

# A Geometric Renormalisation Group in Discrete Quantum Space-Time

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## Abstract

We model quantum space-time on the Planck scale as dynamical networks of elementary relations or time dependent random graphs, the time dependence being an effect of the underlying dynamical network laws. We formulate a kind of geometric renormalisation group on these (random) networks leading to a hierarchy of increasingly coarse-grained networks of overlapping lumps. We provide arguments that this process may generate a fixed limit phase, representing our continuous space-time on a mesoscopic or macroscopic scale, provided that the underlying discrete geometry is critical in a specific sense (geometric long range order).

Our point of view is corroborated by a series of analytic and numerical results, which allow to keep track of the geometric changes, taking place on the various scales of the resolution of space-time. Of particular conceptual importance are the notions of dimension of such random systems on the various scales and the notion of geometric criticality.

# 1 Introduction

Among the various approaches to *quantum gravity* (or (quantum) space-time physics) there exists one which assumes that physics and, in particular, space-time itself are basically discrete on the presumed fundamental Planck level. This working philosophy is shared by a variety of more or less related research programs which, however, employ different technical concepts and follow different lines of reasoning when it comes to the concrete realisation of such a program (for a small and incomplete list of papers of other groups see e.g. [8] to [23], [28], [29], [30] and [36] to [38], for further references see below).

Our own approach has been developed in [1] to [7]. It generalizes the concept of *cellular automata* to so-called *cellular networks* which live on, in general, very large irregular and dynamical *graphs*. That is, both the nodes *and* the bonds are assumed to be dynamical degrees of freedom and interact with each other. An important ingredient of the *dynamical laws* is the possibility that bonds are switched on and off in the course of network evolution so that also the overall wiring or the geometry of the global network is a dynamically changing structure.

If one starts from such discrete model theories, two important points are the following. First, the definition of a (class of) primordial dynamics, which, in one way or the other, have the potential to lead to our wellknown effective (causal) dynamical evolution laws on an emergent continuum space-time. Second (and closely related to the first problem), the control of this continuum limit as a limit of a sequence of increasingly coarse grained intermediate theories. That is, one of the central issues is it, to reconstruct and recover the ordinary continuum physics and mathematics, starting from the remote Planck level. Some steps in this direction have been made in the above mentioned papers. They depend of course crucially on the kind of model theory being adopted and the general working philosophy.

In the following we will develop a kind of *geometric renormalisation process* leading, as we hope, in the end to a fixed point (or rather, phase), representing some continuum theory. Our renormalisation scheme carries the flavor of our particular framework, that is, the global structure and large scale patterns, existing in large networks and graphs. In some qualitative sense it is inspired by the *real-space block variable* approach to renormalisation in the critical regime of statistical mechanics. One should however note that the implementation of such a program on the Planck scale is necessarily much more involved and ambitious as compared to the typical scales of standard physics. The reason is that both the patterns, living in the ambient network or space and the background space itself have to be renormalized, and it turns out to be an ambitious enterprise to keep track of the relevant geometric changes and characteristics on the various scales of resolution of space-time. In particular, among other things, also the dimension of the underlying spaces will change in general during the renormalisation process.

Remark: We want to emphasize that, in the absence of a fixed background space, the clue consists of performing the renormalisation steps in an *intrinsic* way, without referring to some embedding space or other external geometric concepts. On the other hand, the technical methods being developed are expected to be useful also in other areas of modern physics and can be employed in other coarse-graining schemes, for example in the field of *dynamical triangulation* and *simplicial complexes*.

Before we begin with the discussion of the technical details of our program, we want to add some remarks about the wider physical context to which such ideas may belong. Illuminating ideas about discreteness on a fundamental level have already been entertained by Wheeler et al, see e.g. the last pages in [24] or [25],[26] respectively, another early source is Myrheim, [27]. Discrete structures like partial orders have for example been treated by Isham and coworkers, [28]. A broad and general approach towards discrete physics in general has been developed by T.D.Lee and his group (for a collection see vol.3 of his selected papers, [31]). Last but not least, there is the huge body of work subsumed under the catchword *random geometry* or *dynamical triangulation* ([32] or [33]) which is however mostly concerned with the discretisation of a preexisting continuous initial manifold. There may be interesting connections between our framework and these other approaches but, for the time being, we refrain from commenting on them in this paper to keep our paper within reasonable length.

As a last point we want to mention some interesting cross-fertilisation. In the papers mentioned above we based our analysis on a class of dynamical network laws which incorporate a mutual interaction between the local states defined on the nodes of the underlying graph and the near by bonds. This allows us to treat both the dynamics of the ordinary degrees of freedom *on* the graph and the dynamical change of the geometry of the network on the same footing.

We recently observed that similar ideas have been entertained within the framework of cellular automata (see e.g. [34] and [35]), the models being called *structurally dynamic cellular automata* or SDCA. As far as we can see at the moment, the adopted technical framework is not exactly the same but we think, a comparison of both approaches should turn out to be profitable. We conclude this introduction with a brief description of what we are going to do in the following.

In the next section we explain the basics of the framework we are employing. In section 3 we briefly introduce the concept of a *random graph*. To establish some contact to other existing approaches, we show in section 4 that our network naturally carries also the structure of *causal sets*. The concrete construction of the renormalisation steps towards an envisaged continuum theory begins with section 5 which contains also a series of rigorous analytical and numerical results which are of technical relevance in the subsequent reasoning. In section 6 we study some simple toy models which (despite of their simplicity) show that there

indeed do exist fixed points in the category of infinite graphs under our geometric renormalisation process. In section 7 we study the behavior of the particularly important geometric concept of *graph* or *network dimension* and its behavior under renormalisation and in section 8, which is kind of a conclusion, we analyse the kind of *geometric criticality* which is in our view essential in order to arrive at non-trivial macroscopic limit space-times.

We recently came upon a beautiful discussion of some work of Gromov ([47]), which shows that there may be some deep and interesting connections between our framework, developed in the following, and ideas of coarse graining in, for example, geometric group theory by Gromov (see also the references [48],[49],[50] cited in section 7).

## 2 Protogeometry and Protodynamics

In a first step we want to motivate why we choose exactly the kind of model theory, we are discussing in the following. On the one side we have a working philosophy which is similar to the one, expounded by 't Hooft in e.g. [36] to [38]. That is, we entertain the idea that for example quantum theory may well emerge as an *effective (continuum) theory* on the mesoscopic scale of an underlying discrete more microscopic theory. As we want our underlying (pre)geometry to coevolve with the patterns living in this substratum, we developed the above mentioned generalisation of the more regular cellular automata.

Another essential property of such *discrete dynamical systems* is , while the basic ingredients and elementary building blocks are reasonably simple, their potential for the emergence of very complex behavior on the more macroscopic scales, thus supporting the speculation that such systems may be capable of generating viable continuum theories.

We now begin to introduce the necessary technical ingredients. We start with the definition of some notions of graph theory.

**Definition 2.1** *A simple, countable, labelled, undirected graph,  $G$ , consists of a countable set of nodes or vertices,  $V$ , and a set of edges or bonds,  $E$ , each connecting two of the nodes. There exist no multiple edges (i.e. edges, connecting the same pair of nodes) or elementary loops (a bond, starting and ending at the same node). In this situation the bonds can be described by giving the corresponding set of unordered pairs of nodes. The members of  $V$  are denoted by  $x_i$ , the bonds by  $e_{ij}$ , connecting the nodes  $x_i$  and  $x_j$ .*

Remarks: We could also admit a non-countable vertex set. The above restriction is only made for technical convenience. From a physical point of view one may argue that the *continuum* or uncountable sets are idealisations, anyhow. The notions *vertex*, *node* or *edge*, *bond* are used synonymously. Furthermore, the

labeling of the nodes is only made for technical convenience (to make some discussions easier) and does not carry a physical meaning. As in general relativity, all models being invariant under *graph isomorphisms* (i.e. relabelling of the nodes and corresponding bonds) are considered to be physically equivalent.

In the above definition the bonds are not directed (but oriented; see below). In certain cases it is also useful to deal with directed graphs.

**Definition 2.2** *A directed graph is a graph as above, with  $E$  consisting now of directed bonds or ordered pairs of nodes. In this case we denote the edge, pointing from  $x_i$  to  $x_j$  by  $d_{ij}$ . There may also exist the opposite edge, denoted by  $d_{ji}$ .*

**Observation 2.3** *An undirected graph, as in definition 2.1, can be considered as a particular directed graph with  $e_{ij}$  corresponding to the pair of directed edges,  $d_{ij}, d_{ji}$ .*

**Remark 2.4** *We introduced and studied algebraic and functional analytic structures like e.g. Hilbert spaces and Dirac operators on such graphs in [3],[5]. In such situations, the bonds,  $e_{ij}, d_{ij}$ , can be given a concrete algebraic meaning with*

$$e_{ij} := d_{ij} - d_{ji} = -e_{ji} \quad (1)$$

It is now suggestive to regard the edges between pairs of points as describing their (direct) interaction. This becomes more apparent if we impose dynamical network laws on these graph structures so that they become a particular class of discrete dynamical systems. Henceforth we denote such a dynamical network, which is supposed to underly our continuous space-time manifold, by  $QX$  (“*quantum space*”). We want to make the general remark that the *cellular networks*, introduced in the following, can either be regarded as mere models of a perhaps more hypothetical character, encoding, or rather simulating, some of the expected features of a surmised *quantum space-time* or, on the other hand, as a faithful realisation of the primordial substratum, underlying our macroscopic space-time picture. Up to now, this is a matter of taste.

For technical convenience and to keep matters reasonable simple, we choose a discrete overall clock-time (not to be confused with the *physical time* which is rather supposed to be an emergent and intrinsic characteristic, related to the evolution of quasi-macroscopic patterns in such large and intricately wired networks). In principle the clock-time can also be made into a local dynamical variable. Furthermore, we assume the node set of our initial network to be fixed and being independent of clock-time (in contrast to the bonds). We will see in the following sections that this feature will change under the renormalisation steps, i.e. on the higher levels, the class of lumps may become dependent on time.

We assume that each node,  $x_i$ , or bond,  $e_{ik}$ , carries an internal (for simplicity) discrete *state space*, the internal states being denoted by  $s_i$  or  $J_{ik}$ . In simple examples we chose for instance:

$$s_i \in q \cdot \mathbb{Z} \quad , \quad J_{ik} \in \{-1, 0, +1\} \quad (2)$$

with  $q$  an elementary quantum of information and

$$e_{ki} = -e_{ik} \Rightarrow J_{ki} = -J_{ik} \quad (3)$$

In most of the studied cellular automata systems even simpler internal state spaces are chosen like e.g.  $s_i \in \{0, 1\}$ . This is at the moment not considered to be a crucial point. The above choice is only an example.

In our approach the bond states are dynamical degrees of freedom which, a fortiori, can be switched off or on (see below). Therefore the *wiring*, that is, the pure *geometry* (of relations) of the network is a clock-time dependent, dynamical property and is *not* given in advance. Consequently, the nodes and bonds are typically not arranged in a more or less regular array, a regular lattice say, with a fixed near-/far-order. This implies that *geometry* will become to some degree a *relational* (Machian) concept and is no longer a static background.

