $T$. We first match up all vertices of $T$ except for the 8-vertices (recall that these are the vertices which remain under two deflations). We then show that the problem of matching the remaining 8-vertices maps to a perfect matching problem on the twice-deflated tiling $T^{-2}$. On this tiling, we match all but the 8-vertices again (this matches all 8- and 81-vertices on the original $T$). We then use the scale symmetry of $T$ to iterate this procedure and obtain an upper bound on the monomer density of the AB tiling after $n$ deflations. This density vanishes exponentially as $n \to \infty$, corresponding to taking the thermodynamic limit.

Our motivation for separating out the 8-vertices comes from the requirement for a bipartite graph to be charge-neutral in order to admit a perfect matching. This is true of the AB tiling in the thermodynamic limit, because the average vertex connectivity is the same for the two bipartite subsets $U$ and $V$. Note, however, that any $D_8$ local empire has an excess charge of at least one. This follows from the fact that every $D_8$ local empire has an 8-vertex at its centre (by definition), and its eight-fold rotational symmetry mandates that the total number of vertices within the region must be $8m+1$, for some integer $m$. Since this number is odd, there must be an excess of bipartite charge.

In fact, the same argument shows that any symmetric region centred on 8-vertices cannot be perfectly matched without placing at least one dimer outside of the region.

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**III. EXISTENCE OF PERFECT MATCHINGS ON THE AMMANN-BEENKER TILINGS**

We now show that Ammann-Beenker tilings can be perfectly matched. We work in the thermodynamic limit,
Although other dimer inflation tiles could have been chosen, all tile choices that consistently match along boundaries are equivalent up to augmenting cycles in the bulk, and/or reflections such that black and white vertices are exchanged. It is not possible to devise inflation tiles that perfectly match the tiling. This is on account of the previously considered 8-fold symmetry: for example, the local empire of an $S_2$-vertex can be created by attaching eight copies of the rhombus dimer inflation tile — any dimer added to the tile to match the central monomer would be repeated eight times, resulting in a vertex with an 8-fold dimer cover, violating the dimer constraint.

The unpaired 8-vertices already result in an upper bound on the monomer density of $\mathcal{T}$, of

$$\rho^{(0)} \leq \nu_{8v},$$

where $\nu_{8v} = \delta_S^{-4} \sim 0.03$ is the density of 8-vertices on the Ammann-Beenker tiling [61].

Next, we allow these monomers to move around the tiling by augmenting the alternating paths which terminate on them. Moving a monomer along an alternating path cannot create additional monomers, so Eq. (5) remains a good upper bound on the monomer density. The bound will be reduced if we can identify augmenting paths connecting two oppositely charged monomers — augmentation then annihilates the monomers to give a dimer, reducing the bound on number of monomers by two.

We define 8-vertices (all of which host monomers at this stage) to be deflate neighbours on $\mathcal{T}$ if they become true nearest-neighbours under two deflations, i.e. on $\mathcal{T}_{-2}$. On the dimer-decorated $\mathcal{T}$, deflate-neighbouring monomers sit on two of the corner vertices of one of the dimer-decorated tiles in Fig. 10 connected along one of the large tile edges (the monomers have opposite charge). As is clear from the right of Fig. 10 an augmenting path always exists between two monomers on deflate-neighbouring 8-vertices. In addition, augmenting paths between disjoint pairs of deflate-neighbouring monomers can be chosen so as not to intersect. This means that annihilating two deflate-neighbouring monomers does not affect the possibility of further annihilations, except in the obvious way that the annihilated monomers are no longer available for pairing. The paths shown in Fig. 10 are non-intersecting in this way.

Finding a complete set of augmenting paths between deflate-neighbouring monomers is therefore equivalent to finding a perfect matching of the twice-deflated tiling $\mathcal{T}_{-2}$. This follows from our definition of deflate-neighbouring 8-vertices and the existence of non-intersecting augmenting paths between them. We refer the reader back to Fig. 6 to see that the identification of augmenting paths between deflate-neighbouring 8-vertices indeed has the structure of a matching problem at the next scale.

A perfect matching of $\mathcal{T}_{-2}$ is evidently no easier to obtain than for $\mathcal{T}$. However, we can find a partial matching with the same method used previously: by performing
two deflations of $\mathcal{T}_{-2}$ to obtain the tiling $\mathcal{T}_{-4}$, and re-inflating with the dimer inflation tiles. This matches all vertices of $\mathcal{T}_{-2}$ apart from the 8-vertices, and by identifying dimers on $\mathcal{T}_{-2}$ with augmenting paths on $\mathcal{T}$, annihilates all monomers on $8_v$- and $8_1$-vertices of $\mathcal{T}$ (the 8-vertices that deflate to non-8-vertices under two deflations). The remaining unmatched vertices correspond to the $8_{n>1}$-vertices of $\mathcal{T}$, and the bound on the monomer density on $\mathcal{T}$ is decreased by another factor of $\nu_{8v}$:

$$\rho^{(2n)} \leq \nu_{8v}^2.$$  

To complete the proof of perfect matching, we apply this procedure to all scales of the AB tiling. From now on we will refer to a monomer on an $8_v$-vertex as an order-$n$ monomer. Finding augmenting paths between all order-$n$ and order-$(n+1)$ monomers of $\mathcal{T}$ corresponds to finding augmenting paths between all order-$(n-2)$ and order-$(n-1)$ monomers of the $\mathcal{T}_{-2}$ tiling, and by induction, to a matching of the non-8-vertices of the $\mathcal{T}_{-(n+2)}$ tiling (here we identify order-$n$ for $n < 0$ with the non-8-vertices according to Fig. 8). At each matching of the non-8-vertices of $\mathcal{T}_{-(n+2)}$ via the dimer inflation tiles, the density bound on monomers is reduced by a factor of $\nu_{8v}$. Since $\mathcal{T}$ can be deflated an arbitrary number of times and $\nu_{8v} < 1$, the density of monomers must tend to zero in the thermodynamic limit:

$$\rho^{(2n)} \leq \nu_{8v}^{2n}, \quad \lim_{n \to \infty} \rho^{(2n)} \to 0,$$  

and the tiling admits a perfect matching $\square$.

Physically, this hierarchy of perfect matchings arises from the fact that higher-order monomers are placed at the centres of increasingly large $D_8$ regions by the dimer inflation, and, due to the symmetry, have to travel outside of their region to be paired. $D_8$ regions exist at all scales within the AB tiling, and so naturally monomers of equal orders have to be paired together at each step.

This picture of monomers pairing at all orders has an interesting consequence. According to our proof, all finite order monomers are matched after enough iterations of the dimer inflation: any 8-vertices that, for all successive deflations, deflate to an 8-vertex (an ‘order-\infty’ vertex in the terminology of Fig. 8), will never be matched by this process. A vertex that deflates to an 8-vertex, for all successive deflations, must be the 8-fold centre of an infinite large symmetric empire. However, their existence does not spoil our proof: such monomers occur with zero frequency on the infinite tiling, and can be moved arbitrarily far from the centre of the region, as follows from the matching process given above for any finite-order 8-vertex. The monomer can therefore be moved ‘to the boundary’ of the infinite tiling, and the tiling can be said to be perfectly matched.

### IV. MEMBRANES AND PSEUDOMEMBRANES

As we have shown in the preceding section, the AB tiling admits perfect matchings in the thermodynamic limit. However, we also observed that finite regions admit monomers. Indeed, we argued that there must exist at least a single monomer on any finite patch with 8-fold symmetry. A key step in our proof of perfect matchings on the full tiling was to pair up monomers on adjacent patches by augmenting the path connecting them. Now, we argue that this protocol is linked to the existence of ‘pseudomembranes’ — finite closed loops of edges that collectively host exactly one dimer in any perfect matching.

Refs. 58 and 63 identified exact membranes hosting zero dimers separating unmatched regions with an excess of bipartite charge of one sign. In contrast, these pseudomembranes are each comprised of edges which collectively host a single dimer. However, like membranes, pseudomembranes capture how certain aspects of the quasiperiodic graph structure are encoded in the set of perfect matchings. The properties of membranes and pseudomembranes can be formally understood in terms of the Dulmage-Mendelsohn decomposition of the graph and its ‘fine’ generalization as discussed in Appendix A. Here, we provide a more intuitive picture based on first introducing an auxiliary ‘AB* tiling’, on which the existence of exact membranes and perfect matchings can be seen clearly. We then demonstrate that the exact membranes become pseudomembranes on the full AB tiling.

#### A. Membranes in the AB* tiling

In proving the existence of perfect matchings on the AB tiling, at each iteration we first matched all vertices except those 8-vertices preserved by two deflations. In completing the proof, we matched a fraction of these
remaining vertices by associating augmenting paths between 8-vertices with dimers on the twice-deflated tiling. A key aspect of this procedure is that only such augmenting paths between two 8-vertices survive as a dimer at the next double deflation. Crucially, all information that correlates different inflation scales involves the 8-vertices. This observation naturally leads us to consider a simplified dimer problem on an auxiliary tiling that we dub the AB\(^*\) tiling, obtained from the AB tiling by removing all 8-vertices. The proof of perfect matchings on the AB tiling (Sec. II) automatically generates a perfect matching of the AB\(^*\) tiling using the dimer inflation tiles of Fig. 10.

We can construct a set of dimer-decorated tiles for the AB\(^*\) tiling by deleting 8-vertices and their incident edges from the dimer inflation tiles for the AB tiling in Fig. 10. In Fig. 11, the locations of 8-vertices are now marked with solid blue and red circles to emphasize the absence of vertices, and the colours indicate bipartite charge as before. We have coloured plaquettes by their participation in structures that emerge when the tiles are placed on the full tiling. The light-blue- and yellow-shaded plaquettes join to form regions which we call ladders (the colour codes are made clear when we discuss ladders in detail in Sec. V). The green shaded regions form closed loops, which we call stars, of 16 edges and 16 vertices around the missing 8-vertices. To investigate all the different ways in which the ladder segments match up to form ladders in the graph, it is useful to refer to the vertex configurations of such dimer-decorated tiles for the AB\(^*\) tiling, and they are shown in Fig. 12 (compare Fig. 5 for the undecorated tiles). The continuation of light blue and yellow regions into ladder segments, as well as the formation of stars from the green regions, is apparent.

