Life without bounds:
Does the Game of Life exhibit Self-Organized Criticality in the thermodynamic limit?

By

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Abstract

Recently, a class of phenomena known as self-organized criticality (SOC) has been discovered. SOC is characterized by two properties: firstly, the system exhibits power law behavior typical of a critical state, with no characteristic time or length scales; and secondly, this state is approached naturally, without tuning any external parameters. Early studies explained SOC in terms of conserved quantities [1,2]. Then Bak *et al.* [3] suggested that the Game of Life, GL, a cellular automaton lacking any conserved quantities, also exhibited SOC. This sparked a debate as to whether GL truly is SOC; conflicting data suggested it was subcritical [4,5,6].

In this paper I explore both sides of the argument in an attempt to resolve the issue. By finding an explicit form for the scaling function the opposing arguments are reconciled and, with some slight reservations, GL is judged to be subcritical. The differences between the analysis herein and other studies is highlighted.

I also introduce the reader to some other interesting features of GL, and cellular automata in general, in order to elicit the proper respect for these simple yet complex models. In doing so I hope to impress upon the reader the insufficiencies of the available analytical tools. New methods are required to account for the long-range correlations which develop in GL and other deterministic automata.

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Preface

Complexity research is a young field with uncertain goals and high ambitions. It encapsulates studies in biology, mathematics, physics, computers, and even chemistry. As such, mighty paradigms are often expounded with little or no fact to back them up. This sort of soothsaying is probably inevitable in all new fields but it tends to do more harm than good by destroying the field's creditability. Nevertheless, some true scientists prevail here with realistic expectations and meticulous research--and they (attempt to) instill these qualities in their students. My thanks, then to Dr. Birger Bergersen, my supervisor, for supporting and promoting this sort of interdisciplinary research and for his level-headed approach to the subject.

I would also like to thank Dr. E. Evans for unwittingly impressing in me the value of estimating (at least the order of) *all* variables, parameters, probabilities, *et cetera*. Thanks also to Joel Westereng for helping me (or is that *us*?) standardize the usage of the first person singular and plural vernacular. Finally, deep love and thanks to Kathy Blok for her patience and support through my highs and lows over the evolution of this thesis. Science is said to be objective but frankly I'm not sure...

1. Introduction

1.1. Cellular automata

There are a number of ways to model the temporal evolution of spatially extended systems. Differential equations (DEs) are optimal for modelling continuous space-time dynamics. They also have the advantage of being well understood and a large volume of analytical tools have been discovered to predict their behavior. However, not all natural systems fit well into this mold. In some cases either the spatial or temporal dimensions are best discretized. For example, the *logistic map* is a discrete-time model describing global dynamics of a population from one generation to the next. Similarly, evolution near a periodic solution of a differential equation is often easier to analyze by looking at the *Poincaré map*, a cross-sectional slice of space where the periodic orbit is represented by a point, making it easier to visualize in higher dimensions. Discrete time *maps* are chosen when they are mathematically simpler or the natural system being modelled exhibits a periodic or discontinuous temporal behavior. In general, however, there are fewer mathematical tools available for analysis of maps and, surprisingly, they tend to exhibit chaos more often than their continuous cousins. This is often observed in numerical integrations of differential equations, in which the DE is discretized (both spatially and temporally) in order to be solved via computer. Unless very particular preventative measures are taken the numerical simulation often exhibit chaotic behavior not observed in the original equation [7*, pp. 707-752*].

Another possible choice for modelling natural phenomena are cellular automata (CA). They are characterized by not only discrete time, but a discrete lattice space as well. They are well suited for modelling systems with an *atomic* or discrete structure. For example, sand flow has been successfully modelled by CA because of sand's granular nature. Each point, or *cell*, in a CA lattice space can have one of a finite number of states. The physics of this *universe* is the set of rules which govern the transition of cell states.

The transition rules are local, depending only on a cell's neighborhood, $\aleph$, and isotropic, independent of the cell's position. In most CA the entire lattice undergoes parallel (or *synchronous*) updating, but it is also sometimes interesting to observe the effects of removing this constriction. A powerful and easy to implement class of CA apply a *totalistic* law--that is, the cell's state, $s(\mathbf{x},t)$, depends only on the number of live cells in its neighborhood, $\sigma(\mathbf{x},t)$, and not the particular configuration of these neighbors:

$$s(\mathbf{x},t+1) = \mathrm{rule}(s(\mathbf{x},t),\sigma(\mathbf{x},t)) \tag{1.1}$$

where

$$\sigma(\mathbf{x},t) = \sum_{\mathbf{x}'\in\aleph(\mathbf{x})} s(\mathbf{x}',t). \tag{1.2}$$

The transition rule in Eq. (1.1) may be either *deterministic* or *probabilistic*--that is, each transition will occur not with certainty but with some constant probability which depends on the particular transition. In this sense, I will be dealing exclusively with deterministic CA transition rules in this paper (although I will extend the model to explore the effects of randomization in Chapter 4).

This simple structure makes CA models ideal for computer simulation. Simulations can be a good first tool for testing a theory. One can easily change the model parameters and decide which features are necessary for the occurrence of some natural phenomenon and which are irrelevant. Further, CA simulations offer immediate visual feedback which can confirm or discredit a model. However, heavy reliance on CA does incur a penalty: there are no general analytical tools available to predict or verify CA dynamics. For the continued application of these techniques in the scientific community it will be necessary for some independent methods to be developed to confirm the results observed on the computer screen. In isolated cases renormalization group, finite-scaling, and mean field methods have been applied. In this paper I will apply the latter two of these methods to a particular CA, which should demonstrate the difficulties and limitations of these techniques as well as their potentials.

1.1.1. Wolfram classes

As was noted for maps, CA can display a great diversity of behavior. Some rules can lead to dull, predictable dynamics, while other choices may result in wildly chaotic evolution.

Of course, for a deterministic CA on a finite lattice the system must always eventually fall into a periodic loop because there are only a finite number of *microstates* available. Consider an n-state CA on a two dimensional square lattice of length L: then there are n^{L^2} microstates and since the CA is deterministic the evolution must, after an initial transient, cycle repeatedly through a subset of these microstates.

In theory, though, these unwieldy systems may, in the thermodynamic limit, evolve indefinitely without cycling, giving rise to "true" chaos. Wolfram proposed the following qualitative scheme to classify CA by the degree to which they tend to organize: [8]

Class I	evolve to a fixed homogenous state (ordered);
Class II	evolve to simple separated periodic structures (mildly disordered);
Class III	yield chaotic aperiodic patterns (chaotic); and
Class IV	yield complex patterns of localized structures (complex).

Notice that the transition from order to chaos traverses the classes in the order I-II-IV-III. Class IV was singled out by Wolfram because of its special properties: it appears to be "on the edge of chaos". CA belonging to class IV are the most interesting to study because they exhibit the most *complex* dynamics, and those most resembling nature. Class I and II systems tend to be too stable to support any kind of interesting dynamics. Conversely, class III systems are unable to maintain any structure, making them uninteresting as well. Class IV systems, however, do have clear structures but are able to completely rearrange them on demand. In other words, they have the greatest capacity to both store and modify information.

In practice complexity, and hence the Wolfram class, is determined by the dynamics of the transient rather than by the properties of the steady state. Class I and II

CA tend to have short transients before settling down to their equilibrium configurations. Likewise, class III CA, having chaotic attractors, obscure their initial state very quickly. A global quantity, such as population density, will rapidly diverge from its initial value and soon fluctuate chaotically around a mean value which is identical for almost all initial configurations. However, class IV CA exhibit very long transients, and have a very sensitive dependence on their initial configuration. Hence, transient length is a useful measure of complexity. A sample of this definition is represented in Figure 1.1.

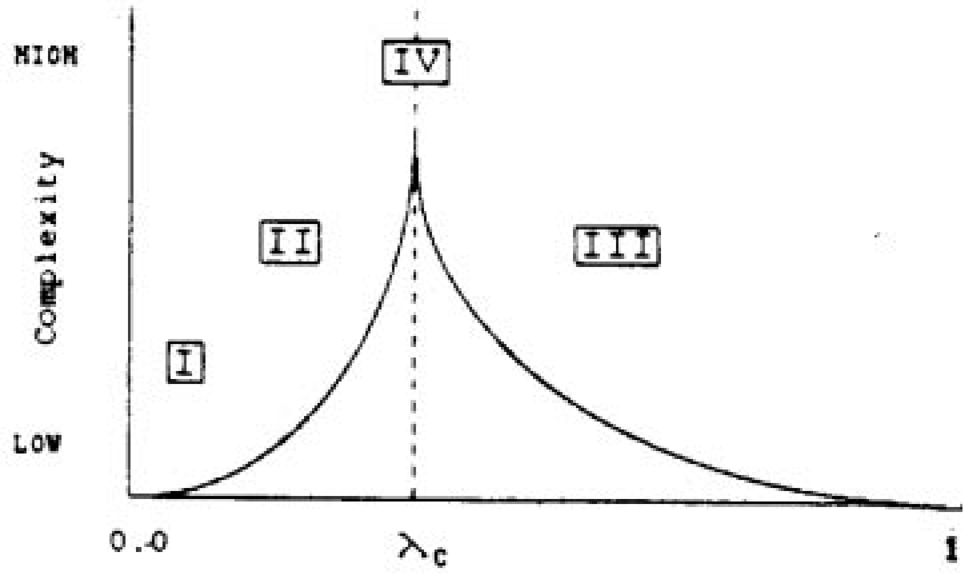


Figure 1.1: Relation between complexity and Wolfram classes as viewed by Langton [9]. Notice the analogy with phase transitions. Complexity is measured by the transient length (stabilization time).

In this figure, the x-axis represents a particular parametrization of the rule-space known as the λ parameter [9]. This parameter is just the fraction of rules which don't map cells to the *dead* state. (Note $\lambda_{GL} = 0.273$.) This parameter has met with limited success in describing CA complexity [10 *and references therein*].

The figure also provides another analogy to describe the differences between the classes: class I and II represent an ordered phase (like a solid), class III represents a disordered phase (fluid), and class IV represents a second-order phase transition between the two. For now we will leave this topic to discuss the particulars of the CA in question but we will expand on this analogy later.

1.2. Life

The *Game of Life* (GL) is a two-dimensional CA invented by John Horton Conway and made famous by Martin Gardner in his 1970 Scientific American articles [11]. This particular CA gained a great deal of attention because of the degree to which it appeared to simulate real-life processes (hence the name). The rules actually have nothing to do with natural systems. In fact, Conway's goal in constructing the rules was to make it difficult to decide whether a particular initial pattern would decay or grow without limit. Naturally, then, GL belongs to class IV by Wolfram's scheme.

GL was also exciting because of the simplicity of the rules which generated the complex dynamics observed. There are only two possible states for each cell: *alive* or *dead*. The neighborhood is defined to be the eight nearest cells on the rectangular lattice (the four adjacent orthogonally and the four adjacent diagonally). With this neighborhood the rules are

- Births. If a cell is currently *dead* and it has exactly three neighbors it will become *alive* in the next time step.
- Survivals. If a cell is currently *alive* and it has either two or three neighbors it will remain *alive* in the next time step.
- Deaths. If neither above condition is satisfied the cell will become *dead* in the next time step.

Note GL is a *synchronous* CA so all the cells in the lattice are updated simultaneously making the evolution deterministic. Mathematically the rules are written as

$$\begin{aligned} \mathrm{rule}(0,\sigma) &= \begin{cases} 1 & \sigma = 3 \\ 0 & \text{otherwise} \end{cases} \\ \mathrm{rule}(1,\sigma) &= \begin{cases} 1 & 2 \le \sigma \le 3 \\ 0 & \text{otherwise} \end{cases} \end{aligned} \tag{1.3}$$

where σ is the neighborhood occupation as defined by Eq. (1.2).

These rules are appealing because of their natural counterparts: the need for multiple parents to produce a child; death from competition arising from overcrowding; and the prospect of death from isolation (suggesting some sort of cooperation enhances survival). It is at least conceivable that these rules could model some simple, androgynous, life form. (I don't claim that they do!)

Early investigations of this simulation focused on the discovery and labeling of "species"--local stable configurations of cells which tended to arise spontaneously and frequently. Some of these configurations are shown below in Figure 1.2. The glider is a particularly interesting animal because it is capable of motion and hence, can transmit information over large distances without degradation. It is responsible for much of the interesting dynamics in GL. Researchers also found a *glider gun*, a configuration which generates gliders at regular intervals, as well as a *pentadecathlon*, which can absorb or reflect gliders. These remarkable species led the way to the discovery that GL can function as a universal computer. This is remarkable because GL is *irreversible*: except under exotic conditions, GL tends to lose information over time.

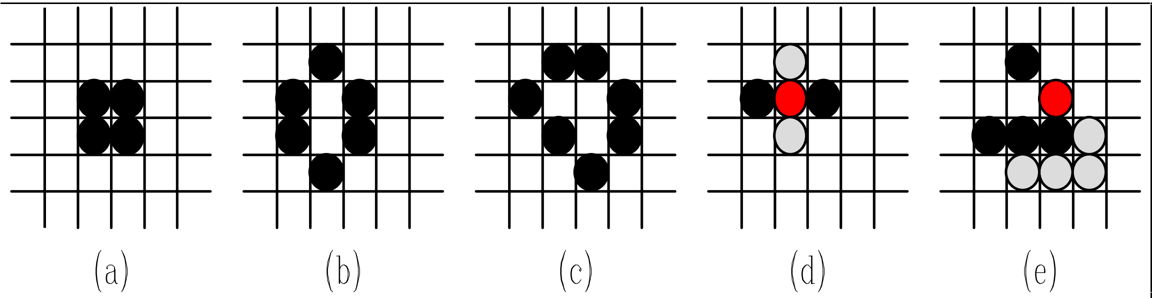


Figure 1.2: Some common recurring species in GL: the block (a) is stable, as are the beehive (b) and the loaf (c). The blinker (d) oscillates with period two (alternate configuration shown in grey) and the glider (e) moves one cell diagonally in four time steps (shown in light grey, the dark grey cell is occupied in both instances).

Later, researchers noticed that GL had more interesting features than just the complex animals which could be produced; its very evolution was something of a conundrum. For example, GL always seemed to stabilize to a particular steady state regardless of the initial configuration. These states are characterized by an average occupation density of roughly 3% and each has the same frequency of the species presented in Figure 1.2. Also, over the course of its evolution, a "nearly stable" configuration could unexpectedly flare up, disrupting the entire system. Many hours of computer time have been spent, the world over, watching--in a semi-hypnotic state--the intricate dynamics play out on a glowing phosphor screen.

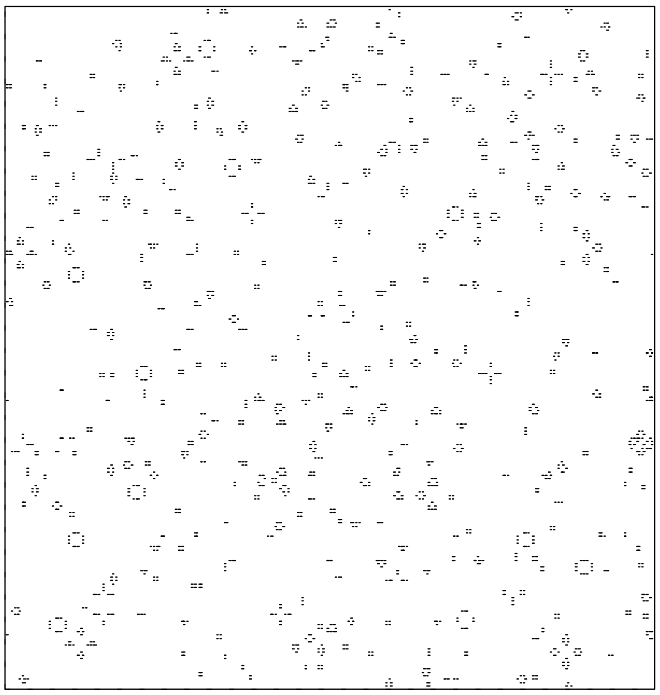


Figure 1.3: Sample stable GL configuration on a 256×256 lattice with periodic boundaries.

1.3. Self-organized criticality

1.3.1. The critical state

Phase transitions, in the context of thermodynamics, are well understood phenomena. The terminology of *order parameter,* a dependent variable which undergoes a "sharp" change, and *control parameter*, the variable which is smoothly adjusted to produce the change, is used to quantify the transition. In the case of first-order transitions (such as melting) the order parameter undergoes a discontinuity--it jumps to a new value. The jump is accompanied by an absorption or liberation of energy (latent heat). Usually, fluctuations within the substance can be ignored for first-order transitions.

To demystify the above definitions, consider a pot of water boiling at 1 atm and 100 °C. If we choose temperature as the control parameter then density could play the role of the order parameter. Below 100 °C water is a liquid with a relatively high density. Above this point, all the water is in the form of steam which has a significantly lower density. At the transition we observe fluctuations in the form of small, uniform steam bubbles. This is a first-order transition.

In contrast, second-order, or *critical*, transitions are characterized by a *discontinuity in the derivative* of the order parameter (see Figure 1.4). Further, near the transition point, properties are dominated by internal fluctuations on all scales. For example, let us revisit our pot of boiling water. We raise the pressure to 218 atm and the temperature to 374 °C (the critical point of water). Again, we observe steam bubbles but in this case the bubbles exist on all scales--from microscopic to the size of the pot itself [12, *p. 5*]. Also, the density (but not its derivative) is continuous across the transition.

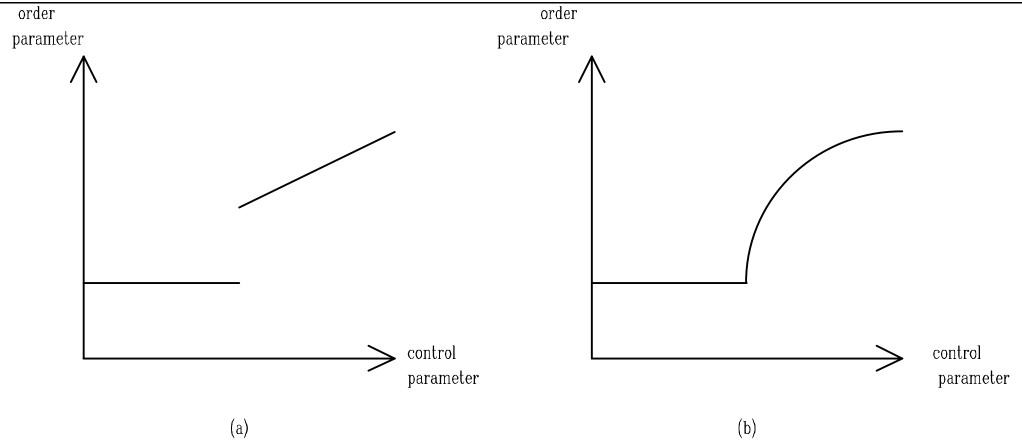


Figure 1.4: Sample phase transitions. A first-order transition (a) is characterized by a discontinuity in the order parameter, while a second-order (critical) transition (b) is discontinuous in the first derivative.

Near a critical point, many thermodynamic properties obey diverging power laws. Early studies of critical phenomena revealed that the characteristic exponents for the power laws clustered around distinct values for a variety of systems. This suggested that some of the features of separate systems were irrelevant --they belonged to the same *universality class*. Some of the irrelevant variables in a universality class are usually the type of local interactions, the number of nearest neighbors, *et cetera*. On the other hand, dimensionality and symmetry, for example, appear to be relevant variables--that is, change the number of dimensions or the symmetry laws and the system changes its class (or may even cease being critical). Critical systems with the same relevant variables but different irrelevant variables have the same critical exponents and are said to belong to the same universality class. If GL can be determined to be critical it may be possible to determine to which universality class it belongs, and hence, determine which variables are significant and which are not.

1.3.2. Self-organization

Many natural systems exhibit self-organizing behavior: the formation of waterways, the network of neurons in the human brain and the evolution of species are some examples. All these spatially extended systems are governed by local interactions, yet they produce interesting global structures. This is the essence of self-organization. Self-organizing systems generate extreme anisotropy from initial randomness. In contrast, a gas also interacts on a local level but in this case the interactions serve to disperse any inconsistencies, bringing the system to equilibrium. Self-organized systems are sometimes said to be *far from equilibrium*.

Often self-organization is called *antichaos* [13] because it appears to reduce entropy, violating the second law of thermodynamics. In fact, this is not the case as all systems exhibiting self-organization are driven by energy reserves. For example, the process of evolution on earth is driven primarily by radiant energy from the sun. However, it is possible to construct artificial models for which there exists no analogue for energy. Such systems can exhibit self-organization without an obvious source. As we will see, this is the case for GL.

1.3.3. Self-organized criticality

Self-organized criticality (SOC) is a merging of the two concepts above. Unlike the pot of water in the example above, for which we had to deliberately adjust the temperature and pressure to reach the critical state, SOC phenomena automatically approach the critical state without any fine-tuning of external parameters. Although it may seem rare and surprising, SOC actually appears to be fairly common in nature. It is seen in systems having self-similar fractal structures [14] and in dynamics with $1/f$ (or *flicker*) noise. Both these observed properties have been poorly understood in the past but now we simply see them as manifestations of the power law behavior seen in critical phenomena. In fact, spontaneously occurring flicker noise and fractal structures are the temporal and spatial fingerprints of SOC seen in the light from quasars, the intensity of sunspots, the current through resistors, the sand flow in an hourglass, the flow of rivers, stock market fluctuations, cosmic structures and turbulence [15 *and references therein*].

Early studies explained SOC in terms of conserved quantities [1,2]. In particular, exact results were achieved for a CA model of a sandpile in which the height of the pile obeyed a local conservation law. It was assumed that conservation laws were integral to SOC. Then Bak *et al.* [3] argued that GL also exhibited SOC. But, as we know, GL is completely artificial, and obeys no known conservation laws--local or global. It was argued that conservation was not a necessary property of SOC. But then doubt was cast upon whether GL was SOC after all. Bennett and Bourzutschky [4] suggested that the observed power law behavior was an artifact of the small system sizes explored in [3], and on larger scales GL is actually *subcritical*. Alstrøm and Leão [5] countered, arguing that the round-offs observed by [4] are boundary effects, and a finite-size scaling analysis demonstrates GL *is* critical. The issue is still not resolved. Since then, Hemmingsson [6] argued that the discrepancy in these results is a product of using different boundary conditions and measuring different statistics. His results agree with those of Bennett and Bourzutschky, that GL is not SOC.

In this paper we will explore whether GL is critical and if these conflicting analyses can be reconciled. We will also explore how GL responds to some variations of control parameters: whether it moves closer to--or further from--SOC.

2. Experimental Design

To study GL I needed a CA evolving program which was both fast and versatile. It must be capable of handling a variety of boundary conditions; changing the dimensionality and lattice size; recording either lattice configurations or just interesting statistics (to save disk space); detecting and perturbing stable states; starting from either random or specific initial lattice configurations; and perhaps most importantly, it must be adaptable to future unforeseen uses. Unfortunately, I could not find any commercial or public domain products that met all these requirements so I chose to design my own. The result is a program I have unimaginatively dubbed *CellBot*, the source code of which is included in Appendix A.

The source was coded on a personal computer running under MS-DOS. It was compiled and debugged on the same computer with Borland Turbo C version 2.01 and later with Borland C++ version 4.02. When sufficiently bug free the source was ported over to a Sun SparcStation running under UNIX where it was recompiled and further tested with Gnu C. Data acquisition runs were performed on four separate SparcStations. Both compilers comply with the ANSI C standard and the resulting source code should be very portable. CellBot should compile and run with any ANSI C compliant compiler in virtually any operating environment.

Graphical interfaces which allow the user to visualize the CA as it evolves are common among this type of program. However, I found it necessary to forgo this feature for the sake of portability. Instead I chose to make the data for a visual display available by recording all live cells in an ordinary text file accessible by a graphing program (I use GnuPlot). One practical advantage this has is that it allows the user to *back up*. Many CA (including GL) are time-irreversible: that is, multiple (degenerate) lattice configurations can evolve to the same particular configuration in a single time step. Unlike some other products, this set-up allows the user to travel back and forth through the time line. Nevertheless, it would be gratifying to have a separate viewer program, optimized for each operating environment, which directly read these data files and graphically represented the system. It has been my personal experience that many subtle *bugs* can be revealed by simply watching the system evolve. For example, the evolution must obey the symmetries imposed by the transition rules (GL has a four-fold rotation and reflection symmetry)--watching the lattice break symmetry constraints is the simplest way of discovering *bugs* in the program. Perhaps the reader would be interested in developing a viewer.

2.1. CA Subrules

CellBot can apply two separate subrules in each step of the CA's evolution. The first is the standard local CA rule, mentioned above in the Introduction, applied synchronously. The second, inspired by epidemic models [16], describing the motion of individual cells, is applied sequentially.

2.1.1. Standard CA subrule

This subrule is described in the Introduction and Eq. (1.1). As it stands, CellBot only accepts totalistic rules of the form given in Eq. (1.3). I have added one minor extension, however. Each cell is selected for updating with some probability *s*, which is defined in the rule file. If s=1 then the system is synchronous, but as s approaches zero fewer and fewer cells are updated in each round. In the limit $s \to 0$, we effectively have a completely asynchronous system.

We can call the evolution asynchronous if no neighboring cells are updated in the same time step. The probability of a specific cell and any of its $|\aleph|$ neighbors being updated is given by the standard binomial expansion:

$$\begin{aligned}\Pr(\text{cell \& neighbors}) &= s\sum_{i=1}^{|\aleph|}\binom{|\aleph|}{i}s^i(1-s)^{|\aleph|-i} \\ &\cong |\aleph|s^2\end{aligned} \tag{2.1}$$

for small *s*. This is true for all of the *N* cells in the system. If, on average, less than one *synchronous update* occurs per time step then the system is effectively asynchronous. This suggests the system is effectively asynchronous if $s < s_{async}$ where

$$s_{\text{async}} = \sqrt{\frac{|\aleph|}{N}}. \tag{2.2}$$

Let us consider as an example GL ($|\aleph| = 8$) on a 256×256 lattice. Then, the evolution should be effectively the same as a completely asynchronous system if $s < s_{\text{async}} = 0.01105$. However, it will be much more efficient than a truly asynchronous evolution because, on average, 724 cells will be updated with each step. We must be careful with terminology here: the rule itself is *deterministic* as discussed in Section 1.1, however, because it is not applied uniformly, the global evolution may not be deterministic if *s*<1.

2.1.2. Mixing subrule

The second subrule allows the extension of CellBot to population models where the motion of the individuals is an important factor in the global evolution such as epidemic models [16] and population dynamics models [17]. After the standard CA subrule is applied a fraction, *m*, of *live* sites are randomly moved to new (previously *dead*) positions. Each cell can be moved only once.

The new position is randomly selected from all sites which lie within a distance R_m for each degree of freedom. Note this restriction generates a cubic bounding box rather than a spherical shell so that the number of available sites is

$$N_m = (2R_m + 1)^d \tag{2.3}$$

where d is the dimensionality of the lattice (assuming there is no interference from the boundaries). In this way, range of motion can be smoothly extended from *short-range* ($R_m = 1$) to *long-range* ($R_m = L$, the length scale of the lattice).

CellBot allows for two methods of moving a cell. The first method simply uses a uniform deviate to jump to a random new location within the above mentioned region. It is computationally efficient but may not describe natural motion very well. Occupied or out-of-bounds sites are not allowed, if an illegal site is chosen a new site is randomly chosen. Note that the original site may be selected resulting in a *null* move. It is important to consider under what circumstances this effect becomes relevant, or even dominant. The probability of an illegal site being chosen in any single attempt is just the average occupation density, $\bar{c}$ (neglecting boundary effects). The probability of a null move on each attempt is $\frac{1}{N_m}$ and the probability of i failed moves followed by a null move is $\frac{1}{N_m}(1-\frac{1}{N_m})^i \bar{c}^i$. Hence, the effective mixing fraction is scaled down by the fraction of null moves:

$$\begin{aligned} m_{eff}^{jump} &= m\left[1 - \tfrac{1}{N_m}\sum_{i=0}^{\infty}(1-\tfrac{1}{N_m})^i \bar{c}^i\right] \\ &= m\left[1 - \frac{1}{N_m(1-\bar{c})+\bar{c}}\right] \end{aligned} \tag{2.4}$$

by the geometric series. As an example, let us consider GL ($\bar{c} = 0.03$) with short-range mixing ($N_m = 9$). In this case, $m_{eff}^{jump} \cong 0.885m$.

The other method of mixing uses a random walk of R_m steps. In each step a new site in the current site's neighborhood, $\aleph$, is chosen. Note that CellBot allows the user to configure the neighborhood in any way, the sites need not even be contiguous or symmetric. This fact, and the fact that the probabilities for motion in orthogonal directions are not independent, make this random walk problem difficult to analyze. Hence, we make the leap of faith that the results for the paradigmatic one-dimensional random walk problem [18, *pp. 7-24*] apply here as well. This tells us the root-mean-square distance traveled in a random walk is proportional to the root of the number of steps so we can determine the *average* distance a cell will be moved:

$$d_m^{walk} = r_{step}(\bar{c})\sqrt{R_m} \tag{2.5}$$

where we define the average distance moved in a single step as

$$r_{step}(\bar{c}) = \frac{1-\bar{c}}{|\aleph|+1}\sum_{\mathbf{x}\in\aleph(\mathbf{0})}|\mathbf{x}|. \tag{2.6}$$

The $1-\bar{c}$ factor arises because a cell will not move into an already occupied site, and the denominator is incremented by one because the *null* move is allowed. For GL this definition gives $r_{step}(0.03) = 1.0408$.

The classical random walk also predicts that the probability distribution will have a Gaussian form with a $(\sqrt{2\pi}\sigma)^{-d}$ prefactor where the standard deviation, σ, is equal to the root-mean-square distance travelled. The probability of no net movement is just this prefactor so we can estimate the effective mixing fraction by scaling it down by the probability that no net movement occurs:

$$m_{eff}^{walk} \approx m\left[1 - \frac{1}{\left(2\pi R_m\right)^{d/2}}\right]. \tag{2.7}$$

Of course, this estimate needs to be taken with a grain of salt, and has no numerical worth in itself. A better result would be obtained by determining the probability distribution explicitly for the particular geometry one wishes to study. However, this information would be of minimal use in this paper so it is left as an exercise for the reader. (I've always wanted to say that!)

The random walk method may seem preferable because it seems more natural, but there are instances when the jump method is preferred. For example, the average distance moved via the *jump* method for *long-range* mixing on a square lattice of side L is $d_m^{jump} = \frac{\sqrt{2}}{3}L$. To achieve this range with the walk method would require

$$R_m = \frac{2L^2}{9r_{step}(\bar{c})} \tag{2.8}$$

or, on a 256×256 lattice, 14,564 steps. Obviously, this would greatly reduce program performance. The random walk method is best suited to shorter-range motion.

In both cases above, the results are slightly complicated by the fact that the dynamics, and hence the average occupation density, depend on the mixing fraction, *m*, so that $\bar{c} = \bar{c}(m)$, as we will see in the next section. Hence, the numerical values of m_{eff} given may be inaccurate. However, this is not a serious problem as $\bar{c}$ can be determined experimentally and the resulting values used in the above formulas. Also, in the derivations we assumed uniform probability densities when we know GL exhibits extreme spatial inhomogeneity. As we will see, though, mixing has the effect of randomizing the distribution and inducing uniform probabilities, so this should be valid for $m \neq 0$.

2.2. Boundaries

Computer models are obviously incapable of modelling systems in the thermodynamic limit--finite boundaries must always be imposed. However, often by choosing appropriate boundary conditions edge effects can be nullified. For example, by applying *periodic* (or *toroidal*) boundaries the evolution resembles the infinite system provided the correlation length does not exceed the size of the system. Unfortunately, the correlation length diverges at a critical point. Hence, the dynamics are dominated by edge effects produced by fluctuations which span the lattice. Knowing GL might be critical it was very important to have a great deal of control over boundaries in CellBot.

For this reason I chose not to use an obvious array structure for the lattice space, but rather CellBot stores the information for each *live* cell in a *hash table* [19]. A hash table is a structure much like a *list* except that it is optimized for speed. The hash table allocates and frees memory dynamically so the only constraint on system size is imposed by physical memory. This technique makes it easy to configure different system sizes for each run, and in fact, even the dimensionality can be configured. For sparse lattices (as in GL), this design also offers a performance advantage because fewer cells need to be updated in each step of a run. Note that the choice of rules in CellBot is constrained by this design. Since CellBot ignores dead sites with all dead neighbors it is imperative that the transition rule maps these configurations to dead.

Boundaries are imposed artificially by inserting the appropriate cells beyond the bounds of the system before each update. In the current version of CellBot, boundaries are simply defined by minimum and maximum coordinates (inclusive). A variety of boundary types can be chosen and even intermixed. For example, periodic boundaries in one dimension can be mixed with reflective boundaries in another (see Figure 2.1). Corner disputes are managed by assigning priorities to the various boundaries; the side with the highest priority imposes its boundary type on the corner. Currently, CellBot supports cold (all cells beyond border are *dead*), hot (a fraction, *h*, of cell's beyond the border are *alive*), periodic, reflective, and even no boundaries.