As in cellular automata, the node and bond states are updated (for convenience) in discrete clock-time steps,  $t = z \cdot \tau$ ,  $z \in \mathbb{Z}$  and  $\tau$  being an elementary clock-time interval. This updating is given by some *local* dynamical law (examples are given below). In this context *local* means that the node/bond states are changed at each clock time step according to a prescription with input the overall state of a certain neighborhood (in some topology) of the node/bond under discussion.

A simple example of such a local dynamical law we are having in mind is given in the following definition (first introduced in [3]).

**Definition 2.5 (Example of a Local Law)** *At each clock time step a certain quantum  $q$  is exchanged between, say, the nodes  $x_i$ ,  $x_k$ , connected by the bond  $e_{ik}$  such that*

$$s_i(t + \tau) - s_i(t) = q \cdot \sum_k J_{ki}(t) \quad (4)$$

(i.e. if  $J_{ki} = +1$  a quantum  $q$  flows from  $x_k$  to  $x_i$  etc.)

The second part of the law describes the back reaction on the bonds (and is, typically, more subtle). We assume the existence of two critical parameters  $0 \leq \lambda_1 \leq \lambda_2$  with:

$$J_{ik}(t + \tau) = 0 \quad \text{if} \quad |s_i(t) - s_k(t)| =: |s_{ik}(t)| > \lambda_2 \quad (5)$$

$$J_{ik}(t + \tau) = \pm 1 \quad \text{if} \quad 0 < \pm s_{ik}(t) < \lambda_1 \quad (6)$$

with the special proviso that

$$J_{ik}(t + \tau) = J_{ik}(t) \quad \text{if} \quad s_{ik}(t) = 0 \quad (7)$$

On the other side

$$J_{ik}(t + \tau) = \begin{cases} \pm 1 & J_{ik}(t) \neq 0 \\ 0 & J_{ik}(t) = 0 \end{cases} \quad \text{if} \quad \lambda_1 \leq \pm s_{ik}(t) \leq \lambda_2 \quad (8)$$

In other words, bonds are switched off if local spatial charge fluctuations are too large or switched on again if they are too small, their orientation following the sign of local charge differences, or remain inactive.

Another interesting law arises if one exchanges the role of  $\lambda_1$  and  $\lambda_2$  in the above law, that is, bonds are switched off if the local node fluctuations are too small and are switched on again if they exceed  $\lambda_2$ .

We make the following observation:

**Observation 2.6 (Gauge Invariance)** *The above dynamical law depends nowhere on the absolute values of the node “charges” but only on their relative differences. By the same token, charge is nowhere created or destroyed. We have*

$$\Delta\left(\sum_{QX} s(x)\right) = 0 \quad (9)$$

( $\Delta$  denoting the change in total charge of the network between two consecutive clocktime steps). To avoid artificial ambiguities we can e.g. choose a fixed reference level, taking as initial condition at  $t = 0$  the following constraint

$$\sum_{QX} s(x) = 0 \quad (10)$$

We resume what we consider to be the crucial ingredients of network laws, we are interested in

1. As in gauge theory or general relativity, our evolution law should implement the mutual interaction of two fundamental substructures, put a little bit vaguely : “*geometry*” acting on “*matter*” and vice versa, where in our context “*geometry*” is assumed to correspond in a loose sense to the local and/or global array of bond states and “*matter*” to the structure of the node states.
2. By the same token the alluded *selfreferential* dynamical circuitry of mutual interactions is expected to favor a kind of *undulating behavior* or *selfexcitation* above a return to some uninteresting *equilibrium state* (being devoid of stable structural details), as is frequently the case in systems consisting of a single component which directly acts back on itself. This propensity for the *autonomous* generation of undulation patterns is in our view an essential prerequisite for some form of “*protoquantum behavior*” we hope to recover on some coarse grained and less primordial level of the network dynamics.

3. In the same sense we expect the large scale pattern of switching-on and -off of bonds to generate a kind of “*protogravity*”.

Remark: The above dynamical law shows that bonds with  $J_{ik} = 0$  at clock time  $t$  do not participate in the dynamics in the next time step. We hence may consider them as being temporally inactive. The shape of the network, neglecting all the internal states on the nodes and bond together with the inactive bonds we call the *wiring diagram*.

If one concentrates solely on this *wiring diagram*, figure 1 describes one clocktime step in the life of a *dynamic graph*. In the picture only a small subgraph is shown and the deletion and creation of edges (that is, elementary interactions among nodes or possible information channels). The new bonds are represented as bold lines. It should be emphasized that the graph is *not* assumed to be a triangulation of some preexisting smooth manifold. This is emphasized by the existence of edges, connecting nodes which are not necessarily close with respect to e.g. the euclidean distance.

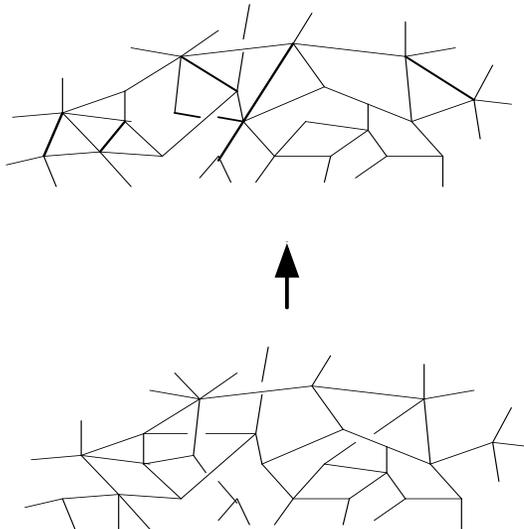


Figure 1:

We have pictured our proto space-time on the Planck scale as a fluctuating network of dynamic relations or exchange of pieces of information between a given set of nodes. At each fixed clock-time step there exist in this network certain subclusters of nodes which are particularly densely entangled and the whole graph can be covered by this uniquely given set of subclusters of nodes and the respective induced subgraphs. We dealt with these distinguished clusters of nodes (called cliques or lumps) in quite some detail in e.g. [4] or [6]. We emphasize the interesting relations to earlier ideas of Menger, Rosen et al, which have been discussed in [6].

One of our core ideas is it that the seemingly structureless (mathematical) points, making up our ordinary continuous manifolds, would display a rich nested internal structure if looked at under a magnification or resolution so that the lumpy structure of space-time became visible. We think this hidden substructure will become particularly relevant when it comes to the interpretation of *quantum phenomena* ([7], where possible relations to some interesting ideas of Connes have been set up).

From a more technical or practical point of view we need a general principle which allows us to lump together subsets of nodes, living on a certain level of resolution of space-time, to get the building blocks of the next level of coarse graining (see below). After a series of such coarse graining steps we will wind up with a nested structure of lumps, containing smaller lumps and so forth, which, after appropriate *rescaling*, may yield in the end some quasi-continuous but nested structure. This principle is provided by the following mathematical concept.

**Definition 2.7 (Subsimplices and Cliques)** *With  $G$  a given fixed graph and  $V_i$  a subset of its vertex set  $V$ , the corresponding induced subgraph over  $V_i$  (that is, its edges being the corresponding edges, occurring in  $G$ ) is called a subsimplex, if all its pairs of nodes are connected by a bond. In this class, which is in fact partially ordered, the order being given by graph inclusion, there exist certain maximal subsimplices, that is, subsimplices so that every addition of another node of the underlying graph (together with the respective bonds existing in  $G$  (pointing to other nodes of the chosen subset) destroys this property. These maximal simplices are usually called cliques in combinatorics (we call them also lumps) and are the candidates for our construction of physical points. Henceforth we denote them by  $C_i$ .*

It has been described in detail in e.g. section 4 of [4] how these cliques can be constructed in an algorithmic way, starting from an arbitrary node. Note in particular that a given node will, in general belong to many different (overlapping) cliques or lumps. The situation is illustrated by the following picture: In this picture we have drawn a subgraph of a larger graph. (1) denotes a clique, i.e. a maximal subsimplex. Subsets of nodes of such a clique support subsimplices (called faces in algebraic topology), the clique being the maximal element in this partial ordered set. (2) and (3) are other, smaller cliques which overlap with (1) in a common bond or node. (4) is an example of a subgraph which is not a clique or subsimplex. Evidently, each node or bond lies in at least one clique. The smallest possible cliques which can occur in a connected graph consist of two nodes and the corresponding edge.

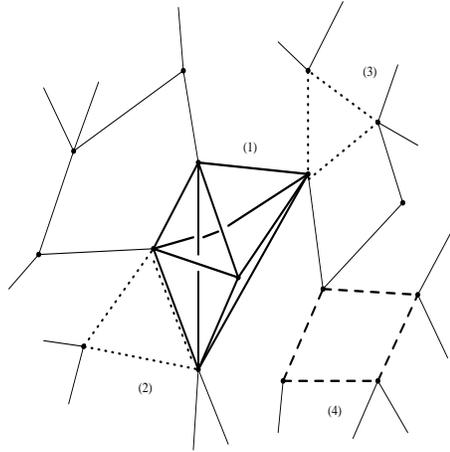


Figure 2:

## 3 Dynamical Networks as Random Graphs

### 3.1 The Statistical Hypothesis

As we are dealing with very large graphs, which are, a fortiori, constantly changing their shape, that is, their distribution of (active) bonds, we expect the dynamics to be sufficiently stochastic so that a point of view may be appropriate, which reminds of the working philosophy of *statistical mechanics*. This does however not imply that our evolving network is nothing but a simple *random graph* as introduced below (cf. the remarks at the end of this section). It rather means that some of its geometric characteristics can, or should, be studied within this well-developed context.

Visualizing the characteristics and patterns being prevalent in large and “typical” graphs was already a notorious problem in *combinatorial graph theory* and led to the invention of the *random graph* framework (see the more complete discussion in [4]). The guiding idea is to deal with graphs of a certain type in a probabilistic sense. This turns out to be particularly fruitful as many graph characteristics (or their absence) tend to occur with almost certainty in a probabilistic sense (as has been first observed by Erdős and Rényi). The standard source is [39] (for further references see [4]).

Another strand of ideas stems from the theory of dynamical systems and cellular automata, where corresponding statistical and ensemble concepts are regularly employed. Typically, we are looking for *attractors* in phase space, which are assumed to correspond to large scale, that is, after *coarse graining* and *rescaling*, quasi continuous or macroscopic patterns of the system. Experience shows, that such a structure or the approach towards attractors is in many cases relatively robust to the choice of initial configurations or microscopic details and, hence, suggests an ensemble picture.

Furthermore, since the early days of statistical mechanics, the ensemble point of view (see for example [46]) is, at least partly, corroborated by the philosophy that time averages transform (under favorable conditions) into ensemble averages. In our context this means the following. Denoting the typical length/time scale of ordinary quantum theory by  $[l_{qm}], [t_{qm}]$ , we have

$$[l_{qm}] \gg [l_{pl}] \quad , \quad [t_{qm}] \gg [t_{pl}] \quad (11)$$

the latter symbols denoting the Planck scale. Under renormalisation the mesoscopic scales comprise a huge number of microscopic clock time intervals and degrees of freedom of the network under discussion.

A fortiori, the networks, we are interested in, correspond to graphs, having a huge *vertex degree*, i.e. channels, entering a given typical node of the graph. That is, we expect large local fluctuations in microscopic grains of space or time. Put differently, the network locally traverses a large number of different microscopic states in a typical mesoscopic time interval,  $[t_{qm}]$ . This observation suggests that, on a mesoscopic or macroscopic scale, microscopic patterns will be washed out or averaged over.