We now argue that in every perfect matching, the stars and ladders of the AB\(^*\) tiling form perfectly matched regions, separated by exact membranes which do not host any dimers. Fig. 11 has dimers residing only on edges that belong to the stars and ladders. Now, we show that all vertices in each star (ladder) must be matched to vertices in the same star (ladder) in all perfect matchings. Therefore, any edges external to the stars and ladders (thick white edges in Fig. 11 and Fig. 12) are never covered by dimers in any perfect matching and hence form exact membranes.

The proof follows from two observations. First, stars are closed loops of 16 vertices, with eight vertices in each bipartite subset (we denote the two subsets \(U\) and \(V\)) and no vertices in the interior (due to the removal of the 8-vertices in constructing AB\(^*\)). For each star, all ‘exterior’ vertices with edges to the rest of the graph (i.e. the ‘points’ of the star) are of the same charge. The ‘interior’ vertices alternate with these and therefore are all of the opposite charge. Since they cannot match with any other vertex, we must match each interior vertex with an adjacent exterior vertex. Therefore each star hosts eight dimers forming one of two possible alternating paths around the star (see Fig. 16b), leaving no exterior vertices unmatched.

Second, ladder segments in the tiles of Fig. 11 always contain the same number of vertices of each charge, a property that is therefore inherited by any section of a ladder built up from these segments. Fig. 12 shows the vertex configurations for the ladder-decorated tiles, allowing us to read off all the ways in which different ladder segments can match up to form ladders. For each

FIG. 12. All vertex configurations of the ladder-decorated tiles of Fig. 11. This shows all possible ways in which ladder segments can join up to form ladders in the AB\(^*\) tiling. The segments shaded with yellow and light blue in Fig. 11 match up to form ladders, whereas the green segments match up to form stars in the bulk of the AB\(^*\) tiling.
ladder section in Fig. 12, all vertices with edges to other ladder segments are of the same charge, say of $U$. While $V$-vertices do have edges connecting them to stars, those edges can never host dimers in a perfect matching, as we have already shown that the vertices in a star are always matched to vertices within the star. Since there are an equal number of vertices of each charge in any ladder, this immediately implies that all $U$-vertices in a ladder must match to $V$-vertices in the same ladder in a perfect matching to avoid a contradiction. Thus, edges outside ladders and stars constitute membranes which never host a dimer in any perfect matching of the AB* tiling.

These results imply that the partition function of the dimer problem on the AB* tiling decomposes into a product of partition functions of ladders of different lengths, and stars. This enables us to make several exact statements about the dimer problem on the AB* tiling in Sec. V.

Ladder regions and membranes in any perfectly matched patch of the AB* tiling can be determined algorithmically by using the Dulmage-Mendelsohn decomposition described in Appendix A. Fig. 15 shows the ladders and stars for an 8-fold symmetric patch of the AB* tiling. All the ladders are closed loops with 8-fold symmetry. Note that a generic finite patch of the AB* tiling can have ladders that span the patch, terminating at the boundaries. However, these ladders will generally close upon completion of the boundary: infinite system-spanning ladders occur with zero frequency on the tiling.

B. Pseudomembranes in the AB tiling

Armed with our results on AB*, we now return to the full AB tiling, and show that the restoration of the deleted 8-vertices transforms the membranes of AB* to pseudomembranes on AB. As we defined earlier, a pseudomembrane is a connected set of edges which collectively host a maximum of one dimer between them in any maximum matching. Pseudomembranes satisfy two additional properties: (i) deleting all the edges in a pseudomembrane disconnects the graph into two components; (ii) pseudomembranes close with $D_8$ symmetry, and are centred on 8-vertices.

Anticipating the second point, we consider local empires of $8_n$-vertices, which we refer to as $8_n$-empires. An $8_n$-empire is generated by inflating the local empire of an $8_0$-vertex (Fig. 9) $n$ times. We first remove the central $8_n$-vertex from a $8_n$-empire, yielding what we term a punctured $8_n$-empire. Certain $D_8$-symmetric annular subregions $H_i$, concentric with the 8-vertex of the punctured $8_n$-empire (to be specified in Appendix B), admit perfect matchings. If we choose boundary conditions to exclude vertices which lie out side the outermost annular subregion $H_n$, then the region so obtained also hosts perfect matchings. In these perfect matchings, vertices in each annular subregion $H_i$ are perfectly matched to other vertices within the subregion $H_i$. The perfectly matched subregions $H_i$ are separated by membranes which are concentric with the deleted 8-vertex. This can be shown using arguments similar to ones used in Sec. III and Sec. IV A. We have relegated the proof of the statement to Appendix B. Here, we display the membranes and perfectly matched regions for punctured $8_2$ and $8_4$-empires in Fig. 13.

If the central 8-vertex is reinstated to this perfect matching, it will host a monomer. Moving this monomer out of any region enclosed by a membrane of the punctured empire converts the membranes to pseudomembranes. This follows since moving the monomer requires the augmentation of alternating paths of even lengths which terminate on the monomer. Since such paths traverse a membrane that originally enclosed the monomer, they will place a single dimer across the former membrane. Since only a single monomer was added to the perfect matching, it follows that there can be no more than one such dimer in any pseudomembrane. One might wonder if a monomer can recross the membrane in the opposite direction and thereby place another dimer across...
the membrane; this is ruled out by some simple observations about the perfectly matched regions. Any two perfectly matched regions separated by a membrane have the property that all edges in the membrane connect vertices of the same bipartite charge in one region to vertices of the opposite bipartite charge in the other region.\(^2\) If the central 8-vertex is an \(U\)-vertex, this implies that each perfectly matched component of a punctured \(8_{n}\)-empire has only \(V\)-vertices on its inner boundary and \(U\)-vertices on its outer boundary. When a monomer is introduced by reinstating the central 8-vertex, the monomer re-crossing a membrane would imply the existence of a perfectly matched region such that its inner boundary is crossed twice by the monomer and its outer boundary is not crossed by the monomer. This matches 2 \(V\)-vertices of that region with vertices outside the region, leaving an excess of 2 \(U\)-vertices in the rest of the region, and is therefore not possible in a maximum matching.

In general, an \(8_n\)-empire hosts \(n + 2\) pseudomembranes concentric with the 8-vertex at the empire’s centre. The \(8_n\)-empire also hosts additional pseudomembranes concentric with other 8-vertices within the empire. These 8-vertices are necessarily of order \(m < n\). The edges comprising the pseudomembranes are those that form membranes in the \(AB^*\) tiling, as described in Sec. IV A.

Note that the results of the previous paragraph also hold for \(8_n\)-empires with generic boundary conditions. Punctured \(8_n\) empires admit a perfect matching only when specific boundary conditions are considered, otherwise they typically host a few monomers at their boundaries depending on the specific choice of boundary conditions. While such monomers have a vanishing density in the thermodynamic limit, our construction of pseudomembranes outlined above does not carry over. However, when such an \(8_n\)-empire is embedded in a larger system, the monomers at the boundaries are annihilated with other monomers in a maximum matching (recall that AB tilings host perfect matchings in the thermodynamic limit), and pseudomembranes appear.

As noted earlier, an \(8_n\)-empire has smaller \(8_m\)-empires \((m < n)\) within it corresponding to 8-vertices of different orders, both concentric and otherwise. All these empires host their own pseudomembranes. The full AB tiling consequently exhibits a rich hierarchical structure of nested pseudomembranes. Further, each region bounded by a pseudomembrane acts as an effective unit which is connected by a single dimer to the rest of the system. This hints at a possible scale invariance in the dimer problem, which we probe numerically in Sec. VI.

V. EXACT RESULTS ON THE \(AB^*\) TILING

So far, we have only considered the single perfect matching that arises from our chosen decoration of the dimer inflation tiles, either from repeated application of the rule specified in Fig. 10 (in the case of the full AB tiling), or single application of the rule specified in Fig. 11 (for the \(AB^*\) tiling). However, in both cases the complete space of dimer configurations is exponentially large in the number of vertices. The most general partition function specified in Eq. (1) is a weighted sum over all dimer configurations. Here we consider a statistical ensemble initially restricted to perfect matchings of the \(AB^*\) tiling, with all such configurations having equal statistical weight. In this way the partition function simply counts perfect matchings.

The nontrivial physics of the dimer problem stems from the matching constraint, which makes the problem of enumerating all configurations on any graph notoriously difficult. The degrees of freedom (dimers) are no longer independent as they are, for example, in spin models. For planar graphs, there is an in-principle exact solution [29, 30, 57, 76]. However, this calculation, requiring the evaluation of a certain Pfaffian, is often computationally demanding. On some periodic lattices, as we have noted, effective long-wavelength ‘height’ representations allow the use of field-theoretic techniques to compute monomer and dimer correlations. While it is possible to construct a height representation for the dimer problem on the AB tiling, there is no clear physical principle (comparable to ‘maximize flippable loops’ for many periodic dimer problems) that would allow us to infer a tractable local free energy density on which to base a systematic height field theory.

Accepting these difficulties, the \(AB^*\) tiling introduced in the preceding section provides a powerful simplification. The constraint that no dimers can sit on membranes dramatically simplifies the enumeration of dimer coverings, since the dimer partition function on the full 2D tiling factorizes into a product of partition functions for lower-dimensional quasiperiodic dimer models. Simply put, there can be no correlation across the membranes. We can leverage this property to obtain an asymptotically exact result for the free energy of dimers on \(AB^*\). While this does not immediately yield an exact result for the AB tiling (since the latter lacks the exact factoring property) it provides important clues to aid our numerical investigation of AB in Sec. VI.

A. Stars and ladders

As explained in Sec. IV, the structure of \(AB^*\) is comprised of stars, ladders and membranes. As the stars and ladders form a subset of the AB tiling, we expect these structures to obey the inflation symmetry. Fig. 11 shows how the ladder tiles of Fig. 11 inflate under \(\sigma\) (technically, to perform inflation on \(AB^*\), the inflation

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\(^2\) This follows from the properties of Dulmage-Mendelsohn decomposition reviewed in Appendix A.
the purpose of matching, we have $A \pi R S \pi$ and $A \pi S$.

Different tile environments that appear in any segment as $R$ represents impermeable membranes. Denoting the three different tile environments that appear in two distinct environments ($S, R,$ and $R'$, and noting that $R'$ is topologically equivalent to $S$ for the purpose of matching, we have $A = SRS, B = S^2R^2S^2$.

The segments are marked on the tiles by coloured arcs of internal angles $\frac{\pi}{4}, \frac{\pi}{4}, \frac{\pi}{2}$ for segments $P, A, B$ respectively, which retain the symmetry of the original segment.

is performed on the AB tiling and then the 8-vertices are once again removed, mapping back to $AB^*$. Rather than work at the level of the tiles, we distinguish three repeating units: the basic 2-edge unit of the star, which we label $P$ (shaded green); a ladder segment with the structure $SRS$ (square-rhombus-square), which we label as $A$ (shaded light blue); and a ladder segment with the structure $S R' R R' S$, which we label $B$ (shaded yellow).

