



Goethe Universität Frankfurt

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Bachelor thesis

Percolation Analysis in Strong Coupling
Lattice QCD

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1 Introduction

Until now there is little known about the phase diagram of QCD, since the usually used methods are only working for a small section of the phase diagram. Nevertheless, it is expected to have a rich phase structure. The essential phase structure is conjectured to consist of a crossover, a first order phase transition and a chiral critical end point. Getting to know more about it is, amongst others, of great interest for examinations of the early universe, compact stars and heavy-ion collisions.

Percolation theory is a purely geometrical theory that deals with clusters on different kind of lattices and the corresponding critical phenomena. The clusters are generated randomly with a certain occupation probability of the lattice points. The main domain of percolation theory is the analysis of these generated clusters. The most interesting clusters are the clusters, which span through the whole lattice, and the dependence of their existence on the probability. Other important properties to analyse are, for example, the mean size of the clusters or the number of clusters per system. All these properties are a function of the occupation probability.

QCD in the strong coupling limit allows for a percolation analysis. In this limit, the gauge coupling goes to infinity. In strong coupling lattice QCD, only two degrees of freedom remain, mesonic degrees of freedom and baryonic degrees of freedom. This makes it possible to study the whole plane of the phase diagram with the methods that can not be used in standard lattice QCD. The phase transitions are not the same as in lattice QCD and due to the massless quarks, a tricritical point exists instead of the chiral critical endpoint. Even though those points are not identical, there may be a connection between them, which still makes it interesting to take a closer look at the tricritical point.

One approach to this is to transfer the two remaining degrees of freedom on a percolation model. This bachelor thesis should establish a basis for this approach by choosing and carrying out an appropriate percolation model.

The first step is to take a closer look at percolation theory and a few percolation models, which will be done in the next chapter. This chapter is based on [1]. Afterwards, the phase diagram of QCD and strong coupling lattice QCD will be described in more detail with [2] and [3] as main sources, and a connection to percolation theory is to be built. In the following chapter the programs for the percolation model and the analysis of it will be described in detail. In the last two chapters the results will be presented and discussed and a short outlook to further work will be given.

2 Percolation theory

This chapter should give an overview on different percolation models and their critical behaviour.

2.1 Percolation models

Percolation theory on a lattice describes models, which develop clusters by random occupation of the sites or links of the lattice. Because the expression 'point' is used for the lattice points and links, the terms 'site' and 'bond' will be used in the following to describe those special cases. Percolation models are purely geometric models without an existing Hamiltonian. The individual points are occupied with a so-called occupation probability p , which refers to a density of points, if occupied sites or bonds are counted as one state and all unoccupied sites or bonds are counted as a different state. This probability is the same for every point and is in this case independent of the occupation state of the adjacent points. Clusters form, when two adjacent points are occupied. If one cluster is spanning through the whole system, that is two ends of the system are connected by at least one path, one talks about a percolating system or cluster. Whether or not a percolating cluster exists depends on the occupation probability p . There is a critical probability p_c , from which a percolating cluster is getting a lot more likely. The bigger the system, the sharper the transition. This means for infinite lattice sizes, that below the critical probability p_c there are no percolating clusters and above p_c , there is most likely a percolating cluster. That means, that this transition can be interpreted as a sort of phase transition. The critical probability p_c depends on the dimension as well as on the chosen model.

In the next section, the for this thesis three most relevant models are introduced.

Site percolation

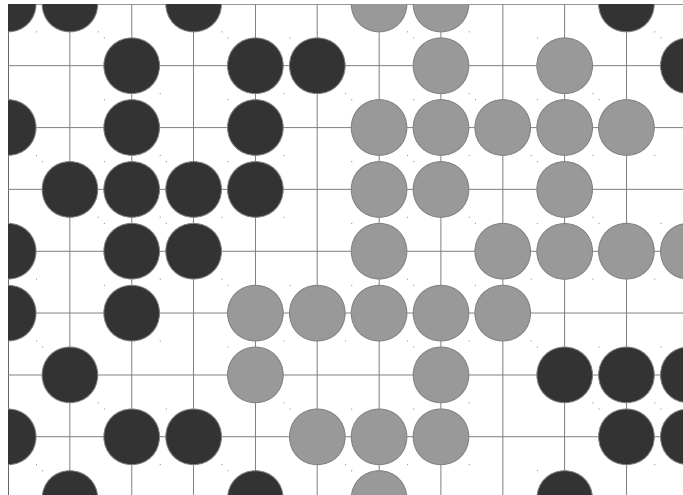


Figure 1: Schematic representation of site percolation

Site percolation on a lattice is described by the occupation of the sites of a lattice. A cluster is characterised by two adjacent occupied sites.