### 3.2 The Random Graph Framework

One kind of probability space is constructed as follows. Take all possible labeled graphs over  $n$  nodes as probability space  $\mathcal{G}$  (i.e. each graph represents an elementary event). The maximal possible number of bonds is  $N := \binom{n}{2}$ , which corresponds to the unique *simplex graph* (denoted usually by  $K_n$ ). Give each bond the *independent probability*  $0 \leq p \leq 1$ , (more precisely,  $p$  is the probability that there is a bond between the two nodes under discussion). Let  $G_m$  be a graph over the above vertex set,  $V$ , having  $m$  bonds. Its probability is then

$$pr(G_m) = p^m \cdot q^{N-m} \quad (12)$$

where  $q := 1 - p$ . There exist  $\binom{N}{m}$  different labeled graphs  $G_m$ , having  $m$  bonds, and the above probability is correctly normalized, i.e.

$$pr(\mathcal{G}) = \sum_{m=0}^N \binom{N}{m} p^m q^{N-m} = (p + q)^N = 1 \quad (13)$$

This probability space is sometimes called the space of *binomially random graphs* and denoted by  $\mathcal{G}(n, p)$ . Note that the number of edges is binomially distributed, i.e.

$$pr(m) = \binom{N}{m} p^m q^{N-m} \quad (14)$$

and

$$\langle m \rangle = \sum m \cdot pr(m) = N \cdot p \quad (15)$$

The really fundamental observation made already by Erdős and Rényi (a rigorous proof of this deep result can e.g. be found in [40]) is that there are what physicists would call *phase transitions* in these *random graphs*. To go a little bit more into the details we have to introduce some more graph concepts.

**Definition 3.1 (Graph Properties)** Graph properties are certain particular random variables (*indicator functions of so-called events*) on the above probability space  $\mathcal{G}$ . I.e., a graph property,  $Q$ , is represented by the subset of graphs of the sample space having the property under discussion.

To give some examples: i) connectedness of the graph, ii) existence and number of certain particular subgraphs (such as subsimplices etc.), iii) other geometric or topological graph properties etc.

In this context Erdős and Rényi made the following important observation.

**Observation 3.2 (Threshold Function)** A large class of graph properties (e.g. the monotone increasing ones, cf. [39] or [40]) have a so-called threshold function,  $m^*(n)$ , with  $m^*(n) := N \cdot p^*(n)$ , so that for  $n \rightarrow \infty$  the graphs under discussion have property  $Q$  almost shurely for  $m(n) > m^*(n)$  and almost shurely not for  $m(n) < m^*(n)$  or vice versa (more precisely: for  $m(n)/m^*(n) \rightarrow \infty$  or 0; for the details see the above cited literature). That is, by turning on the probability  $p$ , one can drive the graph one is interested in beyond the phase transition threshold belonging to the graph property under study. Note that, by definition, threshold functions are only unique up to “factorization”, i.e.  $m_2^*(n) = O(m_1^*(n))$  is also a threshold function.

Calculating these graph properties is both a fascinating and quite intricate enterprise. In [4] we mainly concentrated on properties of *cliques*, their distribution (with respect to their order,  $r$ , i.e. number of vertices), frequency of occurence of cliques of order  $r$ , degree of mutual overlap etc. We then related these properties to the various assumed stages and phases of our space-time manifold.

We can introduce various *random function* on the above probability space. For each subset  $V_i \subset V$  of order  $r$  we define the following random variable:

$$X_i(G) := \begin{cases} 1 & \text{if } G_i \text{ is an } r\text{-simplex,} \\ 0 & \text{else} \end{cases} \quad (16)$$

where  $G_i$  is the corresponding induced subgraph over  $V_i$  in  $G \in \mathcal{G}$  (the probability space). Another random variable is then the *number of  $r$ -simplices in  $G$* , denoted by  $Y_r(G)$  and we have:

$$Y_r = \sum_{i=1}^{\binom{n}{r}} X_i \quad (17)$$

with  $\binom{n}{r}$  the number of  $r$ -subsets  $V_i \subset V$ . With respect to the probability measure introduced above we have for the *expectation values*:

$$\langle Y_r \rangle = \sum_i \langle X_i \rangle \quad (18)$$

and

$$\langle X_i \rangle = \sum_{G \in \mathcal{G}} X_i(G) \cdot pr(G_i = r\text{-simplex in } G). \quad (19)$$

These expectation values were calculated in [4]. We have for example

$$\langle X_i \rangle = p^{\binom{r}{2}} \quad (20)$$

The probability that such a subsimplex is maximal, i.e. is a cliques is then

$$pr(G_r \text{ is a clique}) = (1 - p^r)^{n-r} \cdot p^{\binom{r}{2}} \quad (21)$$

As there exist exactly  $\binom{n}{r}$  possible different  $r$ -sets in the node set  $V$ , we arrive at the following conclusion:

**Conclusion 3.3 (Distribution of Subsimplices and Cliques)** *The expectation value of the random variable ‘number of  $r$ -subsimplices’ is*

$$\langle Y_r \rangle = \binom{n}{r} \cdot p^{\binom{r}{2}} \quad (22)$$

For  $Z_r$ , the number of  $r$ -cliques (i.e. maximal!  $r$ -simplices) in the random graph, we have then the following relation

$$\langle Z_r \rangle = \binom{n}{r} \cdot (1 - p^r)^{n-r} \cdot p^{\binom{r}{2}} \quad (23)$$

These quantities, as functions of  $r$  (the *order* of the subsimplices) have quite a peculiar numerical behavior. We are interested in the typical *order of cliques* occurring in a generic random graph (where typical is understood in a probabilistic sense).

**Definition 3.4 (Clique Number)** *The maximal order of occurring cliques contained in  $G$  is called its clique number,  $cl(G)$ . It is another random variable on the probability space  $\mathcal{G}(n, p)$ .*

It is remarkable that this value is very sharply defined in a typical random graph. Using the above formula for  $\langle Z_r \rangle$ , we can give an approximative value,  $r_0$ , for this expectation value and get

$$r_0 \approx 2 \log(n) / \log(p^{-1}) + O(\log \log(n)) \quad (24)$$

(cf. chapt. XI.1 of [39]). It holds that practically all the occurring cliques fall in the interval  $(r_0/2, r_0)$ . We illustrate this with the following tables. Our choice for  $n$ , the number of vertices, is  $10^{100}$ . The reason for this seemingly very large number is, that we want to deal with systems ultimately simulating our whole universe or continuous space-time manifolds (see the more detailed discussion in [4]). We first calculate  $r_0$ .

$p$	0.9	0.8	0.7	0.6	0.5	0.4	0.3	0.2	0.1
$r_0$	4370	2063	1291	901	664	502	382	286	200

(25)

(for reasons we do not understand we made some numerical errors in the original table 1 in [4], p.2043).

It is more complicated to give numerical estimates of the distribution of cliques, that is  $\langle Z_r \rangle$ . After some manipulations and approximations we arrived in ([4],p.2051f) at the following approximative formula and numerical table (the numerical values are given for  $p = 0.7$ ; note that for this parameters the maximal order of occurring cliques,  $r_0$ , was approximately 1291)

$$\log(\langle Z_r \rangle) \approx r \cdot \log(n) + n \cdot \log(1 - p^r) + r^2/2 \cdot \log(p) \quad (26)$$

(with  $r^2/2$  an approximation of  $r(r-1)/2$ ) for  $r$  sufficiently large).

$r$	600	650	800	1000	1200	1300	1400
$\log(\langle Z_r \rangle)$	$-5.7 \cdot 10^6$	$3.2 \cdot 10^4$	$3.2 \cdot 10^4$	$2.5 \cdot 10^4$	$8.4 \cdot 10^3$	$-0.75 \cdot 10^2$	$-1.1 \cdot 10^4$

(27)

(In the original table 2 of [4] the numerical values for small and large  $r$ 's, lying outside the interval  $(r_0/2, r_0)$ , were wrong as we neglected numerical contributions which are only vanishingly small in the above interval. The above table nicely illustrates how fast the frequency of cliques of order  $r$  drops to zero outside the above interval.

As to the interpretation of these findings, one should remind the reader that the above results apply to the generic situation, that is, do hold for typical graphs (in very much the same sense as in corresponding discussions in the foundations of statistical mechanics). An evaluation of the combinatorial expressions in this and the following sections show that frequently the same kind of extreme probabilistic concentration around, for example, *most probable values* occurs as in ordinary statistical mechanics.

What is not entirely clear is, how far the random graph approach can be applied to our complex dynamical networks. Our working philosophy is that these results serve to show, what we hope, is the qualitative behavior of such systems. As our systems follow deterministic dynamical laws, starting from certain initial conditions, the behavior cannot be entirely random in the strict sense. This holds the more so since we expect the systems to evolve towards *attracting sets*

in phase space and/or generate some large scale patterns. On the other hand, due to the constant reorientation of the bonds, being incident with an arbitrary but fixed node and the generically large vertex degrees of the nodes, one may assume that the system is sufficiently random on small scales, so that the random graph picture reproduces at least the qualitative behavior of such extremely complex systems.

To make this picture more quantitative, the general strategy is the following. We count the typical number of active bonds in our evolving network at a given clock time  $t$ , calculate from this the corresponding bond probability,  $p(t)$ , and relate this snapshot of our network to a random graph with the same! bond probability. This should yield at least some qualitative clues. That is, we expect that qualitative characteristics of our evolving network can, at each given clock time, be related to the characteristics of a corresponding random graph. In this specific sense, one may regard the *bond probability*,  $p(t)$ , as the crucial *order parameter* of our network, regarded as a statistical system. (We note that we implemented such networks on a computer and made detailed studies of their dynamical behavior and stochastic properties, see [41]. Our investigations showed that at least qualitatively the expected phenomena came out correctly).

## 4 Cellular Networks as Causal Sets

In this section we want to make contact with an approach to quantum gravity, being based on the concept of *causal sets*. We again emphasize that, for reasons of technical simplicity, we treat *time* as a global non-dynamical quantity, being well aware that this may be a severe restriction. On the other hand, the notorious so-called *problem of time* has not yet been settled anyhow in quantum gravity and needs an extra and careful treatment. Under this proviso we want to show, that our *cellular networks* and *lump-spaces* automatically have the structure of causal sets, with this extra structure being induced by our local dynamical laws. On the most elementary level we start from our above initial network.

We argued above that we want to neglect the details of the (time dependent) internal states of nodes and bonds and keep only track of the bonds which are in operation at a given clock-time,  $t$ , that is, the bonds with  $J_{ik} \neq 0$ . Doing this, we arrive at the concept of *time dependent graphs*,  $G(t)$ .

**Definition 4.1**  $G(t)$  is a graph with a fixed (time independent) node set,  $V$ , but a time dependent set of active bonds,  $E(t)$ . In principle we could also make the node set time dependent, the above assumption is mainly made for convenience.

The local dynamical laws can as well be viewed as a prescription, by which local pieces (quanta) of information are transported between the active bonds of the network. The nodes, which can be reached from a given node in a single clock

time step, are called its *nearest neighbors*,  $nn$ , the *next-nearest neighbors*,  $nnn$ , are correspondingly defined and so on.