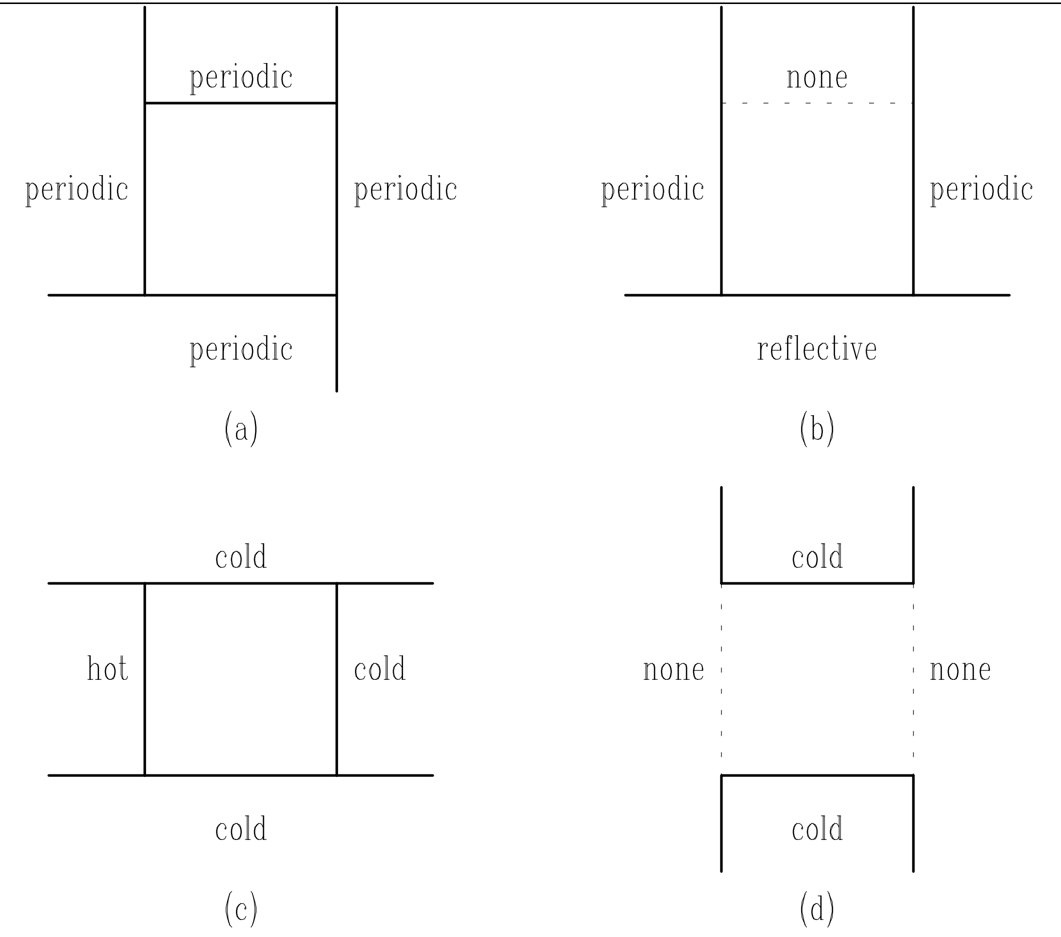


Figure 2.1: Sample boundary conditions on a two-dimensional lattice demonstrate CellBot's versatility: periodic boundaries (a), bin with reflective bottom (b), heat source from side (c), and peep-hole (d).

That boundaries can be eliminated altogether greatly enhances CellBot's potential. Systems can grow or decline as they evolve without being distorted by any edge effects. Of course, if the system grows too large the sheer number of cells will overload the computer's memory. In theory the system size is also constrained by the capacity of the *integer* data type. Coordinates are labelled with integers so when the positions reach the limits of this data type (2^{16} on PCs and 2^{32} on SparcStations) they are subject to the computer's overflow error. In practice I have found that PCs and SparcStations respond by wrapping the integers to the extreme opposite value. Hence, on these machines "no boundaries" effectively means *periodic* boundaries with a length scale of L=65536 and L=4294967296, respectively. My data-gathering runs were all performed on SparcStations at a rate on the order of ten time steps per second. At this rate, the effect of the boundaries would not be felt for some ten years, well beyond the period of this project, making this system effectively infinite.

When implementing different boundary combinations it is best if unbounded edges receive the lowest priority (as in Figure 2.1(b)). A bug in the program may prevent submissive hot, periodic, and reflective boundary types from behaving in the expected manner along these edges. One could not, for example, impose boundaries simulating two large reserves separated by a small peep-hole, like that in Figure 2.1(d), unless it was with cold boundaries.

CellBot is biased towards rectangular lattices by the boundary conditions. When studying other geometries, like triangular neighborhoods, it is best not to impose boundaries for fear of introducing some artifact of this bias (see Figure 2.2). In particular, periodic boundaries will behave very poorly, associating cells on opposite edges with sites the user may not expect. This defect is not a problem here, because GL lies on a rectangular lattice, but it should be remedied for future research.

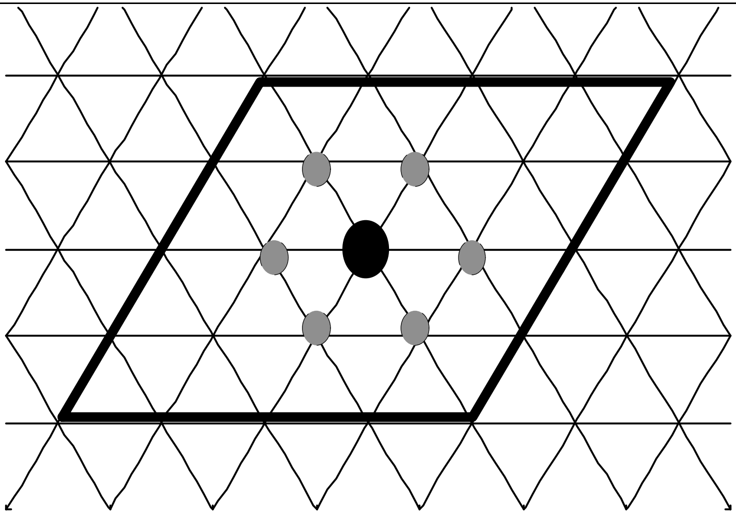


Figure 2.2: Example of rectangular bias imposed by boundaries (thick black lines) on a triangular lattice. The central cell (black dot) is surrounded by six neighbors (grey dots).

2.3. Perturbations

CellBot was generally designed around the following sequence of events:

(A) generate random configuration;

(B) apply boundary constraints;

(C) advance lattice;

(D) record relevant information;

(E) if stable then perturb; and

(F) repeat steps (B) through (E) until stop requested.

As we have already seen CellBot can handle this simple loop and a great deal more. At this point I would like to discuss the particulars of Step (E). First, we need to understand what stability is and how it is recognized.

As an avalanche passes through a region, it leaves in its wake simple stable or periodic species like those seen in Figure 1.2. When the avalanche has completely died, the entire lattice is occupied with these animals. As such, the lattice as a whole, is in a periodic pattern. We call such a configuration stable. In practice, naturally occurring configurations tend to have very short periods, typically from two to six time steps.

To detect stable states one usually uses a moving window to compare the current lattice with those for the last $p_{\max}$ time steps. This allows for the detection of periodic configurations with periods up to $p_{\max}$. This method suffers from two drawbacks: firstly, the memory consumed by the storage of the lattice history may be enormous. Secondly, comparing two lattices for a match site-by-site would significantly reduce system performance. I chose to implement a slightly different method. Instead of a moving window of lattice configurations, I merely store, in a moving window, a particular statistic which is very sensitive to the lattice state. It is important that the statistic of choice is not easily reproducible by different configurations in order to minimize the chance of the program erroneously declaring the lattice stable. Further, the history contains the last $2p_{\max}$ values of the statistic and requires the entire sequence to match before admitting the lattice is stable. The chance of a false positive is negligible (I have never encountered one in any test runs). I have chosen for the statistic the *activity* of the lattice, defined as

$$S(t) \equiv \sum_{\mathbf{x}} \left| s(\mathbf{x},t) - s(\mathbf{x},t-1) \right| \tag{2.9}$$

which is just the count of births and deaths which occurred in the last transition. This quantity is computed by the program anyway, so it requires no extra computer time.

One consequence of using activity to determine stability is that gliders can escape detection. Since they translate one site diagonally in four time steps, gliders are not strictly periodic. Nevertheless, for many situations, one would like to consider them just that. For example, if a glider is traveling away from the general population in a direction which is unbounded, it may well continue forever. A stability detection scheme which did not account for this possibility would generate an infinite loop, never declaring the lattice stable. Since gliders, have a periodic activity count, however, they are determined to be stable with my method, avoiding this trap.

Once CellBot determines a configuration is stable, it tries to incite activity by perturbing a single site. The site can be either *dead* or *alive*, the perturbations flips it to the contrary state. The result is an avalanche as the lattice tries to recover from the disturbance. The perturbation site is recorded in the data file. Actually, perturbations can be applied at regular intervals, not just after the system has stabilized. The latter choice is equivalent to setting the perturbation rate to zero.

As mentioned above, the perturbations implemented are of the form of a reversal of a single site. Other kinds of perturbations may be useful, as well. For example, constructing gliders and sending them into the system provides a method of perturbation which has the advantage of conforming to GL's rules. A single site perturbation violates these rules by spontaneously creating or destroying a cell. A glider, however, could be interpreted as coming from a source at a very large distance, hence, it is consistent with GL's rules. It is not clear whether this or other types of perturbations would modify the dynamics, but they are not implemented in this version of CellBot.

Perturbations will be discussed in more detail in Section 3.2.1.

3. Finite-size scaling

3.1. Introduction

Science in general, is divided into a number of subjects. At first look these subjects may seem unrelated: physics is distinct from biology which is distinct from chemistry, *et cetera*. A better interpretation, however, perhaps may view the separate fields as layers surrounding a central core--like the layers of an onion. These layers are separated by *complexity barriers*, At the core lie the "theories of everything" which attempt to describe all the fundamental interactions in physics. Perhaps the next shell contains the Standard Model of sub-atomic particles. Beyond this we find chemistry, dealing with atoms and molecules. Jumping to the next layer we might find biochemistry, the study of complex molecules like proteins and how they interact. Continuing on our biological bent, we expect to find cellular biology and the study of unicellular organisms. This layering interpretation can be extended indefinitely to include (almost) all science. But what separates these layers? The answer is *complexity*. While in principle it may be possible to describe biomolecular processes in terms of quarks and gluons, in practice it is impossible because of the sheer volume of interacting particles which make up each protein. Having a "theory of complexity" which allows one to reliably extend the basic principles of a fundamental theory to a higher level, at least in isolated cases, could be very advantageous. Any such theory would serve as a link between theories on two successive levels, and by verifying a known phenomenon, would strengthen both theories.

One may wonder why we are interested in GL at all. It has no basis in reality. While it is true GL generates interesting dynamical patterns it doesn't tell us anything about ourselves or the world around us. Or does it? GL is an example of a complex system arising from simple local interactions. There are many natural phenomena with the same criteria. Perhaps, if we can make some headway in exploring GL then the techniques we discover can be adapted to more complex natural systems. GL can serve as a litmus test for theories of complexity--both analytic theories and computer simulations. Until we have made some headway in the investigation of the *Game of Life* we can not expect to understand the complexities of life.

In essence, GL is simply a many-body system with local interactions. There are many exact and approximate methods of solving many-body problems so one may suspect that analysis would be a fairly simple procedure. However, on closer inspection we see that many of the tools at hand are inapplicable for one insurmountable reason or another. One of the main problems for analysis is the lack of a local conservation law. The sandpile model was solved exactly via renormalization-group calculations precisely because of the local conservation law [2]. Further, with a conserved quantity it would be possible to construct a free energy and a Hamiltonian. This would greatly enhance the range of tools at our disposal. Other peculiarities of GL (like the fact that it is deterministic, not stochastic) invalidate other potential tools. The most successful method for studying GL has been to search for the characteristic power law behavior of thermodynamic quantities near a critical point.

Just like the pot of boiling water at the critical point had bubbled of all sizes, critical system are characterized by events of all sizes. The frequency distribution of these events scales as a power law of the size. One fairly simple way to determine if a system is critical is by directly searching for the characteristic power law behavior in some global quantity of the system. We will apply this as our first angle of attack. A simple and effective quantity to explore in GL is the size of an avalanche (or time required to re-stabilize) arising from a perturbation. The basic algorithm runs as follows:

(A) randomly seed lattice, wait for stabilization;

(B) perturb lattice and wait for re-stabilization;

(C) record stabilization time;

(D) repeat (B) and (C) until sufficient statistical population acquired.

When a good statistical data set has been collected the points are grouped by size and the resulting distribution is compared to the suspected power law.

3.2. Considerations

At this point it may seem a simple procedure to make a few thousand runs, get a nice statistical distribution, and test the power law distribution, but in fact, there are a few details which first require our attention.

3.2.1. Perturbations

We must be careful the nature of the dynamics does not arise from the particulars of the perturbation algorithm, but from some intrinsic property of the system itself. Following example [3,20,4,5,6], we implement perturbations by choosing a random site and flipping its state from *dead* to *alive* or vice versa.

There are two points of consideration here. Firstly, notice that GL has a lattice occupancy of about 3%. If we chose our perturbation site completely randomly then the chance of choosing a *dead zone* (a *dead* site surrounded by all *dead* neighbors) is roughly $0.97^9 \cong 0.76$. But GL's rules tell us such a perturbation will result in a *flip-fail* (the lattice immediately reverts back to its original configuration) and the avalanche will be recorded as having lifetime one time step. This will not adversely affect the shape of the frequency distribution, but it will produce a large spike at the low end, completely obscuring any true data for avalanches of size one. Hence, it would be necessary to ignore the low end when analyzing the distribution. The only real problem here is that this leaves us with only 24% of our original data for analysis. It would be more efficient if we could choose our perturbation sites more effectively in order to minimize flip-fails. This is what I have done. I choose a perturbation site from a list of all live cells and those sites in their collective neighborhood. This guaranties the perturbation site will always have at least one live cell in its neighborhood--generating roughly a four-fold increase in productive data.

The second issue of concern also relates to the location of the perturbations. There is a possibility that the evolution of an avalanche depends on the depth of the locus within a cluster. That is, perturbations on the surface of a cluster may evolve differently than perturbations within the body. To test this I compared the lifetimes of avalanches to their locus, the perturbation site. To avoid boundary effects I analyzed data from a GL run that lacked boundaries (see Section 3.12 for more details on this run). Plotting the lifetimes of perturbations against the radial distance of the perturbation sites from the center of mass, a flat line would indicate that the avalanche dynamics were independent of the depth of the perturbation site. Of course, suspecting that GL may be critical we know that there may be a large deviation in avalanche sizes, even for very similar perturbations. Indeed this is what the plot revealed so I needed a smoothing technique which would reveal the underlying average behavior. I chose to use a numerical integration which smoothes nicely, but has the effect of converting flat lines into straight lines with non-zero slopes. The results are shown in Figure 3.1. The x-axis represents the radial distance of the perturbation site from the center of mass scaled by the characteristic length of the system, *L* (defined in Section 3.12.1), and the y-axis represents the integral of the perturbation lifetimes. Notice that, for perturbations within about 10*L* of the center the plot fits a straight line fairly well suggesting that, in this region, avalanche dynamics are independent of the perturbation site--there do not appear to be any surface effects complicating the picture. (It appears that for avalanches very near the center, within 0.3*L*, there is a slight decrease in avalanche activity. It is unclear whether this is a significant effect or simply a statistical fluctuation. In any case, the deviation is slight, so I will call no further notice to it.)

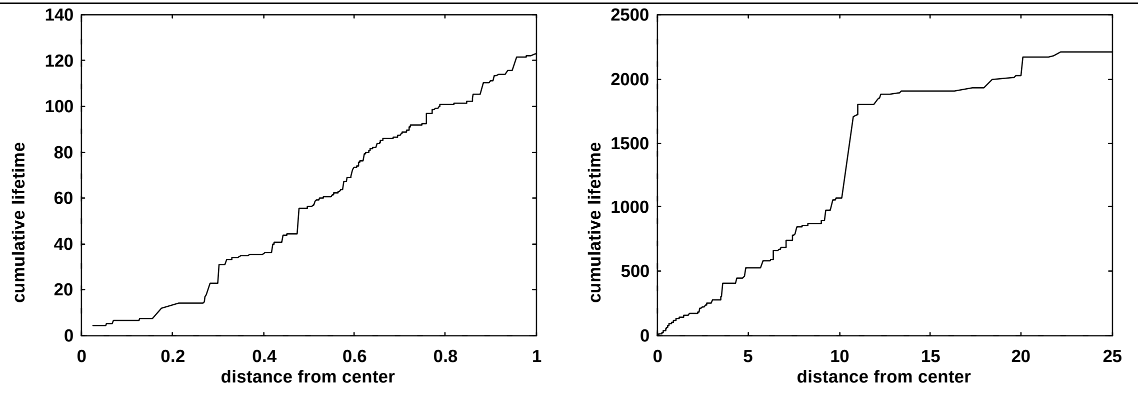


Figure 3.1: Numerical integral of avalanche lifetimes plotted against radial distance of locus from center of mass. Distances are scaled to the characteristic size of the system. The relatively straight line in (a) indicates avalanche lifetimes do not depend on the perturbation site, at least up to the size of the system. On scales much larger than the system (b) avalanches do appear to be affected by the perturbation site, but the results are not statistically reliable.

Beyond this length scale, however, the figure implies there are some surface effects. This is not necessarily the case as the results in this region are statistically unreliable. Most live cells reside in clusters near (within radius L) of the center. Hence, perturbations using the method described above will occur with dropping frequency beyond the system size. For very large radii the perturbations are few and far between. More data points may smooth out the plot shown in Figure 3.1(b) or, on the other hand, they may reveal more interesting dynamics. Perhaps this area is worth further study but most of the systems studied in this paper will be bounded so I will leave it be.

3.2.2. Transient length

When starting a run the lattice is initially seeded with a random population (usually with density 0.5). The system evolves to a stable state and is perturbed at a single site. As the process is repeated, the system evolves into a statistically stationary state, which does not depend on the initial configuration. The properties of this state are the object of our investigations. As such we must consider the possibility of a *transient*–an intermediate behavior as the system slowly obscures information regarding the initial configuration (remember, GL is *irreversible*). Some artifact of the seed may remain for many perturbations after. For example, the spatial distribution of species may be more uniform initially, but become more clustered in the statistically stationary limit. When analyzing GL we would like to skip the polluted data from this *transient period*.

If there is a transient period it should be observable by looking at the evolution of some statistical property (order parameter) of the run. Figure 3.2 shows the temporal (measured by the number of perturbations) evolution of the number of live sites. The raw data is smoothed via a "moving window average" in which each point is average with the first 128 points on either side. The figure suggests that there is no transient period, whatsoever. That is, the system reaches its limiting behavior immediately upon settling down from the initial seed. This is good news because it means all of our acquired data is available for analysis.

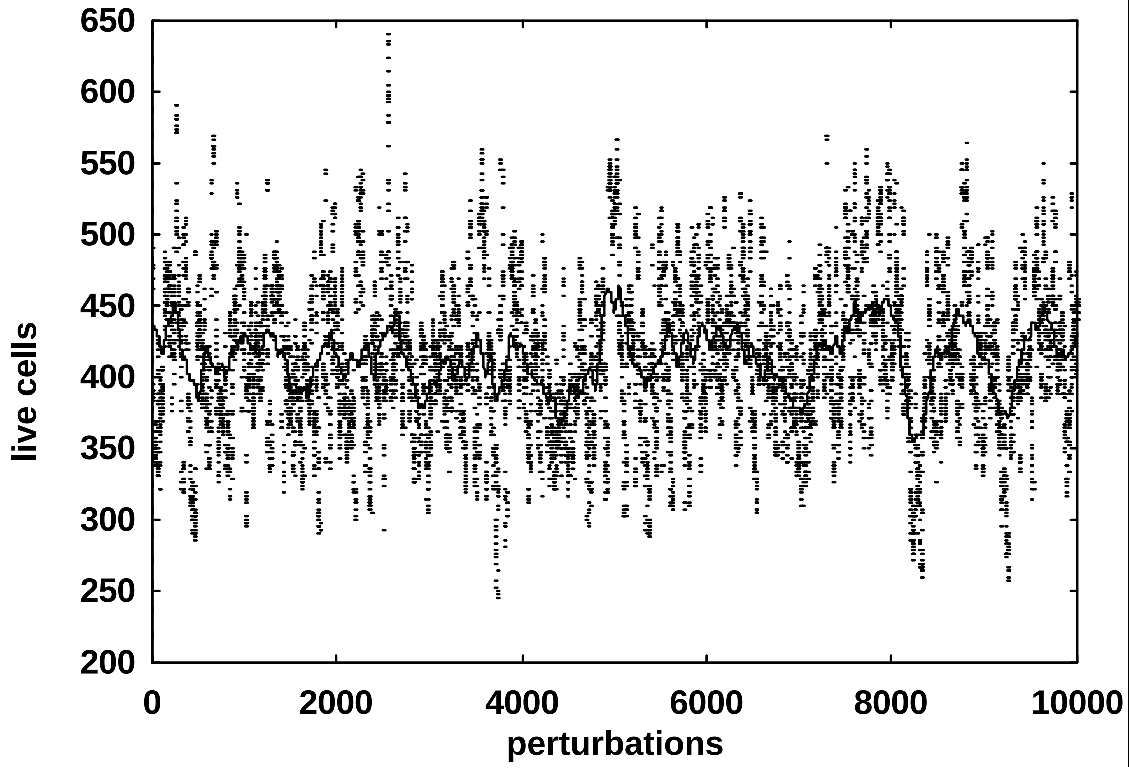


Figure 3.2: Demonstration that GL exhibits no transient behavior. The points show the evolution of the number of live cells over time (perturbations). The line represents a moving window average of width 257 points. Results are for a 128×128 **periodic lattice.**

3.3. Critical exponents: variable-width bins

We are now in a position to test GL for critical behavior. As mentioned above, we are interested in the frequency distribution of avalanche lifetimes, *t*. If GL is SOC the frequencies of lifetimes should decay via a power law with the lifetimes

$$D(t) \propto t^b \qquad \textbf{(3.1)}$$

where *b* is called a *critical exponent*. (We expect *b*<0.) The power law behavior can be seen by plotting the distribution on a log-log graph, so that the power law is mapped to a straight line with a slope *b*. For statistically stable results a great deal of data points is required. I found a typical run containing ten thousand avalanches produces a sufficiently smooth distribution. In the following runs I employed periodic boundary conditions.

Such a run is plotted below in Figure 3.3. Notice the long tail for large avalanches. These points represent extremely large avalanches which occur very rarely (each has a frequency count of one). The raw plot exaggerates these features because it neglects the fact that these points are very sparse and are separated by counts of zero frequency (which are mapped to negative infinity on this graph). To derive meaningful results from this region we need to apply some sort of averaging technique.

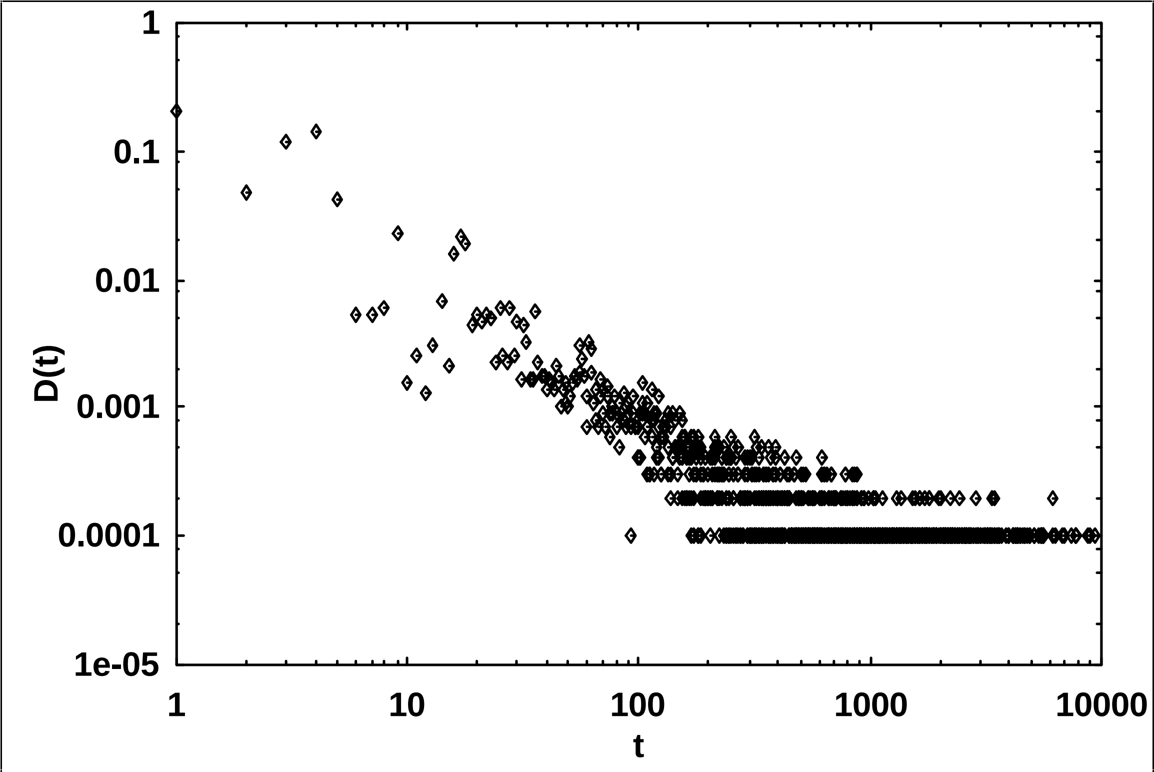


Figure 3.3: Example of a (normalized) raw frequency distribution. The long tail introduces a bias which would influence the critical exponent in an attempted power law fit. This data comes from a 128×128 lattice with periodic boundaries.

One common way of averaging the results is by grouping neighboring values into fixed-width bins such that each bin contains a count of at least one. This does smooth the tail but severely obscures the data for small and intermediate avalanches. Based on this method, I have developed a simple method that preserves the precision in this region and also accurately smoothes out the tail end.. The trick is to use variable-width bins, each of which contains only one data point (x_i, y_i). The *i*'th bin is scaled by the width of the bin, w_i

$$b_i = \tfrac{y_i}{w_i} \tag{3.2}$$

where

$$w_i = \frac{x_{i+1} - x_{i-1}}{2} \tag{3.3}$$

is the distance between the halfway points before and after the current point. This effectively averages y_i with the surrounding "zeroes". The effect is demonstrated in Figure 3.4, below.

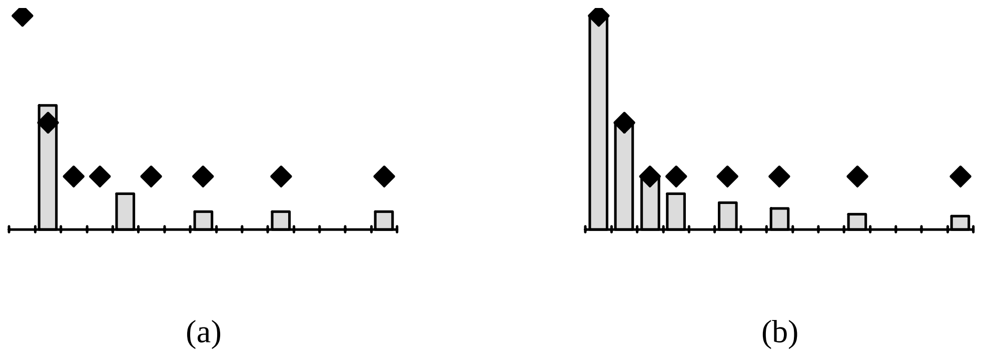


Figure 3.4: Demonstration of two methods of grouping data (points) into bins (bars). Constant-width bins (a) don't work well with irregularly sampled data, losing significant information. Variable-width bins (b), however, preserve the tightly packed region as well as accurately smoothing the sparse region.

Using this grouping method on the data in Figure 3.3 reveals the distribution's underlying power law behavior (dots in Figure 3.5). The graph also shows a line which represents the data smoothed with a low-pass Savitsky-Golay smoothing filter [7]. This filter fits each data point and the nearest 32 points on either side to a polynomial of degree one (a straight line) via a linear least-squares fit on the log-log graph . Fitting this curve to a straight line on the log-log scale may impose an artificial bias towards a power law so the resulting smoothed data is used subsequently only for graphing purposes. For calculations the binned (but not smoothed) data is used.

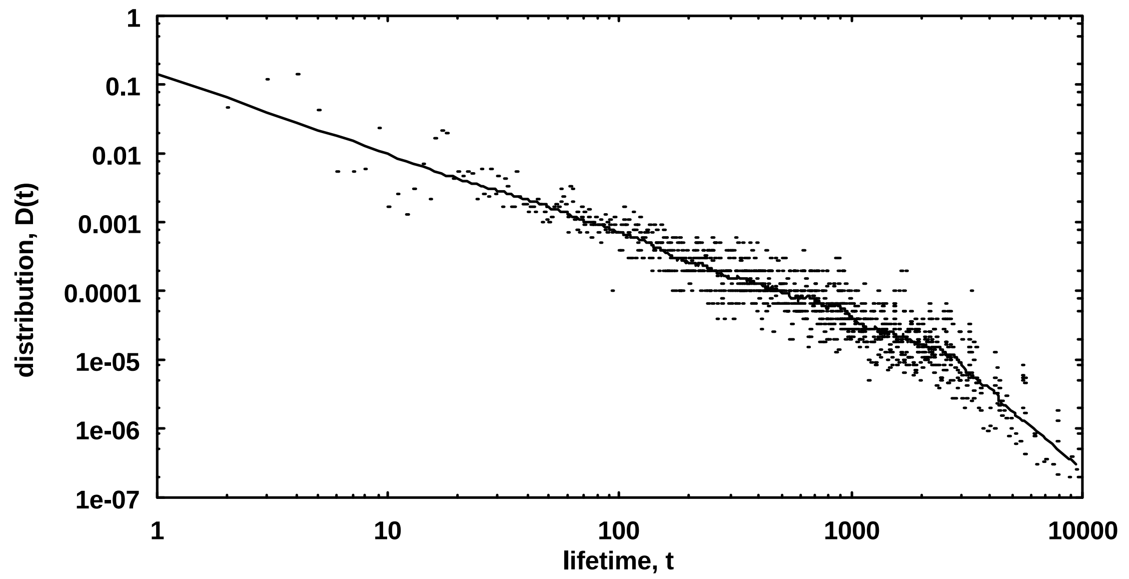


Figure 3.5: Binned lifetime distribution for 128×128 **periodic system (see Figure 3.3). The line represents the smoothed data using a Savitsky-Golay (32,32,1) filter. Notice the drop-off for large avalanches.**

Notice, contrary to the raw plot (Figure 3.3), there appears to be a decay from the power law behavior at large time scales. This deviation has been observed by others [5,6] and is central to the problem of whether GL is critical. As such I am confident it is not an artifact of my averaging method. At this point we assume the deviation is due to the relatively small lattices explored. To estimate the best power law fit, then we must ignore the tail, discarding t>1000.

We also expect the extremely small time scales to cause problems. At this scale the discreteness of the time steps may interfere with the natural distributions of lifetimes. Hence, as a precaution, we also discard data for t<20. As it stands, this should make little difference in the calculations, as these are only 20 points out of some thousands.

Barring these constraints, the plot does indeed seem to fit a power law distribution. The only other point to consider is that the results shown are for a single run on a lattice with a particular length. If GL is critical the above results should hold true for any reasonably sized lattice, and further, the power law parameters should be independent of the lattice size. To test this, a series of runs with differing lengths were analyzed and the results are shown in the figure below. Indeed, the data does appear to conform with a power law distribution, at least within the range mentioned above. In this region the average critical exponent (see Eq. (3.1)) is estimated to be $b = -1.175 \pm 0.012$.

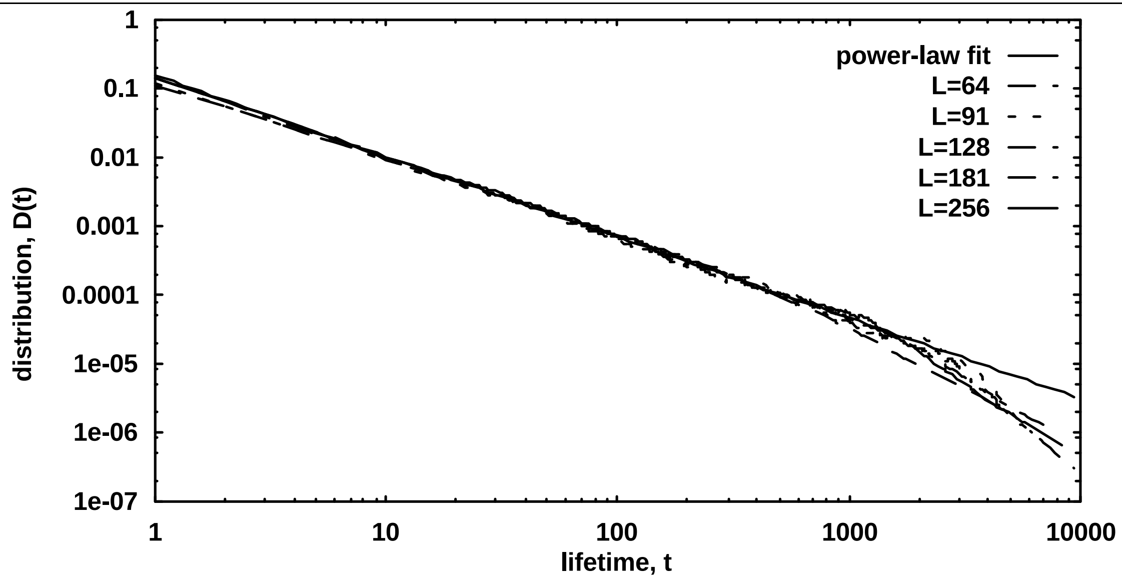


Figure 3.6: Overlapping plot of lifetime distributions for $L \times L$ periodic lattices. The data has been smoothed with a Savitsky-Golay smoothing filter (32,32,1). The average power law fit critical exponent (computed between t=20 and t=1000) is b=-1.175±0.012.