Each unit connects at its two end-points with other units, forming longer segments. We note the basic rhombus tile can appear in two distinct environments ($R$ and $R'$): the $R$ rhombi appear in the $A$ segment or in the centre of the $B$ segment, and have a single vertex which only has edges to two other vertices in the ladder; the $R'$ rhombi appear sandwiched between $S$ and $R$ in $B$. In the graph topology of the ladder, the $R'$ rhombi are equivalent to the $S$. Therefore, for the purposes of matching we may identify $R' \sim S$ and only discuss $S$ and $R$, so that the structure of $B$ is equivalent to $S^2R^2S^2$. We denote a tile or segment $T$ repeated consecutively $n$ times as $T^n$. From Fig. 14 we can read off the inflation of the segments:

$$P \rightarrow A, \quad A \rightarrow B^{1/2} AB^{1/2}, \quad B \rightarrow B^{1/2} A^4 B^{1/2}. \quad (8)$$

Although a one-to-one identification creates fractional-power $B$ segments, two of these always join to form a whole segment: $(B^{1/2})^2 = B$. We are free to shift our inflation rule by $B^{1/2}$ to the right, obtaining the more convenient form

$$\xi : P \rightarrow A, \quad A \rightarrow AB, \quad B \rightarrow A^4B. \quad (9)$$

A 1D inflation rule $\xi$ over the three-letter ‘alphabet’ $(P, A, B)$ is then obtained if we further define

$$\xi(MN) = \xi(M)\xi(N) \quad (10)$$

for any ‘words’ $M, N$. Due to the invertibility of $\sigma$, the inverse of $\xi$ must also exist: we denote it $\xi^{-1}$. The 2D inflation $\sigma$ is therefore reduced to an effective 1D inflation $\xi$ on the $AB^*$ tiling.

The $P$ segments always close into isolated stars with $D_8$ symmetry, i.e. $P^8$ (with periodic boundary conditions). Each ladder either closes in a loop or spans the entire tiling — this follows by noting from the configurations in Fig. 12 that ladders cannot branch or terminate in the tiling. Additionally, if a ladder closes, it does so with $D_8$ symmetry. To see this, observe that the inflation of the ladder tiles (Fig. 14) preserves the symmetry of the segments. Then, given a closed ladder loop, repeated deflation must eventually result in a loop containing $P$ segments, since $\xi^{-1}$ only destroys $Ps$. It follows that ladders can only close with $D_8$ symmetry. The possibility of a system-spanning ladder on the infinite tiling is evident by considering the case of repeated inflation of any single segment; the infinite ladder is obtained in the limit. The possibility of multiple system spanning ladders is more interesting. Similar curves to those in Fig. 14 can be used to decorate the tiles of the Penrose tiling; in that case, Penrose and Conway have independently shown that at most two system-spanning curves can exist in a tiling [92]. We expect there is an infinite $\xi$-symmetry constraint, and assuming periodic boundary conditions, we obtain the structure of the order-$n$ ladder as

$$L_n = (\xi^n(A_0))^8 \equiv A_n^8. \quad (11)$$

Thus the order-$1$ ladder corresponds to $A_8$, the order-$2$ ladder to $(AB)^8$, the order-$3$ ladder to $(ABA^4B)\hat{8}$, and so on.

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3 Since $P$ never occurs after the first inflation the alphabet is effectively two-letter.
The order-$n$ ladders are fractal structures in the limit $n \to \infty$, and their fractal dimension can be derived from the preceding inflation rules. Denoting the number of $A$ ($B$) segments in an order-$n$ ladder as $\alpha_n$ ($\beta_n$), the growth under $\xi$ is specified by the inflation matrix,

$$\begin{pmatrix} \alpha_{n+1} \\ \beta_{n+1} \end{pmatrix} = \begin{pmatrix} 1 & 4 \\ 1 & 1 \end{pmatrix} \begin{pmatrix} \alpha_n \\ \beta_n \end{pmatrix}. \quad (12)$$

The largest eigenvalue of this matrix is 3, and so the number of both $A$ and $B$ segments in a ladder grows by 3 under inflation, in the above limit. It would appear to follow that the length of a ladder likewise increases by a factor of 3 under inflation. However, there is a subtlety here in the fact that the orientations of $A$ and $B$ segments are reversed under a single inflation; this is easily resolved by considering the action under $\xi^2$. Then the length of a ladder increases by a factor of 9, whereas all edge lengths are scaled by the silver ratio $\delta_S^2$. The (box-counting) fractal dimension $d_F$ of the ladders is then found by setting $(\delta_S^2)^{d_F} = 9$, from which

$$d_F = \frac{1}{\log_2 \delta_S} \approx 1.246 \ldots \quad (13)$$

This is similar to the case on the Penrose tiling, where the membranes were found to have fractal dimension $1/\log_2 \varphi \approx 0.8$, where $\varphi$ is the golden ratio.

We show a finite patch of the AB$^*$ stars and ladders in Fig. 15. Observe that an $8_n$-vertex is the centre of concentric ladders of orders $0 \leq m \leq n$. An order-$n$ ladder also encloses other ladders which are not concentric with it, and centred on other $8_m$-vertices of order $m < n$. These properties follow from the fact that all $8_n$-vertices are enclosed by stars, and an order-$n$ ladder inflates from a star. Consequently, the number of ladders at a given order $n$ is in one-to-one correspondence with the number of $8$-vertices of order $m \geq n$. This in turn can be computed by counting the number of all $8$-vertices on the tiling obtained by deflating $n$ times. Given a tiling with $N$ vertices, for $N$ large, the $n$-fold deflated tiling has $\sim N/\delta_S^4$ vertices, a fraction $1/\delta_S^2$ of which are $8$-vertices. These statements become exact as $N \to \infty$. Combining these results, we see that the number $N_n$ of order-$n$ ladders on an $N$-site tiling is given by

$$N_n \equiv \nu_n N \quad \text{with} \quad \nu_n \to \frac{1}{\delta_S^2 + 2} \text{ as } N \to \infty. \quad (14)$$

Here, $\nu_n$ is the frequency of order-$n$ ladders, equal to the sum of frequencies of $8_m$-vertices for $m \geq n$ (so $\nu_0 \equiv \nu_{8}$ in the notation of section III). Note that $N$ refers here to the number of vertices on the ‘parent’ AB tiling; the number of vertices on the AB$^*$ tiling is given by eliminating the $N/\delta_S^4$ 8-vertices, with

$$\lim_{N \to \infty} N_s = N(1 - \delta_S^{-4}). \quad (15)$$

B. Analytic calculation of the free energy of dimers on the AB$^*$ tiling

We now compute the free energy of the dimer model on the AB$^*$ tiling, building on the properties of stars and ladders just described. Starting from a reference perfectly matched configuration, all perfect matchings can be enumerated by a sequence of moves which augment alternating cycles, each leading to a new perfect matching. An alternating cycle cannot intersect a membrane, because augmenting the cycle would lead to the placement of two additional dimers on the membrane, which is impossible in a perfect matching. Therefore, the total number of dimer configurations across the tiling can be obtained as the product over the number of configurations on each ladder. That is, the partition function factorizes over ladders, with each ladder defining an independent 1D dimer problem. Since all ladders of a given order $n$ have the identical partition function $Z_n^\ast$, the partition function in the thermodynamic limit, $Z_s$, is simply

$$Z_s = \prod_{n=0}^{\infty} Z_n^{N_n^\ast}. \quad (16)$$

While the partition function naturally diverges in the thermodynamic limit, the free energy density is directly derivable from the partition function, and is bounded. The edges are the natural degrees of freedom on the tiling. The average edge connectivity on the AB tiling is 4 as all tiles have 4 edges. This is not true for the AB$^*$ tiling, with its 16-edge star tiles. However, in the
thermodynamic limit we have the number of edges of $AB^*$ expressed in terms of $N$, as $N_{E^*} = N(4 - 8\delta S^{-1})/2$. Thus, the free energy per edge of the $AB^*$ tiling in the thermodynamic limit is

$$f_s = \lim_{N \to \infty} \frac{\ln Z_s}{N_{E^*}} = \frac{1}{6(1 + 4\delta S)} \sum_{n=0}^{\infty} \ln Z_n \delta S^n,$$  

where we have used Eq. (14) and Eq. (15), and simplified powers of $\delta S$ using Eq. (3). The factorization of the partition function, so that the free energy density in Eq. (17) can be expressed as a sum over contributions of ‘free ladders’, is a remarkable property of $AB^*$. Note that this decomposition of the partition function is non-trivial: even after the 8-vertex deletions, the $AB^*$ tiling retains a single connected component. The free ladder decomposition emerges from the interplay of the dimer constraint and the quasiperiodic geometry, which disconnects the configuration space of dimers.

The task of computing $f_s$ now reduces to computing the partition function $Z_n$ of the order-$n$ ladder. The ladders and stars are effectively one dimensional, and this suggests that the ladder partition function can be efficiently enumerated in terms of transfer matrices. To construct such transfer matrices, we start with a brief discussion of the dimer configurations of the perfectly matched ladders. Given a perfect matching of any bipartite graph, all other perfect matchings can be obtained by augmenting alternating cycles (Sec. II A). The augmentation of some, but not all, alternating cycles can be achieved by sequentially augmenting alternating cycles on the elementary flippable plaquettes. Recall from Eq. (2) that a plaquette is the set of four edges of a single tile, and a plaquette is flippable if it hosts dimers on parallel edges. These local plaquette flips naturally divide the configuration space into sectors, such that configurations within each sector are reachable from each other by such plaquette flips. For periodic lattices, such sectors are topological in origin, and transitions between sectors are associated with alternating cycles which wind around one of the directions with periodic boundary conditions. Specializing to ladders, the partition function $Z_n$ enumerates configurations that can be reached via alternating cycles remaining within the ladder. The smallest move augments (flips) a single flippable plaquette. Distinct sectors are connected by loops which wind around the whole ladder. We label them by a winding number $w$.