What we have defined up to now corresponds to the *foliation* of space-time into an aggregate of space-like slices. We now form the union of these slices and define

$$G := \bigcup_t G(t) \quad (28)$$

In our above mentioned papers (see in particular [1]) we exploited the fact that graphs carry a natural metric structure

$$d(x_i, x_j) := \inf\{\text{length of paths, connecting } x_i \text{ and } x_j\} \quad (29)$$

where path length is the discrete number of edges of the path. This defines a neighborhood structure on a graph.

$$U_l(x_0) := \{\text{nodes } x_i \text{ with } d(x_0, x_i) \leq l\} \quad (30)$$

We now will transform  $G$  into a *partial ordered set* (*poset*) by introducing additional (*causal*) bonds and relabeling the nodes. From now on we denote the nodes in  $G(t)$  by  $x_i(t)$ , that is, one and the same node  $x_i$  carries an additional time label  $t \in \mathbb{Z} \cdot \tau$ , depending on the time slice  $G(t)$  under discussion and is denoted by  $x_i(t)$ . For each node,  $x_i(t)$  we draw new edges to the nodes  $x_j(t+1)$  lying in  $G(t+1)$ , provided that  $x_j(t)$  is a *nn* of  $x_i(t)$  in  $G(t)$  (including the node  $x_i(t+1)$  itself!). For convenience we usually drop the extra time element  $\tau$ .

**Definition 4.2** *We call the edges lying in  $G(t)$ , that is the original edges of the (time dependent!) graph, the spatial edges (at time  $t$ ), the edges which connect the neighbors in consecutive slices,  $G(t), G(t+1)$ , are dubbed causal edges. That is, an elementary causal neighborhood of, say,  $x_i(t)$  consists of all the nodes,  $x_j(t+1)$ , in  $G(t+1)$ , with  $x_j(t)$ , having spatial distance,  $d(x_i(t), x_j(t)) \leq 1$ , in  $G(t)$  (that is, the node,  $x_i(t+1)$  itself plus the nodes having distance one).*

(It may be helpful to envisage the spatial edges as carrying a red colour and the causal edges a green one).

We can now proceed by introducing the *forward-* or *future cone*, *backward-* or *past cone*, respectively.

**Definition 4.3** *To the forward cone of  $x(t)$  belong those nodes,  $y(t'), t' \geq t$ , which can be connected by a causal edge sequence,  $\gamma$ , starting in  $x(t)$ . Such an admissible sequence consists of  $(t' - t)$  elementary steps. An analogous definition holds for the members of the past cone. Given two nodes,  $x(t), y(t')$  with  $t' \geq t$ , we can intersect the forward cone of  $x(t)$  with the backward cone of  $y(t')$  and get the corresponding double cone.*

Remark: Note that the causal and metric relations are relatively subtle as compared to, for instance, ordinary *special relativity*, where we deal with one and the same topological space structure for all times. In our space-time graph,  $G$ , the spatial wiring is constantly changing on a microscopic scale, due to the imposed local dynamical law. That is, two nodes may become nearest neighbors in  $G(t)$  while being far apart for earlier or later times and vice versa. This can happen since bonds are permanently annihilated and created.

**Conclusion 4.4** *The above causal distance concept has already some of the crucial ingredients of the metric properties, known from general relativity. Furthermore, it is of a markedly stochastic character.*

What we have said above, creates in a natural way some *partial order* on the set of nodes. We do not want to reproduce all the technical notions, which are presumably well known or can be found in e.g. the papers of Sorkin et al, mentioned above, or in, say, [42] or [43]. In the definition of the partial ordered set (poset), only the causal (green) bonds enter (with their (non)existence being a consequence of the respective (non)existence of the spatial (red) bonds).

**Definition 4.5** *We have  $x_j(t') \geq x_i(t)$ ,  $t' \geq t$  if the nodes can be connected by a causal path, lying in the forward cone. The nodes, lying on a causal edge sequence, we call chains, sets of mutually space like nodes are called antichains.*

This order relation is clearly reflexive, antisymmetric and transitive. We remark the following point.

It trivially holds (by assumption) that  $x_i(t') \geq x_i(t)$ , that is, for the same node at different times. This implies that for two nodes,  $x_i, x_j$  it follows

$$x_j(t') \geq x_i(t) \Rightarrow x_j(t'') \geq x_i(t) \quad (31)$$

for all times,  $t'' \geq t'$ , as we can continue the causal path from  $x_i(t)$  to  $x_j(t')$  by the trivial path,  $x_j(t') - x_j(t'')$ .

## 5 The Geometric Coarse-Graining or Renormalisation Process

### 5.1 The General Picture

One of our central hypotheses is it, to regard the ordinary space or space-time as a medium having a complicated internal dynamical fine structure, which is largely hidden on the ordinary macroscopic scales due to the low level of (only mesoscopic) resolution of space-time processes as compared to e.g. the Planck scale. The corresponding process of *coarse graining*, described in the following, may be also called a *geometric renormalisation*, in which the resolution of the

details of space-time is steadily scaled down to the level of ordinary continuum physics. Some preliminary ideas of this renormalisation process have already been described in [4] and [6].

In the following we deal with a generic large network or graph,  $G$ , as a typical representative of the members of the class  $\{G(t)\}$ , described above. The individual renormalisation steps consist of the following constructions.

- Starting from a given fixed graph,  $G$ , pick the (generic) *cliques*,  $C_i$ , in  $G$ , i.e. the subgraphs, forming maximal subsimplices or cliques in  $G$  with their order lying in the above mentioned interval,  $(r^0/2, r^0)$ .
- These cliques form the new nodes of the *clique-graph*,  $G_{cl}$  of  $G$ . The corresponding new bonds are drawn between cliques, having a (sufficient degree of) overlap. Size, overlap and distribution of cliques in a generic (*random*) graph have been analyzed in [4], for more details see the following subsection.
- That is, both *marginal* cliques (if they do exist at all) and *marginal* overlaps are deleted. In this respect a coarse-graining step includes also a certain *purification* of the graph structure.

**Remark 5.1** *What is considered to be a “sufficient overlap” depends of course on the physical context and the general working philosophy. As we noted above, a particular node will in general belong to several, and in the case of densely entangled graphs to many, cliques. The minimal possible overlap is given by a single common node. If, on the other hand, the cliques on a certain level of coarse graining are comparatively large, comprising, say, typically several hundred nodes, it may be reasonable to neglect marginal, i.e. to small, overlaps as physically irrelevant and define a sufficient degree of overlap to consist of an appreciable fraction of the typical clique order. Correspondingly, too small cliques, not lying in the above introduced interval,  $(r_0/2, r_0)$ , are deleted (if they do exist at all!, see the estimates in section 3). The numerical effect of such choices will be studied in the following.*

**Definition 5.2** *We call the graph, defined above, the (purified) clique graph,  $G_{cl}$ , constructed from the initial graph,  $G$ .*

It is an important question whether graphs and networks are connected, that is, if there exists a path or edge sequence, connecting each pair of vertices. This question becomes, a fortiori relevant, in the following (sub)sections if the coarse-graining or renormalisation steps are performed on a given fixed graph. The following lemma is useful.

**Lemma 5.3** *If  $G$  is a connected graph, that is, each pair of vertices,  $x, y$  can be connected by a finite path or edge sequence, depicted as  $x = x_0 - x_1 - \dots - x_n = y$ , then the ordinary (unpurified) clique graph,  $G_{cl}$  is again connected.*

Proof: Let  $x_0$  lie in a certain clique,  $C_0$  and  $y$  in a clique  $C_{n+1}$ . By algorithmic construction (cf. [4]), the vertices  $x_0 - x_1, x_1 - x_2, \dots, x_{n-1} - x_n$  are lying in certain cliques  $C_1, \dots, C_n$  with

$$C_0 \cap C_1 \neq \emptyset, C_1 \cap C_2 \neq \emptyset \dots, C_n \cap C_{n+1} \neq \emptyset \quad (32)$$

by construction ( $x_i \in C_i \cap C_{i+1}$ ). Hence, each pair of cliques,  $C, C'$ , can be connected by a finite sequence of pairwise overlapping cliques. In other words, the ordinary clique graph is again connected.  $\square$

This result is, for example, useful in cases where graphs are so sparsely connected that, viewed in the random graph picture, there is a non-zero probability that they are disconnected. The above construction shows that at least the consecutive sequence of unpurified clique graphs  $G_0 \rightarrow G_1 \rightarrow G_2 \rightarrow \dots$  consists of connected graphs, provided the initial graph,  $G_0$ , is connected, with  $G_{i+1}$  being the clique graph of  $G_i$ . On the other hand, if we take instead the purified clique graph, in which only overlaps of a certain degree are taken into account which are greater than some prescribed value, it may happen that the clique graph is no longer connected.

We want to repeat the above described coarse-graining process several or perhaps many times (if necessary) without the necessity of introducing new principles at each step of the construction. The transition from a graph to its clique graph represents such a *universal principle*, which works on each level of the renormalisation process. In the end we hope to arrive at a (quasi-)continuous manifold, displaying, under appropriate magnification, an intricate internal fine structure. This should (or rather, can only expected to) happen if the original network has been in a (quasi-)critical state as will be described in the following (see in particular section 8).

On each level of coarse-graining, that is, after each renormalisation step, labelled by  $l \in \mathbb{Z}$ , we get, as in the block spin approach to critical phenomena, a new level set of cliques or lumps,  $C_i^l$ , ( $i$  labelling the cliques on renormalisation level  $l$ ), consisting on their sides of  $(l-1)$ -cliques which are the  $l$ -nodes of level  $l$ , starting from the level  $l=0$  with  $G =: G_0$ . That is, we have

$$C_j^l = \bigcup_{i \in j} C_i^{(l-1)}, C_i^{(l-1)} = \bigcup_{k \in i} C_k^{(l-2)} \text{ etc.} \quad (33)$$

( $i \in j$  denoting the  $(l-1)$ -cliques, belonging, as meta nodes, to the  $l$ -clique,  $C_j$ ). These cliques form the meta nodes in the next step.

**Definition 5.4** *The cliques,  $C_i^0$ , of  $G =: G_0$  are called zero-cliques. They become the one-nodes,  $x_i^1$ , of level one, i.e. of  $G_1$ . The one-cliques,  $C_i^1$ , are the cliques in  $G_1$ . They become the 2-nodes,  $x_i^2$ , of  $G_2$  etc. Correspondingly, we label the other structural elements, for example, 1-edges, 2-edges or the distance functions,  $d_l(x_i^l, x_j^l)$ . These higher-level nodes and edges are also called meta-nodes, -edges, respectively.*

The following figure shows how the (meta) nodes and bonds form in two consecutive steps. In this example and in the selected subgraph under discussion the cliques on level 0 are triangles. Some of them have a common bond but all of them are hanging together via a common (central) node. In this example we draw a bond on level 1 if the cliques of level 0 have at least one node in common.