Two previous measures of this quantity gave $b \approx -1.6$ [3] and $b = -1.41$ [5]. It is odd that none of these values agree very closely. It appears Bak *et al.* [3] did not exclude either the low end of the distribution, which is polluted by discreteness, or the high end of the distribution, which is polluted by finite-size effects, when estimating their critical exponent. Further, they only explored lattices with cold boundaries up to 150×150, which may suffer from extreme corrections to scaling. This may account for the discrepancy seen with their result. Alstrøm and Leão [5], however, corrected for both aberrations and they tested lattices up to 1024×1024. The only difference is that they, too, applied cold boundaries, but I am hesitant to attribute the difference in our critical exponents to this fact. This discrepancy hinted that something deeper may be occurring, and it led me to apply another method for determining the critical exponents.

3.4. Critical exponents: cumulative distribution

The disagreement noted above suggested that there may be a flaw in my technique. It was first suspected that the problems arised from a nuisance parameter in the fit. When fitting the binned data to a power-law there are three variables which must be adjusted to get a good fit: the critical exponent (slope, b), the normalization factor (y-intercept), and the high-end cutoff (which we set to 1000). Of these we are only interested in the exponent, b. The other variables are termed *nuisance parameters* because they must be properly adjusted when fitting, but are discarded afterwards. Because a model involving fewer adjustable parameters is considered to have more validity, nuisance parameters impair the confidence one has in a model.

It was proposed that the normalization factor, a nuisance parameter, may be unduly influencing the parameter of interest, the critical exponent. For example, the normalization factor may be estimated too small, decreasing the estimated slope. (In fact we will discover the problem lies elsewhere, I only want to relay the historical development of the new method here.) It is possible to discard the normalization factor with a simple adjustment: instead of analyzing the lifetime distribution, we analyze the cumulative distribution of lifetimes, $C(t)$. The cumulative distribution is defined as the fraction of avalanches *larger* than (or equal to) some lifetime, t:

$$C(t) = \sum_{t' \geq t} D(t') \,. \qquad \textbf{(3.4)}$$

By this definition, $C(1) = 1$ because $D(t)$ is normalized. Hence, we have eliminated one of the nuisance parameters by setting it to one. Another advantage of working with the cumulative distribution is that it acts as a smoothing function, reducing the noise seen in the original distribution. Further, the cumulative distribution is compiled from the original data (see Figure 3.3), not the binned data which has come under suspicion. These attributes make the cumulative distribution an ideal candidate for analysis.

3.4.1. Finite-scaling preview

In the following analysis the determination of the critical exponent is integrated with estimation of finite-size effects. It is necessary to introduce the reader to the concept of finite-size scaling. We assume the distribution of lifetimes in the finite system (Eq. (3.1) represents the infinite system) can be written as

$$D_L(t) \propto t^b f\left(t/_{t_c(L)} \right) \tag{3.5}$$

where *f*, the *scaling function*, obeys $f(x) \to 1$ for *x*<<1 and $f(x) \to 0$ for *x*>>1. This form was originally hypothesized in 1969 and has been used successfully in many cases to extrapolate systems near a critical point [12 *and references therein*]. The *critical lifetime*, t_c, which depends on the system length, *L*, represents the avalanche size above which dynamics are dominated by finite-size effects (boundaries). (The assumption is that longer-lasting avalanches are more likely to interact with the boundaries.)

The cumulative distribution, then, also obeys a finite-scaling law of the form

$$C(t) = t^{1+b} g\left(t/_{t_c} \right) \tag{3.6}$$

where the scaling functions *f* and *g* obey the relation

$$f(x) \propto (1+b)g(x) + xg'(x)\,\textbf{.} \tag{3.7}$$

Notice the equality symbol in Eq. (3.6), indicating we have eliminated the nuisance parameter. Without loss of generality (because the scaling function is strictly positive) we can write *g* as an exponential:

$$g(x) = e^{h(x)}\,\textbf{.} \tag{3.8}$$

The goal is to fit the data to the simplest possible form of *h*. To determine the form of *h* we expand it in a Taylor polynomial:

$$h(x) = h_0 + h_1 x + \ldots\,\textbf{.} \tag{3.9}$$

But we know, from the restriction $C(1) = 1$, that $h_0 = 0$.

We wish to fit the cumulative distribution to the finite-scaling law where the scaling function has the form indicated above. As mentioned above, we prefer to have the fewest possible parameters in our model. As a first attempt, then, we truncate the Taylor expansion at the first order (apparently) giving us three adjustable parameters: h_1, t_c, and b. From the fitting function,

$$C(t) = t^{1+b} e^{h_1 t/t_c} \tag{3.10}$$

however, we see that h_1 and t_c are indistinguishable, so in fact we have only two adjustable parameters: b and h_1/t_c. We can apply an artificial constraint to distinguish the latter of these parameters. For consistency we choose $h_1 = -1$ so that t_c will be strictly positive (we expect $h(x) \to -\infty$ for large x). In this way, t_c indicates the range over which the power law is valid.

By working with the cumulative distribution we have reduced the number of fitting parameters from three to two, eliminating the nuisance parameter. Shown below is a sample fit of the predicted curve to the cumulative distribution data for a 128×128 lattice with periodic boundaries. The fitted parameters are $b = -1.378544$ and $t_c = 1792.96$. The high quality of the fit is encouraging, it suggests we do not need to consider higher order terms in the Taylor expansion of the scaling function.

The other runs fit equally well to this form having an average power law exponent $b = -1.371 \pm 0.008$. Note this agrees much more favourably with Alstrøm and Leão's result of $b = -1.41$ [5] but differs markedly with my previous estimate of $b = -1.175 \pm 0.012$. Which of these two results is correct? Why? These burning questions will be answered in the next section.

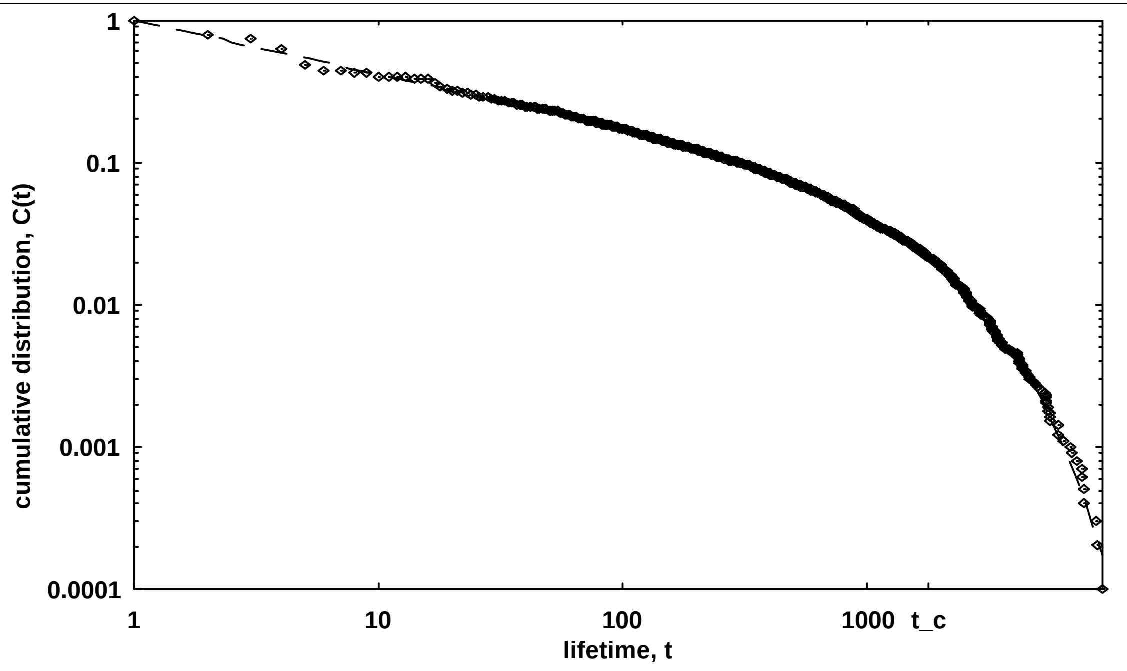


Figure 3.7: Cumulative distribution of lifetimes for GL on a periodic 128×128 lattice. The best fit curve has a power law behavior below $t_c = 1792.96$ with an exponent 1+*b* where *b*=-1.378544.

3.5. Critical exponents: conclusion

The realization that the cumulative distribution fits well to the above form of a scaling function was a fortunate coincidence. Notice, that applying this form to the original distribution would require higher terms in the Taylor expansion due to the relationship in Eq. (3.7). In fact, this relationship predicts some odd behavior for the original lifetime distribution. The analytical derivative of the cumulative distribution suggests that the original distribution scales like

$$D(t) = t^b \left(\tfrac{t}{t_c} - b - 1\right) e^{-t/t_c} \qquad \textbf{(3.11)}$$

or, in terms of the scaling function,

$$f\left(\frac{t}{t_c}\right)=\left(1-\frac{t}{t_c(1+b)}\right)e^{-t/t_c}\,. \qquad \textbf{(3.12)}$$

The linear factor in the scaling function counters the drop-off produced by the decaying exponential, generating a *hump* near t_c (see the figure below). This is very unusual behavior for a scaling function. Traditionally, we expect the function to be monotonically decreasing from one to zero. Nevertheless, it still satisfies the scaling function requirement that as $t_c \to \infty$, *f* converges to one for all *t*.

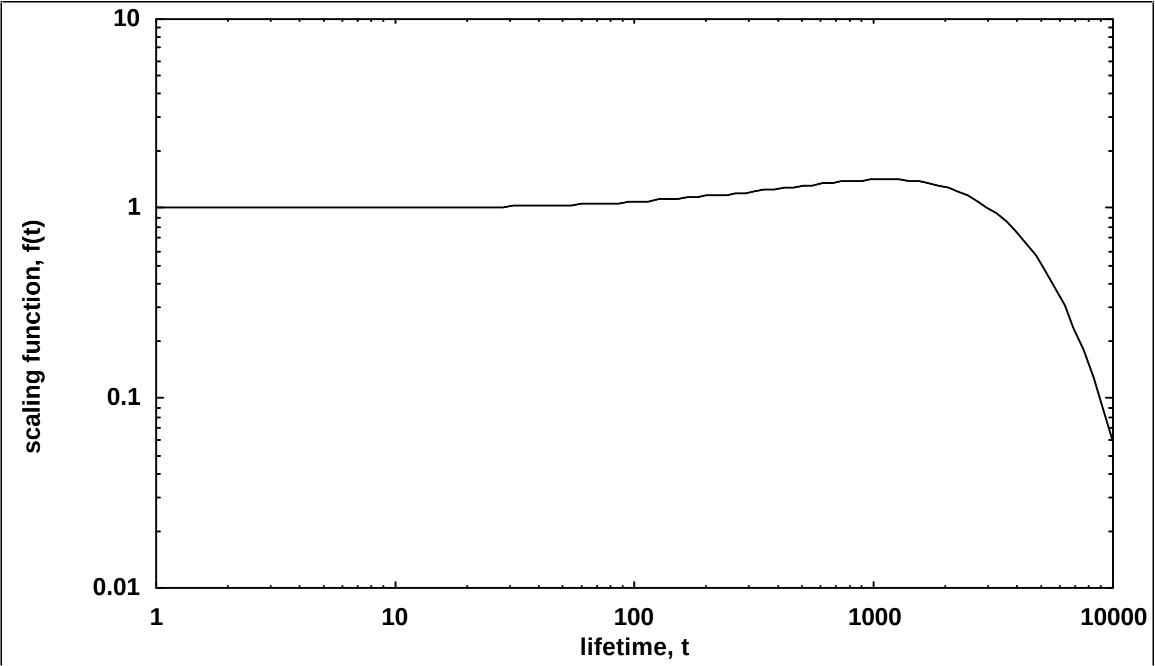


Figure 3.8: Weight of finite-scaling function of original lifetime distribution, *f*, with model parameters $b=-1.378544$ **and** $t_c=1792.96$ **(corresponding to periodic** 128×128 **run). Note the *hump* near** t_c**.**

The effect of the rise in the scaling function is to artificially inflate the lifetime distribution, near t_c, above the true power law. Hence, fitting the raw data to a power law while not taking this factor into account will result in an erroneous critical exponent. Now we understand this as the source of the discrepancy in the two measures of the critical exponent. When we originally fit the binned distribution to a power law with a cut-off we did not expect this unusual behavior from the scaling function and, as a result, estimated too small an exponent. We conclude that the correct power law exponent is the latter estimate of $b = -1.371 \pm 0.008$, in agreement with Alstrøm and Leão's result.

Having established the proper form of the scaling function we can compare the binned data (which generated our first, inaccurate measure of *b*) to the predicted curve in Eq. (3.11). The use of variable-width bins came under suspicion when we observed the disparity in our results. The figure below redeems the method, showing a very good fit. This confirms that the source of error lies only with the unusual form of the scaling function observed above. Note that, given the variance of the distribution, it is very difficult to be sure of one's model and fitted parameters. The cumulative distribution, on the other hand, smoothes the data and reduces the noise level, giving a much stricter data set and making it easier to test the validity of potential models. We will discuss the variance (noise) of the distribution further in Section 3.8.

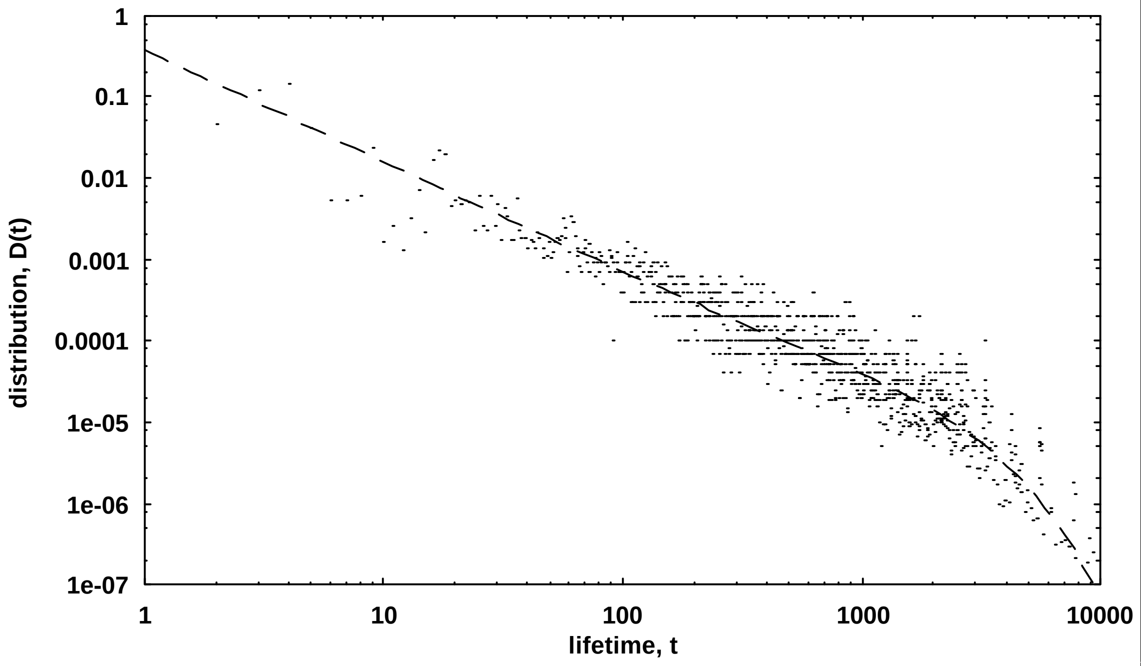


Figure 3.9: Binned lifetime distribution for 128×128 lattice with periodic boundaries. The curve represents the predicted distribution derived from the cumulative distribution.

3.6. Finite-scaling analysis

As stated in the title of this thesis we are interested in GL in the thermodynamic limit, as the system size increases to infinity. Of course, it is impossible to actually know how the infinite lattice would evolve, but it may be possible to extrapolate the behavior from increasingly larger finite systems. In particular, we are curious whether the scaling function (see Eqs. (3.5) and (3.6)) plays a smaller role as the system grows. This can be easily determined by measuring how the critical lifetime, t_c, scales with *L*. We are looking for a trend in t_c as *L* approaches infinity. Traditionally, finite-scaling analyses of critical phenomena reveal that the quantity of interest (critical lifetime) scales as a power law of the system size [12, *pp. 20-1*]:

$$t_c \propto L^z \tag{3.13}$$

where z is called the finite-scaling exponent. Hence, the scaling function, f, approaches one for all t as L increases.

The results for square, periodic lattices of various lengths is plotted below. It appears that GL scales for small L (with scaling exponent $z = 0.355 \pm 0.015$) but stabilizes at $t_c = 1981 \pm 17$ as L increases past 181. This suggests that this configuration probably has a correlation length $\xi \approx 181$ below which the dynamics are dominated by edge effects, but above which boundaries play a minimal role. Having only one data point above the transition makes impossible to extrapolate the behavior with any degree of reliability. It is possible that above the transition, the critical lifetime again scales with L but has a much smaller scaling exponent. More data is required to positively identify the large-scale behavior. I am currently collecting further data on larger lattices, but the results were not available in time for this paper.

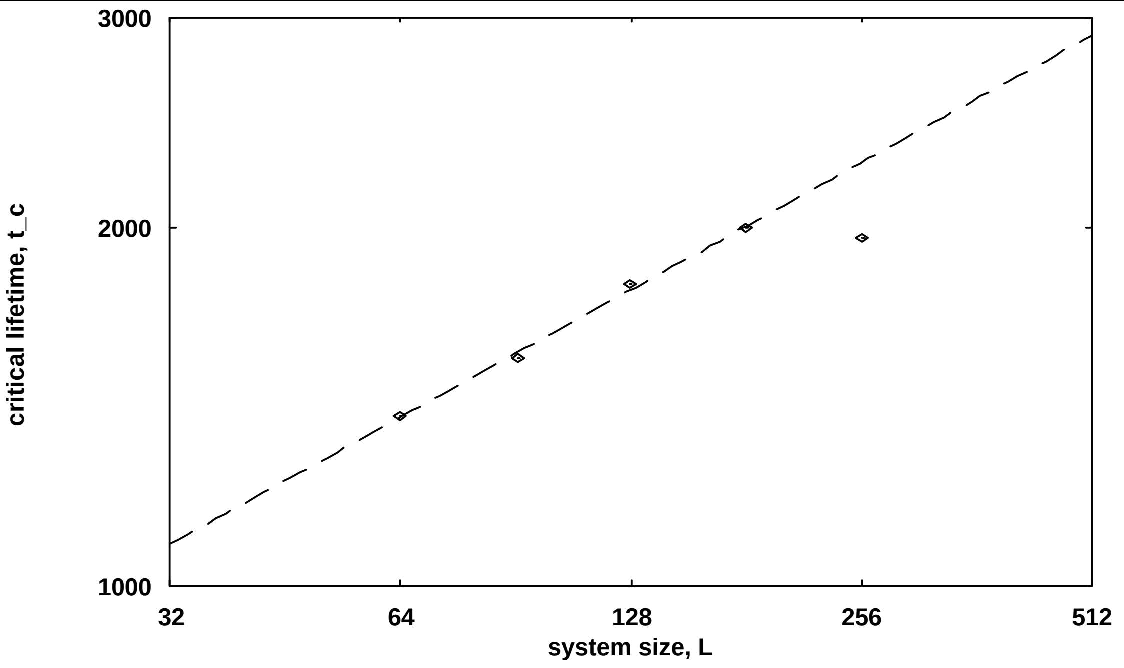


Figure 3.10: Finite-size scaling plot for GL on a square lattice with periodic boundaries. The finite-scaling exponent for small *L* is $z = 0.355 \pm 0.015$ **but GL does not appear to scale for** $L \geq 181$**.**

Although our previous calculation of the critical exponent agreed closely with Alstrøm and Leão's [5], their finite scaling analysis contrasts sharply with the above graph. They conclude that GL does indeed scale with *L*, with a scaling exponent $z \cong 0.52$. There are three possible explanations for this: firstly, they studied GL on square lattices with *open* (or *cold*) boundaries. We expect edge effects to be more severe for these systems so it may be that GL scales as a power law beyond the maximum lattice size they studied (1024×1024). The transition to a constant critical lifetime may occur above *L*=1024.

The second possible explanation is that the level of noise in the distributions reduced the accuracy of their results. It is not an attractive alternative, but I see no account made of the variance in the data so I can not exclude it as a possibility. Their runs consisted of a quantity of data points on the same order as mine, so the variance in their data should be on the order of that seen in Figure 3.5.

Thirdly, it is possible that cold boundaries produce fundamentally different dynamics than do periodic. For example, periodic bounds may impose artificial symmetries on the lattice which obstruct it's natural evolution. Or perhaps, when gliders or other animals interact with the cold bounds they produce new species which dominate the evolution. We will study the statistical properties of systems with other bounds in Section 3.10.

The data presented above suggests GL is subcritical. One may be tempted to believe the following fallacious argument which also comes to this conclusion. We have established that, for finite systems, avalanches have a typical maximum lifetime, t_c. Also for GL we know that an avalanche can expand at a maximum rate of one cell per time step (see Section 1.2) so an avalanche will have a typical maximum radius on the order of t_c. Let us assume the critical lifetime scales via Eq. (3.13) with a scaling exponent $z<1$. Paradoxically, this implies that, for sufficiently large L, the largest avalanches will typically extend only over a subset of the lattice. This appears to be inconsistent with the typical interpretation of finite criticality--that is, a finite system at the critical point has only one length scale, L. Actually, this is not a problem, as a critical point is only strictly defined for the infinite system [12], anomalous finite behavior is not problematic provided it disappears in the thermodynamic limit. More importantly, it has recently been observed [21] that dissipative SOC systems tend to exhibit a characteristic length which diverges slower than the system size. This behavior may be typical of non-conservative SOC, so this argument cannot be used to argue that GL is subcritical.

Jumping to the conclusion that GL does not exhibit SOC may be premature. On larger scales than what we have explored here there may be a crossover to a new scaling behavior or other, more complicated, dynamics. I am not here to refute that. The interesting point is that there have been studies on relatively small systems [3,5] which conclude that GL is *critical*, while other studies [4,6] using virtually the same data, have concluded that GL is *subcritical*. These latter arguments have been made on the basis of the average lifetime of the avalanches (also called average *decay* time).

3.7. Average decay time

If GL is critical then, in the thermodynamic limit, the average lifetime of the avalanches should diverge. For finite lattices it must scale as t_c^{2+b} as we see if we consider the change of variables $u = t/t_c$ in

$$\begin{aligned} \langle t \rangle &\propto \int_0^\infty t^{1+b} f(t/t_c)dt \\ &\propto t_c^{2+b} \int_0^\infty u^{1+b} f(u)du. \\ &\propto t_c^{2+b} \end{aligned} \tag{3.14}$$

Knowing how the critical lifetime scales with the system size (Eq. (3.13), valid for small L) we can predict how the average decay time should scale:

$$\begin{aligned} \langle t \rangle &\propto t_c^{2+b} \\ &\propto L^{z(2+b)} \end{aligned} \tag{3.15}$$

where, from Figures 3.7 and 3.10, $z(2+b) = 0.223 \pm 0.012$. Using this value, we compare the predicted scaling of the average decay time with our data. The results, shown below, seem to indicate that <*t*> does not scale as expected but seems to plateau at $\langle t \rangle = 165 \pm 6$, validating the results for the critical lifetime. This stabilization was also observed by Bennett and Bourzutschky [4] at roughly the same value of $L \approx 181$. They studied square, periodic lattices up to 1024×1024 lattices and observed no further increase in the average decay time on these scales.

Only a subset of the average decay time data fits fairly well to the predicted power law. The first point (*L*=64) does not fit because this run suffered from extreme corrections to scaling -- it did not satisfy Eq. (3.14). The last point (*L*=256) also does not fit the predicted scaling law. In this case, however, we understand this as resulting directly from the informtion in Figure 3.10. This suggests the method of using average decay time as a predictor in scaling analyses is valid, and the results here indicate that GL is subcritical (because the largest lattice does not fit the expected scaling law).

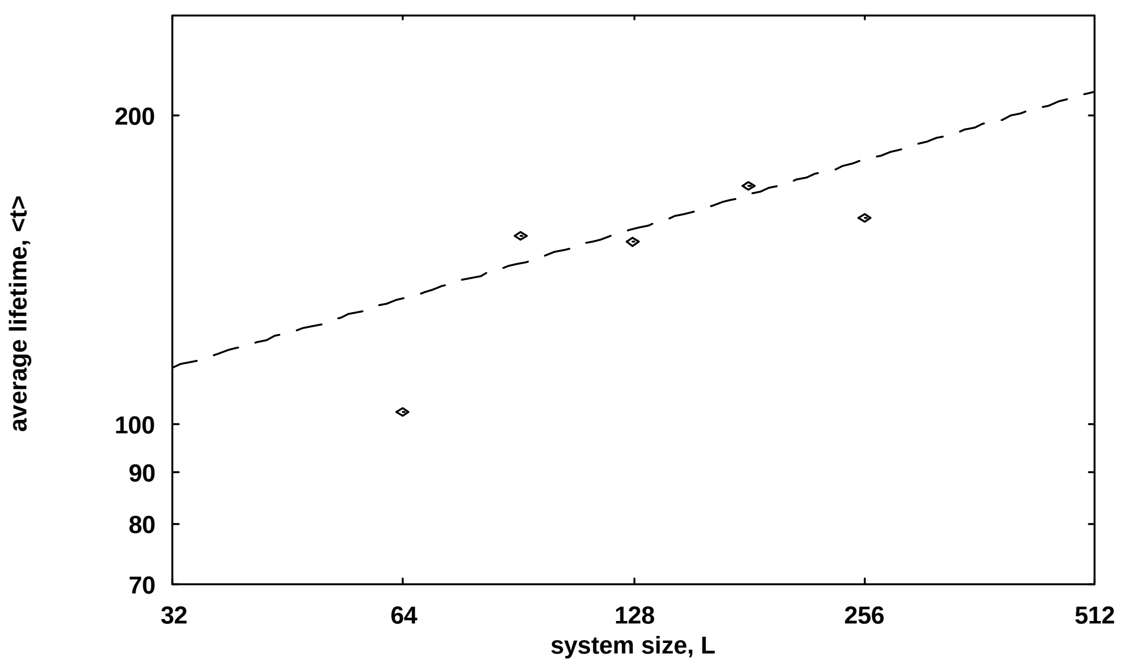


Figure 3.11: Average lifetime as a function of system size for periodic lattices. The predicted scaling exponent, 0.223 ± 0.012**, (line) fits a subset of the actual data (points).**

3.7.1. Other moments of the distribution

Some researchers [4,6] believe this represents clear proof that GL must be subcritical. Alstrøm and Leão [5] offer an alternative explanation: they suggest that the discreteness of small avalanches pollutes the estimation of the average decay time, making it unreliable. The reader will recall that when we first calculated the critical exponents, we explicitly ignored data from small avalanches because of fluctuations caused by the lattice's discrete nature. (These data points were included in our second attempt, however.) Alstrøm and Leão suggest higher moments, which favour large avalanches, would minimize the disturbances caused by the small avalanches and produce fits in agreement with finite-scaling predictions, thus reasserting that GL is critical. (They did not actually include this analysis in their paper, but merely outlined the procedure.)

In parallel with Eq. (3.14) the μ 'th moment of the distribution of lifetimes should scale like

$$\begin{aligned}\left\langle t^{\mu}\right\rangle &\propto t_c^{1+b+\mu} \\ &\propto L^{z(1+b+\mu)}\end{aligned}. \qquad \textbf{(3.16)}$$

We would like to compare this predicted scaling with that determined directly from the data. A convergence of these values for larger moments would suggest, in agreement with Alstrøm and Leão's prediction, that the discrepancy observed in Figure 3.11 is due to the low end of the distribution. However, if the values diverge for larger moments, then the discrepancy is due to the high end above the critical lifetime. Calculating the moments for periodic lattices of various dimensions and fitting them to a finite-scaling power law I have recovered the best fit scaling exponents and plotted them below.

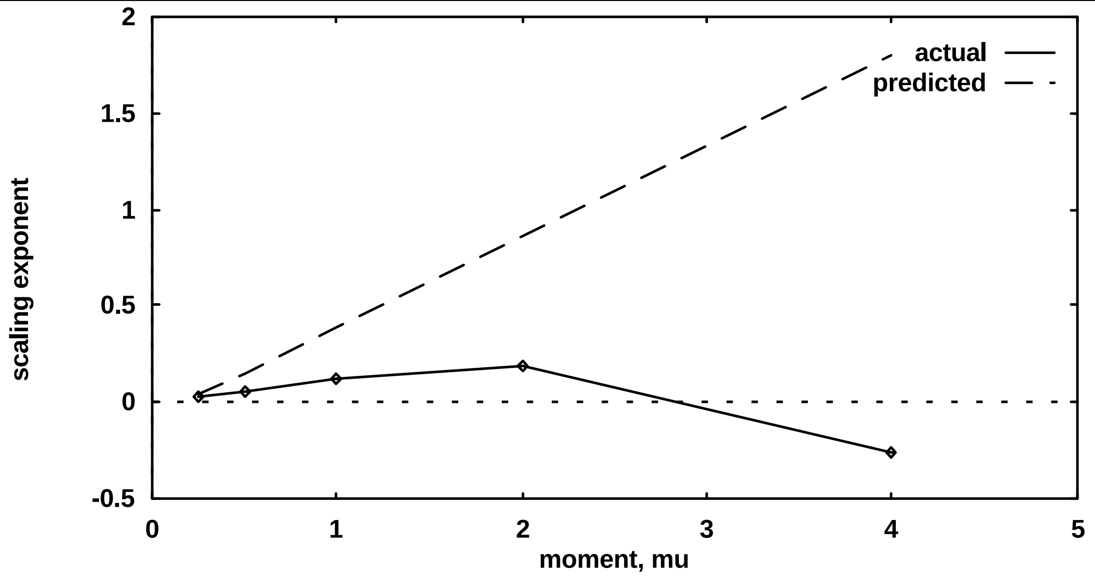


Figure 3.12: Comparison of predicted (from finite-scaling analysis) and actual scaling exponents for various moments of the distribution. The values correlate better for smaller, fractional moments suggesting errors are due to large avalanches.

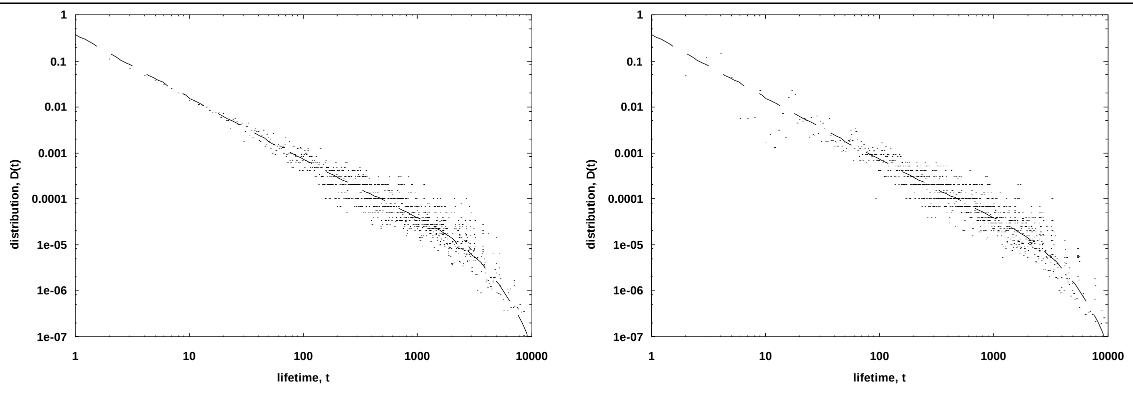
The results clearly show a divergence for large moments. (Note that as $\mu \rightarrow 0$ the values converge with each other faster than they approach zero.) This suggests that the low end of the distribution does not unduly influence the moments. Hence, the average decay time is a valid tool for determining if GL scales or not -- and our result, indicating that the average decay time stabilizes for large lattices, once more confirms our hypothesis that GL is subcritical.

3.8. Noise

We have seen that the cumulative distribution fits the proposed decaying power-law very well. The original distribution also appears to fit the derivative well (see Eq. (3.11)), but we can not be as confident because of the magnitude of the noise which plagues this data. We must question whether the noise reflects some hidden internal mechanism or if it is simply experimental error. The easiest way to test this is by generating a synthetic data set from the theoretical distribution, and comparing the noise levels. The synthetic data set is generated by choosing avalanche lifetimes with the probability given in Eq. (3.11) [7, *pp. 287-8*]. Hence, the events are guaranteed to be independent and the noise will be Gaussian in form (although it may not appear Gaussian on a log-log graph).

If the events (avalanches) are interdependent (suggesting a deeper analysis is required) then we would expect the noise level to deviate from that predicted by the synthetic data set. For example, if avalanches of similar size are positively correlated, we may well expect the noise levels to be smaller than predicted.

Using the theoretical distribution with the parameters for the 128×128 data set, I generated ten thousand data points (the same number as in the experimental runs), and performed the same analysis as for the actual data. The results, shown in the figure below, closely approximate the actual 128×128 distribution. Hence, there does not appear to be any correlation between avalanches and the noise is due to statistical fluctuations.



(a) (b)

Figure 3.13: Comparison of noise levels generated by a synthetic data set (a) and the results of the 128×128 periodic run (b). Both data sets have been binned. The strong similarity confirms our hypothesized form of the distribution function (curve), and suggests that avalanches are indeed independent.

Given that we now know the form of the noise, we could apply this to derive a more precise theoretical distribution. When originally fitting the function to the cumulative distribution I ignored the variance in the data, and treated all points as being equally reliable. A better method would estimate the standard deviation of each data point and include this information for a better fit. Nevertheless, considering how well the curve fits the cumulative distribution even neglecting the deviations (see Figure 3.7), I suspect that implementing this method would not significantly alter the model parameters.

3.9. Activity

The avalanche *size* can be measured by more than just lifetime. If GL is critical, any other property which measures avalanche size should also obey a power law distribution. For example, the total *activity*, defined as the number of births and deaths produced by the avalanche (see Eq. (2.9)), should have the form

$$D(s) \propto s^{\tau} \qquad \textbf{(3.17)}$$

where we expect the critical exponent, τ , to be distinct from *b*.