The 0-ladders (stars) are a special case since they lack plaquettes. They admit only two possible configurations, the two alternating cycles connected by augmentation of the whole loop. Single plaquette flips cannot connect the two configurations. Thus, $Z_0 = 2$ and we label the two sectors by $w = \pm 1$. For the higher-order ladders, let us introduce the terminology ‘rung’ for an edge lying in the ladder interior, and ‘leg’ for an edge on the inner or outer boundary. Choosing any square plaquette on the ladder as a reference, we define the winding number to be the difference in the number of dimers on the inner and outer legs of this square \(^93^\). While the choice of square is arbitrary, the same choice must be made consistently in comparing two configurations. There are then three possible sectors, $w = \pm 1, 0$, and the problem reduces to counting the configurations in each sector on the ladders defined by Eq. (11). We show example configurations for the different winding sectors in Fig. 16.

We start by noting that with $w = \pm 1$, i.e. a square with a dimer on exactly one of its leg edges, the entire ladder configuration is forced, as can be seen in Fig. 16. Thus there are exactly two ‘staggered’ states for each ladder, providing the analogy to the two star states. In the $w = 0$ sector, for an $n$-th order ladder, let us take as a reference configuration $C^{(0)}_n$ the dimer arrangement of the ladder tiles in Fig. 11. This state has the maximum number of flippable plaquettes, maximising dimers on the rungs of the ladder. Such maximally flippable states are often referred to as ‘columnar’ states \(^5^\) in the literature. Owing to the symmetry of each segment about the rhombi, the ladder has $2k_A 3^k_B$ degenerate columnar states, where $k_A (k_B)$ is the number of $A (B)$ segments. Starting from $C^{(0)}_n$, all possible configurations within the $w = 0$ sector can be found using all possible combinations of plaquette flips.

To outline the transfer matrix approach we take on the $AB^*$ ladders, we will first consider the simpler problem of enumerating coverings of a periodic ladder consisting only of square tiles. In the $w = 0$ columnar state with dimers on every rung, every square plaquette is flippable. We can associate each plaquette in this initial configuration with a particle in the ground state, and a flipped plaquette (with dimers on the legs) with the excited state of the particle. Two neighbouring plaquettes cannot then be simultaneously flipped into an ‘excited’ state (with respect to the reference configuration). In other words, two excitations cannot neighbour one other. The same constraint appears in chains of Rydberg atoms \(^97, 98^\). The solution to this problem can be expressed in terms of Fibonacci numbers. The transfer matrix that enforces the neighbour-exclusion constraint is

$$\mathcal{F} = \begin{pmatrix} 1 & 1 \\ 1 & 0 \end{pmatrix},$$  

where the 0 (1) element represents the possibility for a particle to exist in the ground (excited) state. Then, for a closed chain consisting of $M$ plaquettes, the ($w = 0$) partition function is

$$\tilde{Z}^{(0)}_M = \text{Tr}(\mathcal{F}^M) = F_{M+1} + F_{M-1},$$  

\(^4^\) When dealing with dimers on periodic ladders, the equivalent states to our columnar states are also called ‘rung-dimer’ states in the literature, with ‘columnar’ reserved to describe dimers lining up along the ladder legs \(^93, 94^\). More generally, columnar is used to describe the maximally flippable states, which is the terminology we adopt here.
FIG. 16. (a) The two staggered configurations of the star. One can be obtained from the other by augmenting the alternating cycle. (b) The two staggered configurations of a ladder (only a segment of the ladder is shown). The winding number \( w \) is defined to be the difference in the number of dimers on the inner and outer legs of a chosen square plaquette (here marked with black cross). (c) Top: the reference configuration \( C_n^{(0)} \) for an \( n \)-th order ladder in the \( w = 0 \) columnar sector (only a segment of the ladder is shown). We associate each plaquette in \( C_n^{(0)} \) with a particle in its ‘ground’ state (black circles). A plaquette is ‘excited’ by augmenting the minimum 4-edge cycle around the plaquette (‘flipping’ the flippable plaquette): plaquettes that cannot be excited, e.g. the \( S_2 \) plaquette, we show with a red outline. Bottom: exciting plaquettes (teal) results in a new perfect matching, and constrains a new set of plaquettes as unexcitable. For example, exciting the central \( R \) means \( S_2 \) can now be excited, but \( S_1 \) cannot.

with \( F_M \) the \( M \)-th Fibonacci number, and \( F_1 = F_2 = 1 \).

The ladders in \( AB^* \) are not periodic. Their sequences of rhombi and squares contain no repeating part other than that implied by their \( D_8 \) symmetry; the sequences tend to quasiperiodicity in the thermodynamic limit. Consequently Eq. (19) does not hold, but \( \mathcal{F} \) will still be the transfer matrix between two neighbouring square plaquettes (recall that two of the rhombi in the \( B \) segment are treated as squares for this purpose, via the identification \( R' \sim S \)). The rhombi in the ladder segments impose a constraint, distinct from neighbour exclusion, which modifies the exclusion condition. This is easiest to see in the \( A \) segment, where a single rhombus sits between two squares. Our choice of \( C_n^{(0)} \) breaks the symmetry about the rhombus. One of the square plaquettes \( (S_1) \) is flippable in this configuration, while the other \( (S_2) \) is not (see Fig. 16). Flipping the rhombus causes \( S_1 \) to become unflippable, and makes \( S_2 \) flippable. If we again associate every plaquette in the \( C_n^{(0)} \) configuration with the ground state of a particle, the neighbour-exclusion constraint is reversed for plaquette \( S_2 \): only when the preceding rhombus is in the excited state can \( S_2 \) also be excited. The rhombus transfer matrix is therefore the square transfer matrix, \( \mathcal{F} \), multiplied by the Pauli matrix \( \sigma_x \),

\[
\mathcal{W} = \mathcal{F} \cdot \sigma_x = \begin{pmatrix} 1 & 1 \\ 0 & 1 \end{pmatrix}.
\]  

(20)

Note that in the \( C_n^{(0)} \) state, the transfer matrix from a square to a rhombus is still \( \mathcal{F} \). We therefore have two transfer matrices: \( \mathcal{F} \) following a square plaquette, and \( \mathcal{W} \) following a rhombus plaquette. With our definition of \( A \) and \( B \) ladder segments, we will work instead with the two matrices

\[
A_1 \equiv \mathcal{F} \mathcal{W} \mathcal{F} = \begin{pmatrix} 3 & 1 \\ 2 & 1 \end{pmatrix}, \quad B_1 \equiv \mathcal{F}^2 \mathcal{W}^2 \mathcal{F}^2 = \begin{pmatrix} 9 & 7 \\ 5 & 4 \end{pmatrix}.
\]

(21)

The inflation rule \( \xi \) then generalises straightforwardly to the generalized transfer matrices \( A_n \) and \( B_n \) via

\[
A_{n+1} = A_n B_n, \quad B_{n+1} = A_n^4 B_n.
\]

(22)

The dimer partition function of the order-\( n \) ladder in the \( w = 0 \) topological sector is

\[
Z_n^{(0)} = \text{Tr} \left[ A_n^8 \right].
\]

(23)

To see the nontrivial role played by the rhombi, it is useful to compare the partition function of the \( n = 1 \) ladder to the partition function \( Z \) obtained for the periodic ladder obtained by replacing the eight rhombi with squares. From Eq. (19) the partition function \( Z \) is simply

\[
\hat{Z}^{(0)}_{M=24} = \text{Tr}(\mathcal{F}^{24}),
\]

(24)

whence we find that

\[
Z_1^{(0)}/\hat{Z}^{(0)}_{M=24} \approx 0.363.
\]

(25)

In other words, the rhombi remove a large fraction of configurations available to the square-only ladder. The total free energy is now determined via the multiplication of the transfer matrices. Including the two additional staggered configurations contributed to each ladder by the \( w = \pm 1 \) sectors, we find the total free energy density from Eq. (17) to be

\[
f_* = -\frac{1}{6(1 + 4\delta_S)} \ln 2 + \sum_{n=1}^{\infty} \ln \left( \frac{\text{Tr} [A_n^8] + 2}{\delta^8_n} \right).
\]

(26)

When working with transfer matrices in periodic systems, translational invariance permits a closed-form expression for \( Z \) in terms of the transfer matrix eigenvalues. In our case, apart from the eight-fold repetition required by the symmetry of the tiling, there is no periodically repeating unit smaller than \( A_n \). The two matrices \( \mathcal{F} \) and \( \mathcal{W} \) (and therefore \( A_1 \) and \( B_1 \)) do not commute, so cannot be simultaneously diagonalised. Consequently, each \( Z_n^{(0)} \) calculation requires multiplication of an ever-longer (exponentially growing) string of matrices which tends to quasiperiodicity in the thermodynamic limit. However, by iteratively computing in terms of Eq. (22), the
traces can be computed efficiently (approximately linearly in $n$) to arbitrary finite order. Further, the infinite series in Eq. (20) converges exponentially to its limit, on account of the exponential drop-off in the frequency at which higher-order ladders occur.

To prove this, first note that $A_n$ and $B_n$ (and hence $A_n$ and $B_n$ for $n > 1$) are unimodular matrices. Labeling the maximum and minimum eigenvalues of $A_n$ as $a_n^{-}$ and $a_n^{+}$ respectively, and those of $B_n$ as $b_n^{-}$ and $b_n^{+}$, it follows that $a_n^{-} = 1/a_n^{+}$ and $b_n^{-} = 1/b_n^{+}$. The eigenvalues $a_n^{+}$, $b_n^{-}$ are bounded according to Eq. (22) as

$$a_n^{+} < a_{n-1}^{+} b_{n-1}^{-}, \quad b_n^{-} < (a_{n-1}^{+})^{-1} b_{n-1}^{-}. \quad (27)$$

Taking logarithms of Eq. (27) we have the matrix equation

$$\begin{pmatrix} \ln a_n^{+} \\ \ln b_n^{-} \end{pmatrix} < \begin{pmatrix} 1 & 1 \\ 4 & 1 \end{pmatrix} \begin{pmatrix} \ln a_{n-1}^{+} \\ \ln b_{n-1}^{-} \end{pmatrix}. \quad (28)$$

We then write

$$\ln Z_n < 8 \ln a_n^{+} + \ln 2 \quad (29)$$

where we take the $\ln 2$ bound for simplicity. The maximum eigenvalue of the matrix in Eq. (28) is 3, and we have asymptotically $\ln a_n^{+} \sim 3^n$; with $3 < \delta_S^2$, Eq. (29) is bounded by a convergent geometric series. We can use Eq. (29) to bound the total error incurred by truncating the ladder series at finite order $M$. Denoting the error on the free energy by $\delta f^M_*$ we have

$$\delta f^M_* = -\frac{1}{\delta_S^M} \frac{1}{6(1 + 4\delta_S)} \sum_{n=1}^{\infty} \ln Z_{n+M} \delta_S^n. \quad (30)$$

Diagonalising Eq. (28), and using Eq. (29), we have

$$\ln Z_n < 3^{n-1}(4\ln a_1^{+} + 2\ln b_1^{+}) - (-1)^n(4\ln a_1^{-} - 2\ln b_1^{-}) + \ln 2, \quad (31)$$

from which

$$|\delta f^M_*| < \frac{1}{24(1 + 4\delta_S)\delta_S^{2M+1}} (\Gamma_M + \zeta),$$

$$\Gamma_M = 3^{M}(1 + \delta_S)(4\ln a_1^{+} - 2\ln b_1^{+}),$$

$$\zeta = (\delta_S - 1)(4\ln a_1^{-} - 2\ln b_1^{-}) + 2\ln 2. \quad (32)$$

(Here we used $(a_1^{+})^4 > (b_1^{+})^2$ as can be readily checked from Eq. (21)). Taking for example the first 40 terms in the ladder summation, we find $f_* = -0.0688471896847(17)$. The quasiperiodic geometry of $AB^*$ significantly lowers the number of available dimer states.