Figure 1 shows a schematic representation of site percolation. In this example, the occupation probability p is exceeding the critical probability p_c , as the existing percolating cluster indicates.

The critical probability p_c for a site percolation model on a square lattice in two dimensions is $p_c = 0.592746$ [4] and in three dimensions it is $p_c = 0.3116$ [5].

Bond percolation

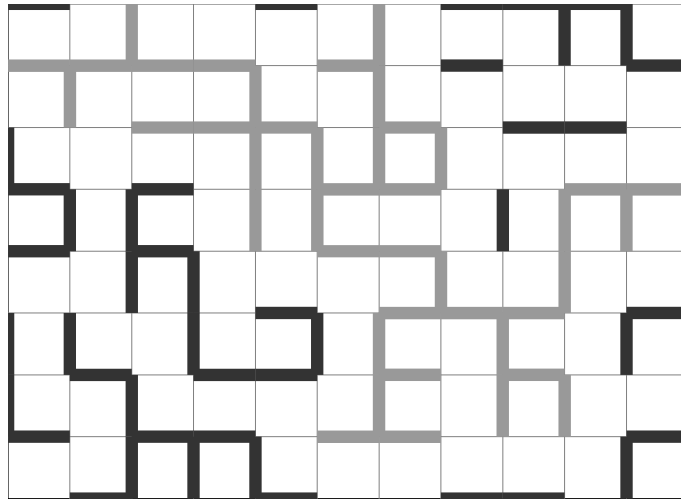


Figure 2: Schematic representation of bond percolation

Bond percolation on a lattice is described by the occupation of the bonds of a lattice. Clusters develop in the case of two occupied adjacent bonds.

A schematic representation for bond percolation can be seen in figure 2. The occupation probability p is as well exceeding the critical probability p_c , which is again indicated by the percolating cluster.

In a bond percolation model on the lattice the critical probability p_c in two dimensions is $p_c = 0.5$ [1] and in three dimensions it is $p_c = 0.2488$ [5].

Mixed percolation

The percolation model, which is most important for this thesis, is a mixed percolation model. This model contains two occupation probabilities. The first occupation probability is p_{bond} , which is the occupation probability for occupying bonds, and the second occupation probability is p_{site} , which is the occupation probability for occupying sites. Clusters start developing when adjacent bonds and the sites in between are occupied. If only adjacent bonds or only adjacent sites are occupied, no cluster will develop.

A schematic representation of a mixed percolation model is shown in figure 3. In this case, p_{site} and p_{bond} have both large enough values to develop a percolating cluster.

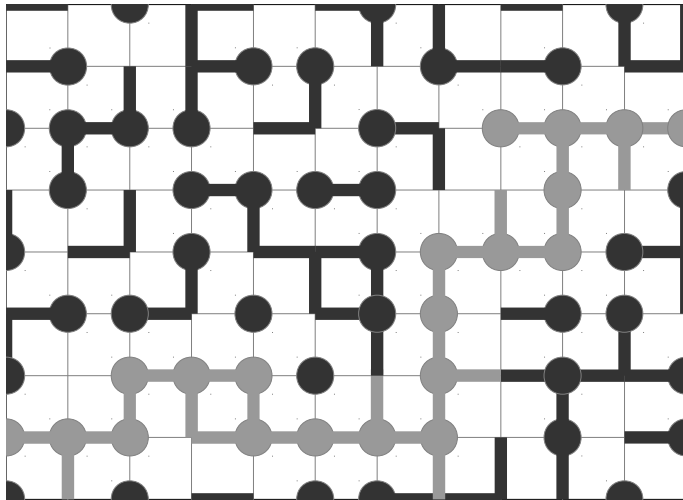


Figure 3: Schematic representation of mixed percolation

The goal of this thesis is to determine the phase boundary for this model on a square lattice in two and three dimensions.