The activity is one of the statistics *CellBot* keeps a record of, so we may test this hypothesis. A plot of the distribution of activities for a variety of systems (all with periodic boundaries) is shown below. Notice the plots are shifted to the right (higher activity) for larger lattices. This does not reveal a remarkable new phenomenon but simply reflects an insufficiency in the program. When counting the births and deaths CellBot does not distinguish between activity within the avalanche and activity arising from simple periodic structures beyond. For example, a *blinker* (see Figure 1.2) has two births and two deaths in each time step, for an activity rate of four. These animals, and others like it will tend to right-shift a distribution.

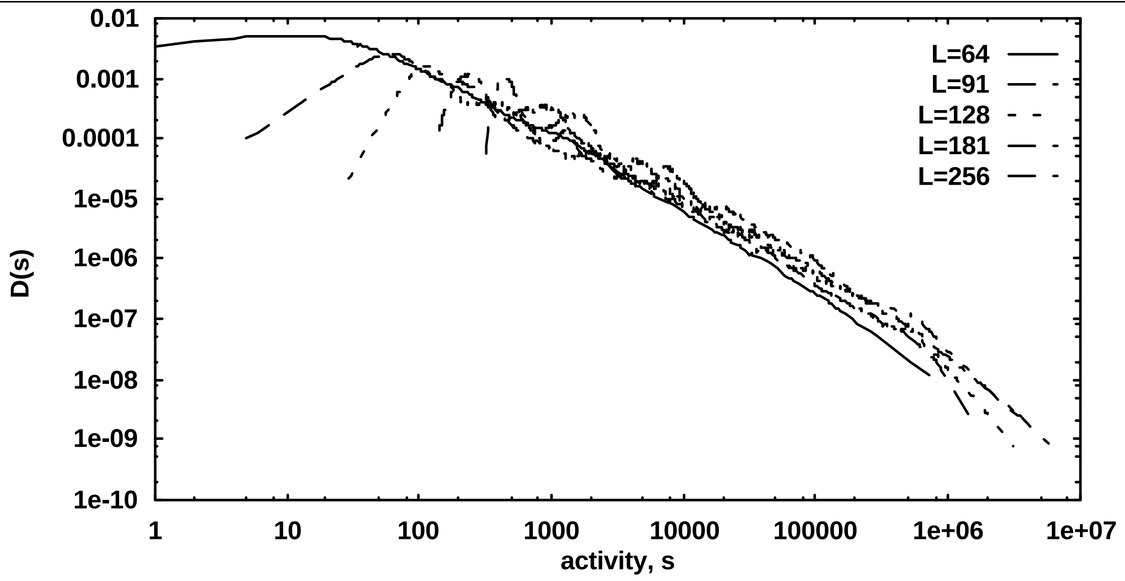


Figure 3.14: Overlapping activity distributions for $L \times L$ periodic lattices. Distribution is right-shifted more severely for larger lattices due to error in measure of activity. The curves represent the binned data smoothed with a Savitsky-Golay filter (32,32,1).

We expect the spatial density of these species to be uniform, and hence the activity for a lattice of dimension L will be inflated by a constant amount on the order of L^2. To correct for this error we must subtract off the estimated activity of the stable structures from that of the avalanche. We can estimate the activity of the underlying lattice by looking at the *flip-fails*, the perturbations which immediately revert to their original state (see Section 3.2.1). In these avalanches only one count of the activity is due to the avalanche itself, the rest represents the activity of the periodic lattice. To correct the activity then, we must subtract the average flip-fail activity once for each time step in the lifetime of the avalanche:

$$s_{correct}(t) = s(t) - t\left[\langle s(1)\rangle - 1\right]. \tag{3.18}$$

The corrected distributions are plotted in Figure 3.15. By fitting the cumulative distribution to a decaying power law analogous to Eq. (3.6) we recover a critical exponent $\tau = -1.293 \pm 0.017$, which agrees favourably with estimates from other studies: -1.4 [3] and -1.27 [5].

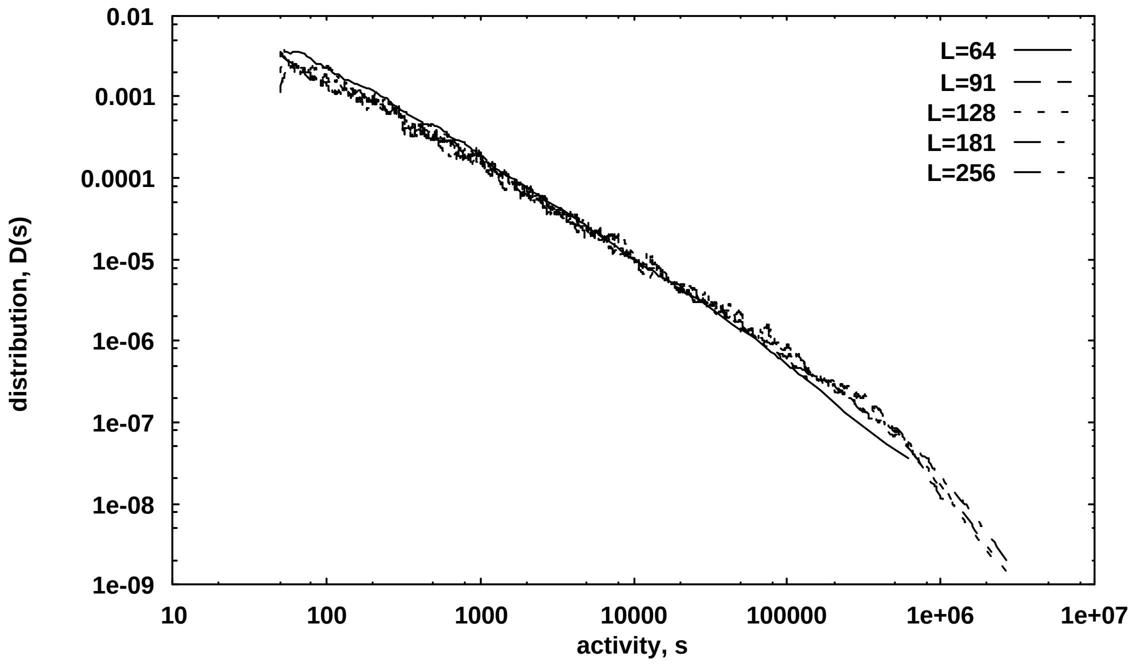


Figure 3.15: Overlapped plots of corrected activity distributions for various $L \times L$ periodic lattices. Best fit critical exponent is $\tau = -1.293 \pm 0.017$ (calculated via fit of cumulative distributions).

The finite-scaling plots of s_c and <*s*> are shown below. In parallel with Eq. (3.13) we assume

$$s_c \propto L^{\delta} \tag{3.19}$$

where, from the graph, $\delta = 0.88 \pm 0.08$. The smallest lattice has been excluded from the fit because of extreme corrections to scaling, and the largest because it appears to have crossed over to a size-independent regime. Note Alstrøm and Leão [5] computed a scaling exponent of 0.69 but let me reiterate--their results apply to *cold* boundaries and we have no reason to expect the same value for *periodic* bounds.

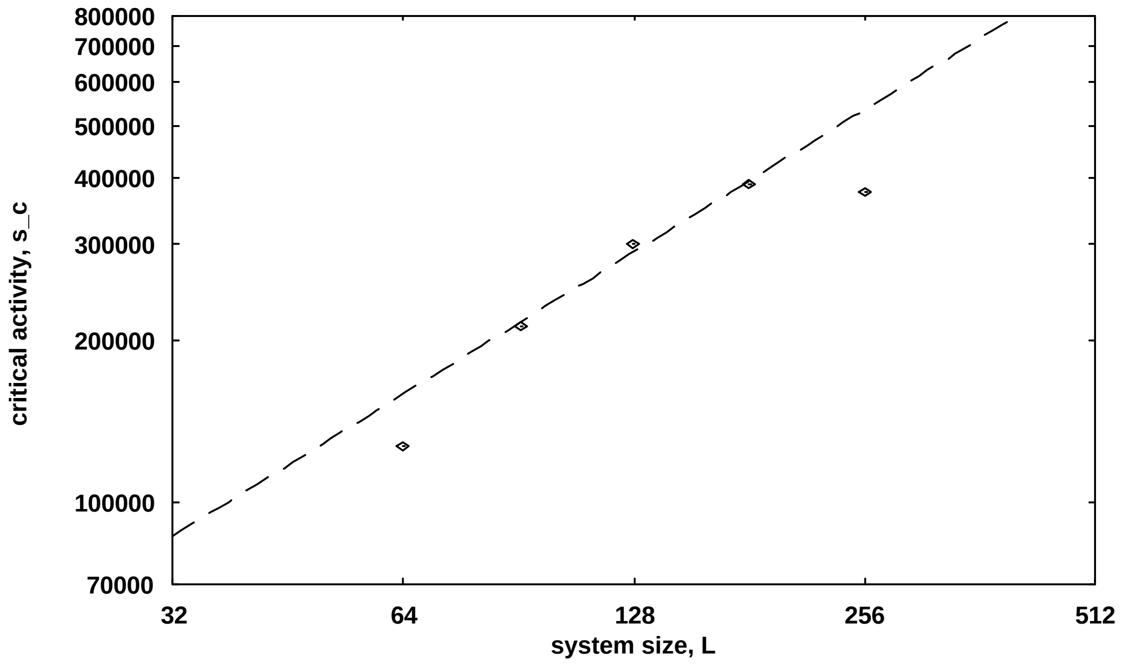


Figure 3.16: Corrected finite-scaling plot for critical activities versus system size for $L \times L$ periodic lattices. Finite-scaling exponent (fit to central three points) is $\delta = 0.88 \pm 0.08$.

In analogue with Eq. (3.15) we compare the scaling of the average (corrected) activity with the predicted scaling exponent $\delta(2+\tau) = 0.73 \pm 0.07$ and observe a good fit for the same lattices as for the above figure.

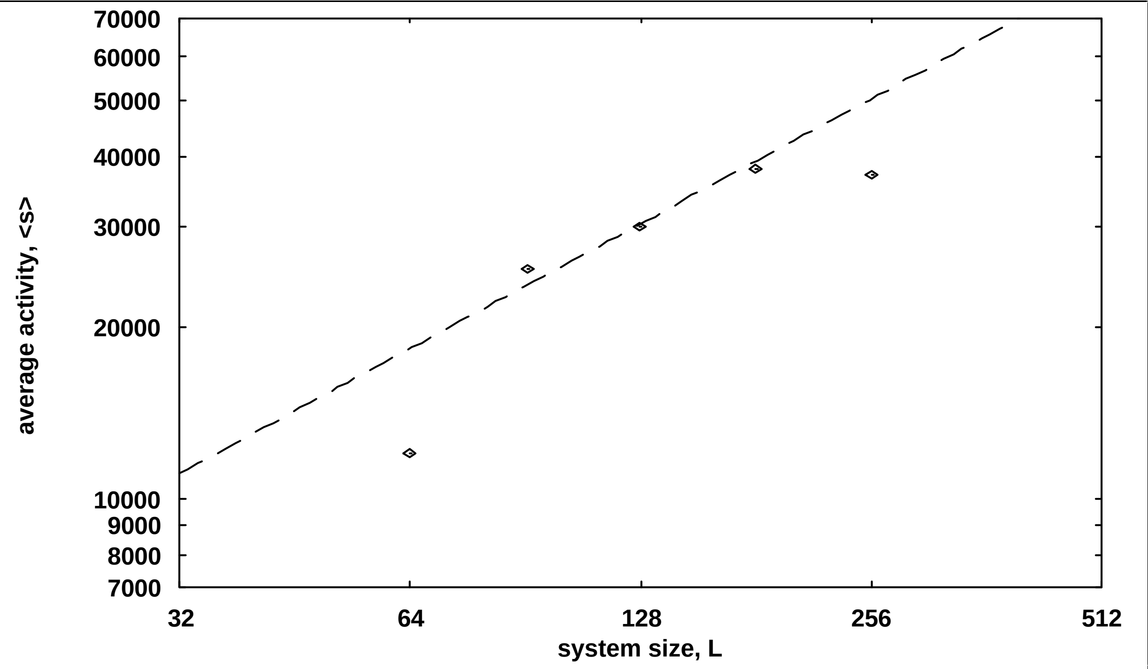


Figure 3.17: Average corrected activity as a function of system size for $L \times L$ periodic lattices. The predicted scaling exponent, 0.73 ± 0.07, fits a subset of the data fairly well.

3.10. Boundary conditions

It has been suggested that the debate over GL's criticality is a result of applying different boundary conditions. In the thermodynamic limit we expect boundary effects to disappear, but they may have important consequences in finite lattices. Bak, *et al*. [3] and Alstrøm and Leão [5] applied cold (also called open) boundaries and they both concluded GL is critical. Bennett and Bourzutschky [4] reached opposite conclusions using periodic boundaries. Later, though, Hemmingsson [6] also concluded GL was subcritical, but he used cold boundaries. Note the general shape of all distributions shown in these references are similar to those shown above in Figures 3.6 and 3.15. I see no evidence in any of these papers that the type of boundaries affect the dynamics significantly. Nevertheless, I would be negligent if I did not explore the possibility for myself.

Figure 3.18 shows the overlapping distribution of lifetimes for several square lattices with cold boundary conditions. The best-fit decaying power law distribution (determined by fitting the cumulative distribution) has critical exponent $b = -1.390 \pm 0.011$. Note this value falls within the margin of error of the value calculated for periodic boundaries. This is satisfying because we expect the power law to represent the behavior of the infinite system, to which the periodic and cold lattices should both converge.

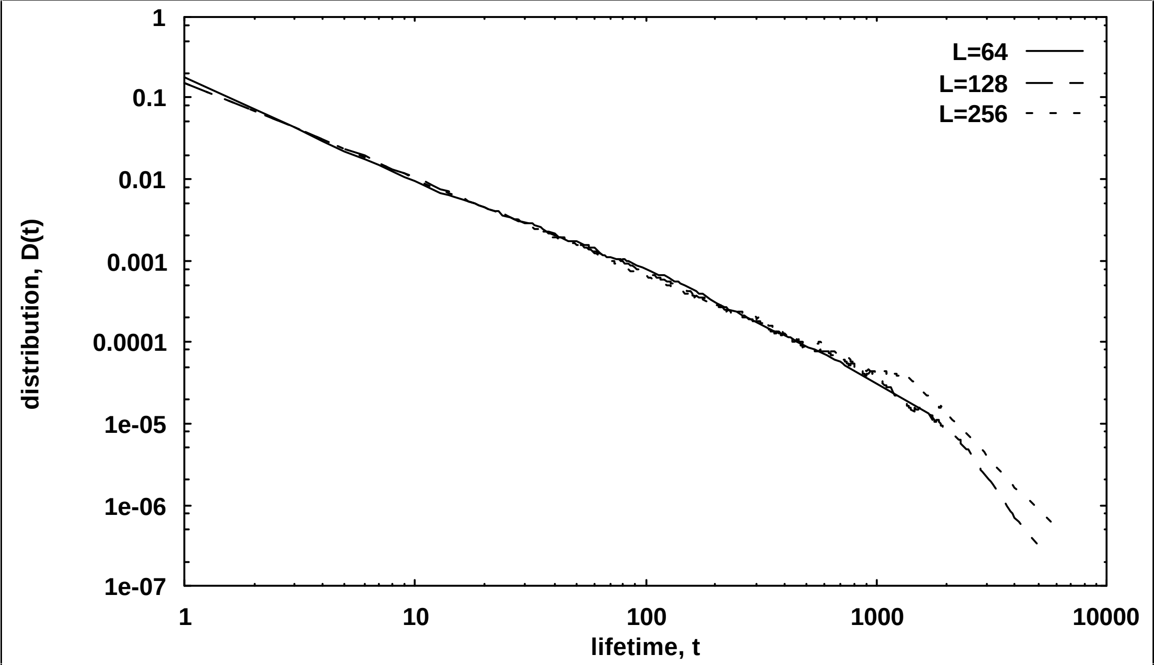


Figure 3.18: Overlapped lifetime distributions for $L \times L$ lattices with cold boundaries. The curves represent smoothed (Savitsky-Golay (32,32,1)) forms of the binned data. The critical exponent is $b = -1.390 \pm 0.011$.

As before, the cumulative distribution simultaneously determines the critical lifetimes, above which finite-size effects dominate the distribution. Unfortunately, only three lattices were tested, making it difficult to reliably fit to a power law (see figure below). Assuming that all three points fit the finite-scaling power law we get a finite-scaling exponent of 0.54. This agrees very nicely with Alstrøm and Leão's estimate of 0.52 [5] using lattices up to L=1024.

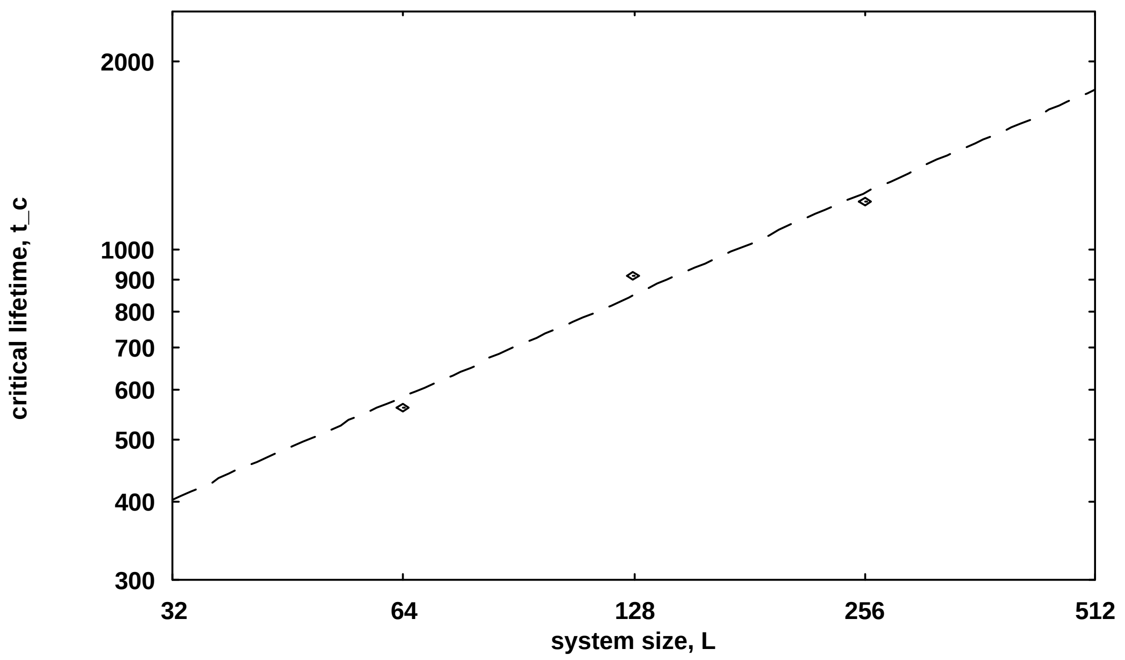


Figure 3.19: Finite-scaling plot of critical lifetimes for $L \times L$ lattices with cold boundaries. The scaling exponent is estimated at $z = 0.54 \pm 0.09$.

If we again plot the average lifetime against system size (below), we observe a good fit to the theoretical result. The only qualitative difference between the cold boundaries and periodic boundaries is that we do not observe any stabilization in the critical lifetime or the average decay time for large lattices.

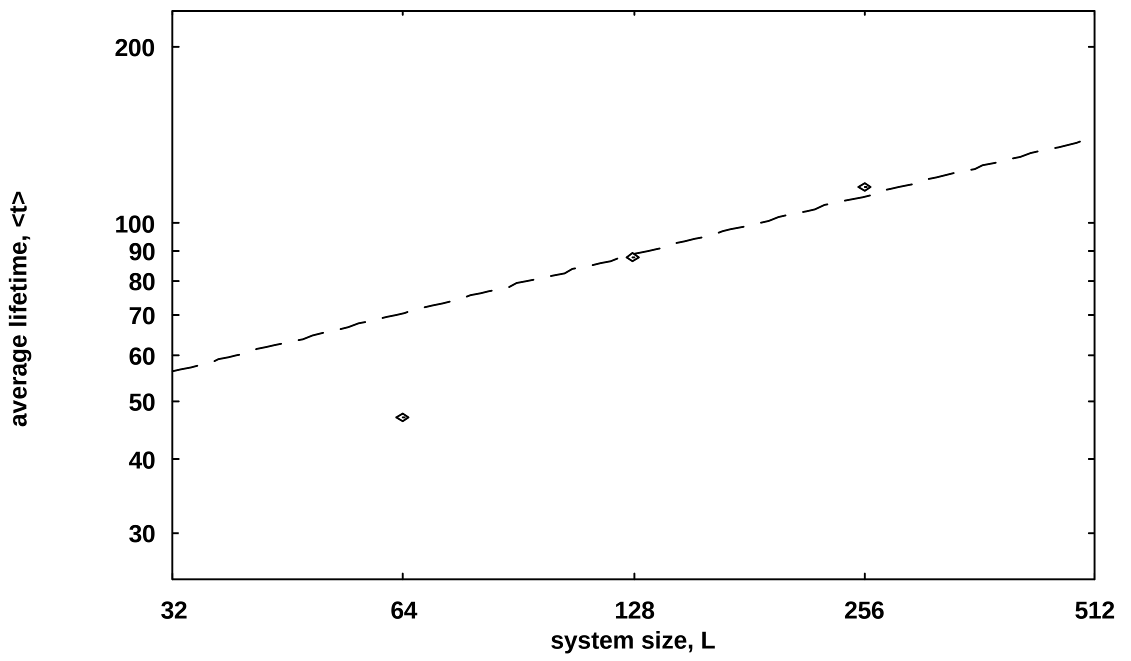


Figure 3.20: Finite-scaling plot of average lifetime for $L \times L$ lattices with cold boundaries. The scaling exponent is predicted to be 0.33 ± 0.06.

In fact, all the properties of the systems seem to be the same as the periodic systems except the finite-scaling exponents and length scales are different. Cold boundaries seem only to differ in that they affect the dynamics more strongly, effectively reducing the system size. Perhaps this is not surprising. On a cold-bounded lattice, an avalanche growing at the speed of light (one site per time step) will interact with the boundaries after $L/4$ time steps, on average. In contrast, a periodic lattice would allow the avalanche to grow for $L/2$ steps before the boundaries affected the course of evolution (via self-interaction of the avalanche). Hence, we expect roughly a halving of the effective lattice length by using cold boundaries. If this holds true then we would not expect to witness crossover from finite-scaling to size-independent dynamics until $L \approx 362$, twice the length at which crossover occurred for the periodic runs.

Alternatively, the quantity of importance may be the critical lifetime. Perhaps crossover occurs when $t_c \geq 1981 \pm 17$ (see Section 3.6). Referring to Figure 3.19 we see this would occur when $L \approx 612$. In either case, it is not surprising that the properties finite-scale as nicely as they do. This does not contradict our previous conclusion that GL is subcritical, but merely indicates that we must study larger lattices before we should expect to observe crossover into a size-independent regime.

3.11. Geometry

So far we have examined square lattices with periodic and cold boundaries. It may be interesting and enlightening to explore some more exotic lattices. My first choice was a strip bounded in only one dimension (with periodic boundaries). To reduce the computational overhead I also imposed a reflective boundary across the width of the strip. The effect is a bin like that shown in Figure 2.1(b). We define the characteristic size of the lattice, *L*, as the width of the bin. The avalanche lifetime distributions for three separate runs are shown in the figure below. Note the critical exponent (calculated by means of the cumulative distribution), $b = -1.372 \pm 0.015$, agrees with the two previous estimates. We see the same drop-off for large avalanches, suggesting a finite-scaling analysis is in order.

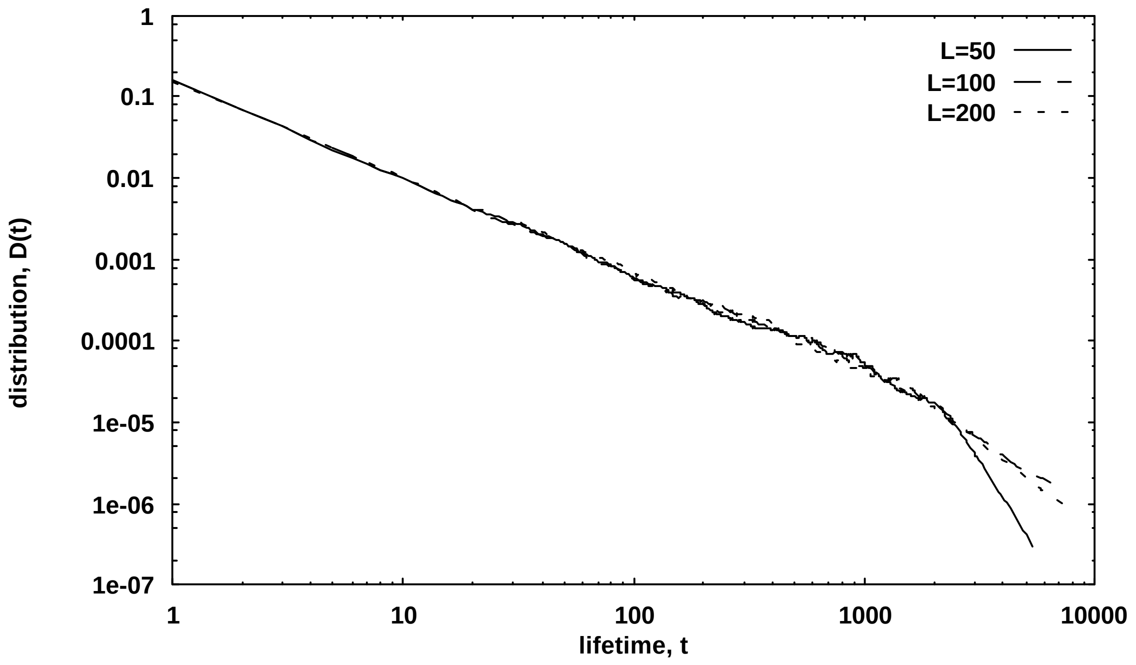


Figure 3.21: Distribution of lifetimes (smoothed) for GL in one-dimensional 'bins' of width *L*. Critical exponent is $b = -1.372 \pm 0.015$.

The standard finite-scaling and average decay time plots are shown below. The finite-scaling exponent, $z = 0.49 \pm 0.09$, fits the data fairly well. Of course, a better analysis would consider more runs with larger lattices.

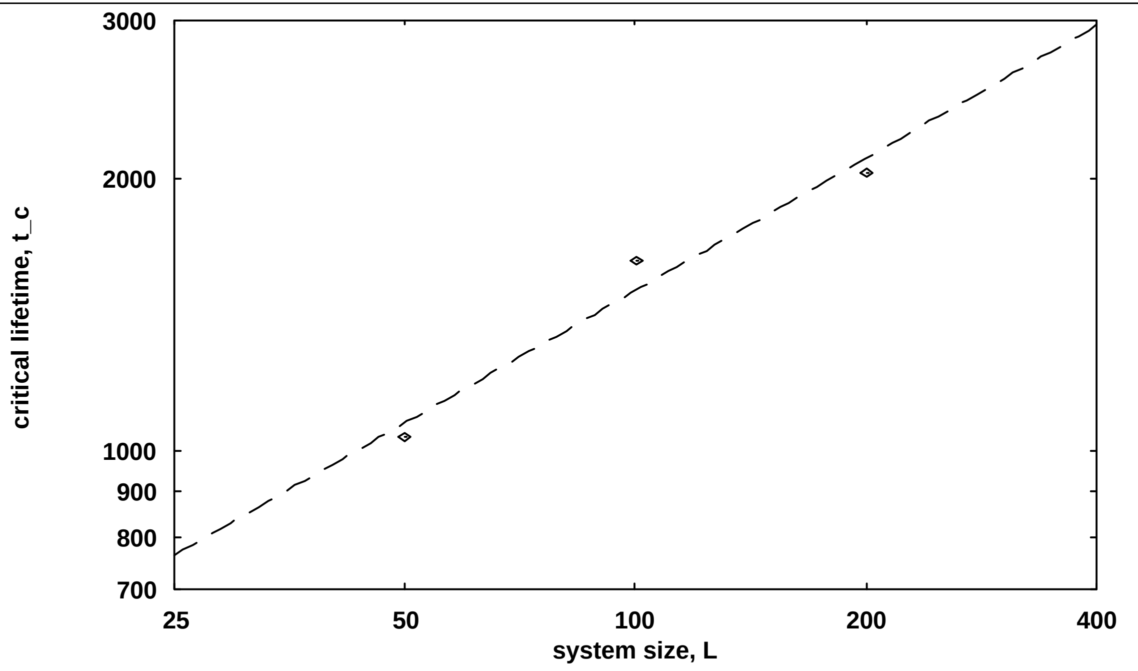


Figure 3.22: Finite-scaling plot of critical lifetimes for GL in one-dimensional 'bins' of width *L*. The scaling exponent is estimated at $z = 0.49 \pm 0.09$.

With this data, we predict the average lifetime should scale with an exponent 0.31 ± 0.06. However, the real data indicates that the system again crosses over from finite-scaling (dominated by boundaries) to a size-independent form near $L \approx 100$, with an average decay time 149 ± 1. However, this result is suspicious because, unlike the periodic lattices in which both scaling plots revealed the same crossover, here the critical lifetime appears to scale even for *L*=200. Whether this disparity is due to statistical fluctuations or hides a deeper discord is a question left unresolved.

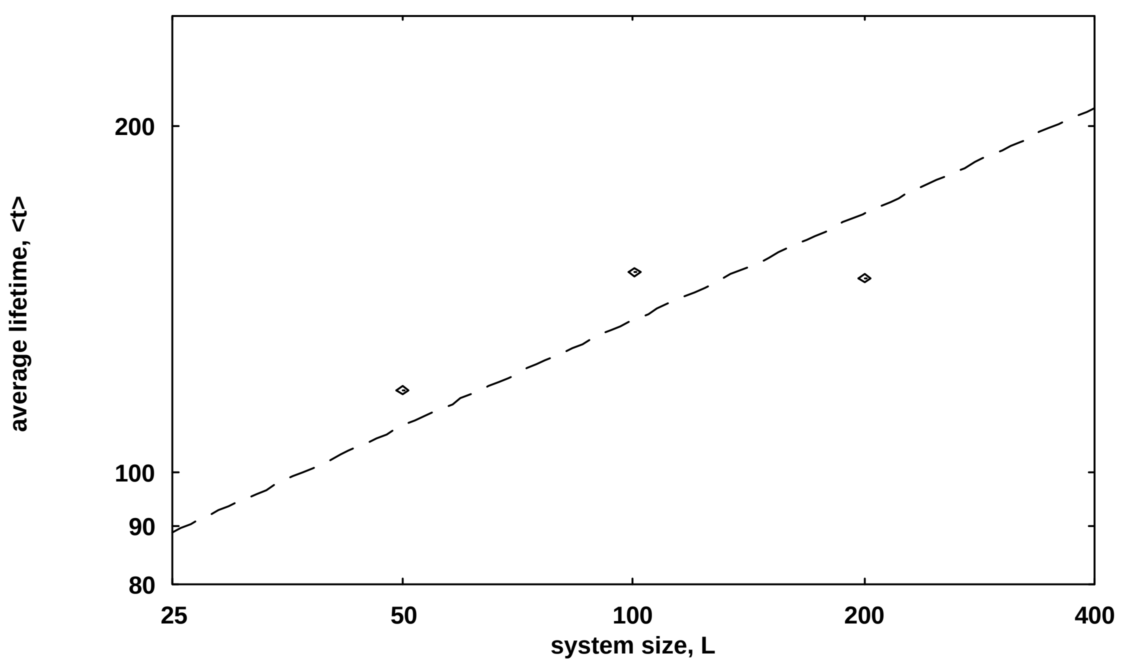


Figure 3.23: Finite-scaling plot of average lifetime as a function of system size for GL in one-dimensional 'bins' of width *L*. The predicted scaling exponent, 0.31 ± 0.06**, (line) does not conform with observed results (points).**

3.12. Unbounded GL

Applying the capabilities of CellBot, I also considered a GL run in which boundaries were removed completely. Starting with a 50×50 block randomly occupied with a 50% density I let the system evolve to a stable state. Then I implemented the same sequence of repeated perturbations used in the other experiments. One of the first things I noticed was that the system quickly grew, and as it did, it slowed down. CellBot's performance is roughly inversely proportional to the number of live cells (which, from the figure below, is proportional to the number of perturbations) so we can estimate the run-time required for P perturbations varies as P^2. The fact that this is polynomial in time (as opposed to exponential) is actually good news. We can realistically expect to acquire sufficient data for our purposes. That said, after having run the program for a few months I had only accumulated 1908 perturbations. Nevertheless, this data is adequate to describe some qualitative features and estimate the critical lifetime and average decay time.

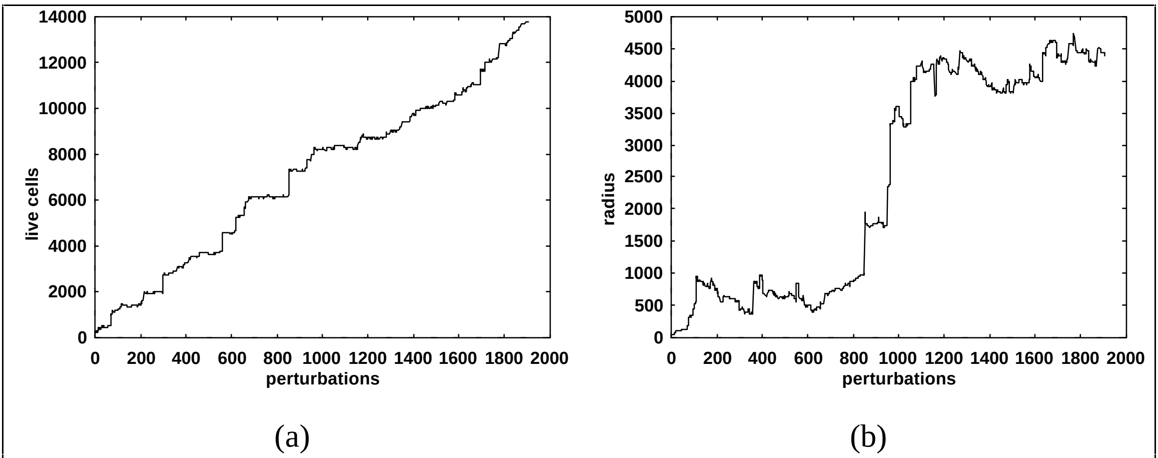


Figure 3.24: Evolution of the unbounded GL run over time (perturbations). The number of live cells (a) grows roughly linearly, but the characteristic size of the lattice (b) looks more like a punctuated equilibrium scenario.