VI. NUMERICAL RESULTS ON THE AB TILING

In Sec. V we used the existence of membranes on the $AB^*$ tiling to factorize the tiling’s dimer partition function into contributions from ladders of different orders. Upon converting $AB^*$ back to $AB$ by reinstating the deleted 8-vertices, the exact membranes become pseudomembranes, and the exact factorization property is lost. Nevertheless, the existence of pseudomembranes suggests that dimer correlations on the full $AB$ tiling could continue to have a rich structure. In this section, we explore these correlations via a numerical study of the classical dimer model on finite patches of the $AB$ tiling using the directed-loop algorithm. Originally introduced to efficiently sample space-time configurations using quantum Monte Carlo algorithms [10, 99, 100], this method has been adapted to sample the configuration space of classical dimer models and to access their monomer correlations [33, 101]. The algorithm involves introducing two monomer defects into a maximum matching, and transporting one of the monomers around an alternating cycle until annihilating it with its partner monomer (or with any other monomer, in graphs not admitting perfect matchings). Since detailed balance is satisfied for these intermediate configurations with two monomers, the corresponding partition function can be sampled. This gives us access to monomer correlations without additional computational effort. For completeness, we review the algorithm in Appendix C.

A. Choice of samples and boundary conditions

As we have noted previously, since quasiperiodic systems are not translationally invariant and do not admit periodic boundary conditions, some care must be taken in choosing appropriate finite patches for our numerical studies of the $AB$ tiling. We consider finite patches with exact $D_8$ symmetry. We anticipate that understanding matching problems on such patches can yield results representative of an arbitrary finite patch of $AB$ tilings, since those are characterized by an effective matching problem of $D_8$ empires. Additionally, every finite patch of tiling is a part of a larger $D_8$ empire of the infinite tiling.

For our largest simulations we consider an $8_4$-empire. We find a small number of vertices near the boundaries of this $8_4$-empire to belong to perfectly matched components of the Dulmage-Mendelsohn decomposition of Appendix A. The central 8-vertex has 6 concentric pseudomembranes around it. We remove the parts of the tiling outside the largest pseudomembrane as they essentially generate boundary effects. As explained in Sec. IV B in any perfect matching of the $AB$ tiling, precisely one dimer straddles the pseudomembrane to correlate the dimer configurations inside and outside the region it encircles. Hence, it is reasonable to expect that calculations of observables defined entirely inside a region enclosed by a pseudomembrane will not be severely affected by the rest of the tiling even in finite patches. With these modifications, the largest $AB$ patch we consider contains 15473 vertices and 30136 edges. In some cases, we consider a smaller patch consisting of the region inside the $4^{th}$ pseudomembrane, which can be derived...
FIG. 17. Left: Dimer occupation densities on an 8\textsubscript{4}-unit, a finite \(D_8\)-symmetric patch of AB tiling. The region is bounded by the 6-th pseudomembrane. The lighter colours indicate a rich nested structure of pseudomembranes associated with different 8-vertices and their local empires. The black lines emphasize the scale symmetry of the lattice (and consequently maximum matchings): they denote sections of the larger AB-tilings \((T_{-2} \text{ and } T_{-4})\) composed of the 8\textsubscript{2} and 8\textsubscript{0}-units. Each 8\textsubscript{n}-unit is surrounded by a pseudomembrane, and hence connected to the rest of the graph by at most one dimer. They sit at the vertices of a larger AB-tiling \((T_{-n})\), and act as effective units. Right: An 8\textsubscript{0}-unit (top) and an 8\textsubscript{2}-unit (bottom), with edges coloured to indicate dimer-occupation densities.

from an 8\textsubscript{2}-empire. This sample contains 481 vertices and 872 edges. For reasons outlined below, we call the larger sample an 8\textsubscript{4}-unit, and the smaller sample an 8\textsubscript{2}-unit. Note that all maximum matchings of this patch host a single monomer with the same bipartite charge as the central 8-vertex. If the finite patch were extended to the infinite tiling, this monomer would annihilate with an oppositely charged monomer in another region, creating the single dimer crossing the pseudomembrane. Unless otherwise specified, when we discuss ‘correlations on the AB tiling’ we mean those obtained on the finite patches just described.

B. Monomer and dimer correlations

First we calculate the dimer occupation densities, with results displayed in Fig. 17. We clearly see that the pseudomembranes of Fig. 13 appear as rings of edges with near-zero dimer density, concentric with the centres of local \(D_8\) symmetry. Every 8\textsubscript{n}-vertex has \(n+2\) pseudomembranes concentric with it (counting the eight edges of the octagon around the 8-vertex as a pseudomembrane). The pseudomembrane structure of the AB tiling can be described as follows. Each pseudomembrane bounds a region (set of edges and vertices) which acts as an effective unit, such that only one dimer connects the region to the rest of the graph. Motivated by this, we define an 8\textsubscript{n}-unit to be the region bounded by the \(n\textsuperscript{th}\) pseudomembrane from the centre of the local empire of any 8\textsubscript{n}-vertex. An 8\textsubscript{n}-unit contains \(n+2\) pseudomembranes. The smallest membrane, the octagon around an 8-vertex, and the eight edges within it, together form the (smallest) 8\textsubscript{2}-unit. From the discussion of scale invariance of the AB tilings in Sec. II B, every 8\textsubscript{0}-unit forms another AB patch, larger by the square of the silver ratio. However, these 8\textsubscript{0}-units are mediated by the ladders (formed of 8\textsubscript{2}-units) of Sec. V. This means that each 8\textsubscript{0}-unit matches to a ladder with a single dimer (living on a pseudomembrane). The edges of this ladder in turn match to other 8\textsubscript{0}-units. Similarly, 8\textsubscript{n}-units form AB tilings mediated by ladders formed of 8\textsubscript{n-2}-units, for all even
n. This effective description in terms of matching up \(8_n\)-units through ladders suggests the possibility of non-trivial long-range dimer correlations.

With this motivation, we investigate the connected correlations \(C(e_i, e_j)\) of dimers on edges \(e_1\) and \(e_2\), defined to be

\[
C(e_i, e_j) = \langle n(e_i)n(e_j) \rangle - \langle n(e_i) \rangle \langle n(e_j) \rangle,
\]

(33)

where \(n(e_i) = 1\) if the edge \(e_i\) hosts a dimer, and \(n(e_i) = 0\) otherwise. For the system sizes under consideration we find a striking result: connected dimer correlations do not decay exponentially, as they would consideration we find a striking result: connected dimer correlations do not decay exponentially, as they would.

Characterizing \(C(e_i, e_j)\) is complicated owing to its lack of translational invariance, and its high degree of inhomogeneity. We have already displayed, in Fig. 2, the dimer-correlation function \(C(e_0, e_j)\) for an edge \(e_0\) which connects a 4-unit to a ladder (formed of 2-units).

While this clearly indicates slowly decaying dimer correlations, we take up a more careful investigation of dimer-correlations here. To characterize the decay of correlations, we calculate \(C_{\max}(e_0, x)\): the maximum value of \(|C(e_0, e_j)|\) such that the edge \(e_j\) has a graph distance of \(x\) edges from \(e_0\). We display this quantity, computed for seven different choices of \(e_0\), in Fig. 18. We see a slow decay consistent with power law asymptotic behaviour.

We conjecture that this slow power law is a manifestation of the description in terms of the effective matching problems, at all scales, in terms of \(8_n\)-units mediated by ladders formed of \(8_{n-2}\)-units as described above. We emphasize that these power-law-like correlations are neither homogeneous nor translationally invariant, and are unrelated to the familiar power laws appearing in bipartite lattices with a continuum Gaussian action. However, not all edges have such power law dimer correlations. For example, inside an \(8_2\)-unit, the edges connecting \(8_0\)-units to \(L_1\) ladders do not have significant connected correlations outside the \(8_2\)-unit. Such bounded correlations are displayed in Fig. 19.

Next we turn to monomer correlations. For dimer problems on bipartite graphs with perfect matchings, the monomer correlation functions can be obtained as the partition function \(Z_{\text{mwm}}(r_1, r_2)\) of two monomers with opposite bipartite charge situated on vertices \(r_1\) and \(r_2\). Our finite patches always have one extra vertex in the bipartite subset of the central 8-vertex. Without loss of generality we denote this the \(\mathcal{U}\)-subset. We define an auxiliary partition function \(Z_{\text{uum}}(r_1, r_2, r_3)\) with three monomers on vertices \((r_1, r_2, r_3)\), where \(r_3\) belongs to the \(\mathcal{V}\)-subset, while \(r_1\) and \(r_2\) belong to \(\mathcal{U}\). We now define monomer correlations for this gas of 3 monomers. Correlations between the two \(\mathcal{U}\)-monomers are dominated by the density of the single \(\mathcal{U}\)-monomer, which our \(D_8\)-symmetric samples host in the maximum matching. To probe the physics associated with the creation of monomer defects in the maximum matching, we measure the correlation function

\[
M^{\mathcal{U}\mathcal{U}}(r_1, r_2) = \sum_{r_3} Z_{\text{uum}}(r_1, r_2, r_3) \delta_{r_3, r_1} \delta_{r_3, r_2}.
\]

(34)

Here, \(M^{\mathcal{U}\mathcal{U}}(r_1, r_2)\) corresponds to a \(\mathcal{U}\)-monomer at \(r_1\) and a \(\mathcal{V}\)-monomer at \(r_2\). We find that \(M^{\mathcal{U}\mathcal{U}}(r_1, r_2)\) is non-monotonic as a function of the graph distance between \(r_1\) and \(r_2\). Irrespective of the location of \(r_1\), \(M^{\mathcal{U}\mathcal{U}}(r_1, r_2)\)
is strongly peaked for $r_2$ within the first few pseudomembranes near the central 8-vertex. A typical profile of $M^{TV}(r_1,r_2)$ for a fixed $(r_1)$ is displayed in Fig. 20. We found similar non-monotonic monomer correlations on Penrose tilings. We conjecture that such correlations are generic to systems with membranes and pseudomembranes. Such non-monotonicities make it tricky to define a sharp notion of monomer confinement. This can be understood in terms of dynamics of the loop algorithm, whose intermediate configurations sample this auxiliary partition function with two monomer defects. The loop spends a lot of time trapped in the first few pseudomembranes near the central 8-vertex. Once a loop enters the region bounded by a membrane, it can only exit through the same edge through which it entered the region. This also holds for pseudomembranes, save when the loop enters the region through the single edge on the pseudomembrane which hosts a dimer.