Percolation and the Ising model

It is also possible to apply percolation with other models, for example the Ising model.

The Hamiltonian of the Ising model is described the following way:

$$\hat{\mathcal{H}} = -\frac{1}{2} \sum_{ij} J_{ij} s_i s_j - H \sum_{i=1}^N s_i \quad (1)$$

One possible way of connecting percolation and the Ising model is the consideration of percolating spin-clusters. If the density for spin up or spin down outweighs the other one, then a percolating cluster can exist. This describes a temperature-dependent percolation model, as for $T = 0$ with or without an external magnetic field, one spin is favoured in a way, that just one spin survives. For $T > 0$, the probabilities for spin up and spin down get more and more alike, until $p_{up} = p_{down} = 0.5$ holds for $T \rightarrow \infty$. This leads to smaller spin-clusters. It is then possible to define a critical percolation probability at a finite T , where the spin-probabilities are both too small to build a percolating cluster. This percolation phase transition can be studied in terms of percolation critical behaviour, which is discussed in the following subsection.

2.2 Critical behaviour

In this subsection we are taking a short look at the critical behaviour of percolation models. The critical behaviour of percolation models is interesting to

study because there are some connections between the critical behaviour of percolation models and the critical behaviour of different other models, for example the Ising model.

The critical exponents of percolation models usually just depend on the dimension of the system. There is no difference in examining a site percolation, a bond percolation or a different kind of percolation model. The only critical parameter, which is not universal for all models is the critical probability p_c . In contrast to the systems that are typically considered, the critical behaviour of percolation models does not depend on the temperature, but on the occupation probability. The order parameter, for example, has the following proportionality in the infinite volume limit:

$$P(p) \sim (p - p_c)^\beta \quad (2)$$

The critical exponent β has the value $\beta = 0.14$ [1] in two dimensions and $\beta = 0.4$ [1] in three dimensions.

Other examples are the mean cluster size, which is analogous to the susceptibility, or the correlation length.

The mean cluster size describes the mean size of the cluster excluding the percolating cluster. This is the reason why the mean cluster size diverges around the critical probability p_c but again decreases at higher occupation probabilities p . This yields the following proportionality:

$$S(p) \sim (p_c - p)^{-\gamma} \quad (3)$$

In two dimensions, the value for γ is $\gamma = 2.43$ [1], and in three dimensions it is $\gamma = 1.6$ [1].

In the usual spin systems this refers to the susceptibility

$$\chi \sim |\tau|^{-\gamma} \quad (4)$$

with $\tau = \frac{T-T_c}{T_c}$, which is analogous to $p-p_c$. The correlation length is describing the mean distance between two points within one cluster. Again, the percolating cluster is excluded. Therefore, the correlation length diverges again around the critical probability p_c and decreases afterwards with increasing p . This leads to the following proportionality:

$$\xi(p) = (p_c - p)^{-\nu} \quad (5)$$

The value for ν in two dimensions is $\nu = 1.34$ [1] and in three dimensions $\nu = 0.8$ [1].

In usual spin systems, this refers to the correlation length

$$\xi \sim |\tau|^{-\nu} \quad (6)$$

with $\tau = \frac{T-T_c}{T_c}$, as stated above.

3 The phase diagram of QCD

In this chapter we will take a closer look at the phase diagram of lattice QCD and we will establish a connection between the phase diagram in the strong coupling limit and percolation theory.