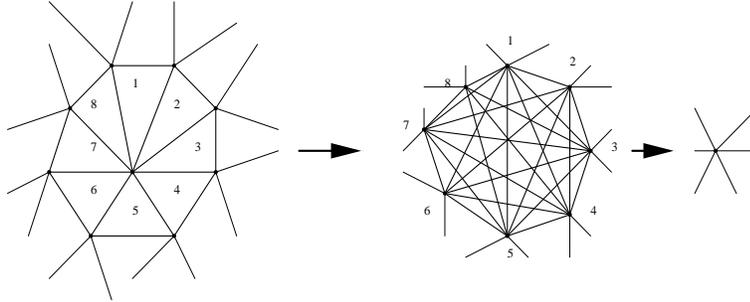


Figure 3:

**Remark 5.5** *The picture may lead to the wrong impression that the network becomes sparser after each step. Quite to the contrary, the number of cliques in  $G_d$  may be much larger than the number of nodes in the original graph,  $G$  (cf. the table in section 3). This happens if there is an appreciable overlap among the occurring cliques, that is, a given node may belong to many different cliques. On the other hand, after several renormalisation steps, the picture becomes stable in the generic case (see the following subsection).*

The above illustration can be understood in two different ways. On the one hand, read from left to right, the resolution of space appears to be reduced. The cluster of cliques on the left happens to be contracted to a single node of the next level. On the other hand, according to our working philosophy, we can regard the node on the right as still containing the structure on the left, which could, in principle, be recovered when increasing the resolving power of our space-time microscope, i.e., by increasing e.g. the energy. This is expressed in the following picture (where for the sake of graphical clarity, the mutual overlaps of the occurring cliques of the same level is not represented!). Understood in this latter sense we call these space-time points also *lumps*, that is, we regard them as objects, having an inner structure. Different aspects of this structure emerge on the respective scale of resolution or magnification. We provided arguments in [7] that in our view even quantum theory is just such an emergent aspect which shows up at the typical quantum scale.

We want to briefly mention the possibly far-reaching interplay on the higher levels of coarse-graining between these deleted, too marginal, overlaps and the more *local* wiring stemming from the non-marginal overlaps. We discussed this

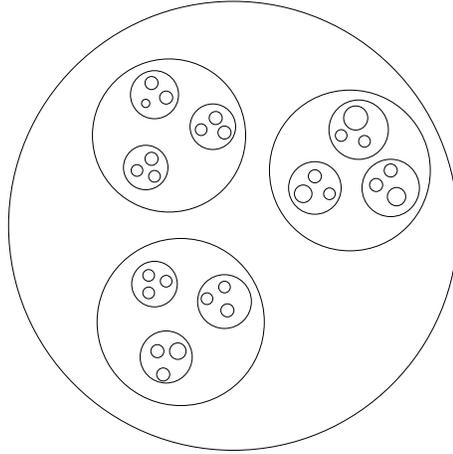


Figure 4:

point at length in [7]. We argued there that these deleted meta bonds are responsible for the translocal behavior of quantum theory. In the following we are, however, chiefly concerned with the emergence of smooth and local behavior, leading, hopefully, to (quasi)classical space-time structures).

## 5.2 The Analytic and Numerical Results

We begin this subsection with a general remark concerning the character of our approximations.

**Remark 5.6** *As the individual terms in our combinatorial expressions are typically either extremely large or small and are frequently, as in statistical mechanics, very sensitive to the given range of parameters, it is a quite delicate matter to make safe estimates. Among other things we usually have to take logarithms and compare them. That is, if for example  $\log(a) \gg \log(b)$ , we sometimes choose to neglect  $\log(b)$  in a contribution like  $\log(a) + \log(b)$  in the further calculations. For the original expression this may have the effect that we replace  $b \cdot a$  by  $a$ . To give an example; we sometimes approximate  $10^2 \cdot 10^{100}$  by  $10^{100}$ . Otherwise we had to take into account a lot of only marginal contributions which would make the calculations rather cumbersome. On the other hand, this is of course only justified, if we are only interested in qualitative results and provided that the final result is insensitive to such an approximation.*

We made more detailed remarks in [4] formulas (62) ff., where we discussed the approximation of e.g. binomial coefficients and their logarithms.

We have seen that the cliques in a large generic random graph of order  $n$  and bond probability  $p$  are with high probability concentrated in the interval  $(r_0/2, r_0)$  with respect to their order,  $r$ , with

$$r_0 \approx 2 \log(n) / \log(p^{-1}) + O(\log \log(n)) \quad (34)$$

and with the expectation of  $r$ -cliques

$$\langle Z_r \rangle = \binom{n}{r} \cdot (1 - p^r)^{n-r} \cdot p^{\binom{r}{2}} \quad (35)$$

We can test our general working philosophy concerning the effects of coarse graining and renormalisation by analytically and numerically calculating various properties of the *clique graph* of a generic random graph. These calculations become increasingly intricate with increasing complexity of the asked questions. Some of the analysis has already been done in e.g. sect. 4.2 of [4] (called ‘*The Unfolded Epoch*’) to which we refer the reader for more technical details.

The meta nodes of the clique graph,  $G_{cl}$ , are the cliques of  $G$ . The meta bonds in  $G_{cl}$  are given by the overlap of cliques in  $G$ . As we want, on physical grounds, to ignore marginal, that is, too small overlaps, it is important to calculate the expected number of  $r'$ -cliques,  $\langle N(C_0; r', l) \rangle$ , having an overlap of order  $l$  with a given fixed  $r$ -clique,  $C_0$  with both  $r$  and  $r'$  lying in the above interval of generic cliques.

In [4] sect. 4.2 we derived the following formula for this stochastic quantity ( $C_0$  being a fixed  $r$ -clique):

$$\langle N(C_0; r', l) \rangle = \frac{\binom{r}{l} \cdot \binom{n-r}{r'-l} \cdot p^{\binom{r'}{2} - \binom{l}{2}}}{(1 - p^r)^{n-r}} \cdot P_{r',l} \quad (36)$$

with  $P_{r',l}$  a lengthy combinatorial expression (formula (69) in [4]) which we can neglect for the parameters  $n, r, r'$ , chosen by us, that is  $n \gg r, r' \gg l$ . That is, in this regime we approximated  $P_{r',l}$  by one. It can however not be neglected if this assumption is violated!

After some manipulations we arrive at the following approximative formula ([4], formula (74)), where we choose, for convenience,  $r' = r$ , as we are at the moment only interested in qualitative or generic results:

$$\begin{aligned} \log \langle N(C_0; r', l) \rangle &\approx (r' - l) \cdot (\log(n) - \log(r' - l)) + 1/2 \cdot (r')^2 \cdot \log(p) \\ &\approx \log \langle Z_{r'} \rangle - l \cdot \log(n) - r' \log(r') \end{aligned} \quad (37)$$

with

$$\log \langle Z_r \rangle \approx r \log(n) + 1/2 \cdot r^2 \cdot \log(p) \quad (38)$$

for this range of parameters (cf. also [4] formula (60)ff).

The total expected number of  $r'$ -cliques, having an overlap  $l \geq l_0$  with a given  $r$ -clique is

$$\sum_{l \geq l_0} \langle N(C_0; r', l) \rangle \quad (39)$$

(the admissible  $l$ 's being bounded by the minimum of  $r$  and  $r'$ ). For  $l = 0$  we get the expected number of  $r'$ -cliques, having zero overlap with the given fixed  $r$ -clique,  $C_0$ , that is we have approximately (remember our simplifying assumption

$r = r'$ ):

$$\log\langle N(C_0; r', l = 0) \rangle \approx \log\langle Z_{r'} \rangle - r' \cdot \log(r') \quad (40)$$

As  $n$  is so large, the total number of  $r'$ -cliques, having overlap  $l \geq l_0$  with  $C_0$  can be approximated by the number of cliques fullfilling the lower bound  $l_0$ . On the other hand, the total number of expected generic cliques,  $N_{cl}$ , in the random graph,  $G$ , that is, the cliques with order lying in the respective interval  $(r_0/2, r_0)$  is roughly

$$N_{cl} \approx r_0/2 \cdot \langle Z_{\bar{r}} \rangle \quad (41)$$

with  $\bar{r}$  an appropriate value in the above interval (this replacement can be made as the numerical values in this interval behave relatively uniformly). We define the *local group* of a generic clique as the set of generic cliques, having non-marginal overlap with the fixed given clique. From the above reasoning we can now infer the following important conclusion

### Conclusion 5.7

$$\langle N_{loc.gr.} \rangle \approx N_{cl}/(n^{l_0} \cdot \bar{r}^{\bar{r}}) \quad (42)$$

with  $n$  the number of nodes in the graph,  $G$ ,  $N_{cl}$  the number of generic cliques in the corresponding clique graph,  $l_0$  the degree of overlap of the generic cliques,  $\bar{r}$  some appropriate value in the interval  $[r_0/2, r_0]$ ,  $n \gg r, r' \gg l_0$  being assumed (where the second  $\gg$  is not so pronounced as the first one;  $n$  is usually gigantic compared to the clique size  $r!$ ).

Such estimates are central in the following as they provide information about the local structure of the clique graph.

From the above formulas and numerical results we can now infer interesting properties of the clique graph of a typical graph of order,  $n$ , and bond probability,  $p$ . The expected order of the *local group* in the clique graph is, by the same token, the *average vertex degree* in the clique graph. That is

$$\langle v_{cl} \rangle \approx N_{cl}/(n^{l_0} \cdot \bar{r}^{\bar{r}}) \quad (43)$$

From this we can immediately infer the bond probability of the clique graph:

$$p_{cl} = \langle v_{cl} \rangle / (N_{cl} - 1) \approx \langle N_{loc.gr.} \rangle / N_{cl} \approx n^{-l_0} \cdot \bar{r}^{-\bar{r}} \quad (44)$$

and see that it is already considerably smaller than the bond probability of the underlying microscopic graph we started from which, in our numerical example, was assumed to be of order one.

We take our above numerical example,  $n = 10^{100}$ ,  $p = 0.7$  which implies  $r_0 = 1291$  and assume that an appreciable overlap for generic cliques should be of the order of, say, 50 nodes. As typical clique size we take  $\bar{r} = r_0/2$  (remember that we are at the moment only interested in qualitative results). The clique graph has roughly  $N_{cl} \approx 10^{10^4}$  generic cliques, that is, meta nodes of the first

level. With the bond probability in the clique graph,  $p_{cl} \approx 10^{-7 \cdot 10^3}$ , we now can calculate the distribution and order of cliques of the first level, that is, cliques of cliques. This provides important information about the near order of the clique graph and the effects of the renormalisation steps.

As the order of these cliques of the first level turns out to be already quite small, it is reasonable to avoid our approximative formulas and determine the respective clique number,  $r_0$ , by explicitly calculating the number where  $\langle Z_r \rangle$  drops from a very large number to effectively zero. The result shows, that for *overlap* = 50 of the original cliques (of the zero level), the cliques of the next higher level comprise only very few cliques of the zero level. That is, the near-order of  $G_1 := G_{cl}$  is already much coarser or less erratic as compared to the near order in the original graph. The results are described in the following observation.

**Observation 5.8** *For the above numerical parameters we get a typical clique size on the first coarse grained level of order  $r = 2$  or  $3$  and an expected number of cliques of the first level of the order of  $\log(N_{cl}) = 10^4$  (which is comparable to the number of cliques of the zero level!).*

We can control the sensitivity of our results to the chosen degree of overlap. We see below that the results do not depend critically on the numerical details as long as the parameters are roughly of the same order. For e.g. *overlap* = 30 we get, performing the corresponding calculations, the following result.