C. Aligning Interactions

Finally, we briefly discuss the role of aligning interactions. To do so, we include an energy function which either favours or disfavours the presence of flippable plaquettes. Specifically, we consider the classical energy function which results when the Rokhsar-Kivelson hamiltonian of Eq. [2] has its kinetic energy $t$ set to zero. We maintain the variable alignment potential $V$ which mimics the diagonal terms in quantum dimer models [2,5]. Taking $V$ positive (negative) penalizes (favourites) configurations with a large number of flippable plaquettes. We work entirely within the manifold of maximum matchings. The partition function is modified to

$$Z = \sum_{\mathcal{C}} e^{-V N_F(\mathcal{C})/T},$$

where $N_F(\mathcal{C})$ counts the number of flippable plaquettes in a dimer configuration $\mathcal{C}$. $T$ is a temperature that we introduce for convenience. Only the combination $V/T$ has physical significance. Regardless of sign, a non-zero
value stabilizes ordered phases which break lattice symmetries. The motivation of our investigation of this classical model is to look for possible ordered phases, and to investigate the form of the the associated transitions, in the absence of periodic lattice symmetries.

To orient the discussion, first consider the effect of aligning interactions on the ladders which make up the AB* tiling. Negative $V$ favours the maximally flippable columnar states on the ladders, while positive $V$ favours the two staggered states, which are in topologically distinct sectors. That is, each staggered state cannot be reached from any other state by a sequence of local plaquette flips. These ladders can be treated exactly using transfer matrices. However, to account for aligning interactions, we must replace Eq. (18) and Eq. (20) with transfer matrices. However, to account for aligning interactions on the ladders which make up the AB patches with $VRK = -3, T = 1$, $VRK = +3, T = 1$...

We calculate the standard deviation $\sigma_{N_F}$ of the number of flippable plaquettes $N_F$ as

$$\sigma_{N_F} = \langle N_F^2 \rangle - \langle N_F \rangle^2.$$  

The results are displayed in the inset of Fig. 22. We see that $\sigma_{N_F}/N$ exhibits a broad feature at $T \approx 1$, which suggests that the dimers settle into configurations resembling staggered states on the ladders without undergoing a phase transition.

$V_{RK} = -3, T = 1$

$V_{RK} = +3, T = 1$

Fig. 23 shows the dimer densities of an AB patch (82-unit) with aligning interactions. Left: at $V = -3.0$, the dimer densities reveal a strong tendency to align along the legs of the ladders, indicating that staggered configurations on the ladders are favoured. Right: at $V = 3.0$, the dimers tend to align along the rungs of the ladders, indicating that columnar states on the ladders are favoured.

Fig. 23 shows the dimer densities of an AB patch in the presence of aligning interactions of both signs. We see that at large negative values of $V$ the dimers align along the rungs of the ladders, while at large positive values of $V$ the dimers align along the legs of the ladders. This suggests that typical dimer configurations of the full...
AB tiling in these limits can be described in terms of the cartoons of columnar and staggered states on the ladders.

VII. CONCLUSIONS

We have demonstrated that classical dimers on the AB tiling admit perfect matchings in the thermodynamic limit, with a rich structure linked to the interplay of constraints with quasiperiodicity. A crucial feature of our analysis is the identification of collections of edges whose dimer content can be strictly bounded from above in any maximum matching. Previous work on the Penrose tiling identified exact membranes, sets of edges that host zero dimers in maximum matchings, separating regions hosting monomers (unmatched vertices) with distinct bipartite charge. The present work extends this analysis in two ways. First, we identified exact membranes on the auxiliary quasiperiodic AB* tiling obtained by deleting 8-vertices from the AB tiling. These membranes can be understood in terms of the fine Dulmage-Mendelsohn decomposition of a bipartite graph, reviewed in Appendix A. Second, returning to the full AB tiling by replacing the 8-vertices, we found that membranes become pseudomembranes, sets of edges that collectively host precisely one dimer in any perfect matching.

The coexistence of perfect matchings and exact membranes allowed us to exactly compute the partition function of the AB* tiling as the product of partition functions for disjoint dimer covers on ‘ladders’, sets of edges on which the dimers are not fully constrained. The pseudomembrane structure of AB implies that there are effective ‘units’ which exist at all scales which are connected by at most one dimer to the rest of the graph, leading to long-range connected dimer correlations that can be understood in terms of the discrete scale invariance of the quasiperiodic tiling. Using classical Monte Carlo simulations we found evidence for long-range and highly heterogeneous connected dimer correlations. Finally, we demonstrated that the introduction of an aligning interaction can favour various subsets of perfectly matched dimer configurations. This allowed us to identify the quasiperiodic analogue of ‘staggered’ and ‘columnar’ states, linked to the dominant correlations along those sets of edges on AB that form ladders on AB*.

The existence of perfect dimer covers on the AB tiling in the thermodynamic limit is in striking contrast with the situation in other two-dimensional quasicrystals. There are six minimal quasicrystals in two dimensions as identified in the classification scheme of Ref. [58]. All vertices of the Penrose tiling belong to regions of one or the other excess bipartite charge. The oppositely charged regions are separated by sets of edges which cannot host dimers in maximum matchings, the prototypes for the AB membranes in the present study. In some sense, however, it is the lack of perfectly matched regions which makes the Penrose tiling unique. The remaining four 2D quasicrystals contain regions with an excess of one or the other bipartite charge alongside perfectly matched regions. The division between different regions is always formed of sets of edges which cannot host dimers in maximum matchings. These cases, while still quasiperiodic and long-range ordered, begin to approach the generic results found in random or disordered bipartite graphs with two-dimensional embeddings, as characterised using the Dulmage-Mendelsohn decomposition. It is in this context that the results in the present study truly stand out. The behaviour of the long-range dimer correlations we have identified in these graphs appears to be related to the discrete scale invariance implied by the quasiperiodic inflation rules of Fig. 1 quantifying this connection more precisely is a worthwhile objective.

Turning to the more thorny issue of quantum fluctuations, the existence of columnar and staggered states for opposing signs of the alignment potential suggests that upon including dimer resonance moves (t > 0 in Eq. (2)), the phase diagram of quantum dimers on quasicrystals will resemble the Rokshar-Kivelson picture for periodic lattices [2, 5]. Therefore we anticipate the existence of at least a point in the quantum dimer phase diagram, between the columnar and staggered limits, where equal-time dimer correlations resemble those of the classical models studied in this work. However, whether this point requires fine tuning, or instead represents the properties of a robust phase of matter, is a much more delicate question. Historically, studies of dimer models on periodic bipartite lattices have made use of the height representation: in the quantum case, the height action must be supplemented by instanton contributions linked to the integer-valued nature of the height field. Instantons destroy the long-range quantum dimer correlations in two spatial dimensions, rendering them exponentially short-ranged: in essence, this is Polyakov’s argument for the absence of a deconfined phase of $U(1)$ quantum lattice gauge theories in three spacetime dimensions. This means that the power law correlations of the RK model require the fine-tuning characteristic of a multicritical point rather than the stability of a robust phase. The situation is less clear in the present case since, as we have noted above, there does not seem to be an obvious local height action that characterizes maximally probable dimer configurations on quasicrystals. Consequently there is a possibility that long-wavelength dimer correlations persist in the quantum problem. Verifying this is challenging, since in order to make precise statements one must approach the thermodynamic limit via a discrete sequence of inflations, and we are forced by quasiperiodicity to work with open boundary conditions. This means that the relevant computational cost likely becomes prohibitive before finite-size effects have been suppressed. In light of this, further study of the classical problem to determine if there is a convenient, possibly non-local, characterization of maximally probable dimer configurations seem warranted, as this might open a route to an analytical treatment. A more numerically tractable direction is to explore dimer models on
the $D_8$-symmetric ladders introduced in the context of the AB$^*$ tiling in Sec. 1. Recall that each of the eight symmetry-related segments of the ladder forms a system which tends to quasiperiodicity in the thermodynamic limit in its own right. This presents an interesting avenue for investigating quasiperiodic quantum dimer ladders. Periodic ladders, and closely associated frustrated spin ladders, have long been studied to shed light on the phases and transitions of quantum dimers [44–63, 104–106]. We expect studies of quasiperiodic quantum matching problems have been mapped to exact zero-energy modes of the hopping problem on the same graph [63, 107]. Here, the number of monomers hosted in a maximum matching is associated with the number of zero modes, while the monomer-confining regions are associated with wave functions whose support is confined within a compact subgraph. The computed monomer densities and geometry of monomer-confining regions on the Penrose tiling [58] are consistent with density of zero modes and the nature of confined states obtained from investigations of hopping problems on the Penrose tiling [108–110]. Ref. [71] has recently computed a finite density of confined zero modes on the AB tiling; naively, this appears to be in conflict with our results that demonstrate that the AB tiling can be perfectly matched with vanishing monomer density in the thermodynamic limit. This apparent contradiction may be resolved by noting that the zero modes obtained in Ref. [71] are what we term ‘fragile’: they move away from $E = 0$ on introducing arbitrarily weak disorder in the hopping matrix elements. In contrast, the Penrose tiling hosts ‘strong’ zero modes that survive to any disorder strength. Formally, the monomer density computed in the dimer cover problem exactly equals the density of strong zero modes, but is not linked to the density of fragile zero modes. The fragility of the AB zero modes may be explicitly verified by computing the spectrum of the random-hopping problem: for any nonzero randomness, exactly one zero mode from Ref. [71] survives (the strong mode associated with the unavoidable central monomer on 8-fold symmetric patches), with all the remaining modes moving to finite energy.