3.1 The structure of the phase diagram

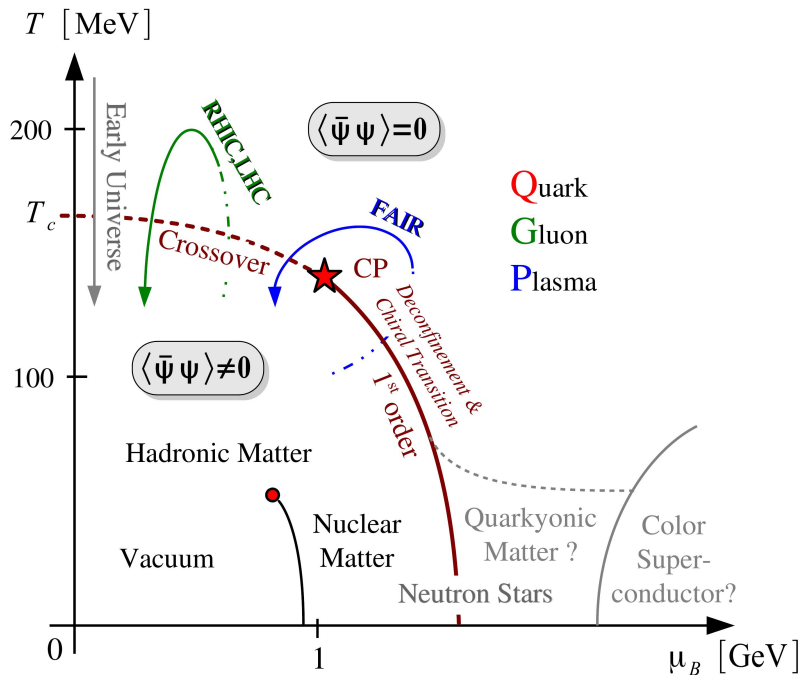


Figure 4: Assumed structure of the phase diagram of QCD for massless quarks; [2] s.3

The phase diagram of QCD is suspected to have a rich phase structure. An example for the assumed structure can be seen in figure 4. The first important phase for this thesis is the phase found at low temperatures and low baryonic chemical potentials, which is the phase of hadronic matter. It is split in a vacuum phase and the phase of nuclear matter. In this phase, the chiral symmetry is broken. The other important phase is found at high temperatures and/or high chemical potentials. In that phase confinement is absent, instead the so-called Quark-gluon plasma can be found and the chiral symmetry is restored. For even higher chemical potentials, speculations on further phases, like a colour-superconducting phase or a phase of quarkyonic matter, exist. Between the two phases, two different transitions are suspected. At high temperatures there should be a crossover, which is strictly speaking not a true phase transition, and at high chemical potential there probably is a first order phase transition. If the first order phase transition exists, there also must be a critical

end point.

However, it is still not possible to verify this phase structure. The main problem with verifying the phase structure is the sign problem. This problem arises because the weight for the fermion determinant becomes complex. This leads to problems with the mainly used methods, like Monte Carlo simulations. Those methods are just available for $\mu/T \lesssim 1$, with $\mu = \frac{1}{3}\mu_B$.

3.2 The phase diagram in the strong coupling limit

Considering the phase diagram in the strong coupling limit of lattice QCD is one possibility to avoid this problem. In the strong coupling limit, the gauge coupling parameter goes to infinity, $g \rightarrow \infty$. This means, that the gauge action $\beta = \frac{2N_c}{g^2}$ is going to zero, $\beta = 0$. This makes it possible, to first integrate out the gauge variables and then the Grassmann variables. Normally, first the fermions would be integrated out, which leads to the fermion-determinant, that leads to the problems stated in the above section. In order to make those integrations possible, the QCD action [7]

$$S = \int d^4x \left(\frac{1}{4} F_{\mu\nu} F^{\mu\nu} - \bar{\Psi} D \Psi \right) \quad (7)$$

has to be discretised to get to the lattice representation of QCD. After that, doing the integrations yields the following partition function [2]:

$$Z_{SC}(m_q, \mu, \gamma) = \sum_{\{k,n,l\}} \prod_{b=(x,\mu)} \frac{(N_c - k_b)!}{N_c! k_b!} \gamma^{2k_b \delta_{\mu 0}} \prod_l w(l, \mu) \quad (8)$$

The first term of the partition function describes meson hoppings and the second term describes baryon world lines. The meson hoppings, or spatial dimers, are favoured at low temperatures because of the anisotropy $\gamma = \frac{a}{a_t}$. It favours temporal dimers, so the spatial dimers are disfavoured, which leads to static mesons. In this case, the baryonic loops are always static.