**Observation 5.9** *For clique-overlap = 30 the clique size on the first level increases slightly to a value of  $r_0 = 4$ .*

In the following we present some more characteristics of the clique graph with overlap 50.

- average vertex degree  $\approx 10^{(10^4 - 7 \cdot 10^3 + 3)}$
- expected number of bonds =  $\langle v_{cl} \rangle \cdot 0.5 \cdot \langle n_{cl} \rangle \approx 0.5 \cdot 10^{5 \cdot 10^3 + 10^4 + 6}$

An important question is whether the (purified) clique graph,  $G_1$ , is still connected. In [4] we gave the threshold value for the corresponding  $p^*(n)$ , which is

$$p^*(N_{cl}) = \log(N_{cl})/N_{cl} \approx 10^4/10^{10^4} = 10^{-(10^4-4)} \ll p_{cl} \approx 10^{-7 \cdot 10^3} \quad (45)$$

that is,

$$p_{cl}/p^*(n) \approx 10^{3 \cdot 10^3} \quad (46)$$

**Conclusion 5.10** *For the numerical data we employed the web of lumps is almost surely connected. On the other hand, after one renormalisation step, the purified net of cliques is much sparser connected than the initial microscopic net.*

Summing up, what we have accomplished so far in this subsection, we have the following row of graph characteristics for the particular set of numerical parameters we employed.

- $l = 0$ : number of nodes  $n_0 = 10^{100}$ , bond probability  $p_0 = 0.7$ , clique number  $r_0 = 1291$ .
- $l = 1$ :  $n_1 \approx 10^{10^4}$ ,  $p_1 \approx 10^{-7 \cdot 10^3}$ ,  $r_1 = 3$ ,  $\langle \text{vertex degree} \rangle \approx 10^{0.3 \cdot 10^4}$

The respective values were calculated by using the following approximative formulas:

$$p_1 = n_0^{-l_0} \cdot \bar{r}^{-\bar{r}}, \quad l_0 = 50, \quad n_1 \approx r_0/2 \cdot \langle Z_{\bar{r}}^{(0)} \rangle \quad (47)$$

( $\langle Z_{\bar{r}}^{(0)} \rangle$  the distribution function of cliques in the initial graph,  $G_0$ ,  $\bar{r}$  some average or typical value).

The expected order of cliques on level 1 is only 2 or 3. That is, taking the next step from level 1 to level 2 we may assume an overlap  $l_1 = 1$ , i.e., we may take the ordinary clique graph. With this value we can calculate the corresponding characteristics of  $G_2$ , the graph having as nodes cliques, consisting of nodes of level 1. Before we proceed with the numerical estimates we first have to check whether the approximations we have made above are still valid for this new regime of parameters!

Now,  $r, r', l$  are both very small and of comparable size. That is, our above approximative formulas are no longer valid. On the other hand, for  $r, r', l$  near one, it becomes possible to evaluate the combinatorial expressions directly. For the expected number of nodes on level 2, that is, expected number of cliques on level 1, we insert our parameters into the formula for  $\langle Z_r^{(1)} \rangle$  (cf. formula (35)) and get an approximate value,  $n_2 \approx 10^{10^4}$  (which is of the same order as  $n_1$ !).

The calculation of the vertex degree, that is,  $\langle N^{(1)}(C_0, r', l) \rangle$  with e.g.  $r' = 2, l = 1$ , is numerically more delicate since now we have to take into account also the term  $P_{r', l}$  in formula (36), we up to now approximated by one. Furthermore we now face the problem of having to deal with small differences of extremely large numbers in the various occurring expressions and/or factors which are extremely small or large and tend to cancel each other.

Fortunately, there is a more direct way to get sufficiently precise results in this regime. We saw that typical cliques in  $G_1$  are of order two or three. The assumed overlap is  $l = 1$ . We can hence infer that the expected number of cliques, overlapping with a fixed given clique,  $C_0$ , is roughly the same as the number of nodes, being connected with one of the nodes of  $C_0$ . We conclude that

$$p_2 = \langle N^{(1)}(C_0, r', l) \rangle \approx p_1 \approx 10^{-7 \cdot 10^3} \quad (48)$$

With these values for  $n_2, p_2$ , we can calculate  $r_2$  and again get  $r_2 = 3$ . We hence have for  $l = 2$ :

- $n_2 \approx 10^{10^4}$  (number of cliques of level 1)
- $p_2 \approx p_1 \approx 10^{-7 \cdot 10^3}$ ,  $r_2 = 3$

For the following levels the parameters are now stable and the same as for level two.

**Conclusion 5.11** *We see that after only two steps we have arrived at a coarse grained graph with a large number of nodes, a very small bond probability and small cliques, which shows that the geometric near- and far-order has unfolded. We further conclude that the following renormalisation steps would no longer alter appreciably the graph characteristics calculated above for the levels  $G_1, G_2$ . That is, at least as far as these particular graph properties are concerned, we have already reached a quasi-stable regime, so that the assumption of the existence of fixed phases or attractors does not seem too far-fetched. We can also infer that all the graphs are almost shurely connected.*

*On the other hand, we do not expect that a smooth limit manifold, having e.g. a fixed integer dimension, does emerge quasi automatically in the pure random graph framework. A further important ingredient will be the action of some appropriately chosen local law as we have introduced it above. (see the corresponding discussions in our mentioned prior work).*

## 6 Fixed Point Behavior

Starting from a sufficiently large network or graph,  $G = G_0$ , and performing the consecutive steps, described above, denoting the transition from  $G_l$  to  $G_{l+1}$ , i.e. from a graph to its (purified) clique graph, by  $R$  (standing for *renormalisation*), we have

$$R : G_l \rightarrow G_{l+1}, \quad G_l = R^l G_0, \quad R^l = R \cdots R \text{ (} l\text{-times)} \quad (49)$$

The philosophy of the renormalisation group is, that initial systems, lying on the *critical submanifold*, approach a *fixed point* under  $R^l$  for  $l \rightarrow \infty$ . In statistical mechanics the limit systems represent rather a *limit phase*, i.e. a statistical system with the finer details still fluctuating. In the same sense we can at best hope that our presumed limit network of lumps represents a similar limit phase, that is, a network which is only invariant and homogeneous on a larger scale of resolution, while the fine structure is still constantly changing.

The geometric concepts, which have to be further clarified, are the notions of *geometric (fixed) phase* and *critical network state*. We want to emphasize that we cannot expect that these characterisations will be a simple task. Quite to the contrary, both concepts represent subtle and delicate properties. In general, the emerging array of lumps will not fit automatically into something which does resemble a smooth macroscopic manifold, having for example a well-defined and integer (macroscopic) dimension (among other things). Possible obstacles are

already well-known on the much simpler level of simplicial complexes. In order that such a complex has the chance to approximate a manifold, a variety of subtle incident relation between the occurring individual simplices have to be fulfilled (see e.g. [44]).

In our context these relations on the more coarse-grained scales will depend on the appropriate choice of the microscopic local dynamical laws on the Planck scale we started from. Experience with complex systems in general and cellular automata in particular tells us, that the class of appropriate laws will be a very small and peculiar set in the space of possible interaction laws. See the corresponding findings in the regime of *selforganized criticality* ([45]), the catchword being *complexity at the edge of chaos*.

In other words, as the whole approach appears to be relatively new and the task formidable, we will make what are perhaps only some first steps towards a solution of these problems. In a first step we will convince ourselves that the renormalisation procedure described by us does not lead to nonsensical results (we have already previously seen that some gross characteristics of the network seem to become stable after only a few renormalisation steps). We show that there do exist examples of graphs which display fixed point or fixed phase behavior in a more microscopic sense. These graphs are however simple and very regular and are not meant to represent possible examples of networks, underlying our continuum space-time. They rather serve at best as illustrative toy models.

In the following section we then introduce a geometrical core concept designed to classify such irregular network structures, i.e. the notion of *graph dimension*. We show, how it behaves under our renormalisation process. The corresponding analytic results indicate what kind of *critical behavior* is presumably needed to have a physically reasonable limit behavior.

We illustrate our framework with the help of some simple examples (see also the following figure 5). Note that in the following examples the minimal admissible clique overlap is assumed to be one common node!

1) *The graph  $\mathbb{Z}^2$ :*

The set of nodes are parametrized as  $V = \{(i, j), i, j \in \mathbb{Z}\}$ . Edges are drawn between the following nodes:

$$(i, j), (i', j') \text{ with } |i' - i| + |j' - j| = 1 \quad (50)$$

We determine the cliques at the various levels, given by  $G_l$  (see also the following figure).

$G_0$ ) A node,  $(i, j)$ , belongs to the following 0-cliques:

$$\{(i + 1, j), (i, j)\} \{(i, j + 1), (i, j)\} \quad (51)$$

and  $+$  replaced by  $-$ . That is, the order of the 0-cliques is 2, the diameter (that is, the maximal distance between two nodes) is 1, the maximal mutual overlap is

1.

$G_1$ ) A 0-node,  $(i, j)$  belongs to the following 1-cliques

$$\{(i, j), (i \pm 1, j)(i, j \pm 1)\} \quad (52)$$

and the cliques, formed around the  $nm$ -nodes of  $(i, j)$ . The order relative to  $G_0$  is 5, the diameter is 2, maximal overlap is 2.

$G_2$ ) The order of 2-cliques relative to  $G_0$  is 13, diameter is 3, maximal overlap is 8.

Remark: Note that the above values of order and diameter refer to the start graph  $G_0$ .

With increasing  $l$ , the maximal overlap becomes large, due to the particular structure of the graph,  $\mathbb{Z}^2$ . One sees that for large  $l$  the hierarchical structure of the corresponding tower of graphs,  $G_l$ , becomes very dense and entangled, a feature one would also expect from something like a *continuum*.

On the other side, it is instructive, to perform also the above mentioned rescaling and compare the various levels at the same scale, viz., inspect the pure graph structure. This will make explicit the fixed point behavior, we are particularly interested in.

$G_0 \rightarrow G_1$ ) The 1-nodes of  $G_1$  (i.e. the 0-cliques) we represent by the midpoints of the edges of the start graph,  $G_0 := \mathbb{Z}^2$ . Four of these 0-cliques meet at a common node,  $(i, j)$ , say. We represent the 1-edges as the line segments, connecting these midpoints. This yields a new, rotated lattice (pus two extra diagonal edges).

$G_1 \rightarrow G_2$ ) These four 1-nodes (the 1-cliques) form now the 2-nodes. They form a simplex having 6 1-edges. We inscribe these 2-nodes in  $G_0$  by placing them in the centers of the 1-cliques, that is the original lattice points of  $G_0$ . We draw a 2-edge if two of these 1-cliques have a common 1-node (that is, a 0-clique!). We can convince ourselves that the emerging graph,  $G_2$  is isomorphic to the start graph,  $G_0$ . We hence make the interesting observation:

**Observation 6.1** *Starting from  $G_0 = \mathbb{Z}^2$ , we see that  $G_2$  is combinatorially isomorphic to  $G_0$ , meaning that there exists an invertible map,  $\Phi : G_0 \rightarrow G_2$ , mapping nodes on nodes and bonds on bonds and preserving the combinatorial structure in the following way (with  $e_{ij}$  an edge of  $G_0$ )*

$$e_{ij} \in E(G_0) \leftrightarrow \Phi(e_{ij}) \text{ connects } \Phi(x_i), \Phi(x_j) \quad (53)$$

The same holds for  $G_1, G_3$  etc.