Note that the term *unbounded* does not mean *infinite*. Typically, we have a localized cluster of live cells surrounded by a sea of dead sites. In the truly infinite system, to which we aspire, there would be a roughly uniform spatial distribution of live cells. The dynamics are affected, albeit more subtly, by this island structure and we expect finite-size effects to play a role in avalanche evolution.

Figure 3.24(b) demonstrates the size of this island is continually growing. It is possible that earlier avalanches are constrained more tightly by the smaller size of the system, in which case the earlier avalanches should not be fitted to the same distribution as the later ones. The figure below shows the raw sequence of avalanche lifetimes and the same data smoothed. The smoothed data reveals no trend but seems to fluctuate randomly around a mean value. (Note this mean value does not represent the average avalanche lifetime because the log-scale was used in the smoothing process.) The lack of a transient should satisfy the reader that all the data can be included in a single distribution.

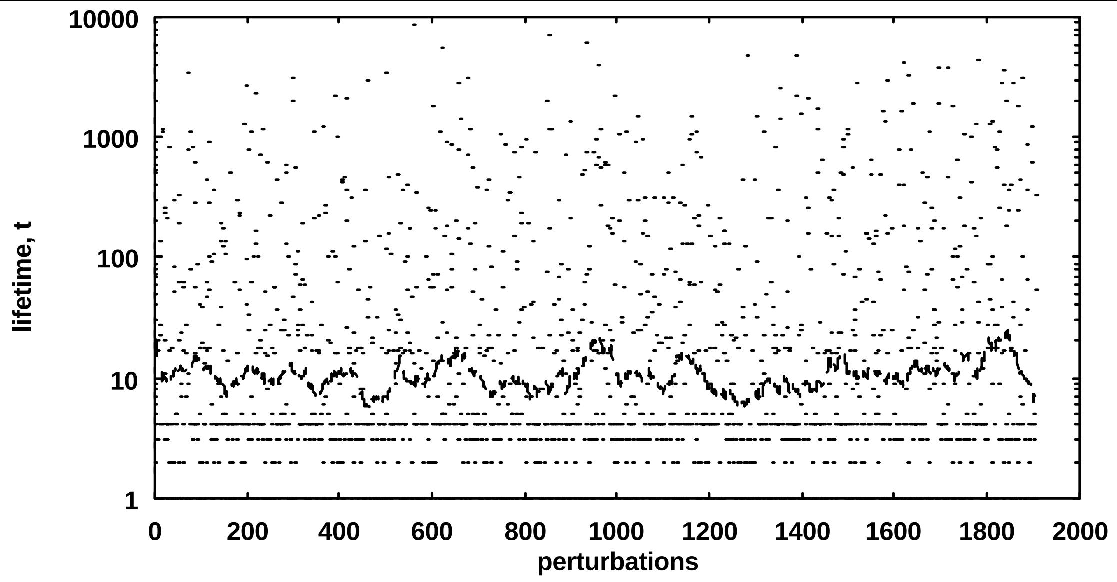


Figure 3.25: Demonstration that avalanches exhibit no transient. The line represents a Savitsky-Golay smoothing filter (32,32,1) applied to the raw data (dots). No trend in avalanche size is observed. Note the average value of the line does not represent the average avalanche lifetime.

The distribution of lifetimes for the unbounded system is plotted below. The critical exponent is $b \cong -1.376$, in close agreement with the critical exponent for the square lattices with periodic boundaries. We observe the same drop-off noted for bounded lattices, perhaps not surprisingly because we suspect GL to be subcritical. (We may still see a drop-off even if GL is critical because this run is not equivalent to an infinite lattice). The drop-off occurs at $t_c \cong 1857$, on the same order as the stable (large L) value of 1981 ± 17 observed for periodic lattices. The fact that this quantity is slightly less than that for large periodic systems suggests that the unbounded run may suffer from finite-size effects due to the small size of the initially filled lattice. The average decay time, 152, being smaller than expected, also confirms that the run is inhibited by the small initial seed. It would be interesting to study this run at later times to determine if the critical lifetime and average decay time have increased.

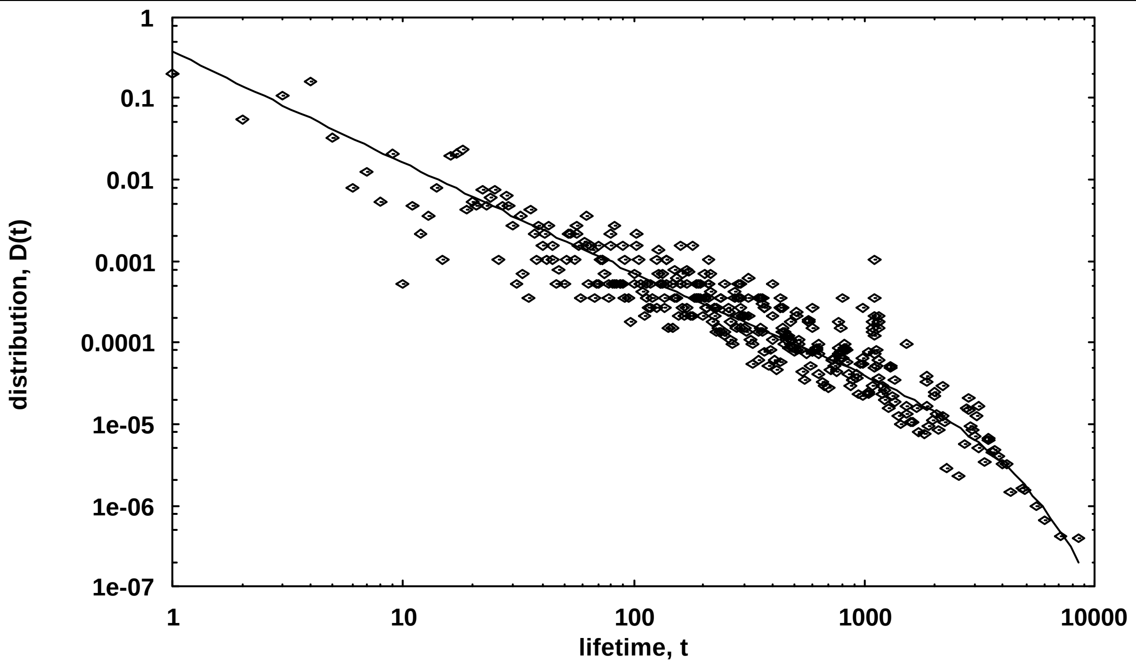


Figure 3.26: Distribution of lifetimes for the unbounded GL. The power law fit exponent is $b \cong -1.376$. The critical lifetime is estimated at $t_c \cong 1857$ and the average avalanche lifetime is $\langle t \rangle \cong 152$.

3.12.1. Gliders and the characteristic radius

Up to now I have discussed the *system size* without mentioning how it was measured. For bounded lattices this is trivial, but for the unbounded system it becomes slightly more complicated. At first guess one would simply define a bounding box which is the minimum size to contain all live cells. Unfortunately this does not accurately represent GL very well because, looking at Figure 3.27, we see that the unbounded system consists of two domains: the *cluster domain* and the *glider domain*. The glider domain arises from the central cluster periodically spitting out gliders as it evolves. Initially, these gliders, spreading out diagonally in all four directions from the origin, account for only a very small fraction of the population. We can reliably estimate the radius of the system (ignoring these few gliders) with the radius of gyration (from inertial mechanics):

$$R_g = \sqrt{\frac{1}{N}\sum_{i=1}^{N} r_i^2} \qquad \textbf{(3.20)}$$

where N is the number of live cells and r_i is the distance from the center-of-mass of the *i*'th live cell. This measure gives accurate results when the gliders are few and near the center but as the glider domain grows its weight inflates the radius of gyration.

A new measure which could distinguish between the cluster and glider domains was needed. In response, I constructed the θ-*count radius*. The principle behind this measure is that the cluster domain has a relatively uniform density. This being the case, one estimates the θ-count radius by performing a binary search for the radius from the center-of-mass, r_θ, of a circle such that the circle encompasses a fraction, θ, of the live cells:

$$N(r_\theta) = \theta N \qquad \textbf{(3.21)}$$

where $N(r)$ is the number of live cells within a radius r and $N \equiv N(\infty)$ is the total number of live cells. The density of live cells within this circle is assumed to be the density of the central cluster, and the radius of the entire cluster (the θ-count radius) is estimated by extrapolating this radius to include what would be all N cells if they belonged to the cluster domain (assuming a uniform density):

$$R_\theta = \frac{r_\theta}{\sqrt{\theta}}\,. \qquad \textbf{(3.22)}$$

I chose $\theta = \frac{1}{2}$ (half-count radius) because it provides a nice balance. Too small a fraction would give rampantly fluctuating measures because the population within the circle would not be statistically stable. On the other hand, too large a fraction runs the risk of including part of the glider domain within the circle. As long as the cluster domain accounts for more than half of the live cells in the system this choice gives a good measure of the characteristic radius. In the figure below, the half-count radius would give an even better estimate except that the center-of-mass is being shifted by the weight of the glider domain.

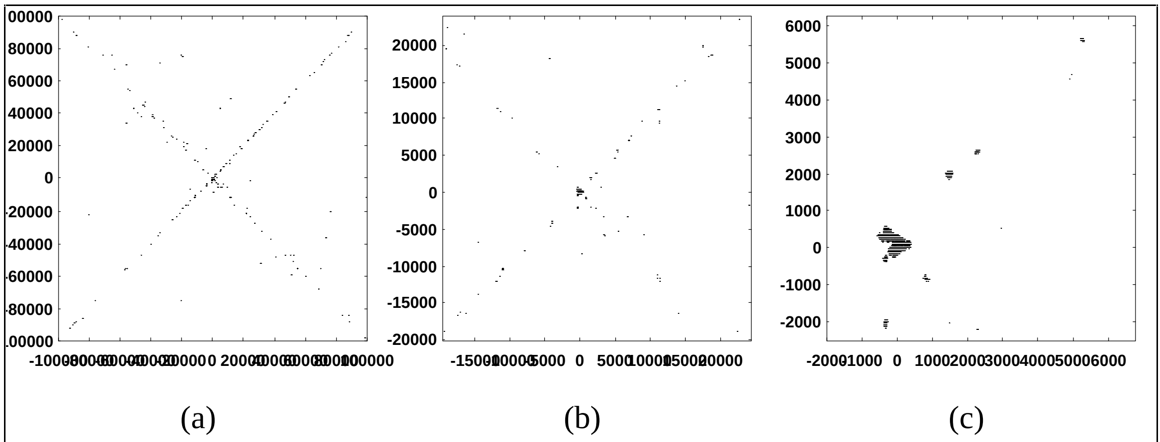


Figure 3.27: Sample unbounded GL configurations. Snapshots taken at perturbation 1906, time step 4314. The full system (a) is dominated by the glider domain. The radius of gyration (b) and half-count radius (c) attempt to filter out this region.

The gliders also complicate the dynamics in other ways. One important property of SOC systems is that the driving rate approaches zero (see Section 5.2.2). This implies that all gliders should have moved off to infinity (disappeared) before the system is perturbed. As it stands the system is perturbed when it reaches stability, even though the gliders are still active. The problem is that, using the perturbation method mentioned in Section 3.2.1, it is possible that these gliders could be perturbed. In fact, as the glider domain grows, it may become the dominant force in the evolution and accrue most of the perturbations. I had not considered this possibility when collecting the above data. The effect of perturbations in the glider domain is to form clusters at unnaturally large distances from the central cluster, weighting the glider domain even more. If I had it to do over again, I would restrict perturbations to occur within the half-count radius of the center-of-mass. It is unclear whether this would significantly alter the distribution of avalanches.

4. Mean-field and mixing

4.1. Introduction

We now turn our attention to another method developed for analyzing the many-body problem. *Mean-field theories* have been successful in predicting critical transitions in such systems as the *Ising model*--a mathematically idealized magnet [22]. The Ising model is relevant because it shares some commonalities with GL: namely, it is consists of a spatially-extended lattice of finite-state points which are constricted to interactions with only nearest neighbors. Perhaps, then, a mean-field analysis would provide some insight for us.

As the name implies, mean-field theory proceeds by replacing the particulars of an interaction with an expectation value which represents the system as a whole. Each site is assumed to be identical, and as such, any particular site's interactions with its neighbors can be approximated by a *mean field*. Further, because this site is identical to the others, the field is self-consistent. That is, the field represents some parameter of the neighboring sites, and this parameter must also describe the central site itself. This last requirement makes the transcendental problem easily solvable.

4.2. GL's mean field map

In GL, transitions are determined by the number of live cells in a neighborhood. This suggests we use the probability of each cell being *alive* as our mean field. On a large scale, this parameter is just the population density, c. Given such a field, the probability of exactly σ live neighbors surrounding a site is given by the binomial distribution:

$$p(\sigma,c)=\binom{8}{\sigma}c^{\sigma}(1-c)^{8-\sigma}. \quad \textbf{(4.1)}$$

Of course, the central site is also going to have an occupation probability c (self-consistency requirement). Using this information we can determine the occupation probability in the next time step from Eq. (1.3):

$$c(t+1)=c(t)\sum_{\sigma=2}^{3}p(\sigma,c(t))+[1-c(t)]p(3,c(t)). \quad \textbf{(4.2)}$$

This form is called the mean-field map and it describes not just the local probabilities, but the evolution of the global population. The map is plotted below in Figure 4.1, showing the fixed points and their stabilities. These values suggest that if the system was started from an initial population in the range $c(0)\in(0.192,0.564)$ then it will evolve to a final population of $c(\infty)=0.370$. Otherwise, the system will decay and eventually disappear altogether.

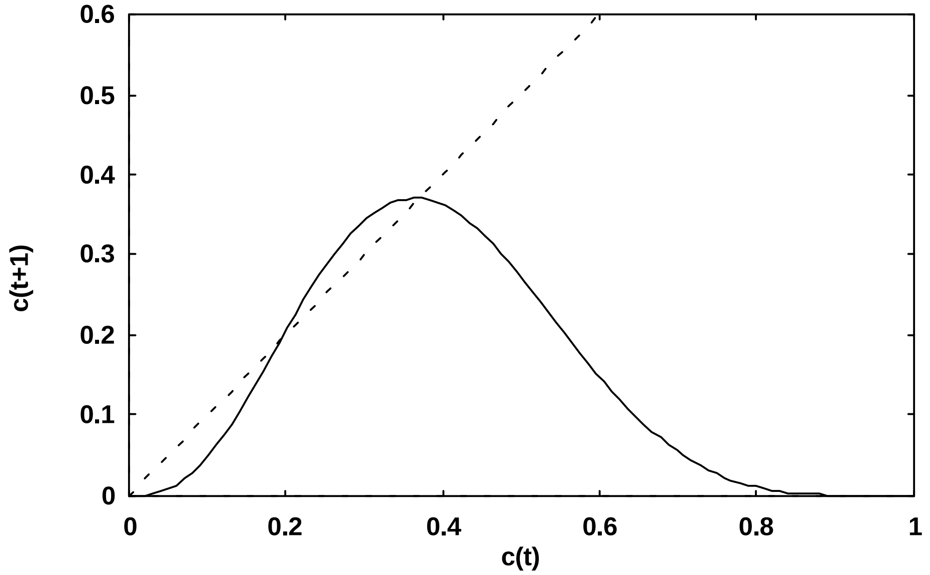


Figure 4.1: Projected mean-field map for GL. Fixed points lie at 0 (stable), 0.192 (unstable) and 0.370 (stable). These results are incompatible with experimental observations.

Of course, we know GL has a stable population density of roughly 0.03, in disagreement with the predicted value of 0.370, above. One may question why mean-field theory makes incorrect predictions for GL. By replacing particular interactions with an average field which ignores spatial inhomogeneity we must be losing information significant to GL's evolution. In fact, GL is dominated by spatial correlations which mean-field theories ignore. As a GL population evolves, each of the cells strives to reach a state compatible with its neighbors. The final, stable configuration consists of cells which are correlated over very long distances. (If GL is critical we expect the correlation length to diverge.)

4.3. Long-range mixing

We know mean-field theory ignores spatial correlations, and hence fails to properly represent GL. It may be interesting to explore the effect of modifying GL in order to destroy correlations and test the validity of this assumption. Correlations can be broken by mixing the cells (see Section 2.1.2). We consider the simplest case of long-range mixing via random jumps. (Other forms of mixing tend to complicate the results [17].)

We expect, in the limit of complete mixing, $m \to 1$, that the global dynamics should conform with mean-field predictions.

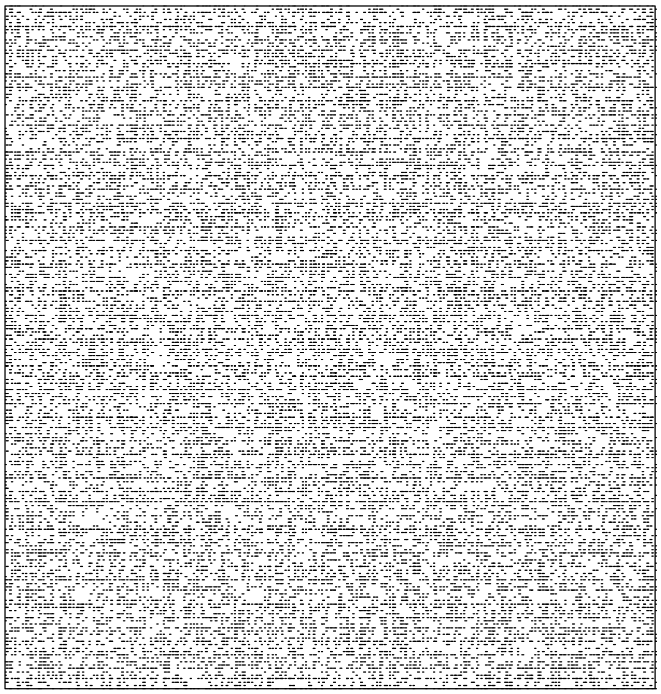


Figure 4.2: Sample equilibrium configuration of GL with long-range, m=1.0 mixing on a 256×256 **lattice with periodic boundaries.**

Observing how GL metamorphoses from the sparse, deterministic system seen in Figure 1.3 to the results observed above may reveal some insights into GL's nature. In fact, GL lies at one limit point on a bifurcation diagram where *m* plays the role of the bifurcation parameter. This may reveal insights into GL's critical nature. For small *m*, we expect the lattice to respond like GL with occasional perturbations. Large *m*, on the other hand, should have the effect of adjusting the dynamics to conform with the mean-field map. These predictions are confirmed in the figure below. Also, we observe a phase transition in the intermediate values of *m*.

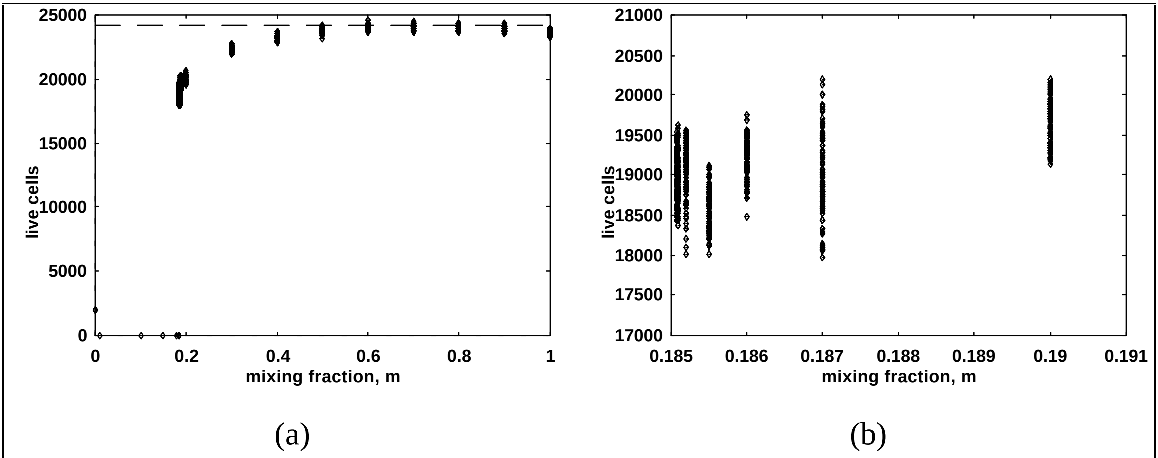


Figure 4.3: Bifurcation diagram for GL with long-range mixing on a 256×256 lattice with periodic boundaries. As the mixing fraction approaches 1 (see (a)), the population grows to the mean-field prediction (line). There appears to be a second-order transition at m=0.18508, but on closer inspection (b) it may be first-order.

According to Eq. (2.4) the actual mixing fraction is somewhat smaller than the assumed value, due to possible null moves. The error is calculated from $\bar{c} \sim 0.4$ and $N_m = 256^2$. Applying these quantities reveals a negligible error on the order of 10^{-5}. Hence, the results already shown do not need adjustment because null moves play an infinitesimal role in the dynamics.

The natural occurrence of the phase transition at $m_c = 0.18508$ may be surprising at first. However, similar transitions have been observed in other stochastic extensions of GL [23] and, in other CA, even more complex bifurcations are sometimes observed [17]. In this case, we may conceptually interpret the bifurcation as the point where a *disordering force* (a monotonically increasing function of the mixing fraction) exceeds a constant *ordering force* represented by GL's rules. Unfortunately, this interpretation fails to predict the value of m_c.

As mentioned above, the dynamics near the transition point seem to be defined by the balance of the ordering and disordering subrules. It may be possible to quantify this behavior, at least roughly. Consider a block which consists of a central site and its eight neighbors. The first subrule attempts to correlate the block. However, if any of the cells in the block are moved, it becomes impossible to organize. Hence, as a first approximation, we consider m_c to lie at that point such that, on average, one cell in each block has been moved. We expect this to destroy correlations as fast as the ordering subrule forms them. The number of cells moved in such a block is just nine times the probability of each cell being moved. To calculate this probability we must consider the possibility of a live cell moved out of the block (to first order this is just *m*) or a dead cell being replaced by a live cell from elsewhere. This latter probability is given by

$$\begin{aligned}\Pr(\text{dead gets live}) &= \underbrace{mcN_m}_{\#\text{ moves}} \times \underbrace{\frac{1}{(1-c)N_m}}_{\substack{\text{chance of receiving}\\ \text{cell per move}}} \\ &= \frac{mc}{1-c}\end{aligned} \quad . \qquad \textbf{(4.3)}$$

Now, the probability of any single cell being moved is just the combination of the probabilities for the live and dead cells respectively:

$$\begin{aligned}\Pr(\text{cell moved}) &= mc + (1-c)\Pr(\text{dead gets live}) \\ &= 2mc\end{aligned} \quad . \qquad \textbf{(4.4)}$$

We are now in a position to estimate the critical mixing fraction. As I mentioned above, we suspect this to occur at the point when correlations are being destroyed as fast as they can be constructed. This suggests that, on average, one cell in each block is moved. Since the number of cells moved is just nine times the value given in Eq. (4.4) we expect a transition at

$$m_c = \frac{1}{9 \cdot 2c} \cong 0.150 \tag{4.5}$$

We take c to be the mean-field population density because we are interested in the equilibrium dynamics and the mean-field dynamics represent an equilibrium configuration . This estimate agrees roughly with the observed value of 0.18508. A better estimate would also consider the possibility that the move does not affect the transition--for example, a neighborhood containing eight live cells would evolve in the same way regardless of whether another cell was added or one of the eight removed. In this case correlations could still grow, but we assume these situations are rare.

4.4. Asynchrony

In GL, correlations are set up not only spatially, but over time as well. We may expect, then, that breaking temporal correlations should produce dynamics similar to those observed in the last section. At first glance one may guess the figure below, which shows a GL configuration with a low synchronisity, looks like Figure 4.2, a sample mean-field configuration. On closer inspection, however, the reader will notice patterns of vertical and horizontal lines which are not seen in the mean-field configuration. This supports claims in reference [24] that asynchrony induces order in cellular automata.

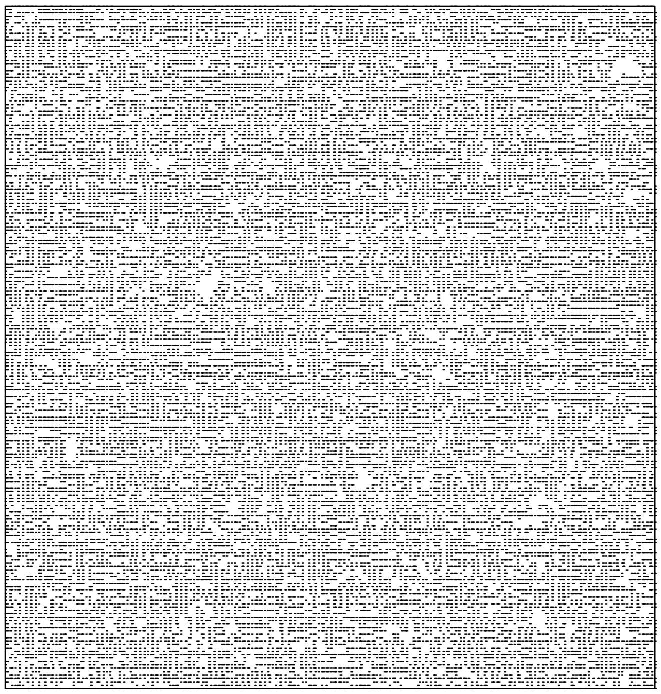


Figure 4.4: Sample equilibrium GL configuration with asynchronous updating (s=0.10) on a 256×256 lattice with periodic boundaries. Notice the pattern of vertical and horizontal lines emerging.

Again, curiosity prompts us to explore the transition from GL (s=1) to asynchrony. The figure below indicates another second-order phase transition. The dynamics responsible for this transition and the transition observed with mixing deserve closer inspection. For now, let me only say that we see from the graph that asynchrony is a markedly different property than mixing and the transitions must arise from different forces.

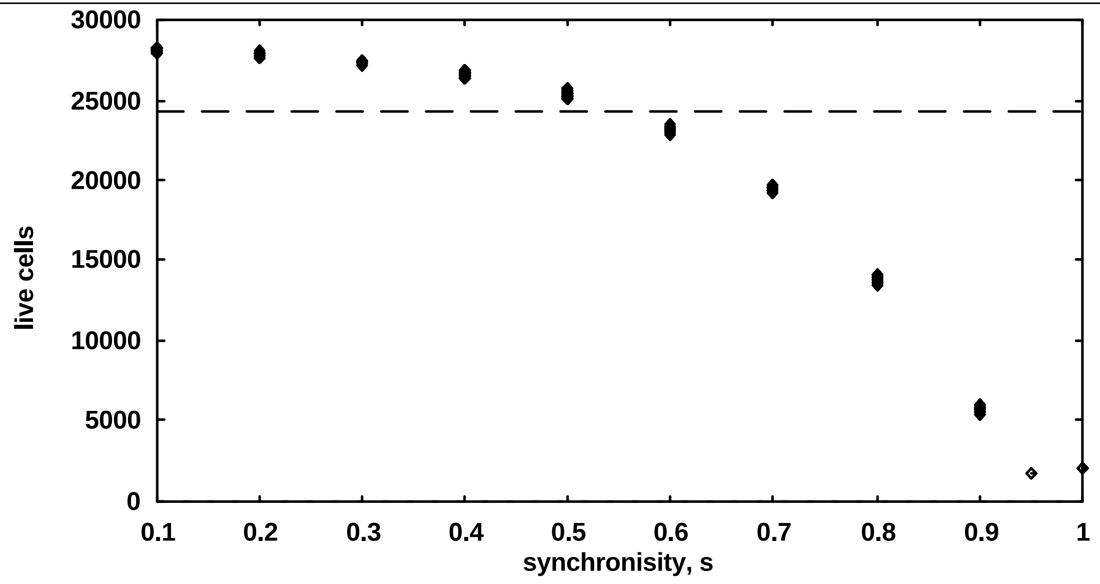


Figure 4.5: Bifurcation diagram for population density as a function of synchronisity for GL on a 256×256 periodic lattice. A second-order transition occurs between s=0.9 and 0.95. Notice that, in the extreme, the dynamics do not correspond to mean-field predictions (line).

5. Conclusions

5.1. Is GL SOC?

In this paper we have explored evidence which suggests the Game of Life (GL) is self-organized critical (SOC) as well as evidence which suggests it is not. In an attempt to reconcile these conflicting views we stumbled upon a tool -- a simple scaling form of the cumulative distribution -- which clarified much of the vague and subjective evidence supporting either claim. With this tool we were able to apply a rigorous finite-scaling analysis and discovered that the evidence points to GL falling short of criticality. Unfortunately, we have very little data beyond the length-scale where GL crosses over from finite-scaling to stability -- larger lattices must be studied to confirm that GL is subcritical.

In making the discovery that GL is subcritical we have reconciled arguments from both camps -- we have applied a finite-scaling analysis and observed that it is in agreement with the lack of scaling observed in the average of the distribution. We have explored a variety of boundary conditions and alternate geometries and found no indication that these variations affect the dynamics in any way except in the size of the lattice at which crossover occurs. We have also discovered an unusual and perplexing scaling function in that it increases above one before falling off to zero.

One must always constrain one's conclusions to scales which have been explored, and hence, we will never know if GL is truly critical on all scales. The best we can say is that GL is subcritical, at least up to such-and-such a system size.

Regardless of whether GL does exhibit SOC or not, I hope this paper conveys to the reader the problems with the analytical tools at our disposal. New methods need to be developed, or old methods adapted, to the exploration of spatially extended dynamical systems far from equilibrium. In the following sections I present some of my own ideas in the pursuit of this goal.

5.2. Unexplored avenues

5.2.1. Renormalization group

The renormalization group is an elegant new theory developed in the 1970s by Wilson [25, *p. 18*] and others to study spatio-temporal dynamics of phenomena lacking a length-scale. It is well suited to critical phenomena, providing a method for approximately computing the critical exponents, and provides a conceptual framework for understanding that enigma of criticality--universality.

The basic idea behind (real space) renormalization is that of coarse-graining,. The lattice space of cells is partitioned into blocks of linear dimension *l*. Then, each block is replaced by a single site which represents some sort of average of the block. Self-similar properties of the transformation are exploited revealing fundamental properties of the underlying system.

Each iteration of renormalization decreases the length scale by a magnitude *l*. Hence, for systems off the critical manifold the correlation length is also rescaled, $\xi \to \xi/l$, pulling near-critical systems further and further from criticality ($\xi = \infty$) and making them easier to analyze with traditional methods.

Unfortunately, in GL no conserved quantities have been discovered, and in particular, there is no analogue for energy. Hence, it is impossible to construct a Hamiltonian (the preferred quantity to obey self-similar scaling). Nevertheless, despite my abysmal understanding of the subject, intuition tells me a renormalization approach would go far in the deciphering of GL's mysteries.

5.2.2. Mapping onto criticality

Recently, Sornette *et al* [26] have described a method of mapping specific SOC models onto dynamical critical phenomena. SOC is viewed as a result of tuning the *order* *parameter* (instead of the *control parameter*) to approach a vanishingly small non-zero value, which has the effect of forcing the control parameter to the critical point (see Figure 1.4(b)). Mapping SOC onto criticality has the advantage of not requiring any conservation laws and it explains the *very slow driving rate* observed in all SOC systems.

In their paper Sornette *et al* give an example of how this mapping is implemented on the canonical SOC model--the sandpile. They consider a physical system of a drum containing sand which is rotated at a rate $\frac{d\theta}{dt}$. The rotation is driven by a torque, *T*. At some critical torque, T_c, avalanches of all sizes are observed in the sand with a decaying power law frequency. This suggests the system is at a critical point. Below this point the torque is insufficient to rotate the drum, while above this point a non-zero average rotation rate, $\left\langle \frac{d\theta}{dt} \right\rangle$, is observed. SOC is seen as controlling the order parameter, $\frac{d\theta}{dt}$, instead of the control parameter, *T*. If we require $\frac{d\theta}{dt} \to 0^+$ then we incidentally force $T \to T_c$, the critical value. The important point here is that there is no manual tuning of any parameters, the critical point is found automatically.

One could explore GL in these terms. As we will see, the dynamics are driven by site perturbations which occur only after very long times (after the system has stabilized). This suggests, in analogy with the sandpile mapping, that the perturbation rate plays the role of the order parameter. However, the question of what plays the role of control parameter comes to light. I can find no clear way of interpreting GL as a critical system, in this manner.

On a different tack, GL is suspected to be SOC because of the apparent power law behavior observed. No experiments have been done which place GL at a critical point on a bifurcation diagram. The problem has been finding a suitable control parameter which is continuous and yet describes GL for some value. GL has a discrete neighborhood, discrete rules, and a discrete alphabet (*dead* or *alive*), making it difficult to parameterize. One method is to consider the rule space of probabilistic CA of which GL is a member. For GL we determine the transition probabilities from Eq. (1.3):

$$\begin{aligned} p^{\mathrm{GL}}_{0\to 1}(\sigma) &= \mathrm{rule}(0,\sigma) \\ p^{\mathrm{GL}}_{1\to 1}(\sigma) &= \mathrm{rule}(1,\sigma) \end{aligned} \tag{5.1}$$

and

$$\begin{aligned} p^{\mathrm{GL}}_{0\to 0}(\sigma) &= 1 - p^{\mathrm{GL}}_{0\to 1}(\sigma) \\ p^{\mathrm{GL}}_{1\to 0}(\sigma) &= 1 - p^{\mathrm{GL}}_{1\to 1}(\sigma) \end{aligned}. \tag{5.2}$$

Now we construct a two-parameter family of rules which includes GL.