It follows from this partition function that the only degrees of freedom are mesons and baryons. It is now possible to obtain the phase diagram in the strong coupling limit of lattice QCD with Monte Carlo simulations, which is shown in figure 5.

The phase boundary has the same structure as in figure 4, but there are differences. Again, the most important phases are the phase of hadronic matter, where baryons and mesons represent all degrees of freedom, and the Quark-Gluon-Plasma, where the confinement dissolves. Firstly, instead of a crossover there is a second order phase transition at high temperatures, at high chemical potentials the phase transition stays first order. In the strong coupling limit there lies a tricritical point in between the two phase transitions. The tricritical point is the analogon to the critical endpoint for massless quarks.

3.3 Connection between the phase diagram in the strong coupling limit and percolation theory

One approach to this problem is to transfer the $\mu - T$ plane to a mixed percolation model. This is possible, since in the strong coupling limit, which was

discussed in the last subsection, only two degrees of freedom exist, the mesons and the baryons. Those are linked to the temperature and the baryonic chemical potential. At low temperatures, a lot of spatial meson hoppings are taking place, and at high baryonic chemical potential there are many baryons. Between sites without a baryon, spatial meson hoppings are possible.

This leads to a representation on a lattice, where the spatial meson hoppings are occupied bonds and the baryons are unoccupied sites. This clarifies the connection to a mixed percolation model, in a way that mesons refer to bond percolation and baryons refer to site percolation. It is now possible to assign an occupation probability to every temperature T and every baryonic chemical potential μ_B . This yields the following correlations

$$\mu_B \sim n_B \sim 1 - p_{site} \quad (9)$$

$$T \sim 1 - n_{MH} \sim 1 - p_{bond} \quad (10)$$

with n_B the density of baryons and n_{MH} the density of spatial meson hoppings. n_B increases with increasing baryonic chemical potential and n_{MH} decreases with increasing temperatures. Every occupied bond then defines a spatial meson hopping and every unoccupied site defines a baryon.

This mapping of percolation theory to LQCD is not entirely accurate. Firstly, it just considers a three dimensional model without a time axis, so the considered baryons are static and are point-shaped. As well, the occupation of the sites is, in contrary to the assumed case, not completely random, as the interaction between the baryons is not truly random. Hence, the percolation model is a simplification. However, due to the similarity of dynamic and geometric second order phase transitions, a percolation analysis is appropriate. So, as it still describes the model relatively well, it is possible to use this simple percolation model to get an impression of the phase diagram of strong-coupling QCD. To get a percolation phase boundary that can be connected to the $\mu - T$ plane, p_{site} and p_{bond} must be varied from 0 to 1. The percolating phase should correspond to the phase of broken chiral symmetry. The reason for this are the mesons and spatial mesons hoppings that spread over the whole system in the percolating phase. When the spatial meson hoppings are spreading over the whole lattice, the chiral condensate diverges, which means, that the chiral symmetry is broken. In the non-percolating phase no spatial meson hoppings take place or at least, they can not spread through the whole system, because there are too many baryons or not enough spatial meson hoppings are possible.

This phase boundary refers to mesonic percolation, which means, that the percolating phase is defined over the occurring spatial meson hoppings, that has to spread over the whole system. For this, it is important, that there are enough mesons on the lattice, so that the spatial meson hoppings can take place. The baryon density n_B is therefore just of secondary interest, because the hole density, or the density of sites without a baryon, is of actual interest, because spatial meson hoppings can only take place between two holes. The reason why the baryon density is considered above is the relation $1 = n_B + n_M$ or $n_M = 1 - n_B$, so it does not matter if the baryon density n_B or the density of holes is considered, but one has to keep in mind, that for this phase boundary the density of holes is of interest. The reason for considering the baryon density instead of the hole density is, that it is more convenient to consider the density of a present quantity than the density of an absent quantity.