Finally, we comment on a relationship between the ideas explored in this paper and fracton phases of matter [111–117]. The latter are usually defined on translationally invariant lattices, and blend topological features with sensitivity to geometry. Type-I fracton phases host quasiparticle excitations which cannot move individually, but which can combine into pairs or quadruplets to move along lines or planes. There is a passing resemblance to the membranes in AB$^*$, in which the minimum excitation out of a perfect matching would be the deletion of a single dimer, creating a monomer-antimonomer pair. Membranes restrict each individual monomer to move on a subset of vertices of the same bipartite charge. But the pair together is free to move anywhere, with one or other monomer ‘opening a door’ through a membrane which the other closes. However, a key feature of mobile fracton pairs is that their separation is fixed, while the monomer pair has no such constraint. Very recent work [118] has extended the duality between fractons and elasticity theory [119] to quasicrystalline systems, but as yet it is unclear whether this has direct implications for the results presented here. In type-II fracton phases the excitations can only move along fractal subsets of the full system. Loosely speaking, they are an instance where a complicated set of gauge constraints on a simple lattice leads to emergent low-energy behaviour in which the natural gauge-charged objects are fractals. Contrast this with the present example, where a conventional Gauss-law-like structure (imposed by the dimer constraint) leads to a setting where ‘gauge lines’ are themselves subject to fractal — and fractally distributed — barriers. It seems therefore that the study of dimer models on quasicrystals presents an intriguing counterpoint to fractons. In future, it will be interesting to explore whether properties such as unusual topological robustness at finite temperature and glassy dynamics characteristic of fractonic phases also emerge in the quasiperiodic dimer setting.

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Appendix A: Membranes in general bipartite graphs and the Dulmage-Mendelsohn decomposition

We provide a graph-theoretic picture of monomer-confining regions and their associated membranes in maximum matchings. These regions turn out to be components of the Dulmage-Mendelsohn decomposition, which we will briefly review here.

A bipartite graph can be represented by a matrix $G$ with rows denoting one bipartite subset $U$, and columns denoting the other subset $V$. An edge between an $U$-vertex $i$ and a $V$-vertex $j$ corresponds to a nonzero value of the element $G_{ij}$. Readers may be more familiar with the graph adjacency matrix $A$, a square matrix labelled by vertices of the graph, and whose nonzero entries correspond to edges. In terms of $G$, the adjacency matrix
The Dulmage-Mendelsohn decomposition can be succinctly expressed in terms of a block-triangular factorisation (BTF) of the matrix $G$, achieved by a permutation of its rows and columns. In general, such a BTF is of the form

$$G = \begin{pmatrix} G^h & M^{hs} & M^{hv} \\ 0 & G^v & M^{sv} \\ 0 & 0 & G^c \end{pmatrix}. \tag{A2}$$

The Dulmage-Mendelsohn decomposition can be succinctly expressed in terms of a block-triangular factorisation (BTF) of the matrix $G$, achieved by a permutation of its rows and columns. In general, such a BTF is of the form

$$A = \begin{pmatrix} 0 & G \\ G^T & 0 \end{pmatrix}. \tag{A1}$$

The matrix $G_h$ has dimensions $U_h \times V_h$ with $U_h \times V_h$ and the matrix $G_v$ has dimensions $U_v \times V_v$ with $U_v > V_v$. $G_h$ is a square matrix with dimensions $U_h \times V_h$, with $U_h = V_h$. The subscripts $h, v, s$ denote horizontal, vertical and square respectively.

In a maximum matching, all the $U$-vertices in $G_h$ are matched to $V$-vertices in $G_h$, leaving behind $V_h - U_h$ monomers. Similarly all the $V$-vertices in $G_v$ are matched to $U$-vertices in $G_v$, leaving behind $U_v - V_v$ monomers. $U$-vertices in $G_s$ are perfectly matched to $V$-vertices in $G_s$. This implies that none of the edges in the off-diagonal blocks $M^{hv}, M^{hs}, M^{sv}$ are matched in any maximum matching: these edges constitute membranes. Note that for a particular bipartite graph, some of these blocks might not appear in the BTF: a graph with a perfect matching would only have the block $G^s$, while the Penrose tiling (which decomposes into monomer-confining regions) would only have the matrices $G^h, G^v$ and $M^{hv}$ in its BTF. This is the content of the coarse Dulmage-Mendelsohn decomposition.

Monomer-confining regions (such as those studied Refs. [58 63]) as well as perfectly matched regions separated by membranes in our problem are components of the fine Dulmage-Mendelsohn decomposition [64 67]. This involves a further decomposition of the matrices $G_h, G_v$ and $G^s$ by row and column permutations. Monomer regions correspond to a block-diagonalisation of $G_h$ and $G_v$.

$$G_h = \begin{pmatrix} G_1^h & 0 & 0 \\ 0 & G_2^h & 0 \\ \vdots & \vdots & \ddots \\ 0 & 0 & G_n^h \end{pmatrix}. \tag{A3}$$

Each rectangular block $G_i^h$ corresponds to a monomer-confining region with more $V$ vertices than $U$ vertices, and hosting a corresponding number of monomers on $V$-vertices. All vertices on the boundary of such regions belong to the $U$-subgraph, and all edges connecting such boundary vertices to the rest of the graph constitute membranes which never host a dimer.

$G^v$ can be similarly block diagonalized into $G_i^v$. These blocks correspond to regions confining monomers on $U$-vertices. Each block now has an excess of $U$-vertices and host a corresponding number of monomers on $U$-vertices.

The boundary vertices of $G_i^v$ belong to the $V$-subgraph, and the edges connecting the boundary vertices to the rest of the graph constitute membranes. Membranes separating perfectly matched regions correspond to a finer decomposition of the perfectly matched region $G^v$. $G^s$ can be further block-triangularised as

$$G^s = \begin{pmatrix} G_1^s & M_{12}^s & \cdots & M_{1n}^s \\ 0 & G_2^s & \cdots & M_{2n}^s \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & G_n^s \end{pmatrix}. \tag{A4}$$

Each block $G_i^s$ corresponds to a region of the graph such that all vertices in $G_i^s$ are perfectly matched to vertices within $G_i^s$ in all maximum matchings. This implies that edges in the off-diagonal blocks $M_{ij}$ are never matched in any maximum matching, and correspond to membranes separating perfectly matched regions.

Having identified different kinds of membranes and monomer-confining regions with components of the Dulmage-Mendelsohn decomposition, we outline the procedure to compute the decomposition. Given any maximum matching, find all vertices reachable from the $U$-monomers by alternating paths. $G^v$ is the subgraph induced by these vertices. Similarly, $G^h$ is the subgraph induced by the vertices reachable from $V$-monomers by alternating paths. $G^s$ is the subgraph induced by vertices unreachable from monomers by alternating paths. The further decomposition of $G^h$ and $G^v$ into monomer-confining regions (Eq. [A3]) corresponds to computing their connected components.

The decomposition of the perfectly matched $G^s$ (Eq. [A4]) requires a bit more work. Given two $U$-vertices in $G^s$, being a part of a closed alternating path defines an equivalence relation. Let the corresponding equivalence classes be $C_{1}^d \cdots C_{m}^d$. Further, we denote the set of $V$-vertices matched to $U$-vertices in $C_{i}^d$ by $C_{i}^v$. The subgraph induced by $C_{i}^d$ and $C_{i}^v$, for each $i$, correspond to the blocks $G_i^s$ appearing in the decomposition of $G^s$ (Eq. [A4]). These are perfectly matched regions separated by membranes (sets of edges which do not host dimers in any maximum matching). These equivalence classes can be determined by first forming a directed graph $G_d$ corresponding to the perfectly matched subgraph $G^s$. To construct $G_d$, given a perfect matching of $G^s$, we first direct all unmatched edges from $U$-vertices to the $V$-vertices. Then all matched edges are collapsed to a single vertex, labelled by the $U$-site. This specifies the directed graph $G_d^s$, with vertices labelled by $U$-vertices. The strongly connected components of this directed graph give us the equivalence classes $C_{i}^d$. Strongly connected components of a directed graph can be efficiently determined using Tarjan’s algorithm. [120] This allows an efficient determination of the components $G_i^s$ of the perfectly matched subgraph $G^s$ — all $U$-vertices in each component are perfectly matched to $V$-vertices in the same component, and the components are separated by membranes, which never host a dimer in any maximum matching.
FIG. 24. Starting from $\mathcal{H}_1$, the order-1 ladder, an inflation rule $\lambda$ generates concentric, $D_8$-symmetric regions $\mathcal{H}_i = \lambda^i(\mathcal{H}_1)$ which can be perfectly matched, such that all sites in an $8_n$-empire belong to one of the $\mathcal{H}_i$ for some $i$. We have presented the inflation rules in terms of ladder segments of Fig. 11. As before, the ladder segments are represented by coloured arcs of internal angles $\pi/4, \pi/2$ for the segments $P$, $A$ and $B$ respectively. Each region $\mathcal{H}_i$ is comprised of closed ladders as well as the links connecting those ladders. For clarity, we have suppressed both the 8-vertices located at the centre of the green circles (stars) and the links between the ladder segments.

Appendix B: Membranes in punctured $8_n$-empires

In Sec. IV A we showed that the AB* tiling hosts a perfect matching, and membranes separate stars and ladders, which host dimers in the perfect matching. Here, we consider punctured $8_n$-empires, obtained by removing the central 8-vertex from the $8_n$-empire, and prove that when such $8_n$-empires are terminated with certain $D_8$-symmetric boundary conditions they host a perfect matching. Further, concentric membranes around the absent central 8-vertex separate perfectly matched components, which we label as $\mathcal{H}_i$. These statements can be proven as follows:

- Starting with $\mathcal{H}_1$, which we take as the first closed ladder ($L_1$, in the language of Sec. IV A) which surrounds the absent 8-vertex and the star around it, there exists an inflation rule $\lambda$ such that $\mathcal{H}_{i+1} = \lambda^i(\mathcal{H}_1)$ are mutually exclusive $D_8$-symmetric regions, concentric with the central 8-vertex, and all vertices of the punctured $8_n$-empire belong to one of the $\mathcal{H}_i$ for some $i$. In an $8_n$-empire, the central 8-vertex is surrounded by a star (we define $\mathcal{H}_0$ to be the star, $\mathcal{H}_0 \equiv \mathcal{L}_0$), which in turn is surrounded by $\mathcal{H}_1$, and a region $\mathcal{H}_i$ is surrounded by the region $\mathcal{H}_{i-1}$. The inflation rule $\lambda$ can be easily read off from the inflation of the ladder tiles in Fig. 11. Vertices in a ladder are no longer entirely matched to vertices within the same ladder (dimers are placed on the membranes). However, it is convenient to describe the inflation rules in terms of the ladder segments. A region $\mathcal{H}_i$ is comprised of certain closed ladders that follow from the inflation, as well as the links connecting them, which can be read off from Fig. 12 (previously membranes on the AB* tiling). We present the $\lambda$ inflation rule in Fig. 24. From $\lambda$, all regions $\mathcal{H}_i$ can be constructed starting from $\mathcal{H}_1$. The first two regions constructed using the inflation rules of Fig. 24 are displayed in Fig. 25.