σ	$p_{0\to 1}(\mu_1,\sigma)$	$p_{1\to 1}(\mu_2,\sigma)$
0	0	0
1	0	$\max(0,-\mu_2)$
2	$\max(0,-\mu_1)$	$\min(1,1-\mu_2)$
3	$1-\lvert\mu_1\rvert$	$\min(1,1+\mu_2)$
4	$\max(0,\mu_1)$	$\max(0,\mu_2)$
$5+$	0	0

(5.3)

for $\mu_1,\mu_2 \in (-1,1)$. The other probabilities are exclusive as in Eq. (5.2). Upon close examination we observe that GL corresponds to $(\mu_1,\mu_2)=(0,0)$. Physically, the above table can be interpreted as meaning that the CA prefers a more heavily occupied neighborhood for larger values of the parameters and a sparser neighborhood for smaller values. The parameters are responsible for shifting the location of the crest in Eq. (5.3).

It is unclear whether this method will give any meaningful results but I intend to study it in the future. I foresee difficulties, however, because GL differs in one crucial way from the CA nearby in the parameter-space: it is deterministic. Hence, it may set up long-range correlations and large-scale structures which probabilistic systems tend to smear out. We have already seen examples of this when we studied mixing and asynchrony in Chapter 4.

5.2.3. Directed Percolation

To study the dynamics in GL we considered the effect of a single site perturbation--flipping the state of a cell and watching the resulting avalanche. Statistically speaking, the avalanche has a chance of either growing or shrinking at each time step, as it evolves. Perhaps this evolution can be interpreted in terms of a directed percolation problem.

Directed percolation [27] is used to model the flow of fluid through a porous material. At each time step the fluid can penetrate further into the material with some probability, p. If we consider the family of all such models, then we observe a critical transition as p increases past some probability p_c. For small p, the fluid penetration is inevitably halted, eventually. Above p_c, however, there will always be at least one path which permeates the entire length of the substance. The value of p_c depends on the dimensionality, geometry, *et cetera*.

It is possible that the evolution of an avalanche can be modelled in these terms. If we can determine that GL avalanches are guaranteed the possibility of traversing the entire lattice space, does this not put some lower bound on GL's complexity? One of GL's sticking points, the strong correlations which extend over the lattice may not apply (in the same way) to the avalanche as it does to the space itself. If this is true, a mean-field theory, like directed percolation, may be applicable to the avalanches.

5.3. Summary

As can be seen, GL holds a wealth of possible future research topics. Remember, though, we are interested in GL not for its own sake, but in order to find tools which may be useful for the analysis of natural spatially extended dynamical systems--particularly those near a critical point. We have seen that spatio-temporal correlations strongly affect the dynamics of the system. Breaking these correlations, by either spatial or temporal mixing, reduces GL's complexity and makes it more readily solvable. But natural systems with internal chronometers do exist, and may exhibit the same complexity seen in GL. Complexity sometimes occurs even without synchronization. In these cases, the experience we have gained from the study of GL will be useful.

A. CellBot source code

CellBot copyright © Hendrik J. Blok 1994, 1995

This is the source code, in C, for the program CellBot. All files included here may be freely copied and redistributed, without modification, provided the copyright notice is not removed. This program is for non-commercial use only and may not be sold for profit.

The files nr.h and ran1.c can be found in Numerical Recipes [7] and are not included here. However, nrutil.c and nrutil.h are included because they include important modifications to the original code (placed into the public domain by Numerical Recipes Software). To compile CellBot simply copy all these files to the same directory and compile them. Then link the object files to create an executable. Note: the function **main()** which contains the heart of the algorithm, can be found in the file cb.c.

bounds.c

```
/*
  CellBot - bounds.c

        Copyright 1994,1995 Hendrik J. Blok

  Routines for analyzing boundary conditions.  Note that ALL systems are
  bounded, even btype=NONE.  In fact these behave as PERIODIC systems
  with lengths equal to MAXINT.  This is because large integers loop
  around to their maximal negative value (and vice versa).

  Note: on DOS MAXINT=65535 while on Unix MAXINT=4294967295.

  Modifications:

  v2.05a  Aug 12/94
     - changed btype[] to a float in preparation for HOT boundaries
     - added Hot boundaries

  v2.04a  Aug 11/94
     - in initbounds() btype is now read as a string instead of a coded
        integer

  v2.02a  Aug 10/94
     - added routine initbounds() which reads boundary info. from config.
        file

  v2.01a  Aug 9/94
     - changed boundary type REFLECT to REFLECT_EVEN and REFLECT_ODD

  v2.00e  Aug 9/94
     - deleted routine single_applybounds().  Now always uses
        applyboundaries() for consistency.
     - reactivated map_inbounds() under the new name map_across().
  v2.00d  Aug 9/94
     - in apply_boundaries() changed PERIODIC & REFLECT routines to only
        duplicate cells within range of border (see isonborder).
  v2.00c  Aug 8/94
     - fixed bug in how REFLECT handled corners. (It didn't!)  Required
        complete rewrite of subroutine in applyboundaries().
     - deleted map_cell().  No longer used.
     - temporarily disabled map_inbounds() and single_applybounds().
  v2.00a  July 21/94
     - now can handle separate conditions for each boundary.  Corner
        disputes are handled by choosing priorities for boundaries.
*/

#include <stdlib.h>         /* defines abs()    */
#include <string.h>                             /* defines stricmp()       */
#include "bounds.h"         /* defines NONE, COLD, PERIODIC, REFLECT_EVEN, REFLECT_ODD, LOOP_OVER_BOUND(), inbounds()
        */
```

```
                                                                   /* includes stdio.h ==> defines FILE          */
#include "cb.h"          /* defines LOOP_OVER_CELLS(), LOOP_OVER_FLIP_NBRS() */
#include "rules.h"        /* defines dim, live(), maxnbrs, nbrx   */
#include "nrutil.h"       /* defines ivector(), free_ivector(), ivector_cmp(), CMP_LESS, CMP_GREATER  */
#include "fileio.h"       /* defines fstrip() */
#include "pandora.h"       /* defines runtime_err()   */
#include "rrandom.h"       /* defines flip()   */

int *minx, *maxx;     /* boundaries      */
float *btype;        /* array of boundary types (by descending priority) */
int *bcode;          /* array of boundaries (")  */


int beyondbound(int bc, int *x)
/*
    Tests if x is outside a particular boundary.  bt is of the form indicated
    in the configuration file.

    Note: this routine ignores the possibility that btype==NONE.
*/
{
    if (bc<0)                          /* minx */
        if (x[-bc] < minx[-bc]) return 1;
        else                  return 0;
    else                               /* maxx */
        if (x[bc] > maxx[bc])      return 1;
        else                  return 0;
}


int inbounds(int *x)
/*
    Tests whether x is within [minx..maxx].  Always returns TRUE if no
    boundaries.

    Modifications:

    v2.00a July 21/94
        - now compatible with multiple boundary conditions
*/
{
    int p;

    /* check boundaries (by priority)   */
    for (p=1; p<= 2*dim; p++)
        if (beyondbound(bcode[p], x))
            if (btype[p] == NONE)      return 1;
            else                      return 0;

    /* else (is inside all bounds)  */
    return 1;
}


void map_across(int bc, float bt, int *x)
/*
    Maps x across the boundary bc according to the boundary type, bt.

    Modifications:

    v2.05a  Aug 12/94
        - changed switch() to if..else because switch doesn't accept floats

    v2.01a  Aug 9/94
        - added support for REFLECT_EVEN and REFLECT_ODD

    v2.00e  Aug 9/94
        - renamed from map_inbounds() to map_across()
        - flipped boundary which PERIODIC maps across to reflect new use
            of routine (now designed to map in-bounds cells to
            out-of-bounds).
*/
{
    if (bt==PERIODIC) {
        if (bc<0)
            x[-bc] = minx[-bc] - (maxx[-bc] - x[-bc]) -1;
        else
            x[+bc] = maxx[+bc] + (x[+bc] - minx[+bc]) +1;
    } else if (bt==REFLECT_EVEN) {
        if (bc<0)
            x[-bc] = minx[-bc] - (x[-bc] - minx[-bc]) -1;
        else
            x[+bc] = maxx[+bc] + (maxx[+bc] - x[+bc]) +1;
    } else if (bt==REFLECT_ODD) {
        if (bc<0)
            x[-bc] = minx[-bc] - (x[-bc] - minx[-bc]);
        else
            x[+bc] = maxx[+bc] + (maxx[+bc] - x[+bc]);
    }
}


int pri_beyondbound(int p, int *x)
/*
    Tests if x is outside a particular boundary.  b is of the form indicated
    in the configuration file.  If beyond a higher priority border or not
    beyond border b then returns 0.  Else returns 1.

    Note: you can't choose the boundary like you can in beyondbound() because
        if you choose one other than b[p] then it may be a higher priority
        boundary in which case this routine could return a false 0.

    Note: this routine ignores the possibility that btype==NONE.
*/
{
    int i;

    for (i=1; i<p; i++) if (beyondbound(bcode[i], x))   return 0;
    /* else */  if (beyondbound(bcode[p], x))           return 1;
    /* else */                                          return 0;
}


int is_on_border(int *x)
/*
    Assumes x is out-of-bounds.  Returns 1 if x is a neighbor to an
    in-bounds cell, else returns 0.
*/
{
    int temp = 0;
    int *nx = ivector(1,dim);

    LOOP_OVER_FLIP_NBRS(x,nx)
        if (inbounds(nx))       temp = 1;
    }

    free_ivector(nx,1,dim);
    return temp;
}


void applyboundaries(void)
/*
    Modifies cell states on border to reflect boundary conditions.
    Deals with each edge separately handling corners according
    to the priorities of the boundaries.

    Modifications:

    v2.05a  Aug 12/94
        - changed switch() to if..else because switch() doesn't work on
            floats
        - added Hot boundaries
*/
{
    int p;
    cell *c, *like;
    int *x = ivector(1,dim);

    for (p=2*dim; p>=1; p--) {

        if (btype[p]==COLD) {
            LOOP_OVER_CELLS(c)
                if (pri_beyondbound(p,c->x))    delete_cell(&c);
            }

        } else if (btype[p]==PERIODIC    ||
                   btype[p]==REFLECT_ODD ||
                   btype[p]==REFLECT_EVEN) {
            /*
                These types map cells across boundaries.  They set out-
                of-bounds cells to mimic the state of the corresponding
                in-bounds (sort of) cell.

                This bit has been entirely rewritten in v2.00c.
            */
            LOOP_OVER_CELLS(c)
                if (live(c) && !pri_beyondbound(p,c->x)) {

                    /* map c->x to out-of-bounds equivalent (x) */
                    ivector_cpy(x,c->x,1,dim);
                    map_across(bcode[p], btype[p], x);

                    /* if just outside boundary then duplicate c    */
                    if (pri_beyondbound(p,x) && is_on_border(x)) {
                        like = getcell(x);
                        like->state = c->state;
                    }
                }
            }
        } else if (btype[p]>=0.0 && btype[p]<=1.0) {    /* HOT  */
            int *outx = ivector(1,dim);

            LOOP_OVER_BOUND(bcode[p], x)
                LOOP_OVER_NBRS(x,outx)
                    if (pri_beyondbound(p,outx)) {
                        c = getcell(outx);
                        c->state = flip(btype[p]) ? x_flipstate(deadstate) : deadstate;
                    }
                }
            }
            free_ivector(outx,1,dim);
        }
    }
    free_ivector(x,1,dim);
}


void initbounds(FILE *f)
/*
    Read boundary information from f (configuration file).  Reads
    bcode, x, and btype.

    Modifications:

    v2.06a  Aug 21/94
        - error trapping

    v2.05a  Aug 12/94
        - read HOT boundaries

    v2.04a  Aug 11/94
        - btype is now entered as a string instead of a coded integer

    v2.02a  Aug 10/94
        - initial version
```

```
*/
{
    int p;
    char bs[20];

    /* allocate arrays  */
    minx = ivector(1,dim);
    maxx = ivector(1,dim);
    bcode = ivector(1,2*dim);
    btype = vector(1,2*dim);

    for (p=1; p<=2*dim; p++) {
        /* read bcode   */
        fscanf(f, "%i", bcode+p);              fstrip(f);
        if (bcode[p]==0 || abs(bcode[p]) > dim) runtime_err("Configuration File: bcode must be in the range +/-1 ... +/-dim");

        /* read minx/maxx   */
        if (bcode[p] < 0) {
            fscanf(f, "%i", minx - bcode[p]);   fstrip(f);
        } else {
            fscanf(f, "%i", maxx + bcode[p]);   fstrip(f);
        }

        /* read btype   */
        fscanf(f, "%s", bs);                   fstrip(f);

        if      (stricmp("None",bs)==0)         btype[p] = NONE;
        else if (stricmp("Cold",bs)==0)         btype[p] = COLD;
        else if (stricmp("Periodic",bs)==0)     btype[p] = PERIODIC;
        else if (stricmp("Reflect_Odd",bs)==0)  btype[p] = REFLECT_ODD;
        else if (stricmp("Reflect_Even",bs)==0) btype[p] = REFLECT_EVEN;
        else if (stricmp("Hot",bs)==0) {        /* next no. is temperature  */
            /*
                                                Note: COLD==0.0 so applybounds() will use COLD (erase out-
                of-bounds cells) if this number is 0.0
            */
            fscanf(f, "%f", btype+p);   fstrip(f);
            if (btype[p]<0.0 || btype[p]>1.0)
                runtime_err("Configuration File: Hot boundaries must be in the range 0.0 ... 1.0");
        } else
            runtime_err("Configuration File: boundary type not recognized");
    }

    for (p=1; p<=dim; p++)
        if (minx[p]>maxx[p])    runtime_err("Configuration File: maxx must be >= minx");
}

/* turn off "'____' declared but never used" warning    */
#pragma warn -use
•
```

bounds.h

```
/*
                CellBot - bounds.h

                Copyright 1994,1995 Hendrik J. Blok

                Modifications:

                v2.14a      Jun 18/95
                            - #include stdio.h so that FILE is defined in rules.c

                v2.05a      Aug 12/94
                            - changed boundary types to floats in preparation for HOT boundaries

                v2.01a      Aug 9/94
                            - changed boundary type REFLECT to REFLECT_EVEN and REFLECT_ODD
*/

#ifndef _BOUNDS_H_
#define _BOUNDS_H_

#include <stdio.h>       /* defines FILE             */
/*#include "hash.h"*/

/* boundary types         */
#define NONE                                    -1.0
#define COLD                                    0.0
#define PERIODIC        2.0
#define REFLECT_ODD                             3.0
#define REFLECT_EVEN            4.0

/*
                The following is a control structure like the ones found in cb.h.  This
                one loops over all possible x-values of a boundary.

                Modifications:

                v2.05a      Aug 15/94
                            - new
*/
static int bndcarry;
static int bndrun;
#define LOOP_OVER_BOUND(b,x)                ivector_cpy(x,minx,1,dim);                        \
                                                                                    if (b>0)      x[b]=maxx[b];                        \
                                                                                    if (abs(b)==dim)          x[dim-1]--;
\
                                                                                    else
                x[dim]--;                       \
                                                                                    while (1) {                                    \
                                                                                                bndcarry=1;
\
                                                                                                for  (bndrun=dim;  bndrun>=1  &&
bndcarry; bndrun--) {    \
                                                                                                                    if  (bndrun  !=  abs(b))  {
\
                x[bndrun]++;                              \
                                                                                                                                    if
(x[bndrun] > maxx[bndrun]) {            \
                x[bndrun] = minx[bndrun];               \
                bndcarry = 1;                           \
                                                                                                                                    }          else
\
                bndcarry = 0;                           \
                                                                                                                    }
\
                                                                                                          }                                   \
                                                                                                          if (bndcarry)                break;

/* global vars.              */
extern float *btype;                        /* boundary type (by descending priority)          */
extern int *bcode;                                          /* boundary code (by descending priority)         */
extern int *minx, *maxx;                  /* coordinates of boundaries          */

/* function prototypes    */
extern int inbounds(int *x);
extern void applyboundaries(void);
extern void initbounds(FILE *f);

#endif        /* _BOUNDS_H_         */•
```

cb.c

```
/*
   CellBot - cb.c

                Copyright 1994,1995 Hendrik J. Blok

   MAIN PROGRAM

   Modifications:

                v2.14a      Jun 18/95
                            - in advance() mixing routine modified to work with new move_cell()

                v2.13d      Jun 8/95
                            - sum count_live in fillgrid() so record_sps() works on zeroth step.
                v2.13c      May 19/95
                            - now handles both DOS and Unix filename formats in configuration
                                          file.  See configure().
                v2.13b      May 13/95
                            - fixed bug which halted program when t>sync*ntime.  Should halt
                                          when sync*t>ntime.
                v2.13a      May 9/95
                            - replaced t by sync*t in record_cps(), record_sps(), record_spp()
                                          and when comparing length of last pert.  Changed ntime to a
                                          float.

                v2.12a      Apr 2/95
                            - don't use random walk when mixing cells in advance()

                v2.11a      Mar 15/95
                            - prevent repeat moves of each cell by flagging moved cells

                v2.10a      Mar 12/95
                            - advance() now randomly mixes cells by moving some of them

   v2.06a  Aug 21/94
      - error trapping

   v2.05a  Aug 12/94
      - in version_cmp() now checks that input file isn't newer than the
          CellBot program
      - in fillgrid() now uses control structure LOOP_OVER_SPACE() defined
          in cb.h

   v2.03a  Aug 11/94
      - added routine version_cmp() which confirms that the file being
          read is a recent enough version and the right type of file.

   v2.02a  Aug 10/94
      - in configure() now swaps to initbounds() to read boundary info.

   v2.00b  July 27/94
      - if not recovering from crash then record initial data in files
          (.cps & .sps)
*/

/* my e-mail address    */
#define CB_MAILTO   "blok@physics.ubc.ca"


/*#include <stdio.h>*/
#include <string.h>                                                   /* defines strlen(), strnicmp(), stricmp()            */
#include <stdlib.h>             /* defines abs()    */
#include "pandora.h"            /* defines runtime_err(), time_t, time()    */
#include "rrandom.h"            /* defines flip(), rrandom(), time_t    */
#include "fileio.h"             /* defines fexist(), fstrip(), expand_fn()   */
#include "bounds.h"             /* defines applyboundaries(), minx, maxx, btype, inbounds() */
#include "cb.h"                 /* defines LOOP_OVER_CELLS(), LOOP_OVER_NBRS(), LOOP_OVER_FLIP_NBRS(), LOOP_OVER_SPACE(),
cell  */
#include "record.h"             /* defines fscan_dump(), fprint_dump(), record_cps(), record_sps(), record_cpp(), record_spp()  */
#include "rules.h"                  /*  defines  initrules(),  dim,  deadstate,  x_flipstate(),  dead(),  live(),  maxnbrs,  nbrx,  sync,  applyrules(),  mixing,
move_cell()             */
#include "stable.h"             /* defines stable(), maxperiod, stablewin   */
```

```
#include "nrutil.h"             /* defines ivector(), free_ivector(), ivector_cpy(), ivector_cmp(), CMP_GREATER */

/* global variables */
long nperts;            /* max. # perts (nperts<0 ==> loop forever) */
float ntime;                        /* max. # time steps on last pert   */
int rec_cps,            /* record cells per step (boolean)  */
    rec_sps,            /* record stats per step (boolean)  */
    rec_cpp,            /* record cells per perturb (boolean)   */
    rec_spp;            /* record stats per perturb (boolean)   */
char prefix[255];       /* prefix (path+partial filename) for all data files.   */
char dumpfname[255];    /* (path &) name of dumpfile    */
float dens;             /* initial fill density within bounds   */
time_t dumptime;        /* keeps current time, to test if dump needed   */
long dump_period;       /* time between dumps in seconds    */
int delete_flag;        /* used in LOOP_OVER_CELLS  */
int dump_flag;          /* modify dumpfile? (boolean)   */
long count_live,        /* # of live, inbounds cells    */
    count_activity;     /* sum of changes to system over one step   */
long sum_activity=0;    /* sum of 'count_activity' over one pert.   */
int *pertx;             /* location of perturbation */

void main(int argc, char *argv[])
{
    /* function prototypes  */
    void configure(char cfgfname[]);
    void fillgrid(void);
    void advance(void);
    void addneighbors(void);
    void perturb(void);
    void notice(void);

    /* variable declaration */
    long pert;                  /* pert = 0..nperts.    */
    unsigned long t;            /* time index   */
    int lastpert;               /* is last pert? (boolean)  */

    /* copyright notice */
    notice();

    /* Parse command-line.  */
    if (argc != 2)  runtime_err("Usage: CB <filename.ext>\n\n\twhere <filename.ext> is the name of the configuration file.");

    /* initialize */
    rrandomize();
    configure(argv[1]);

    /* Fill hash table. */
    if (fexist(dumpfname))
        fscan_dump(&pert, &t);      /* read dumpfile and update pert & t    */
    else {
        fillgrid();
        pert = 0;
        t = 0;
        /* If not recovering then record data. First included in v2.01a */
                                if (rec_cps)    record_cps(pert, sync*t);
                                if (rec_sps)    record_sps(pert, sync*t);
    }
    time(&dumptime);

    /* main loop */

    /*  Crashes are expected to occur at applyboundaries()...advance() and
        at stable().  Want recordings at positions such that after recovering
        from a crash no info will be lost or recorded twice.  Placing all
        suspect routines before recordings should work. With the current
        configuration stable() may be executed twice in a row if there is a
        crash.  */

    while (nperts < 0 || pert <= nperts) {  /* nperts<0 ==> loop forever    */
        lastpert = (nperts >=0 && pert+1 > nperts);
        do {
            if (dump_flag && elapsed(&dumptime, (time_t) dump_period)) {
                fprint_dump(pert, t);
            }

            t++;
                                        if (lastpert && sync*t > ntime)  /* if last step on last pert then exit  */
                break;

            /* H:   - live cells
                    - maybe neighbors              */
            applyboundaries();
            /* H:   - live cells
                    - boundaries                   */
            addneighbors();
            /* H:   - live cells
                    - boundaries
                    - neighbors                    */
            advance();
            /* H:   - live cells                   */

                                        if (rec_cps)    record_cps(pert, sync*t);
                                        if (rec_sps)    record_sps(pert, sync*t);
        } while (!stable());

        if (rec_cpp)    record_cpp(pert);
                                if (rec_spp)    record_spp(pert,sync*t);

        perturb();
        /* H:   - live cells
                - neighbors (except nbrs of pert.)  */
        pert++; t=0;
        sum_activity = 0;   /* for tabulation   */
    };
    if (dump_flag)
        remove(dumpfname);      /* Completed execution; delete dumpfile */
}
```

```
void configure(char cfgfname[])
/*
   Reads all necessary information and sets up arrays, etc.

   Modifications:

              v2.13c      May 19/95
                          - calls expand_fn() to convert DOS<-->Unix filename formats.
                                  Applied to argv[1], rulefname, dumpfname, and prefix.
              v2.13a      May 9/95
                          - changed ntime to a float

   v2.06a  Aug 21/94
      - error trapping

   v2.02a  Aug 10/94
      - now uses initbounds() to read boundary info.

   v2.00a  July 22/94
      - now reads multiple boundary conditions from configuration file
         (by descending priority)

              v1.01a  July 16/94
      - dimension new variable pertx[] and initialize to 0.
*/
{
   FILE *cfgfile;
   char rulefname[80];
   int i;

              cfgfile = fopen(expand_fn(cfgfname),"r");
   if (!cfgfile)   runtime_err("Configuration file not found");

   version_cmp(cfgfile, "Configuration", CFG_MAJOR, CFG_MINOR);

   fstrip(cfgfile);
   fscanf(cfgfile,"%s", rulefname);    fstrip(cfgfile);
              initrules(expand_fn(rulefname));                     /* get dim, etc.    */

   initbounds(cfgfile);

   /* stopping conditions  */
   fscanf(cfgfile,"%li", &nperts);     fstrip(cfgfile);
              fscanf(cfgfile,"%f", &ntime);      fstrip(cfgfile);

   fscanf(cfgfile,"%f", &dens);        fstrip(cfgfile);
   if (dens<0.0 || dens>1.0)   runtime_err("Configuration File: dens must be >= 0.0 and <= 1.0");

   /* read maxperiod & allocate stablewin  */
   fscanf(cfgfile,"%i", &maxperiod);   fstrip(cfgfile);
   if (maxperiod > 0)  stablewin = (long *)lvector(0,2*maxperiod-1);

              fscanf(cfgfile,"%s", dumpfname);    fstrip(cfgfile);
              expand_fn(dumpfname);
   fscanf(cfgfile,"%i", &dump_flag);   fstrip(cfgfile);
   fscanf(cfgfile,"%li",&dump_period); fstrip(cfgfile);
   if (dump_period<0)  runtime_err("Configuration File: dump_period must be >= 0");

              fscanf(cfgfile,"%s", prefix);       fstrip(cfgfile);
              expand_fn(prefix);
   fscanf(cfgfile,"%i", &rec_cps);     fstrip(cfgfile);
   fscanf(cfgfile,"%i", &rec_sps);     fstrip(cfgfile);
   fscanf(cfgfile,"%i", &rec_cpp);     fstrip(cfgfile);
   fscanf(cfgfile,"%i", &rec_spp);     fstrip(cfgfile);

   fclose(cfgfile);

   pertx = ivector(1,dim);
   for (i=1; i<=dim; i++)
      pertx[i]=0;
}


void fillgrid(void)
/*
   Fills a fraction (dens) of cells within the boundaries to random states
   other than dead.

   Modifications:

              v2.13d      Jun 8/95
                          - tally count_live so that record_sps() works on zeroth step.

   v2.05a  Aug 15/94
      - now uses LOOP_OVER_SPACE() defined in cb.h which loops from minx[]
         to maxx[]
*/
{
   int *x = ivector(1,dim);
              cell *c;

              count_live=0;
   LOOP_OVER_SPACE(x)
      if (flip(dens)) {
         c = getcell(x);                  /* insert cell into hash table  */
                                           c->state = x_flipstate(deadstate);  /* set state to anything but dead   */
                                           count_live++;                                                          /* tally live cells
              */
      }
   }
   free_ivector(x,1,dim);
}


void addneighbors(void)
/*
   Strips off all dead cells and re-adds only neighbors of live cells
```

```
    (possibly boundaries).

    Modifications:

    v2.05a  Aug 15/94
        - caught bug: addneighbors() should LOOP_OVER_FLIP_NBRS() not
            LOOP_OVER_NBRS()
*/
{
    cell *c;
    int *x = ivector(1,dim);

    /* Delete dead cells.   */
    LOOP_OVER_CELLS(c)
        if (dead(c))    delete_cell(&c);
    }

    /* Restore neighbors.   */
    LOOP_OVER_CELLS(c)
        if (live(c)) {
            LOOP_OVER_FLIP_NBRS(c->x,x)
                getcell(x);         /* with insertions */
            }
        }
    }

    free_ivector(x,1,dim);
}


void advance(void)
/*
    Advance system.  Assumes boundary conditions have already been applied.
    Also does some statistical tabulation to save time.

    Operates in 2 steps: first it figures out what each the cell's new state
                will be.  Then it sets all current states to these values.

                Modifications:

                v2.14a      Jun 18/95
                            - mixing routine modified to work with new move_cell()

                v2.12a      Apr 2/95
                            - no longer uses random walk but just picks new random site in
                                        random_move().

                v2.11a      Mar 14/95
                            - added support for mixflag (to prevent repeat moves) and simplified

                v2.10a      Mar 12/95
                            - added mixing
*/
{
    cell *c, *nbr;
                int *x = ivector(1,dim);
                int *n = ivector(0,maxnbrs);
                cell *newc;                                                     /* new cell allocated after move      */

    /* Get next state of each cell and put in c->newstate.  */
    LOOP_OVER_CELLS(c)
        if (flip(sync)) {
            n[0]=c->state;              /* fill n[] */
            LOOP_OVER_NBRS(c->x,x)
                nbr = ni_getcell(x);
                                                    n[nbrcount] = dead(nbr) ? deadstate : nbr->state;
            }
            c->newstate = applyrules(n);    /* set c->newstate  */
        } else
            c->newstate = c->state;
    }
                /*
                            Move newstate to state and tabulate statistics.  Also delete dead and
                            out-of-bounds cells.  Also reset mixflag in preparation for mixing.
                */
    count_activity=0;
    count_live=0;
    LOOP_OVER_CELLS(c)
        if (inbounds(c->x)) {
            count_activity += abs(c->newstate - c->state);
            c->state = c->newstate;
                                        if (live(c)) {
                                                    count_live++;
                                                    c->mixflag = 0;
                                        }
            if (dead(c))    delete_cell(&c);
        } else
            delete_cell(&c);
    }
                sum_activity += count_activity;

    free_ivector(n,0,maxnbrs);

                /*
                            New to v2.10.
                            Apply mixing rules to a cell with probability mixing.  Don't move
                            each cell more than once.
                */
                if (mixing > 0.0) {
                            LOOP_OVER_CELLS(c)
                                        if (flip(mixing) && c->mixflag==0) { /* mix a fraction of live cells            */
                                                    newc = move_cell(c);
                                                    if (newc != c)              delete_cell(&c);
                                        }
                            }
                }

                free_ivector(x,1,dim);
```

```
}


void perturb(void)
/*
   Perturbs a random cell in the hash table by toggling its state.  We
   only want to toggle in-bounds cells so first delete all out-of-bounds
   cells.

   After a crash the system will follow a different route because
   the index used by rrandom() will have been re-initialized.  If
              sync==1 and deterministic, this effect will only be noticed in perturb().

   This routine does not generate the most general single-site
   perturbations possible.  Ideally one would want to perturb ANY random
   site within the boundaries but this has 2 problems: (1) if there are
   no boundaries then how do you decide on a valid region, and (2) there
   would be a large number of "flip fails" (when the system immediately
   returns to its previous rest state) for some common rules (eg. Life).
   These can consume a lot of computer time, so we would like to minimize
   their occurence.  Thus we choose the only available sites for flipping
   to be in the neighborhood of live cells.

   Modifications:

   v1.01a  July 16/94
      - save location of perturbation on pertx[]
*/
{
   unsigned long countcells(void);

   unsigned long p,q;
   cell *c;

   addneighbors();

   /* Delete out-of-bounds cells    */
   LOOP_OVER_CELLS(c)
      if (!inbounds(c->x))    delete_cell(&c);
   }

   /* Perturb  */
   q = 1 + rrandom(countcells());            /* 1..countcells */
   p=0;
   LOOP_OVER_CELLS(c)      /* Don't use a break statement because it may   */
                    /*  not behave properly in this abstract loop.  */
      p++;
      if (p==q) {
         c->state=x_flipstate(c->state);
         ivector_cpy(pertx, c->x, 1,dim);
         return;
      }
   }
}


unsigned long countcells(void)
/*  Counts the number of cells in the hash table including dead cells
and out-of-bounds cells.    */
{
   cell *c;
   unsigned long i = 0;

   LOOP_OVER_CELLS(c)
      i++;
   }
   return i;
}

void notice(void)
/*  Copyright notice    */
{
   printf("\n");
   printf("----------------------------------------------\n");
   printf("CellBot - CB - v%i.%02i%c\n", CB_MAJOR, CB_MINOR, CB_BUGFIX);
              printf("Copyright 1994,1995 Hendrik J. Blok\n\n");

   printf("%s\n\n", __DATE__);

   printf("Send comments, suggestions and bug reports to:\n");
   printf("       %s\n", CB_MAILTO);
   printf("----------------------------------------------\n");
}

void version_cmp(FILE *f, char *ftype, int major, int minor)
/*
   Compares first line in file with ftype, major and minor to make sure the
   file being read is valid.  Designed to work with "Configuration" and
   "Rule" files.

   v2.05a  Aug 12/94
      - now reports error if file is NEWER than CellBot program

   v2.03a  Aug 11/94
      - new
*/
{
   char s[255];
   char errmsg[255];
   char line[255];
   char *lp = line;
   int fmajor, fminor;

   fgets(line, 255, f);

   /* Check for comment char.  */
   sprintf(errmsg, "Invalid comment character in %s File", ftype);
   if (lp[0] != remc)
```

```
        runtime_err(errmsg);

    /* Check for " CellBot v"   */
    lp++;
    sprintf(s, " CellBot v");
    sprintf(errmsg, "Not a valid %s File", ftype);
    if (strnicmp(lp, s, strlen(s)) != 0)
        runtime_err(errmsg);

    /* Read version number (assume proper format) and file type */
    lp += strlen(s);
    sscanf(lp, "%i.%i %s", &fmajor, &fminor, s);

    /* Check file type  */
    if (stricmp(ftype, s) != 0)
        runtime_err(errmsg);

    /* Check version numbers    */
    sprintf(errmsg, "Incompatible %s File", ftype);
    /* is file too old? */
    if (fmajor < major || (fmajor==major && fminor < minor))
        runtime_err(errmsg);
    /* is file too new? */
    if (CB_MAJOR < fmajor || (CB_MAJOR==fmajor && CB_MINOR < fminor))
        runtime_err(errmsg);
}

/* turn off "'___' declared but never used" warning */
#pragma warn -use
•
```