**Conclusion 6.2** *The sequence of graphs,  $G_0, G_1, G_2, \dots$ , decomposes in exactly two sets of isomorphic graphs,*

$$\{G_0, G_2, \dots\}, \{G_1, G_3, \dots\} \quad (54)$$

under the renormalisation group

$$\mathcal{R} := \{R^i\}, \quad R^i : G_0 \rightarrow G_i, \quad R^2 : G_i \rightarrow G_{i+2} \quad (55)$$

**Corollary 6.3** *A corresponding observation can be made for a general lattice,  $\mathbb{Z}^n$ .*

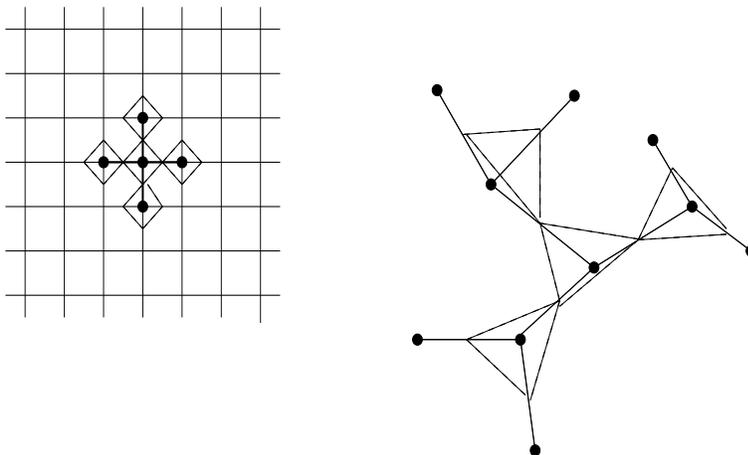


Figure 5:

2) *The trivalent infinite tree:*

In order to get a better feeling for what can happen, we study some more elementary examples. Let us take an infinite trivalent tree. The 0-cliques are again 2-sets of vertices or line segments, connecting  $nn$ . The graph,  $G_1$ , is again represented by connecting the midpoints of these line segments. The resulting 1-cliques are 3-sets or triangles. Taking them as the 2-nodes of  $G_2$ , we see that  $G_2$  is again isomorphic to  $G_0$  as in the  $\mathbb{Z}^2$ -case.

**Observation 6.4** *For a trivalent infinite tree, the sequence of graphs,  $G_0, G_1, G_2, \dots$ , decomposes into two subsets. The situation is the same as for the preceding example.*

3) *The triangulated  $\mathbb{R}^2$ :*

We introduce another simple example. We triangulate  $\mathbb{R}^2$  by using the above lattice,  $\mathbb{Z}^2$ , and complement it by drawing the diagonals, pointing from  $(i, j)$  to  $(i + 1, j + 1)$ . The 0-cliques are these triangles. Without a purification, bonds in the graph,  $G_1$ , are drawn if two 0-cliques meet at a common node or 0-edge. The emerging 1-cliques have the shape of hexagons, i.e. they are 6-simplices. Repeating this process, one sees that  $G_2$  is isomorphic to  $G_1$ .

**Observation 6.5** *In the case of the above triangulation of  $\mathbb{R}^2$ , we have a start graph,  $G_0$ , while all the graphs,  $G_1, G_2, \dots$ , are isomorphic. In other words, we now have a fixed point of the renormalisation group.*

**Conclusion 6.6** *We have seen that there exist examples in the category of graphs which display phenomena like invariant sets or fixed points under our geometric renormalisation group.*

These observations open up interesting vistas. While we have not yet shown that the above invariant sets or fixed points have the character of *attracting sets*, that is, whether there exist large *basins of attraction* in the category of graphs under the repeated application of the map,  $R$ , we strongly surmise that this is true. Furthermore, the concept of *selfsimilarity* suggests itself (see also the next section), a notion we have already introduced and studied in [1], to construct graphs with *fractal dimension*.

## 7 Graph Dimension under the Renormalisation Group

We repeatedly mentioned the possibility of *geometric* or *topological phase transitions* in evolving networks of the kind we are having in mind. In [1] we developed and studied the concept of *graph dimension* in quite some detail. We concluded that, from the physical point of view, the number of nodes which can be reached by, say,  $l$  steps starting from a given node, is an important characteristic as is its limiting and scaling behavior as a function of  $l$ . This is the crucial and *intrinsic* property, which underlies implicitly most of the calculations in the physics of phase transitions and many other phenomena, which are triggered by the collective interaction of many constituents. Its true significance is however frequently hidden as the reasoning is usually performed by using the properties of the embedding space (viz., its ordinary dimension).

Remark: We learned recently that such growth properties are also important characteristics in geometric group theory and related subjects in pure mathematics (see e.g. [48],[49] or [50]).

We will investigate the behavior of this quantity under the application of our renormalisation group. In [1] we introduced the two variants, defined below. They are not strictly equivalent but coincide in the more regular situations. In the following, for the sake of brevity, we only use the first notion.

**Definition 7.1 (Internal Scaling Dimension)** *Let  $x$  be an arbitrary node of  $G$ . Let  $\#(U_n(x))$  denote the number of nodes in  $U_n(x)$ . We consider the sequence of real numbers  $D_n(x) := \frac{\ln(\#(U_n(x)))}{\ln(n)}$ . We say  $\underline{D}_G(x) := \liminf_{n \rightarrow \infty} D_n(x)$  is the*

lower and  $\overline{D}_S(x) := \limsup_{n \rightarrow \infty} D_n(x)$  the upper internal scaling dimension of  $G$  starting from  $x$ . If  $\underline{D}_S(x) = \overline{D}_S(x) =: D_S(x)$  we say  $G$  has internal scaling dimension  $D_S(x)$  starting from  $x$ . Finally, if  $D_S(x) = D_S \forall x$ , we simply say  $G$  has internal scaling dimension  $D_S$ .

**Definition 7.2 (Connectivity Dimension)** Let  $x$  again be an arbitrary node of  $G$ . Let  $\#(\partial U_n(x))$  denote the number of nodes in the boundary of  $U_n(x)$ . We set  $\tilde{D}_n(x) := \frac{\ln(\#(\partial U_n(x)))}{\ln(n)} + 1$  and define  $\underline{D}_C(x) := \liminf_{n \rightarrow \infty} \tilde{D}_n(x)$  as the lower and  $\overline{D}_C(x) := \limsup_{n \rightarrow \infty} \tilde{D}_n(x)$  as the upper connectivity dimension. If lower and upper dimension coincide, we say  $G$  has connectivity dimension  $D_C(x) := \overline{D}_C(x) = \underline{D}_C(x)$  starting from  $x$ . If  $D_C(x) = D_C$  for all  $x$  we call  $D_C$  simply the connectivity dimension of  $G$ .

Remark: The above does not imply, that this notion is the only relevant topological characteristic of large networks. It clearly is not sufficient, to describe *all* of the mesoscopic or macroscopic properties, but we think it is, as in the continuum, a very important concept.

We already proved in [1] that this kind of dimension is stable under a variety of transformations, in particular under *local* ones. In section 5.2.5 of [1] we showed that, in order to change the dimension of a graph, we have to introduce long-range effects or interactions. This reminds one of the behavior of *critical systems*.

We now compare the dimension of a graph,  $G$ , with the dimension of its clique graph,  $G_{cl}$ , where, for the time being, we take the clique graph in its original meaning. That is, we draw a bond if two cliques have a non-void overlap of arbitrary size.

Let us assume, for convenience, that  $G$  has the scaling dimension,  $D$ , that is, for every node,  $x_0$ , we have

$$\lim_l \ln(\#(U_l)) / \ln l = D \quad (56)$$

Furthermore, we assume for simplicity that the node degree of  $G$  is globally bounded, i.e.

$$v_i \leq v < \infty \text{ for all } x_i \quad (57)$$

We choose a fixed node,  $x_0$ , lying in a fixed clique,  $C_0$ . We have to calculate the number of 1-nodes, that is, the number of 0-cliques,  $\#(U_l^{cl}(C_0))$ , lying in  $U_l^{cl}(C_0)$  with the distance,  $d_1$  now measured in the clique graph,  $G_{cl}$ . That is, a clique,  $C_l$ , lies in  $U_l^{cl}(C_0)$  if  $C_0$  and  $C_l$  can be connected by a sequence of  $l'$  cliques with  $l' \leq l$  so that two consecutive cliques have a non-zero overlap. For each 0-node,  $x'_l$ , lying in some  $C_{l'}$  with  $d_1(C_0, C_{l'}) \leq l$ , we can estimate the distance to the node  $x_0$  in  $C_0$ . There exists, by definition, a sequence of overlapping cliques,

$$C_0, C_1, \dots, C_{l'} , l' \leq l \quad (58)$$

For two neighboring cliques,  $C_i, C_j$ , we have

$$d_0(x_i, x_j) \leq 2, \quad x_i \in C_i, x_j \in C_j \quad (59)$$

For each intermediate consecutive pair of cliques we need one step (a bond from a node in the overlap  $C_{i-1} \cap C_i$  to a node in  $C_i \cap C_{i+1}$ ), for the initial and final pair we need at most two steps, we hence get

$$d_0(x_0, x_{l'}) \leq l' + 2 \quad (60)$$

**Lemma 7.3** *For two arbitrary nodes*

$$x_0 \in C_0, x_{l'} \in C_{l'} \text{ with } d_1(C_0, C_{l'}) \leq l \quad (61)$$

we have

$$d_0(x_0, x_{l'}) \leq l' + 2 \quad (62)$$

and hence

$$|U_l^{cl}(C_0)| \subset U_{l+2}(x_0) \quad (63)$$

with  $|U_l^{cl}(C_0)|$  the set of 0-nodes, lying in  $U_l^{cl}(C_0)$  (the latter set now understood as the set of its 0-nodes). This implies

$$\#(|U_l^{cl}(C_0)|) \leq \#(U_{l+2}(x_0)) \quad (64)$$

From observation 4.2 of [4] we know that each node,  $x_i$ , can lie in at most  $2^{v_i}$  different cliques, with  $v_i \leq v$ . This yields the crude, but apriori estimate

$$\#(U_l^{cl}(C_0)) \leq \#(U_{l+2}(x_0)) \cdot 2^v \quad (65)$$

which is the desired upper bound on the number of cliques, lying in  $U_l^{cl}(C_0)$ . We conclude that, for an infinite graph with  $v_i \leq v < \infty$ , we have for the dimension of its clique graph:

$$\overline{D}_{cl} \leq D \quad (66)$$

since

$$\ln(\#(U_l^{cl}(C_0))) / \ln(l) \leq \ln(\#(U_{l+2}(n_0))) / \ln(l) + v \cdot \ln(2) / \ln(l) \quad (67)$$

For  $l \rightarrow \infty$  we get the above result.