- Second, each component $\mathcal{H}_i$ generated by the inflation rule $\lambda$ can be perfectly matched. Such a perfect matching can be constructed following the arguments of Sec. IV A used to construct a perfect matching of the AB* tiling: $\mathcal{H}_i$ contains ladder segments which can be perfectly matched, using the dimer-decorated ladder tiles displayed in Fig. 11. The 8-vertices (located at the centres of green circles in Figs. 24 and 25, not shown) now lie at the vertices of the component $\mathcal{H}_{i-2} = \lambda^{-2}(\mathcal{H}_i)$, with edge-lengths larger by a factor of $\delta_0^2$. Each edge of the larger $\mathcal{H}_{i-2}$ component implies an odd-length alternating path between the corresponding 8-vertices in $\mathcal{H}_i$, and can be augmented to match the 8-vertices. This follows directly from applying the augmenting paths for the dimer-inflation tiles, Fig. 10 to connect up the (now reintroduced) 8-vertices in the ladder tiles (Fig. 11). Since both the star and order-1 ladder can be perfectly matched, all $\mathcal{H}_i$ can be perfectly matched. If boundary conditions are imposed on an $8_n$-empire such that all vertices outside the largest component $\mathcal{H}_n$ are excluded, then the bounded empire hosts a perfect matching. Now we argue the existence of membranes within the perfect matching.

- Each component $\mathcal{H}_i$ has the property that if the central 8-vertex is (say) a $U$-vertex, all vertices on the inner boundary of $\mathcal{H}_i$ (towards the central 8-vertex) are $V$-vertices while those on the outer boundary are $U$-vertices. This can be seen by first noting that this is true for $\mathcal{H}_1$. If $\mathcal{H}_i$ has ladder segments with $U$-vertices at a boundary, inflations of Fig. 24 result in segments with $U$-vertices at the boundary.

In a perfect matching, vertices in the smallest component $\mathcal{H}_0$ (the star surrounding the absent 8-vertex) must be perfectly matched to vertices.
FIG. 25. Using the inflation rules of Fig. 24, we construct the first two inflated regions $\mathcal{H}_2$ and $\mathcal{H}_3$, starting from the order-1 ladder $\mathcal{H}_1 \equiv L_1$. Ladder segments $P$, $A$, and $B$ are represented by coloured arcs as in Fig. 14. The $\mathcal{H}$ regions are comprised of closed ladders as well as the links connecting those ladders. Each $\mathcal{H}_i$ region admits a perfect matching.

within $\mathcal{H}_0$. $\mathcal{H}_0$ has an equal number (8) of $U$- and $V$-vertices, with only $U$-vertices having edges connecting them to the rest of the graph. In a perfect matching, this constrains the $U$-vertices to match to $V$-vertices on the interior of $\mathcal{H}_0$, lest the $V$-vertices remain unmatched. For the component $\mathcal{H}_1$, the outer boundary has only $U$-vertices having edges connecting them to vertices in $\mathcal{H}_2$. At the inner boundary, only $V$-vertices have edges connecting them to vertices in $\mathcal{H}_0$, but these edges cannot be matched as vertices in $\mathcal{H}_0$ are always matched to vertices within $\mathcal{H}_0$. This implies that vertices in $\mathcal{H}_1$ are matched to other vertices in $\mathcal{H}_1$ in all perfect matchings.

Extending this argument implies that for all components $\mathcal{H}_i$, vertices of $\mathcal{H}_i$ are matched to vertices within $\mathcal{H}_i$. $\mathcal{H}_i$ are the perfectly matched components $G^*_s$ of the Dulmage-Mendelsohn decomposition reviewed in Appendix A.

We have shown that if we choose boundary conditions of the $8_n$-empire which exclude vertices lying outside the outermost component $\mathcal{H}_n$, then the $8_n$-empire hosts a perfect matching with $n$ concentric membranes.

Appendix C: The directed loop algorithm

In this appendix, we summarize the directed-loop algorithm for sampling dimer configurations/maximum matchings. Note that this approach works both for maximum as well as perfect matchings, so we develop the discussion without specializing to the perfect-matching case. Given a maximum matching, the algorithm generates new maximum matchings as follows:

1. **Start** with a maximum matching. Randomly pick a matched vertex $s_0$. Let $s_0$ be matched to $s_1$. Set $s_i = s_0$ and $s_j = s_1$.

2. **Pivot**: Randomly choose a neighbour of $s_j$, say $s_k$. (The probability governing this choice is described below.) Remove the dimer on the edge $(s_i, s_j)$ and place a dimer on the edge $(s_j, s_k)$. This is the elementary step of the update, where a dimer ‘pivots’ over the vertex $s_j$ from the edge $(s_i, s_j)$ to the edge $(s_j, s_k)$. Note that in the first step, the dimer-pivoting move leaves an extra monomer at $s_0$.

3. **Grow**: if $s_k$ hosted a monomer before the pivot.

4. **Grow**: if $s_k$ hosts a dimer $(s_k, s_m)$ with $s_m \neq s_j$, the intermediate configuration has a monomer at the starting vertex $s_0$, and an antimonomer (two dimers touching a site) at the vertex $s_k$. Set $s_i = s_k, s_j = s_m$, and go to Step 2 (Pivot).

Intuitively, each step of the algorithm creates a monomer-antimonomer defect-pair and moves the antimonomer around until it annihilates with another monomer. The value of $s_k$ when the procedure terminates determines which of two possible updates have been implemented:
\( s_k = s_0 \) corresponds to flipping the dimer-occupancies in a closed alternating path of edges (a loop update), while \( s_k \neq s_0 \) corresponds to transporting a monomer from \( s_k \) to \( s_0 \) (string update).

The utility of the algorithm lies in the fact that any two maximum matchings can be connected by a sequence of loop or string updates, and so it can sample the whole configuration space of maximum matchings.

To ensure detailed balance in the space of maximum matchings generated by the update, we implement it in the enlarged configuration space that includes all maximum matchings as well as the intermediate configurations generated by the algorithm. The latter correspond to configurations which have an extra monomer-antimonomer pair relative to a maximum matching. Imposing detailed balance at each step of the update yields the transition probabilities \( P_{ijjk} \) for a dimer to pivot on a vertex \( j \) from the edge \( (s_i, s_j) \) to the edge \( (s_j, s_k) \):

\[
    w_{ij} P_{ijjk} = w_{jk} P_{jk:ij} \quad (C1)
\]

\[
    \sum_{(jk)} P_{ijjk} = 1. \quad (C2)
\]

\( w_{ij} \) is the weight contributed to the partition function by a dimer on the edge \( (s_i, s_j) \). In general, the system of equations (C2) subject to the constraints (C1) is under-determined. It is necessary to look for solutions which minimize the probabilities \( P_{ij:j} \) of the loop retracing itself. Such solutions can be found using linear programming techniques \[12\]. If the dimers are non-interacting, as is the case in most of this paper, the backtracking is closely coordinated vertex \( s_j \). \( P_{ijjk} = 1/(n - 1) \) for all edges \( (s_j, s_k) \neq (s_i, s_j) \).

Since the algorithm respects detailed balance in the extended configuration space with the monomer-antimonomer pair created while making the loop, it affords access to the partition function \( Z_{ma} \). This involves configurations with the same number of dimers as the maximum matching, but with one additional monomer and one additional antimonomer. The loop update samples this partition function with the correct weights. This is very nearly the quantity we are interested in when understanding questions of confinement, though there one usually considers a closely related partition function \( Z_{mm} \), which involves two more monomers than the maximum matching. In fact, the loop-construction procedure outlined above could equivalently be described as creating two monomers in a maximum matching, and propagating one of the monomers until it annihilates with another monomer to give a new maximum matching. To be precise, a step where the dimer pivots on the vertex \( s_j \) from the edge \( (s_i, s_j) \) to the edge \( (s_j, s_k) \) can be equivalently described in terms of a monomer hopping from the vertex \( s_j \) to the vertex \( s_m \) (which is matched to \( s_k \)), while another monomer is fixed at the starting vertex \( s_0 \). The dimer on the edge \( (s_k, s_m) \) is moved to the edge \( (s_j, s_k) \) during this hop. However, the detailed balance equations are satisfied with respect to the partition function \( Z_{ma} \) instead of \( Z_{mm} \). To sample from \( Z_{mm} \) correctly we weight each intermediate configuration generated in the loop update (with monomers at \( s_j \) and \( s_0 \)) with a factor of \( (\sum w_{jk})^{-1} \). Measurement of \( Z_{mm} \) closely corresponds to the monomer correlations as discussed in the main text.

Appendix D: Source edges for dimer correlations

To investigate connected correlations of dimers, we investigated the quantity \( C_{Max}(e_0, x) \), the maximum absolute value of the dimer correlation function at a distance of \( x \) edges from \( e_0 \), in Sec. VI B. Fig. 18 shows slow decay of \( C_{Max}(e_0, x) \), consistent with power laws, for many different source edges \( e_0 \). Fig. 19 shows that for some other choices of source edges, the connected correlations are bounded within pseudomembranes. For a 6-unit considered in Sec. VI B we label the source edges considered in Fig. 18 and Fig. 19 in Fig. 26.

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FIG. 26. Top: The set of source edges $e_0$ considered in Fig. 18, which are representative of edges for which connected correlations of dimers decay as power laws. Bottom: The set of source edges $e_0$ considered in Fig. 19, for which connected correlations of dimers are bounded within pseudomembranes. The colour of the edges indicate dimer occupation density to reveal the structure of pseudomembranes. We use the $D_8$-symmetry to choose (and display) source edges within a wedge—eight of these wedges make up the whole sample.

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