cb.h

```
/*
    CellBot - cb.h

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    Modifications:

            v2.14b      Jun 23/95
                        - in rules.c move_cell() doesn't change c->state and c->newstate
                                anymore
            v2.14a      Jun 18/95
                        - in rules.c random_move() extended to handle either jumps or random
                                walks.  Also renamed random_move() to move_cell().
                        - in rules.c renamed mix_radius to mix_range

            v2.13d      Jun 8/95
                        - in cb.c fixed fillgrid() so record_sps() doesn't give nulls on
                                zeroth step.
            v2.13c      May 19/95
                        - in cb.c configure() now handles both DOS and Unix filename formats
            v2.13b      May 13/95
                        - fixed bug which prematurely halted run on last pert.
            v2.13a      May 9/95
                        - time is scaled by sync so that the rate of events is conserved

            v2.12a      Apr 2/95
                        - in cb.c advance() now just calls random_move() for long_range
                                moves (in rules.c).  random_move() doesn't use random walk but
                                randomly picks point within distance mix_radius (in each
                                coordinate).

            v2.11a      Mar 15/95
                        - in cb.c prevent repeat moves of each cell when mixing in
                                advance() by flagging moved cells

            v2.10a      Mar 12/95
                        - added mixing to advance() in cb.c.  Moves a fraction of cells
                                to break correlations.

    v2.06a  Aug 21/94
        - added error checking in cfg & rul file.  Also checks for illegal
            rule case

    v2.05a  Aug 12/94
        - in bounds.c changed btype[] to a float in preparation for HOT
            boundaries
        - in cb.c version_cmp() now checks that the input file isn't newer
            than the CellBot program
        - added new control structure LOOP_OVER_SPACE() in cb.h
        - added new control structure LOOP_OVER_BOUND() in bounds.h
        - added HOT boundaries in which the cells beyond a boundary randomly
            fluctuate.  Note: Hot 0.0 == Cold.
        - in cb.c fixed bug in addneighbors() which should
            LOOP_OVER_FLIP_NBRS() instead of LOOP_OVER_NBRS()

    v2.04a  Aug 11/94
        - use "Cold", "Periodic", etc. to describe boundary types in
            configuration file instead of integers

    v2.03b  Aug 11/94
        - added DMP_MAJOR and DMP_MINOR to use version_cmp() in fscan_dump()
    v2.03a  Aug 11/94
        - in cb.c added routine version_cmp() which confirms that the file
            being read is a recent enough version and the right type of file.
        - added CFG_MAJOR and CFG_MINOR to use this routine in configure()
        - added RUL_MAJOR and RUL_MINOR to use this routine in initrules()

    v2.02a  Aug 10/94
        - added routine initbounds() which reads boundary info. from config.
            file.  Called by configure().

    v2.01a  Aug 9/94
        - changed boundary type REFLECT to REFLECT_EVEN and REFLECT_ODD
    v2.00e  Aug 9/94
        - in bounds.c deleted routine single_applybounds().  Now always uses
            applyboundaries() for consistency.
        - in bounds.c reactivated map_inbounds() under the new name
            map_across().
    v2.00d  Aug 9/94
        - in cb.h changed LOOP_OVER_NBRS() and LOOP_OVER_FLIPNBRS() to use
            c->x as the first argument instead of c itself.  Makes it possible
            to loop over the neighbors of x without allocating a cell.
        - used this in bounds.c to only duplicate cells if they are within
            range of the border.  Faster, less memory.
    v2.00c  Aug 8/94
        - in bounds.c fixed bug in how REFLECT handled corners. (It didn't!)
            Required complete rewrite of subroutine in applyboundaries().
        - in bounds.c deleted map_cell().  No longer used.
        - in bounds.c temporarily disabled map_inbounds() and single_applybounds().
    v2.00b  July 27/94
        - if not recovering from crash then record initial data (.cps & .sps)
    v2.00a  July 22/94
        - now can handle separate conditions for each boundary.  Corner
            disputes are handled by choosing priorities for boundaries.

    v1.02d  July 21/94
        - in nrutil.c modified the vector_cmp() routines to increase speed.
            They now exit as soon as the criterion is met instead of looping
            through all elements.
        - changed nperts so that nperts=0 means loop through once (previously
            was nperts=1).
    v1.02c  July 20/94
        - in record.c modified cutoff_radius() to calculate SMALLEST radius
            which satisfies criteria.
        - in record.c added line in fprint_header() to record CellBot version
            number in data files.
    v1.02b  July 19/94
        - in record.c rewrote cutoff_radius().  New version is faster and
            simpler.
    v1.02a  July 18/94
        - in record.c added routine cutoff_radius()
        - in record.c eliminated double checking of live() and inbounds().
            Assumes all cells in hash table are both live and in bounds.
        - in record.c erased routine packingdens() which assumed hash table
            consisted of live cells and neighbors.

    v1.01a  July 16/94
        - added pertx[] for recording position of perturbation in .spp file
        - erased all duplicate #includes
        - added rrandomize() as seed for rrandom()

    v1.00a  June 19/94
        - initial release
*/

#ifndef _CB_H_
#define _CB_H_

/* CellBot version numbers (format: #.##c)  */
#define CB_MAJOR    2
#define CB_MINOR    14
#define CB_BUGFIX   'b'

/* lowest versions of input files compatible with present version   */
#define CFG_MAJOR   2
#define CFG_MINOR   04
#define RUL_MAJOR   2
#define RUL_MINOR   14
#define DMP_MAJOR   1
#define DMP_MINOR   00

#include <stdio.h>      /* defines FILE */
#include <stddef.h>     /* defines NULL */
#include "hash.h"


/*  The following control structures are designed to make the source
code more readable.  They must be used with caution!  Nested loops are not
allowed because of the reference to the global variables hashcount and
nbrcount.  Also, in LOOP_OVER_CELLS be very careful of how insertions and
deletions of cells are handled.  Inserted cells may or may not be looped over!
Finally, each structure has the opening bracket included within.  Be sure not to
forget the closing bracket at the end of the loop!
*/
static int hashcount;              /* used in LOOP_OVER_CELLS  */
extern int delete_flag;
#define LOOP_OVER_CELLS(c)
                                                  \
        for (hashcount=0; hashcount<HASHSIZE; hashcount++)                        \
                for (c=H[hashcount]; c != NULL; (delete_flag ? (c=c) : (c=c->next))) {  \
                        delete_flag = 0;


/*  Be sure that x is allocated with ivector() before calling LOOP_OVER_NBRS(). */
static int nbrcount;                      /* used in LOOP_OVER_NBRS & LOOP_OVER_FLIP_NBRS */
static int nbrrun;
#define LOOP_OVER_NBRS(cx,x)                                                                       \
        for (nbrcount=1;nbrcount<=maxnbrs;nbrcount++) {             \
                for (nbrrun=1; nbrrun<=dim; nbrrun++)                  \
                        x[nbrrun] = cx[nbrrun] + nbrx[nbrcount][nbrrun];


/* LOOP_OVER_FLIP_NBRS loops over all cells TO WHICH c IS A NEIGHBOR.  This
is NOT necessarily the same as LOOP_OVER_NBRS if the neighborhood is asymmetric.    */
#define LOOP_OVER_FLIP_NBRS(cx,x)                                                                  \
        for (nbrcount=1;nbrcount<=maxnbrs;nbrcount++) {             \
                for (nbrrun=1; nbrrun<=dim; nbrrun++)                  \
                        x[nbrrun] = cx[nbrrun] - nbrx[nbrcount][nbrrun];
```

```
/*
    LOOP_OVER_SPACE(x) loops from x=minx to x=maxx.  x must be defined
    before calling this structure.

    Modifications:

    v2.05a  Aug 15/94
        - new
*/
static int spccarry;
static int spcrun;
#define LOOP_OVER_SPACE(x)                                                          \
        ivector_cpy(x,minx,1,dim);                          \
        x[dim]--;                                   \
        while (1) {                                 \
                spccarry=1;                         \
                for (spcrun=dim; spcrun>=1 && spccarry; spcrun--) { \
                        x[spcrun]++;                        \
                        if (x[spcrun] > maxx[spcrun]) {             \
                                x[spcrun] = minx[spcrun];               \
                                spccarry = 1;                   \
                        } else                              \
                                spccarry = 0;                   \
                }                                   \
                if (spccarry)   break;


/* global vars. */
extern char prefix[255];        /* output file(s) prefix    */
extern char dumpfname[255];     /* name of dumpfile */
extern long count_live;         /* statistic: count of live cells   */
extern long count_activity;     /* statistic: sum of changes    */
extern long sum_activity;       /* statistic: sum of count_activity */
extern int *pertx;              /* location of perturbation */

/* function prototypes  */
extern void addneighbors(void);
extern void version_cmp(FILE *f, char *ftype, int major, int minor);

#endif  /* _CB_H_   */
•
```

fileio.c

```
/*
        fileio.c

        Copyright 1994,95 Hendrik J. Blok

        Routines to simplify file input/output operations.
*/
#include <stdlib.h>                     /* defines getenv()        */
#include "fileio.h"                     /* includes <stdio.h>     */
#include "strops.h"                     /* includes <string.h>    */

char *expand_fn(char *fn)
/*
        Expands filename by replacing "~" with the contents of environment
        variable home.  If in MSDOS then replaces occurences of "/" with "\\"
        else replaces "\\" with "/".
*/
{
        char *home=getenv("HOME");

        /* replace "~" with home (just the first occurence)              */
        str_replace_str(fn,"~",home,1);

        /* replace path separators (ie. "/" and "\\")         */
        #ifdef __MSDOS__
                str_replace_str(fn,"/","\\",-1);
        #else
                str_replace_str(fn,"\\","/",-1);
        #endif          /* __MSDOS__ */

        return fn;
}

FILE *_fopen(char *fname, char *mode)
/*
        Interactive file open with some error trapping.
*/
{
        FILE *f;
        for (f = fopen(fname, mode); f == NULL;) {
                if (strchr(mode,'w') || strchr(mode,'a') || strchr(mode,'+'))
                        printf("Error: Unable to open output file '%s'.\nEnter new path and name: ", fname);
                else
                        printf("Error: Unable to find file '%s'.\nEnter new path and name: ", fname);
                scanf("%s", fname);
                f = fopen(fname, mode);
        }
        return f;
}

int fnextc(FILE *f)
/*
        Preview next character from file without skipping over it.
*/
{
        int c;
        c = fgetc(f);
        ungetc(c, f);
        return(c);
}

void fstrip(FILE *f)
```

```
/*
        Strips comment lines (lines beginning with remc) from the input file.

        Modifications:

        May 19/95
                - replace fgets() with search for "\n".  Don't need STRLEN anymore.
*/
{
        char c;
        while (((c = fnextc(f)) == remc) || c_in_s(c,softspaces)) {
                if (c == remc) {
                        while (c != '\n' && c != EOF)       c=fgetc(f);
                } else {
                        fgetc(f);
                }
        }
}

int _feof(FILE *f)
/*
        Check if end-of-file is imminent.  Strips comments.
*/
{
        fstrip(f);
        return(feof(f) || fnextc(f) == EOF);
}

char fnextline(FILE *f)
/*
        Jump to next line of input file.  Returns last character read (can be
        used to check for end-of-file).
*/
{
        char c;

        c=fgetc(f);
        while (c != '\n' && c != EOF)       c=fgetc(f);
        return c;
}
•
```

fileio.h

```
/*
        fileio.h

        Copyright 1994,95 Hendrik J. Blok

        Utilities to simplify file input/output.  Designed to work under MSDOS
        and UNIX.
*/
#ifndef _FILEIO_H_
#define _FILEIO_H_

#include <stdio.h>      /* defines FILE         */

#define remc            '#'

#ifdef __MSDOS__        /* needed for access()  */
        #include <io.h>
        #define F_OK            0
        #define W_OK            2
#else
        #include <unistd.h>     /* for F_OK & W_OK    */
#endif

/* these use access() */
#define fexist(fname)   (access(fname, F_OK) == 0)
#define fwritep(fname)  (access(fname, W_OK) == 0)

char *expand_fn(char *);
int fnextc(FILE *);
void fstrip(FILE *);
int _feof(FILE *);
char fnextline(FILE *f);

#endif  /* _FILEIO_H_           */
•
```

hash.c

```
/*
        CellBot - hash.c

        Copyright 1994 Hendrik Jan Blok

        Functions for referencing and updating hash table.
*/
#include <stdlib.h>                             /* defines malloc(), free(), labs()     */
#include "cb.h"                                         /* defines delete_flag, includes hash.h        */
#include "rules.h"                              /* defines dim, deadstate               */
#include "pandora.h"                    /* defines runtime_err()                */
#include "nrutil.h"                             /* defines ivector(), free_ivector(), ivector_cpy(), ivector_cmp(), CMP_EQUAL       */

Hashtable_type H;

int Hash(int *x);       /* prototype */

cell *getcell(int *x)
/*
        Returns the cell with coordinates (x,y).  If cell not found then create
        it.
        Modifications:

        v2.11       Mar 14/95
                    - initialize mixflag to 0
*/
{
        int location;
        cell *p;

        p=ni_getcell(x);
        if (p!=NULL)        return p;
        /* Else must create a new cell, initialize it, and insert it into the
        hash table. */
        p=(cell *)malloc(sizeof(cell));
        if (p==NULL)        runtime_err("Out of memory in getcell()");      /* abort */
        p->x=ivector(1,dim);
        ivector_cpy(p->x, x, 1,dim);
        p->state=deadstate;
        p->newstate=deadstate;
        p->mixflag=0;
        location=Hash(x);                               /* insert in front of H[]   */
        if (H[location] != NULL)
                (H[location])->prev=p;
        p->next=H[location];
        p->prev=NULL;
        H[location]=p;
        return p;
}

cell *ni_getcell(int *x)
/*      Returns the cell with coordinates (x,y).  If cell not found then return
NULL (no insertions).   */
{
        int location;
        cell *p;

        location=Hash(x);
        p=H[location];
        while (p != NULL) {
                if (!ivector_cmp(p->x,x,1,dim, CMP_LESS | CMP_GREATER))         return p;
                else
                        p=p->next;
        }
        return p;
}

void delete_cell(cell **c)
/* Deletes a cell from the hash table.  Returns a pointer to the next cell
in the hash table.      */
{
        cell *prev, *next;
        int location;

        prev = (*c)->prev;      next = (*c)->next;

        /* update links (including hash)      */
        if (next != NULL)       next->prev = prev;
        if (prev != NULL)       prev->next = next;
        else {                                                          /*  if  prev==NULL  then
set H   */
                location = Hash((*c)->x);                       /*          to next node
        */
                H[location] = next;
        }

        /* free memory          */
        free_ivector((*c)->x,1,dim);
        free(*c);

        delete_flag = 1;
        *c = next;
}

int Hash(int *x)
/* Returns the hash-key for accessing H[].  This routine is optimized for
two dimensions.  In higher dimensions this choice may not maximize the
spread or minimize collisions.        */
{
        if (dim >= 2)
                return (int) (labs(x[1]+FACTOR*x[2]) % HASHSIZE);
        else
                return (int) (labs(x[1]) % HASHSIZE);
}

/* turn off "'___' declared but never used warning              */
#pragma warn -use
•
```

hash.h

```
/*
        CellBot - hash.h

        Copyright 1994 Hendrik Jan Blok
*/

#ifndef _HASH_H_
#define _HASH_H_

#define FACTOR                  101
#define HASHSIZE        997

typedef struct cell_tag {
        int state;
        int newstate;
        int mixflag;                                    /* new in v2.11         */
```

```
		int *x;
		struct cell_tag *prev, *next;
} cell;

typedef cell *Hashtable_type[HASHSIZE];

extern Hashtable_type H;

/* function prototypes */
extern cell *getcell(int *x);				/* with insertions	*/
extern cell *ni_getcell(int *x);		/* w/o insertions	*/
extern void delete_cell(cell **c);

#endif		/* _HASH_H_		*/
•
```

nr.h

This file can be found in Numerical Recipes [7].

nrutil.c

```
#ifdef __TURBOC__
		#include <mem.h>
#endif
#include <stdio.h>
#include <stddef.h>
#include <stdlib.h>
#include "nrutil.h"
#define NR_END			1
#define FREE_ARG	char*

/* turn off "Conversion may lose significant digits" warning */
#pragma warn -sig

void nrerror(char error_text[])
/* Numerical Recipes standard error handler */
{
		fprintf(stderr, "Numerical Recipes run-time error...\n");
		fprintf(stderr, "%s\n", error_text);
		fprintf(stderr, "...now exiting to system...\n");
		exit(1);
}

/***********************
		ALLOCATE VECTOR
***********************/

float *vector(long nl, long nh)
/* allocate a float vector with subscript range v[nl..nh] */
{
		float *v;

		v=(float *)malloc((size_t) ((nh-nl+1+NR_END)*sizeof(float)));
		if (!v)		nrerror("allocation failure in vector()");
		return v-nl+NR_END;
}

int *ivector(long nl, long nh)
/* allocate an int vector with subscript range v[nl..nh] */
{
		int *v;

		v=(int *)malloc((size_t) ((nh-nl+1+NR_END)*sizeof(int)));
		if (!v)		nrerror("allocation failure in ivector()");
		return v-nl+NR_END;
}

unsigned char *cvector(long nl, long nh)
/* allocate an unsigned char vector with subscript range v[nl..nh] */
{
		unsigned char *v;

		v=(unsigned char *)malloc((size_t) ((nh-nl+1+NR_END)*sizeof(unsigned char)));
		if (!v)		nrerror("allocation failure in cvector()");
		return v-nl+NR_END;
}

unsigned long *lvector(long nl, long nh)
/* allocate an unsigned long vector with subscript range v[nl..nh] */
{
		unsigned long *v;

		v=(unsigned long *)malloc((size_t) ((nh-nl+1+NR_END)*sizeof(unsigned long)));
		if (!v)		nrerror("allocation failure in lvector()");
		return v-nl+NR_END;
}

double *dvector(long nl, long nh)
/* allocate an double vector with subscript range v[nl..nh] */
{
		double *v;

		v=(double *)malloc((size_t) ((nh-nl+1+NR_END)*sizeof(double)));
		if (!v)		nrerror("allocation failure in dvector()");
		return v-nl+NR_END;
}

fcomplex *Cvector(long nl, long nh)
/* allocate a complex vector with subscript range v[nl..nh] */
{
		fcomplex *v;
```

```
	v=(fcomplex *)malloc((size_t) ((nh-nl+1+NR_END)*sizeof(fcomplex)));
	if (!v)		nrerror("allocation failure in Cvector()");
	return v-nl+NR_END;
}

dcomplex *dCvector(long nl, long nh)
/* allocate a double complex vector with subscript range v[nl..nh] */
{
	dcomplex *v;

	v=(dcomplex *)malloc((size_t) ((nh-nl+1+NR_END)*sizeof(dcomplex)));
	if (!v)		nrerror("allocation failure in dCvector()");
	return v-nl+NR_END;
}

float **matrix(long nrl, long nrh, long ncl, long nch)
/* allocate a float matrix with subscript range m[nrl..nrh][ncl..nch] */
{
	long i, nrow=nrh-nrl+1, ncol=nch-ncl+1;
	float **m;

	/* allocate pointers to rows */
	m=(float **) malloc((size_t) ((nrow+NR_END)*sizeof(float*)));
	if (!m)		nrerror("allocation failure 1 in matrix()");
	m += NR_END;
	m -= nrl;

	/* allocate rows and set pointers to them */
	m[nrl]=(float *) malloc((size_t) ((nrow*ncol+NR_END)*sizeof(float)));
	if (!m[nrl])	nrerror("allocation failure 2 in matrix()");
	m[nrl] += NR_END;
	m[nrl] -= ncl;

	for (i=nrl+1;i<=nrh;i++) m[i]=m[i-1] + ncol;

	/* return pointer to array of pointers to rows */
	return m;
}

double **dmatrix(long nrl, long nrh, long ncl, long nch)
/* allocate a double dmatrix with subscript range m[nrl..nrh][ncl..nch] */
{
	long i, nrow=nrh-nrl+1, ncol=nch-ncl+1;
	double **m;

	/* allocate pointers to rows */
	m=(double **) malloc((size_t) ((nrow+NR_END)*sizeof(double*)));
	if (!m)		nrerror("allocation failure 1 in dmatrix()");
	m += NR_END;
	m -= nrl;

	/* allocate rows and set pointers to them */
	m[nrl]=(double *) malloc((size_t) ((nrow*ncol+NR_END)*sizeof(double)));
	if (!m[nrl])	nrerror("allocation failure 2 in dmatrix()");
	m[nrl] += NR_END;
	m[nrl] -= ncl;

	for (i=nrl+1;i<=nrh;i++) m[i]=m[i-1] + ncol;

	/* return pointer to array of pointers to rows */
	return m;
}

int **imatrix(long nrl, long nrh, long ncl, long nch)
/* allocate a int imatrix with subscript range m[nrl..nrh][ncl..nch] */
{
	long i, nrow=nrh-nrl+1, ncol=nch-ncl+1;
	int **m;

	/* allocate pointers to rows */
	m=(int **) malloc((size_t) ((nrow+NR_END)*sizeof(int*)));
	if (!m)		nrerror("allocation failure 1 in imatrix()");
	m += NR_END;
	m -= nrl;

	/* allocate rows and set pointers to them */
	m[nrl]=(int *) malloc((size_t) ((nrow*ncol+NR_END)*sizeof(int)));
	if (!m[nrl])	nrerror("allocation failure 2 in imatrix()");
	m[nrl] += NR_END;
	m[nrl] -= ncl;

	for (i=nrl+1;i<=nrh;i++) m[i]=m[i-1] + ncol;

	/* return pointer to array of pointers to rows */
	return m;
}

/* turn off "Parameter never used" warning	*/
#pragma warn -par

float **submatrix(float **a, long oldrl, long oldrh, long oldcl, long oldch, long newrl, long newcl)
/* point a submatrix [newrl..][newcl..] to a[oldrl..oldrh][oldcl..oldch] */
{
	long i,j, nrow=oldrh-oldrl+1, ncol=oldcl-newcl;
	float **m;

	/* allocate array of pointers to rows */
	m=(float **) malloc((size_t) ((nrow+NR_END)*sizeof(float*)));
	if (!m)		nrerror("allocation failure in submatrix()");
	m += NR_END;
	m -= newrl;

	/* set pointers to rows */
	for (i=oldrl,j=newrl;i<=oldrh;i++,j++)		m[j]=a[i]+ncol;

	/* return pointer to array of pointers to rows */
	return m;
```

```
}

float **convert_matrix(float *a, long nrl, long nrh, long ncl, long nch)
/* allocate a float matrix m[nrl..nrh][ncl..nch] that points to the matrix
declared in the standard C manner as a[nrow][ncol], where nrow=nrh-nrl+1
and ncol=nch-ncl+1.  The routine should be called with the address
&a[0][0] as the first argument. */
{
		long i,j,nrow=nrh-nrl+1,ncol=nch-ncl+1;
		float **m;

		/* allocate pointers to rows */
		m=(float **) malloc((size_t) ((nrow+NR_END)*sizeof(float*)));
		if (!m)		nrerror("allocation failure in convert_matrix()");
		m += NR_END;
		m -= nrl;

		/* set pointers to rows */
		m[nrl]=a-ncl;
		for (i=1,j=nrl+1;i<nrow;i++,j++)	m[j]=m[j-1]+ncol;

		/* return pointer to array of pointers to rows */
		return m;
}

/********************
		FREE VECTOR
********************/
void free_vector(float *v, long nl, long nh)
/* free a float vector allocated with vector()	*/
{
		free((FREE_ARG) (v+nl-NR_END));
}

void free_ivector(int *v, long nl, long nh)
/* free an int vector allocated with ivector()	*/
{
		free((FREE_ARG) (v+nl-NR_END));
}

void free_dvector(double *v, long nl, long nh)
/* free a double vector allocated with dvector()	*/
{
		free((FREE_ARG) (v+nl-NR_END));
}

void free_Cvector(fcomplex *v, long nl, long nh)
/* free a complex vector allocated with Cvector()		*/
{
		free((FREE_ARG) (v+nl-NR_END));
}

void free_dCvector(dcomplex *v, long nl, long nh)
/* free a double complex vector allocated with dCvector()	*/
{
		free((FREE_ARG) (v+nl-NR_END));
}

void free_matrix(float **m, long nrl, long nrh, long ncl, long nch)
/* free a float matrix allocated with matrix()	*/
{
		free((FREE_ARG) (m[nrl]+ncl-NR_END));
		free((FREE_ARG) (m+nrl-NR_END));
}

/* turn on "Parameter never used" warning	*/
#pragma warn +par


/********************
		COPY VECTOR
********************/
float *vector_cpy(float *dest, float *src, long nl, long nh)
/* copies vector src to dest.  Returns dest.	*/
{
		return (float *)memcpy((void *)(dest+nl), (void *)(src+nl), (nh-nl+1)*sizeof(float));
}

int *ivector_cpy(int *dest, int *src, long nl, long nh)
/* copies vector src to dest.  Returns dest.	*/
{
		return (int *)memcpy((void *)(dest+nl), (void *)(src+nl), (nh-nl+1)*sizeof(int));
}

unsigned char *cvector_cpy(unsigned char *dest, unsigned char *src, long nl, long nh)
/* copies vector src to dest.  Returns dest.	*/
{
		return (unsigned char *)memcpy((void *)(dest+nl), (void *)(src+nl), (nh-nl+1)*sizeof(unsigned char));
}

unsigned long *lvector_cpy(unsigned long *dest, unsigned long *src, long nl, long nh)
/* copies vector src to dest.  Returns dest.	*/
{
		return (unsigned long *)memcpy((void *)(dest+nl), (void *)(src+nl), (nh-nl+1)*sizeof(unsigned long));
}

double *dvector_cpy(double *dest, double *src, long nl, long nh)
/* copies vector src to dest.  Returns dest.	*/
{
		return (double *)memcpy((void *)(dest+nl), (void *)(src+nl), (nh-nl+1)*sizeof(double));
}

fcomplex *Cvector_cpy(fcomplex *dest, fcomplex *src, long nl, long nh)
/* copies vector src to dest.  Returns dest.	*/
{
		return (fcomplex *)memcpy((void *)(dest+nl), (void *)(src+nl), (nh-nl+1)*sizeof(fcomplex));
}
```

```
dcomplex *dCvector_cpy(dcomplex *dest, dcomplex *src, long nl, long nh)
/* copies vector src to dest.  Returns dest.        */
{
        return (dcomplex *)memcpy((void *)(dest+nl), (void *)(src+nl), (nh-nl+1)*sizeof(dcomplex));
}

/*********************
        COMPARE VECTORS
*********************/
/*      Compares two vectors, v1 and v2, over the range [nl..nh].  Compares
        each element in turn, returning a 1 or 0 depending on whether ANY
        elements match the mask.

        For example,

        if vector_cmp(v1,v2,...,CMP_LESS | CMP_GREATER) == 0 then v1 == v2,
                (note: this would have returned 1 if ANY elements of v1 had been
                                either less than or greater than v2.  We don't require
                                that there exist both elements which are less than and
                                elements which are greater than v2!)

        if vector_cmp(v1,v2,...,CMP_LESS) == 1 then at least 1 element of v1
                is less than v2,

        So, to check if v1 (strictly) <= v2 you might use

                !(vector_cmp(v1,v2,...,CMP_GREATER)

        which means that it is not the case that any of the elements of v1
        are larger than v2.
*/

/* Generic vector comparison routine.  Use in all vector comparisons
where < and > valid for comparing elements of v1 and v2.  */
#define GEN_VECTOR_CMP          long j;
                \
                                                int m = 0;
                                \

                                                \
                                                for (j=nl; j<=nh; j++) {
        \
                                                        if              (v1[j] < v2[j])         m       |=
CMP_LESS;                       \
                                                        else if (v1[j] > v2[j])   m |= CMP_GREATER; \
                                                        else
        m |= CMP_EQUAL;                 \

                                                \
                                                        /* if m contains mask then break    */
        \
                                                        if (mask & m)           return 1;
                \
                                                }
                                                \
                                                return 0;

int vector_cmp(float *v1, float *v2, long nl, long nh, int mask)
{
        GEN_VECTOR_CMP;
}

int ivector_cmp(int *v1, int *v2, long nl, long nh, int mask)
{
        GEN_VECTOR_CMP;
}

int cvector_cmp(unsigned char *v1, unsigned char *v2, long nl, long nh, int mask)
{
        GEN_VECTOR_CMP;
}

int lvector_cmp(unsigned long *v1, unsigned long *v2, long nl, long nh, int mask)
{
        GEN_VECTOR_CMP;
}

int dvector_cmp(double *v1, double *v2, long nl, long nh, int mask)
{
        GEN_VECTOR_CMP;
}

/* turn on "Conversion may lose significant digits" warning */
#pragma warn +sig

/* turn off "'___' decalred but never used" warning             */
#pragma warn -use
•
```

nrutil.h

```
#ifndef _NR_UTILS_H_
#define _NR_UTILS_H_

typedef struct FCOMPLEX {float r,i;} fcomplex;
typedef struct DCOMPLEX {double r,i;} dcomplex;

static float sqrarg;
#define SQR(a)                  ((sqrarg=(a)) == 0.0 ? 0.0 : sqrarg * sqrarg)

static double dsqrarg;
#define DSQR(a)                 ((dsqrarg=(a)) == 0.0 ? 0.0 : dsqrarg * dsqrarg)

static double dmaxarg1, dmaxarg2;
#define DMAX(a,b)   (dmaxarg1=(a), dmaxarg2=(b), dmaxarg1 > dmaxarg2 ? dmaxarg1 : dmaxarg2)
```

```
static double dminarg1, dminarg2;
#define DMIN(a,b)   (dminarg1=(a), dminarg2=(b), dminarg1 < dminarg2 ? dminarg1 : dminarg2)

static float maxarg1, maxarg2;
#define FMAX(a,b)   (maxarg1=(a), maxarg2=(b), maxarg1 > maxarg2 ? maxarg1 : maxarg2)

static float minarg1, minarg2;
#define FMIN(a,b)   (minarg1=(a), minarg2=(b), minarg1 < minarg2 ? minarg1 : minarg2)

static long lmaxarg1, lmaxarg2;
#define LMAX(a,b)   (lmaxarg1=(a), lmaxarg2=(b), lmaxarg1 > lmaxarg2 ? lmaxarg1 : lmaxarg2)

static long lminarg1, lminarg2;
#define LMIN(a,b)   (lminarg1=(a), lminarg2=(b), lminarg1 < lminarg2 ? lminarg1 : lminarg2)

static int imaxarg1, imaxarg2;
#define IMAX(a,b)   (imaxarg1=(a), imaxarg2=(b), imaxarg1 > imaxarg2 ? imaxarg1 : imaxarg2)

static int iminarg1, iminarg2;
#define IMIN(a,b)   (iminarg1=(a), iminarg2=(b), iminarg1 < iminarg2 ? iminarg1 : iminarg2)

#define SIGN(a,b)       ((b) >= 0.0 ? fabs(a) : -fabs(a))

/* ANSI C compatible function prototypes. */
void nrerror(char error_text[]);

float                           *vector(long nl, long nh);
int                                     *ivector(long nl, long nh);
unsigned char           *cvector(long nl, long nh);
unsigned long           *lvector(long nl, long nh);
double                          *dvector(long nl, long nh);
fcomplex                *Cvector(long nl, long nh);
dcomplex                *dCvector(long nl, long nh);

float           **matrix(long nrl, long nrh, long ncl, long nch);
double          **dmatrix(long nrl, long nrh, long ncl, long nch);
int                     **imatrix(long nrl, long nrh, long ncl, long nch);
float           **submatrix(float **a, long oldrl, long oldrh, long oldcl, long oldch, long newrl, long newcl);
float           **convert_matrix(float *a, long nrl, long nrh, long ncl, long nch);
float           ***f3tensor(long nrl, long nrh, long ncl, long nch, long ndl, long ndh);

void free_vector(float *v, long nl, long nh);
void free_ivector(int *v, long nl, long nh);
void free_cvector(unsigned char *v, long nl, long nh);
void free_lvector(unsigned long *v, long nl, long nh);
void free_dvector(double *v, long nl, long nh);
void free_Cvector(fcomplex *v, long nl, long nh);
void free_dCvector(dcomplex *v, long nl, long nh);

void free_matrix(float **m, long nrl, long nrh, long ncl, long nch);
void free_dmatrix(double **m, long nrl, long nrh, long ncl, long nch);
void free_imatrix(int **m, long nrl, long nrh, long ncl, long nch);
void free_submatrix(float **b, long nrl, long nrh, long ncl, long nch);
void free_convert_matrix(float **b, long nrl, long nrh, long ncl, long nch);
void free_f3tensor(float ***t, long nrl, long nrh, long ncl, long nch, long ndl, long ndh);

float                           *vector_cpy(float *dest, float *src, long nl, long nh);
int                                     *ivector_cpy(int *dest, int *src, long nl, long nh);
unsigned char           *cvector_cpy(unsigned char *dest, unsigned char *src, long nl, long nh);
unsigned long           *lvector_cpy(unsigned long *dest, unsigned long *src, long nl, long nh);
double                          *dvector_cpy(double *dest, double *src, long nl, long nh);
fcomplex                *Cvector_cpy(fcomplex *dest, fcomplex *src, long nl, long nh);
dcomplex                *dCvector_cpy(dcomplex *dest, dcomplex *src, long nl, long nh);

#define CMP_LESS                        0x1
#define CMP_EQUAL                       0x2
#define CMP_GREATER                             0x4

int             vector_cmp(float *v1, float *v2, long nl, long nh, int mask);
int             ivector_cmp(int *v1, int *v2, long nl, long nh, int mask);
int             cvector_cmp(unsigned char *v1, unsigned char *v2, long nl, long nh, int mask);
int             lvector_cmp(unsigned long *v1, unsigned long *v2, long nl, long nh, int mask);
int             dvector_cmp(double *v1, double *v2, long nl, long nh, int mask);

#endif /* _NR_UTILS_H_ */
•
```

pandora.c

```
/*
 *              Pandora.c
 *                      A "Pandora's Box" of useful functions and utilities.
 */
#include <ctype.h>
#include <stdio.h>
#include <stdlib.h>
#include <string.h>
#include <time.h>

#ifdef __MSDOS__
                #include <conio.h>

int query(const char *s)
/*
 * Asks a question and waits for a y/n response.
 */
{
                int c;
                do {
                        printf("%s (y/n)  ",s);
                        c = toupper(getche());
                } while ((c != 'Y') && (c != 'N'));
                if (c == 'Y') return 1;
                /* else */                  return 0;
}
```

```
#endif		/* __MSDOS__		*/

int elapsed(time_t *was, time_t seconds)
/* if "seconds" or more seconds have elapsed since last call to elapsed()
 * returns 1, else 0.  If true then also resets was to current time.
 */
{
		time_t now;
		time(&now);
		if (now - *was >= seconds) {
				*was = now;
				return 1;
		}
		/* else */	return 0;
}

void runtime_err(char error_text[])
/*		Run-time error handler.			*/
{
		fprintf(stderr,"Run-time error...\n");
		fprintf(stderr,"%s\n", error_text);
		fprintf(stderr,"...now exiting to system...\n");
		exit(1);
}

void switchptr(void **a, void **b)
/* Switches the pointers a & b.		*/
{
		void *temp;
		temp=(*a);
		*a=*b;
		*b=temp;
}
```

pandora.h

```
/*
 *		Pandora.h
 *				A "Pandora's Box" of useful functions and utilities.
 */

#ifndef _PANDORA_H_

#define _PANDORA_H_

#include <time.h>

/* returns a % b.  Gives a positive result even if a < 0. */
#define absmod(a,b)	((a) % (b) + (((a) < 0) ? (b) : 0))
/* min & max */
#ifndef __MSDOS__
		#define min(a,b)	((a) < (b) ? (a):(b))
		#define max(a,b)	((a) > (b) ? (a):(b))
#endif

/* the variable swap needs to be declared		*/
#define SWAP(a,b)	{swap=(a);(a)=(b);(b)=swap;}

/* function prototypes */
int				query(const char *s);	/* Asks a question and waits for a y/n response. */
int		elapsed(time_t *was, time_t seconds);
										/* returns non-neg if seconds or more have
elapsed since last call */
void		runtime_err(char []);	/* Run-time error handler.		*/
void		switchptr(void *, void *);		/* Switches 2 pointers */

#endif		/* _PANDORA_H_		*/
```

ran1.c

This file can be found in Numerical Recipes [7].