The difference between the models, that in the strong coupling limit bonds are just occupied when the adjacent sites are occupied as well, while in the mixed percolation model sites and bonds are occupied independently from each other, is not a problem. This difference only has an effect on the number and the size of the clusters, but not on the critical probability p_c . Due to the restriction, that clusters are only able to form when the bonds and the adjacent sites are occupied, the occupied bonds without occupied adjacent sites are counted as clusters of size 1. Those clusters are never able to percolate and do not affect the percolation threshold.

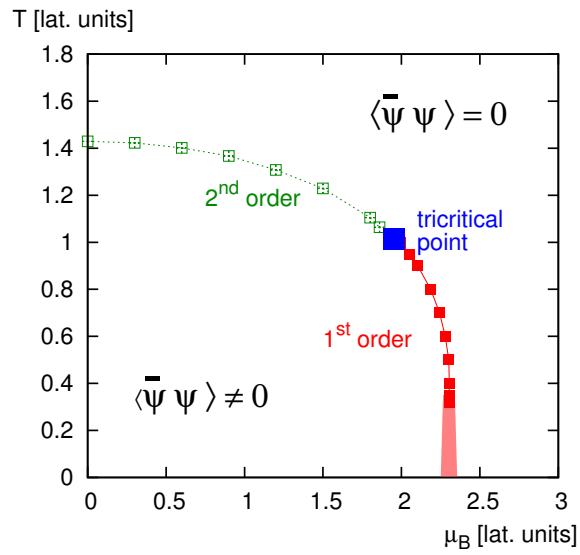


Figure 5: The phase diagram of lattice QCD in the strong coupling limit for massless quarks; [3] p.3

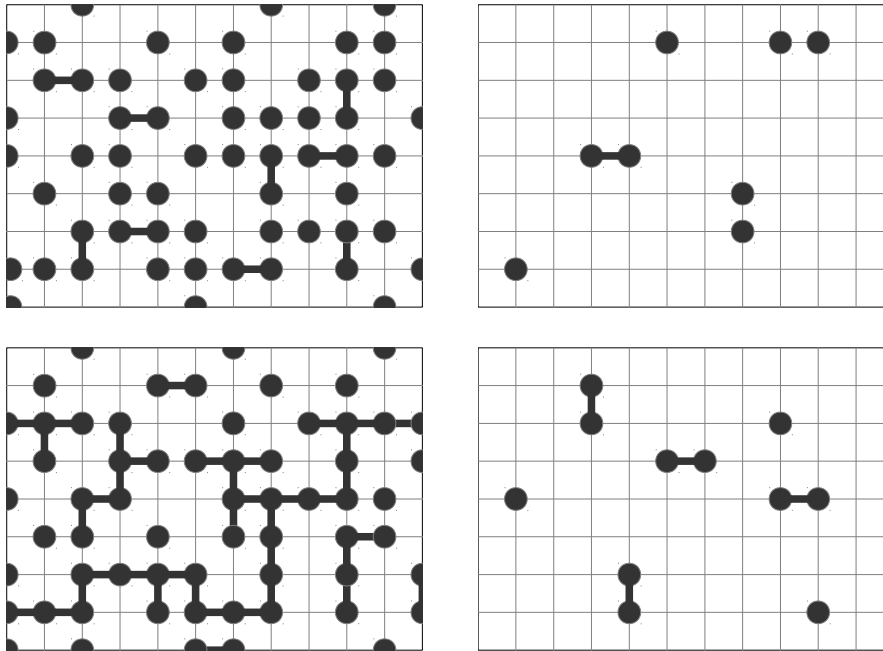


Figure 6: Schematic representations for different occupation probabilities p_{site} and p_{bond} . In the upper left figure, T is large and μ is small, that means p_{site} is large and p_{bond} is small. In the upper right figure, T and μ are large, that means p_{site} and p_{bond} are small. In the lower left figure, T and μ are small, that means p_{site} and p_{bond} are large, one can see the percolating phase. In the lower right figure, T is small and μ is large, that means p_{site} is small and p_{bond} is large, but the bonds can only be occupied between two occupied sites.

4 Numerical background

In this chapter, the developed program for the percolation model as well as the program for the data analysis are discussed.