We want to prove a corresponding lower bound. Take an arbitrary node,  $x_{l'}$ , in  $U_l(x_0)$ . By definition, there exists a node- (edge-)sequence

$$x_0 - x_1 - \dots - x_{l'} \text{ with } l' \leq l \quad (68)$$

On the other side, there exists a sequence of cliques,  $C_i$ , with each consecutive pair of nodes,  $(x_{i-1}, x_i) \in C_i$ . These cliques do exist because, starting from the

connected pair,  $(x_{i-1}, x_i)$ , we get such a clique by extending this germ in one of (possibly) several ways to a clique (cf. section 4 of [4]). We can conclude that for each node,  $x_{l'} \in U_l(x_0)$ , and  $x_0 \in C_0$ , we have

$$x_{l'} \in |U_{l+1}^{cl}(C_0)| \quad (69)$$

(note that the clique, containing both  $x_0$  and  $x_1$  may be different from the start clique,  $C_0!$ ).

We then have

$$U_l(x_0) \subset |U_{l+1}^{cl}(C_0)| \quad \text{and} \quad \#(U_l(x_0)) \leq \#(|U_{l+1}^{cl}(C_0)|) \quad (70)$$

With  $v_i \leq v$  for all  $x_i$ , the maximal order of a clique is bounded from above by  $(v + 1)$ . This implies

$$\#(|U_{l+1}^{cl}(C_0)|) \leq (v + 1) \cdot \#(U_{l+1}^{cl}(C_0)) \quad (71)$$

and

$$\#(U_{l+1}^{cl}(C_0)) \geq \#(U_l(x_0))/(v + 1) \quad (72)$$

We hence get

$$\ln(\#(U_{l+1}^{cl}(C_0)))/\ln(l + 1) \geq \ln(\#(U_l(x_0)))/\ln(l + 1) - \ln(v + 1)/\ln(l + 1) \quad (73)$$

With

$$\ln(l + 1) = \ln(l \cdot (1 + l^{-1})) = \ln(l) + \ln(1 + l^{-1}) \quad (74)$$

and  $l \rightarrow \infty$ , we see that

$$\underline{D}_{cl} \geq D \quad (75)$$

and get the important theorem:

**Theorem 7.4** *Assuming that  $G$  has dimension  $D$  and globally bounded node degree,  $v_i \leq v < \infty$ , we have that  $D_{cl}$  also exists and it holds*

$$D_{cl} = D \quad (76)$$

*Note that this result does hold for the ordinary clique graph, viz. arbitrary overlap, viz., no purification. In other words, under these assumptions, the renormalisation steps do not change the graph dimension.*

This result is reminiscent of a similar observation in statistical mechanics where the non-coarse-grained Gibbsian entropy happens to be a *constant of motion*. The same happens here. In the ordinary clique graph each original bond occurs in at least one clique, i.e. there is no real (or, more precisely, not enough) coarse graining.

## 8 Critical Network States

In subsection 5.2 we derived formulas for the size of the so-called local group of a clique in a random graph, that is the set of cliques with which a given clique has a (sufficient) common overlap. If one is in the parameter regime in which the cliques are still densely and complicately entangled (typically the first renormalisation steps) and compares the number of bonds in the *purified* clique graph, that is, bonds being defined by a sufficient! overlap, with the number of bonds in the corresponding (unpurified) clique graph, the latter number exceeds the former one by many orders. Put differently, in this situation the number of *marginal* overlaps of cliques is much bigger. All these marginal overlaps are deleted in the purification or renormalisation process.

The last theorem in the preceding section shows that we will not get a dimensional reduction without sufficient purification. If we go through the proof we see that the first part does hold unaltered for the purified clique graph. In the second part, however, we used an argument which does only hold for ordinary clique graphs (see the remarks following formula (68)). The existence of the row of overlapping cliques, employed there, can only be guaranteed if the degree of overlaps are left arbitrary. We hence can infer:

**Corollary 8.1** *For the purified clique graph, with overlaps exceeding a certain fixed number,  $l_0$ , we can only prove*

$$D_{cl} \leq D \tag{77}$$

Having for example the picture in mind, frequently invoked by Wheeler and others, of a space-time foam, with a concept of dimension depending on the scale of resolution (see e.g. Box 44.4 on p.1205 in [24]), we infer from our above observations that this may turn out to be both an interesting and not entirely trivial topic. We have to analyze under what specific conditions the dimension can actually shrink under coarse-graining, so that we may start from a very erratic network on, say, the Planck scale, and arrive in the end at a smooth macroscopic space-time having perhaps an integer dimension of, preferably, value 4 or so.

We remarked already in the introduction that geometric change or geometric phase transitions are supposed to be related to some sort of *critical state* of the network. Our previous observations about the possibility of dimensional change under coarse graining together with an interesting observation already made in [1], lemma 4.10, allows us to *almost rigorously* prove what kind of criticality is in fact necessary to achieve this goal.

We showed there that it is not so easy to modify the dimension of a graph by *local* alterations.

**Proposition 8.2** *Additional insertions of bonds between arbitrarily many nodes,  $y, z$ , having original graph distance,  $d(y, z) \leq k$ ,  $k \in \mathbb{N}$  arbitrary but fixed, do not change  $\underline{D}(x)$  or  $\overline{D}(x)$ .*

From this we learn the following. Phase transitions in graphs, changing the dimension, have to be intrinsically *non-local*. That is, they necessarily involve nodes, having an arbitrarily large distance in the original graph. We think, this is a crucial observation from the physical point of view. On the one side, it shows that systems have to be *critical* in a peculiar way, that is, having a lot of distant correlations or, rather, correlations on all scales (cf. also Smolin's discussion in e.g. [11] and elsewhere). On the other side, it fits exactly with our working philosophy that quantum theory is a *residual* and *coarse grained* effect of such largely hidden long range correlations ([7]).

If we apply these findings to our renormalisation steps, that is, passing from a graph to its associated (purified) clique graph, this implies the following. We saw that assuming a network or graph,  $G$ , having a dimension,  $D$ , the unpurified clique graph still has

$$D_{cl} = D \quad (78)$$

On the other hand, denoting the purified clique graph by  $\hat{G}_{cl}$ , we have the estimate

$$\hat{D}_{cl} \leq D_{cl} = D \quad (79)$$

The transition from  $G_{cl}$  to  $\hat{G}_{cl}$  consists of the deletion of marginal overlaps among cliques (with the necessary criteria provided by the physical context). That is,  $\hat{G}_{cl}$  lives on the same node set (the set of cliques) but has fewer (meta)bonds. The above proposition shows that this does *not* automatically guarantee that we really have

$$\hat{D}_{cl} < D_{cl} \quad (80)$$

Quite to the contrary, we learned that this can only be achieved if the bond deletions happen in a very specific way.

On  $G_{cl}$  we have, as on any graph, a natural distance or neighborhood structure, given by the canonical graph metric,  $d_{cl}(C_i, C_j)$ . Note that the above proposition holds as well for bond deletions instead of insertions. We thus infer that bond deletions in  $G_{cl}$  between cliques which are not very far apart in the final purified graph  $\hat{G}_{cl}$  cannot alter the final dimension of  $\hat{G}_{cl}$ . More precisely, only bond deletions between cliques having distances in  $\hat{G}_{cl}$  which approach infinity in a specific way, can have an effect.

**Conclusion 8.3** *We conclude that only the bond deletions between very distant cliques (with respect to  $\hat{G}_{cl}$ ), with this distance being unbounded, can decrease the dimension of  $\hat{G}_{cl}$  as compared to  $G_{cl}$ . More precisely, there has to be a substantial bond deletion on all scales up to infinity.*

The above observation reminds one of the *scale invariance* of *critical systems* in other contexts. We exemplify this by a simple but instructive example.

This (inhomogeneous; it slightly depends on the reference point  $(0, 0)$ ) construction has already been given in section 5.2.5 of [1]. One takes the lattice,

$\mathbb{Z}_2$ , inscribes in it, starting from the point  $(0, 0)$ , two non-intersecting outwardly spiraling edge sequences:

$$(0, 0) \rightarrow (1, 0) \rightarrow (1, 1) \rightarrow (0, 1) \rightarrow (-1, +1) \rightarrow (-2, +1) \rightarrow (-2, 0) \rightarrow \dots \quad (81)$$

and

$$(0, 0) \rightarrow (-1, 0) \rightarrow (-1, -1) \rightarrow (0, -1) \rightarrow (+1, -1) \rightarrow (+2, -1) \rightarrow (+2, 0) \rightarrow \dots \quad (82)$$

We consider this inscribed graph as a representation of the one-dimensional

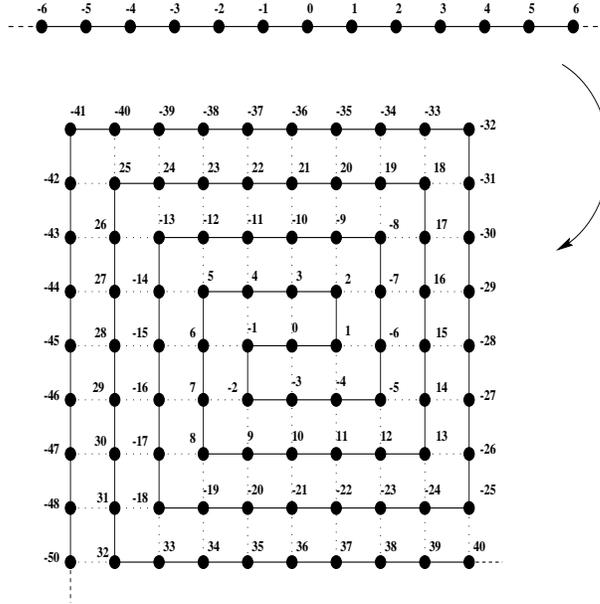


Figure 6:

lattice,  $\mathbb{Z}_1$ , with the node labelling running from  $-\infty$  to  $+\infty$ .

$$0 \rightarrow 1 \rightarrow 2 \rightarrow 3 \rightarrow 4 \rightarrow 5 \rightarrow \dots \quad (83)$$

and

$$0 \rightarrow -1 \rightarrow -2 \rightarrow -3 \rightarrow -4 \rightarrow -5 \rightarrow \dots \quad (84)$$

**Remark 8.4** *The embedded graph, being isomorphic to  $\mathbb{Z}_1$ , is in fact a spanning tree relative to the ambient graph,  $\mathbb{Z}_2$ .*

One can now see that the extra bonds, occurring in  $\mathbb{Z}_2$ , not belonging to the representation of  $\mathbb{Z}_1$ , connect nodes of a larger and larger distance with respect to the labelling of  $\mathbb{Z}_1$ . We have for example bonds in  $\mathbb{Z}_2$  between pairs of nodes with the  $\mathbb{Z}_1$ -labels,

$$0, 3; 3, -10; -10, 21; 21, -36 \dots \quad (85)$$

and correspondingly for other sequences of nodes. That is, the embedded graph is one-dimensional, lying in a two-dimensional graph, while the node sets are identical. The preceding discussion and the figure illustrate and confirm what we have said above about the type of necessary criticality and long-range correlations.

To employ this example for our renormalisation group approach, we can replace the original nodes (with the  $\mathbb{Z}_1$ -labelling) by certain cliques of arbitrary order, choose the overlaps appropriately, so that the above representation of  $\mathbb{Z}_1$  becomes the *purified* clique graph of the total graph. We arrive at a coarse-grained graph of dimension one, starting from an unpurified graph of dimension two or a larger dimension.

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