record.c

```
/*
   CellBot - record.c

   Copyright 1994 Hendrik Jan Blok

   Routines for analyzing system and recording results.

   Note: The hash table MUST CONTAIN ONLY LIVE CELLS when calling these
      routines!  See Modifications: v1.02a.

   Modifications:

		v2.13a	May 9/95
				- changed parameter t in record_cps(), record_sps(), record_spp()
						to a float

   v2.06a  Oct 1/94
      - renamed radius_squared() to dist_sqr() and modified so now
         calculates separation between any two points
      - renamed cutoff_radius() to halfcount_radius()

   v2.03b  Aug 11/94
      - now writes "# CellBot v#.## Dump File" on first line of dump
         file to support version_cmp()
      - fscan_dump() supports version_cmp()
    v1.02c  July 20/94
        - cutoff_radius() now finds SMALLEST r which satisfies criteria.
        - print version number in data file headers

    v1.02b  July 19/94
        - new (simpler) version of cutoff_radius()

    v1.02a  July 18/94
        - added routine cutoff_radius()
        - eliminated double checking of live() and inbounds().  Assumes all
            cells in hash table are both live and in bounds.
        - erased routine packingdens() which assumed hash table consisted
            of live cells and neighbors.
*/
#include <math.h>           /* defines sqrt()   */
#include "cb.h"             /* defines LOOP_OVER_CELLS(), count_live, count_activity, prefix, dumpfname, addneighbors() */
#include "rules.h"          /* defines dim, sync  */
#include "stable.h"         /* defines maxperiod    */
#include "pandora.h"        /* defines runtime_err(), time_t, time(), ctime()   */
#include "fileio.h"         /* defines fstrip(), remc, _feof()  */
#include "nrutil.h"         /* defines SQR(), vector(), free_vector(), ivector(), free_ivector()    */

/* These are placed at the heads of files to describe the columns of data.
See fprint_cells() & fprint_stats().    */
#define CELLS_HEADER    "<position ...>\t<state>"
#define STATS_HEADER    "<live>\t<center ...>\t<r_cut>\t<r_g>"

/* used by halfcount_radius() to determine fractional accuracy of r    */
#define EPS 1e-2

/* function prototypes  */
void fprint_header(FILE *f, char *s);
void fscan_cells(FILE *f);


/***** BEGIN STATISTICS *****/


void center_of_mass(float *x)
/*
    Calculates the center of mass of the system.  Weights all live cells
    equally.
*/
{
    int i;
    cell *c;

    for (i=1; i<=dim; i++)  x[i]=0.0;

    /* error trap   */
    if (!count_live)    return;

    LOOP_OVER_CELLS(c)
        for (i=1; i<=dim; i++)
            x[i] += c->x[i];
    }

    for (i=1; i<=dim; i++)  x[i] /= 1.0 * count_live;
}


float dist_sqr(float *x1, int *x2)
/*
    Calculates distance squared from center of mass.  Returns 0
    if x is NULL.  Assumes first arg. is float array and second is integer
    array.

    Modifications:

    v2.06a  Oct 1/94
        - renamed from radius_squared() to dist_sqr()
        - assumes second argument is integer vector.
*/
{
    int i;
    float sum2 = 0.0;

    /* error trapping   */
    if (!x1 || !x2) return 0.0;

    for (i=1; i<=dim; i++)
        sum2 += SQR(x1[i]-(float)x2[i]);

    return sum2;
}


float radius_gyration(float *cm)
/*
    Returns the radius of gyration of the system (as in inertia).  We assume
    Euclidean geometry (d^2 = x^2 + y^2 + ...) and weight all non-dead states
    equally.  The radius of gyration is measured around cm (typically the
    center of mass) to give a characteristic "length" for the system.

    NOTE: halfcount_radius() seems to give better results for "Life", but
        this is kept for error checking.
*/
{
    float sum2 = 0.0;
    cell *c;

    /* error trap   */
    if (!count_live)    return 0.0;

    LOOP_OVER_CELLS(c)
        sum2 += dist_sqr(cm, c->x);
    }
    return sqrt(sum2/count_live);
```

```
}

long r_countlive(float *cm, float maxr2)
/*
   Used by halfcount_radius() to count the number of live cells within a
   radius r of the center of mass.
*/
{
   cell *c;
   long count = 0;

   /* We want to work in r^2 so we first square maxr2. */
   maxr2 *= maxr2;

   /* Count all cells with r^2 <= maxr2    */
   LOOP_OVER_CELLS(c)
      if (dist_sqr(cm,c->x) <= maxr2)  count++;
   }
   return count;
}


float halfcount_radius(float *cm)
/*
   Another measure of the characteristic size of the system.  In 'Life'
   gliders cause a gross overestimation of the radius of gyration so we
   try this.

   It works by assuming the system is a localized cluster with a uniform
   distribution.  Then the volume within a radius r is proportional to the
   count of live cells in that area.  This function does a binary search
   for the radius which gives a count of half the total number of live
   cells.  Doubling the area would then encompass the entire cluster, so
   we return the radius of this doubled area.

   This is useful for systems which are fairly localized with long tendrils
   which invalidate the radius of gyration.

   Modifications:

   v1.02b  July 19/94
      - rewrote routine.  Is now faster and simpler.
*/
{
   const infinity = -1.0;

   static float rsave = 1e3;       /* initial guess    */

   float r = rsave,
      r_lo = 0.0,
      r_hi = infinity;
   long countr;            /* count of live cells within radius r  */

   /* binary search    */
   do {
      countr = r_countlive(cm,r);

      if (2*countr < count_live)  r_lo = r;

      /* if too big or perfect then decrease (find smallest)  */
      else                          r_hi = r;

      if (r_hi == infinity)   r *= 2.0;
      else                   r = (r_lo + r_hi) / 2.0;


   /* only break when r found to EPS fractional accuracy   */
   } while (r_hi==infinity || r_hi-r_lo > r*EPS);

   /* Full radius is such that full area is twice that spanned by r.   */
   return pow(2.0,1.0/dim) * r;
}


/***** END STATISTICS *****/


void fprint_cells(FILE *f)
/*  Prints a list of live cells within boundaries to file.  Records a list
of coordinates separated by tabs followed by the cells state.   */
{
   cell *c;
   int i;

   LOOP_OVER_CELLS(c)
      for (i=1; i<=dim; i++)                  /* print coordinates    */
         fprintf(f,"%i\t", c->x[i]);
      fprintf(f,"%i\n", c->state);        /* print state  */
   }
}

void fprint_stats(FILE *f)
/*
   Prints a list of statistics to file.  Does not print decay time--that
   is done in record_spp().  Modify this to choose the desired statistics.

   Modifications:

   v1.02a  July 18/94
      - now prints cutoff_radius() as well as radius_gyration()
*/
{
   int i;
   float *cm = vector(1,dim);
   float r_g;

   fprintf(f,"%li\t", count_live);
```

```
    center_of_mass(cm);
    for (i=1; i<=dim; i++)
        fprintf(f,"%.2f\t", cm[i]);

    r_g = radius_gyration(cm);
    fprintf(f,"%.2f\t%.2f\n", halfcount_radius(cm), r_g);

    free_vector(cm,1,dim);
}

void record_cps(long pert, float t)
/*  Record cells each time step.  Records to a new file with each call. */
{
    char s[255];
    FILE *f;

                /* Note: this won't work in DOS because of the 8.3 filename
                                    restriction.  */
                sprintf(s,"%s%li-%.2f.cps",prefix,pert,t);
    f = fopen(s,"w");
    if (f==NULL)    runtime_err("Could not open .cps file");
    sprintf(s, "Cells Per Step\n%s", CELLS_HEADER);
    fprint_header(f,s);
    fprint_cells(f);
    fclose(f);
}


void record_sps(long pert, float t)
/*  Record stats each time step.  Record time index in first column and
activity in second.  Records to same file with multiples calls. */
{
    char s[255];
    FILE *f;
    static long initpert = -1;      /* always want to write header on first */
                                   /*  call.  Assumes pert != -1.          */
    sprintf(s,"%s%li.sps",prefix,pert);
    f = fopen(s,"a");
    if (f==NULL)    runtime_err("Could not open .sps file");
    /* If first call to this file then print header.    */
    if (initpert==pert || initpert==-1) {
        sprintf(s, "Statistics Per Step\n<t>\t<activ>\t%s", STATS_HEADER);
        fprint_header(f,s);
        initpert = pert+1;
    }
                fprintf(f, "%.2f\t%li\t",t,count_activity);
    fprint_stats(f);
    fclose(f);
}

void record_cpp(long pert)
/*  Record cells each perturbation.  Records to a new file with each call.
*/
{
    char s[255];
    FILE *f;

    sprintf(s,"%s%li.cpp",prefix,pert);
    f = fopen(s,"w");
    if (f==NULL)    runtime_err("Could not open .cpp file");
    sprintf(s, "Cells Per Perturbation\n%s", CELLS_HEADER);
    fprint_header(f,s);
    fprint_cells(f);
    fclose(f);
}

void record_spp(long pert, float t)
/*
    Record stats each perturbation.  In addition to stats recorded by
    fprint_stats(), it also records the perturbation count and the decay time
    (in the second column).  Records to same file with all calls.

    Note: the decay time is t-2*maxperiod because the system must have been
    stable for 2*maxperiod steps before it is recognized as stable.

    Modifications:

                v2.13a  May 9/95
                                    - t is scaled by sync so also have to scale maxperiod by sync below.

                v1.01a        July 19/94
        - record location of perturbation
*/
{
    char s[255];
    FILE *f;
    static init=1;
    int i;

    sprintf(s,"%s.spp",prefix); /* prefix must contain filename */
    f = fopen(s,"a");
    if (f==NULL)    runtime_err("Could not open .spp file");
    if (init) {
        sprintf(s, "Statistics Per Perturbation\n<prt>\t<time>\t<activ>\t<pert site ...>\t%s", STATS_HEADER);
        fprint_header(f,s);
        init = 0;
                }
                fprintf(f, "%li\t%.2f\t%li\t", pert, t-2.0*sync*maxperiod, sum_activity);
    for (i=1; i<= dim; i++)
        fprintf(f, "%i\t", pertx[i]);
    fprint_stats(f);
    fclose(f);
}

/*
    Dumping routines.
*/
```

```
void fscan_dump(long *pert, unsigned long *t)
/*
    Reads in the dumpfile.  Sets pert & t to the values found therein and
    fills the hash table.

    Modifications:

    v2.03b  Aug 11/94
        - added support for version_cmp()
*/
{
    FILE *f;

    f = fopen(dumpfname, "r");
    version_cmp(f, "Dump", DMP_MAJOR, DMP_MINOR);

    /* get pert & t */
    fstrip(f);
    fscanf(f, "%li", pert);     fstrip(f);
    fscanf(f, "%lu", t);        fstrip(f);
    fscan_cells(f);         /* get list of cells & insert into Hash */
    fclose(f);
}

void fprint_dump(long pert, unsigned long t)
/*
    Records current pert & t in first line of file.  Following lines are
    a list of live cells.

    Modifications:

    v2.03b  Aug 11/94
        - now prints "# CellBot v#.## Dump File" on first line to support
            version_cmp()
*/
{
    FILE *f;

    f = fopen(dumpfname, "w");          /* overwrite file   */
    fprintf(f, "%c CellBot v%i.%02i Dump File\n", remc, CB_MAJOR, CB_MINOR);
    fprint_header(f, "Dump file");
    fprintf(f, "%li\t%lu\n\n", pert, t); /* put pert & t    */
    fprint_cells(f);                        /* put cells    */
    fclose(f);
}

void fprint_header(FILE *f, char *s)
/*
    Prints a header line to the desired file.  Uses remc which defines
    a comment line (found in fileio.h).  Also adds date & time stamp.
*/
{
    char *c;
    time_t stamp;

    fprintf(f, "%c CellBot v%i.%02i%c Data File\n", remc, CB_MAJOR, CB_MINOR, CB_BUGFIX);
    time(&stamp);
    fprintf(f,"%c %s", remc, ctime(&stamp));    /* ctime() adds '\n'    */
    fprintf(f,"%c ",remc);
    for (c=s; *c != '\0'; c++) {
        fprintf(f,"%c",*c);
        if (*c=='\n')   fprintf(f,"%c ",remc);
    }
    fprintf(f, "\n");
}

void fscan_cells(FILE *f)
/*  Reads list of cells (and their states) from a file into the hash table. */
{
    int *x,
        s,
        i;
    cell *c;

    x = ivector(1,dim);
    while (!_feof(f)) {
        for (i=1; i<=dim; i++) {              /* read position    */
            fscanf(f, "%i", x+i);   fstrip(f);
        }
        fscanf(f, "%i", &s);        fstrip(f);  /* read state       */
        c = getcell(x);     /* insert cell into hash table  */
        c->state = s;       /* set cell state   */
    }
    free_ivector(x,1,dim);
}

/* turn off "'___' declared but never used" warning */
#pragma warn -use
•
```

record.h

```
/*
    CellBot - record.h

                Copyright 1994 Hendrik Jan Blok

                Modifications:

                v2.13a      May 9/95
                            - in record_cps(), record_sps(), record_spp() changed t to a float
*/

#ifndef _RECORD_H_
#define _RECORD_H_
```

```
void record_cps(long pert, float t);
void record_sps(long pert, float t);
void record_cpp(long pert);
void record_spp(long pert, float t);

void fscan_dump(long *pert, unsigned long *t);
void fprint_dump(long pert, unsigned long t);

#endif  /* _RECORD_H_   */
•
```

rrandom.c

```
/*
   rrandom.c

   A collection of random number routines designed to work with the
   generators in Numerical Recipes.  To switch random number generators
   change the called function in rrand() and link with the new routine.
*/
#include <stdlib.h>
#include <time.h>
#include "rrandom.h"
#include "nr.h"

static long rr_idum = 0;

float rrand(void)
/*  Returns a random number between 0.0 and 1.0 using one of the routines
   in Numerical Recipes.  To switch routines, change it in here.
   NOTE: ran1() excludes endpoints.
*/
{
   float r;

   r = ran1(&rr_idum);
   if (r >= 1.0)   r=0.0;      /* ensure r<1   */
   return r;
}

void rrandomize(void)
/*  Initializes the random number generator.  Initializes by setting
   rand_idum to a negative number which depends on the time.  Also
   randomizes internal random number generator with srand().
*/
{
   rr_idum = (long)time(NULL);
   if (rr_idum >= 0)
      rr_idum = -rr_idum;
   srand((unsigned)time(NULL));    /* this may be called randomize() in stdlib.h   */
}

int flip(float prob)
/*  Returns a 1 with probability prob, else returns 0.  */
{
   if (prob <= 0.0)    return 0;
   if (prob >= 1.0)    return 1;
   if (rrand() < prob) return 1;
   /* else */          return 0;
}

unsigned long rrandom(unsigned long num)
/*  Returns an unsigned long between 0 and num-1.   */
{
   return (unsigned long)(rrand()*num);
}
```

rrandom.h

```
/*
           rrandom.h

           A collection of random number routines designed to work with the
           generators in Numerical Recipes.
*/

extern float rrand(void);
extern void rrandomize(void);
extern int flip(float prob);
extern unsigned long rrandom(unsigned long num);
•
```

rules.c

```
/*
   CellBot - rules.c

           Copyright 1994,1995 Hendrik J. Blok

   I want to keep the use of rules in CellBot as general as possible so that
   the rules may be adaptable.  The best way to do this is to keep the
   variables and types in a separate file, accessed only via non-specific
   functions.

   The only restriction we must have is that a deadstate cell with all deadstate
   neighbors maps to deadstate.

   In this case the rule file will be organized as indicated in life.rul.

   Modifications:

           v2.14a      Jun 18/95
```

```
                        - expanded random_move() and renamed it to move_cell().  Now can
                                choose either a jump or a random walk.
                        - added mix_type to rule file.
                        - renamed mix_radus to mix_range

                v2.12a  Apr 2/95
                        - random_move() now can handle long-range moves.  mix_radius is
                                the maximum distance (in each coordinate).

                v2.10a  Mar 12/95
                        - added support for mixing.  Defined mixing, mix_radius and
                                random_move().

    v2.06a  Aug 21/94
        - tests whether rules are legal (ie. tests "dead + 0 nbrs --> dead")

    v2.03a  Aug 11/94
        - added support for version_cmp() in initrules()
*/

#include <string.h>                                     /* defines stricmp()      */
#include "bounds.h"                                     /* defines inbounds()     */
                                                                                /* includes stdio.h ==> defines FILE
                */
#include "cb.h"             /* defines version_cmp()    */
#include "fileio.h"         /* defines FILE, fopen(), NULL, fstrip(), fscanf(), fclose()    */
#include "nrutil.h"         /* defines imatrix(), ivector() */
#include "pandora.h"            /* defines runtime_err()    */
#include "rules.h"                                      /* defines live()             */
#include "rrandom.h"            /* defines rrandom()    */

/* for mix_type             */
#define JUMP                0
#define WALK                1

int dim;                /* dimensionality   */
int maxnbrs;                /* # neighbors  */
int **nbrx;             /* matrix of integers, representing all a cell's neighbors  */
int minstate,           /* all cell states are in minstate..maxstate    */
    maxstate,
                deadstate;          /* cells in this state are dropped from the hash table */
float sync;             /* degree of synchronisity  */
int bornmin,
    bornmax,
    livemin,
    livemax;
float mixing;                                   /* mixing fraction          */
int mix_range;                                  /* range of moves when mixing       */
int mix_type;                                   /* type of mixing: JUMP or WALK   */

void initrules(char rulefname[])
/*
    Reads the rule file and interprets it.

    Modifications:

                v2.14a  Jun 18/95
                        - added mix_type to rule file

                v2.10   Mar 12/95
                        - reads mixing and mix_radius

    v2.06a  Aug 21/94
        - branches to testrule() to make sure rules are legal
        - added error checking

    v2.03a  Aug 11/94
        - added support for version_cmp()
*/
{
    void testrules(void);

    int i,j;
                FILE *rulefile;
                char ms[20];

    rulefile = fopen(rulefname, "r");
    if (rulefile == NULL)   runtime_err("Rule file not found.");
    version_cmp(rulefile, "Rule", RUL_MAJOR, RUL_MINOR);
    fstrip(rulefile);

    /* read dimensions  */
    fscanf(rulefile, "%i", &dim);       fstrip(rulefile);
    if (dim < 1)    runtime_err("Rule File: dim must be >= 1");

    /* read range of states and dead state  */
    fscanf(rulefile, "%i", &minstate);  fstrip(rulefile);
    fscanf(rulefile, "%i", &maxstate);  fstrip(rulefile);
    fscanf(rulefile, "%i", &deadstate); fstrip(rulefile);
    if (minstate>maxstate)  runtime_err("Rule File: maxstate must be >= minstate");
    if (minstate>deadstate) runtime_err("Rule File: deadstate must be >= minstate");
    if (deadstate>maxstate) runtime_err("Rule File: maxstate must be >= deadstate");

    /* read maxnbrs */
    fscanf(rulefile, "%i", &maxnbrs);   fstrip(rulefile);
    if (maxnbrs<0)  runtime_err("Rule File: maxnbrs must be >= 0");

    if (maxnbrs > 0) {
        nbrx=imatrix(1,maxnbrs,1,dim);
        for (i=1; i<=maxnbrs;i++) {
            /* read integer sets into nbrx[i][j]. */
            for (j=1; j<=dim; j++) {
                fscanf(rulefile, "%i", &(nbrx[i][j]));  fstrip(rulefile);
            }
        }
    }

    /* read sync    */
```

```
            fscanf(rulefile, "%f", &sync);          fstrip(rulefile);
    if (sync<0.0 || sync > 1.0)     runtime_err("Rule File: sync must be >= 0.0 and <= 1.0");

    /*
                        This block is specific to Conway's LIFE and similar rules (outer
                        totalistic laws).  In the future I may want to generalize this to
                        accept a string representing a symbolic expression with operators,
                        etc.
    */
    /* read bornmin, bornmax, livemin, & livemax    */
    fscanf(rulefile, "%i", &bornmin);   fstrip(rulefile);
    fscanf(rulefile, "%i", &bornmax);   fstrip(rulefile);
    fscanf(rulefile, "%i", &livemin);   fstrip(rulefile);
    fscanf(rulefile, "%i", &livemax);   fstrip(rulefile);

            /* read mixing and mix_range         */
            fscanf(rulefile, "%f", &mixing);                fstrip(rulefile);
            if (mixing<0.0 || mixing > 1.0)         runtime_err("Rule File: mixing must be >= 0.0 and <= 1.0");
            fscanf(rulefile, "%i", &mix_range);    fstrip(rulefile);
            if (mix_range<0)                                                    runtime_err("Rule File: mix_range must be >=
0");

            /* read mix type            */
            fscanf(rulefile, "%s", ms);                                 fstrip(rulefile);
            if              (stricmp("Jump",ms)==0)             mix_type = JUMP;
            else if (stricmp("Walk",ms)==0)      mix_type = WALK;
            else
                        runtime_err("Rule File: mixing type not recognized");

            fclose(rulefile);

    testrules();
}


int applyrules(int *n)
/*
    Returns the cell's next state.  n[0..maxnbrs] holds the current state of
    the cell in question, n[0], and all its neighbors, n[1]..n[maxnbrs],
    ordered as specified by the rule file.

    This block is specific to Conway's LIFE and similar rules.  In the
    future I may want to generalize this to accept a string representing
    a symbolic expression with operators, etc.
*/
{
    int sum=0;
    int i;

    for (i=1; i<=maxnbrs; i++)  sum += n[i];
    if ( n[0] && sum>=livemin && sum<=livemax)  return maxstate;
    if (!n[0] && sum>=bornmax && sum<=bornmax)  return maxstate;
    /* else */                                  return deadstate;
}

int flipstate(void)
/*  Returns a random, valid cell state.
*/
{
    return minstate + (int)rrandom(maxstate-minstate+1);    /* full range   */
}

int x_flipstate(int s)
/*  Returns a random, valid cell state other than s.
*/
{
    int rnd;

    rnd = minstate + (int)rrandom(maxstate-minstate);       /* range - 1    */
    if (rnd < s)    return rnd;
    /* else */      return rnd+1;
}

void testrules(void)
/*
    There is only one illegal rule case in this program.  This routine tests
    if that case is encountered.  If it is ithalts the program with an error
    message.

    The illegal rule case is "dead + 0 nbrs --> live".  This is illegal
    because the dead state is chosen by exactly this criterion.  If this is
    not true then CellBot will fail to handle it properly.  Hence, choose
    your "deadstate" with care!

    Modifications:

    v2.06a  Aug 21/94
        - new
*/
{
    int *n = ivector(0,maxnbrs);
    int i;

    for (i=0; i<=maxnbrs; i++)    n[i] = deadstate;
    if (applyrules(n) != deadstate)
        runtime_err("Illegal rule detected.  Choose new deadstate.");

    /* else Ok  */
    free_ivector(n,0,maxnbrs);
}

cell *move_cell(cell *c)
/*
            Chooses new random position in the range

                        newx = oldx[]-mix_range .. oldx[]+mix_range

            for each coordinate.  Includes possible zero move.  Sets new cell's state
```

```
	and mix flag.  Can move via jump or random walk through neighbors
	depending on mix_type.

	Modifications:

	v2.14b	Jun 23/95
		- don't modify c->state or c->newstate
	v2.14a	Jun 18/95
		- can move via walk or jump (see mix_type)
		- does bounds and error checking internally
		- renamed random_move() to move_cell()
		- now takes in old cell and returns new cell

	v2.12a	Apr 2/95
		- no longer restricted to first neighbors.  Now range=mix_radius
		- function type set to void.  No returns.

	v2.10a	Mar 12/95
		- new
*/
{
	cell *newc;
	int *oldx;
	int *newx = ivector(1,dim);
	int i,j,k, state;

	state = c->state;
	c->state = deadstate;	/* make cell available	*/

	if  (mix_type==JUMP) {
		oldx = c->x;
		/* repeat until valid site found		*/
		do {
			/* get new site			*/
			for (i=1; i<=dim; i++)
				newx[i]=oldx[i]-mix_range + (int)rrandom(2*mix_range+1);
			newc=ni_getcell(newx);
		} while (!inbounds(newx) || live(newc));
	} else if (mix_type==WALK) {
		oldx = ivector(1,dim);
		ivector_cpy(newx,c->x,1,dim);		/* copy c->x to newx	*/
		/* do a random walk of mix_range steps		*/
		for (i=1; i<=mix_range; i++) {
			ivector_cpy(oldx,newx,1,dim);		/* copy newx to oldx	*/
			do {						/* repeat until valid site found		*/
				/* take a step			*/
				j=(int)rrandom(maxnbrs+1);
				if (j!=0) {
					for (k=1; k<=dim; k++)
						newx[k]=oldx[k]+nbrx[j][k];
				}
				newc=ni_getcell(newx);
			} while (!inbounds(newx) || live(newc));
		}
	}
	newc = getcell(newx);
	newc->state = state;
	newc->newstate = c->newstate;
	newc->mixflag = 1;
	return newc;
}

/* turn off "'___' declared but never used" warning */
#pragma warn -use
•
```

rules.h

```
/*
	CellBot - rules.h

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	Modifications:

	v2.14a	Jun 18/95
		- random_move() replaced by move_cell()

	v2.12a	Apr 2/95
		- mix_radius made local to rules.c

	v2.10a	Mar 12/95
		- dead(c) & live(c) now test if c==NULL
		- added prototypes for mixing, mix_radius & random_move()
*/

#ifndef _RULES_H_
#define _RULES_H_

#define dead(c)		((c) == NULL || (c)->state == deadstate)
#define live(c)		((c) != NULL && (c)->state != deadstate)

extern int		dim;				/* dimensionality		*/
extern int		**nbrx;				/* relative locations of all neighbors		*/
extern int		maxnbrs;			/* number of neighbors */
extern float sync;					/* synchronisity		*/
extern int		minstate;			/* possible states are		*/
extern int		maxstate;			/*		minstate..maxstate		*/
extern int		deadstate;			/* must be within range */
extern float mixing;					/* mixing fraction		*/

/* function prototypes */
void initrules(char rulefname[]);
int applyrules(int *n);
int flipstate(void);
int x_flipstate(int s);
```

```
cell *move_cell(cell *c);

#endif      /* _RULES_H_          */
•
```

stable.c

```
/*
        CellBot - stable.c

        Copyright 1994 Hendrik Jan Blok

        Determines whether the system has stabilized or not.  If so, then
        returns period, else returns 0.  Actually tests periodicity of a
        statistic of the system.  Assumes that if this is periodic then
        it is reasonable to assume the system is also periodic.

        The statistic I have chosen is count_activity which is calculated in
        advance().  It is the sum of the magnitudes of all changes to the
        cells (ie. sum(abs(c->newstate - c->oldstate))).

*/

#include "cb.h"                         /* defines count_activity          */

int maxperiod;                          /* maximum detectable period       */
long *stablewin;                /* stability window     */

int stable(void)
/*
        Returns 0 if system has not stabilized, else non-zero (returns
        system period).  Also adjusts sum_activity to eliminate the
        effects of overlap.

        Note: we are not recording stability data in the dumpfile so in the
        event of a crash the decay time may not be accurate.  This would
        occur if the system has stabilized but stable() hasn't recognized it
        yet.  After the crash, all stability data is reset so we must advance at
        least 2*maxperiod steps before the system can be recognized as stable.
*/
{
        int testperiod(int p);

        static int next=0;
        static int filled=0;
        int p;

        /* first check if user wants to test stability at all.          */
        if (maxperiod <= 0)     return 0;

        /* Fill stablewin[].  count_activity set in advance() so that must be called
        first.          */
        stablewin[next] = count_activity;
        if (++next == 2*maxperiod) {
                next=0;
                filled=1;
        }

        /* if not filled then can't test stability              */
        if (!filled)    return 0;

        /* else test periodic      */
        for (p=1; p<=maxperiod; p++)
                if (testperiod(p)) {

                        /* Adjust sum_activity.  */
                        for (next=0; next < 2*maxperiod; next++)
                                sum_activity -= stablewin[next];

                        /* Reset stablewin[].    */
                        next=0;
                        filled=0;

                        /* Exit.        */
                        return p;
                }

        /* else not periodic       */
        return 0;
}

int testperiod(int p)
/*
        Tests if stablewin[] periodic with period p.
*/
{
        int i;

        for (i=p; i<2*maxperiod; i++) {
                if (stablewin[i] != stablewin[i-p])     return 0;
        }
        /* else        */                                                                    return p;
}

/* turn off "'___' declared but never used" warning             */
#pragma warn -use
```

stable.h

```
/*
        CellBot - stable.h

        Copyright 1994 Hendrik Jan Blok
```

```
	Determines whether the system has stabilized or not.
*/

#ifndef _STABLE_H_
#define _STABLE_H_

extern int maxperiod;			/* maximum detectable period	*/
extern long *stablewin;			/* stability window	*/

int stable(void);

#endif	/* _STABLE_H_	*/
```

strops.c

```
/*
	strops.c

	Copyright 1994,95 Hendrik J. Blok

	Routines to enhance string operations.
*/

#include "strops.h"			/* includes <string.h>, defines _strlen()	*/

void str_insert(char *ptr, char *substr)
/*
	Insert substring at ptr.
*/
{
	unsigned int l=_strlen(substr);
	int i;

	if (!substr)	return;
	for (i=_strlen(ptr); i>=0; i--)		/* shift characters out	*/
		*(ptr+l+i)=*(ptr+i);
	for (i=0; i<l; i++)			/* insert substr		*/
		*(ptr+i)=*(substr+i);
}

void str_delete(char *ptr, unsigned int count)
/*
	Delete count characters at ptr.
*/
{
	unsigned int n=_strlen(ptr);

	if (!count)	return;
	if (count>=n)
		*ptr='\0';	/* simply truncate string pointer	*/
	else			/* move characters to overwrite deleted substring	*/
		strcpy(ptr,ptr+count);
}

int str_replace_str(char *ptr,char *find, char *replace, int freq)
/*
	Find occurances of find, and replace with replace up to freq
	times.  Returns -1 if ptr or find strings are null.  Else returns 0.
	If initial freq<0 then replace all occurances.
*/
{
	unsigned int findlen=_strlen(find);
	unsigned int ptrlen=_strlen(ptr);
	char *match_ptr;

	/* argument checking	*/
	if ((findlen*ptrlen) == 0)
		return -1;

	match_ptr=strstr(ptr,find);
	while ((match_ptr != 0) && (freq != 0)) {
		freq--;
		/* remove string found	*/
		str_delete(match_ptr, findlen);
		/* replace it with new string		*/
		if (replace)
			str_insert(match_ptr,replace);
		/* find next matching strings		*/
		match_ptr=strstr(ptr,find);
	}
	return 0;
}
```

•

strops.h

```
/*
	strops.h

	Copyright 1994,95 Hendrik J. Blok

	Some routines to simplify string operations.
*/
#ifndef _STROPS_H_
#define _STROPS_H_

#include <string.h>

#define softspaces	" \t\n"

#define c_in_s(c, s)			(strchr(s,c)!=NULL)
#define itos(value)				itoa((int) value, str, 10)
#define ltos(value)				ltoa((long) value, str, 10)
```

```
#define ultos(value)                    ultoa((unsigned long) value, str, 10)
#define gtos(value, ndig)               gcvt((double) value, ndig, str)
#define etos(value, ndig)               ecvt((double) value, ndig, str)
#define ftos(value, ndig)               fcvt((double) value, ndig, str)

/*
        Use _strlen() instead of strlen() for portability onto Unix machines.
        Unix doesn't like strlen(NULL).
*/
#ifdef __MSDOS__
        #define _strlen(s)              strlen(s)
#else
        #define _strlen(s)              ((s)!=NULL ? strlen(s) : 0)
#endif

/* Routines from Mosich, Shammas and Flamig (see strops.c)         */
void str_insert(char *, char *);
void str_delete(char *, unsigned int);
int str_replace_str(char *, char *, char *, int);

#endif  /* _STROPS_H_       */•
```

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