4.1 Programming the percolation model

In the first step, the program calculates the volume $\text{Vol} = L * \text{dim}$ and the numbers of sites and/or bonds dof :

$$\text{dof}_{\text{site}} = \text{Vol} \quad (11)$$

$$\text{dof}_{\text{bond}} = \text{dim} * \text{Vol} \quad (12)$$

$$\text{dof}_{\text{mixed}} = (\text{dim} + 1) * \text{Vol} \quad (13)$$

It also assigns an array $\text{direction}[\text{dim}]$, which has one component for every dimension.

Because the points of the lattice will be saved in a single array and it is necessary to reconstruct clusters out of those numbers, it is important to know how the points are arranged among each other. This can be accomplished as a function of the model, even before it is assigned to the array, which points are occupied, and before the clusters are reconstructed.

4.2 Forward and backward functions

First, two arrays fwx and bwx are generated. For site percolation and mixed percolation they both have the size $\text{dof} * \text{dim}$ and for bond percolation $2 * \text{dof} * \text{dim}$. It becomes clear later, why a different size was chosen for bond percolation. The arrays are assigned a value corresponding to two different functions, the **forward** and **backward** functions:

$$\text{fwx}[\text{v} * \text{dim} + \text{d}] = \text{forward}(\text{v}, \text{d}, \text{model}, \text{fb}) \quad (14)$$

$$\text{fwx}[(\text{v} * \text{dim} + \text{d}) * 2 + \text{fb}] = \text{forward}(\text{v}, \text{d}, \text{model}, \text{fb}) \quad (15)$$

The first equation describes site percolation and mixed percolation and the second equation describes bond percolation. The array bwx is assigned in a similar way, just the **forward** function is changed to the **backward** function.

The variable v is the number of the current point in the array, d is the dimension for which the neighbour should be determined. model tells the functions, for which model the neighbours should be calculated, because these functions are one of the few parts of the program, that contain explicitly the information about the model. fb is an additional variable, that is only important for bond percolation and will be described in the section for bond percolation.

In the following, the **forward** and **backward** functions are described in more detail for every model.

For a site percolation model the points are sorted according to the following scheme:

$$\text{v} = \text{x}_0 + \text{x}_1 L + \text{x}_2 L^2 + \dots + \text{x}_n L^n \quad (16)$$

To determine the neighbours of this number, the individual values for $\text{x}_0, \text{x}_1, \text{x}_2, \dots, \text{x}_n$ are saved in the array $\text{direction}[\text{n}]$. The value x_{dir} belongs to the dimensions

that should be changed. This value is increased by 1 by the forward function and is decreased by 1 by the backward function. That causes a shift to the nearest neighbour in the given dimension. Finally, the number of the neighbour is put together like in the above scheme and is saved in `fwx[v*dim+d]` or `bwx[v*dim+d]`, depending on the used function.

Considering bond percolation, the fourth input parameter `fb` is needed. The reason for this are the two ends of a bond, which both contain neighbours. Because of this, a given dimension is not unique and there are twice as many directions as in a site percolation model, one for every end of a bond. To solve this problem, a further input parameter is needed, which differentiates between the two directions of a dimension. The two ends of the bond are varied with the `forward` and `backward` functions, the `forward` function considers the front end of the bond and the `backward` function considers the back end.

This also leads to a variation in the sorting of the points compared to site percolation:

$$v = d \cdot \text{Vol} + x_0 + x_1L + x_2L^2 + \dots x_nL^n \quad (17)$$

Here `d` describes the direction of the bond and takes a value between 0 and `(dim - 1)`. This factor is needed, as every point of the lattice contains one bond in every direction, which leads to `dim`-times more bonds than there would be sites.

Similar to site percolation, the individual parameters `d, x_0, x_1, x_2, ... x_n` are determined and saved, `d` as a single variable and `x_0, x_1, x_2, ... x_n` in the array `direction[n]`. The saved numbers `x_0, x_1, x_2, ... x_n` correspond to the back end of the bond.

Therefore, when considering the forward function, the parameter `x_d`, which is the value for the direction of the bond, has to be increased by 1 independently of the direction of the sought neighbour. According to `fb`, `x_dir` is decreased by 1 or is not changed at all. This determines the direction within the chosen dimension. The second part of the number is put together after the above scheme. In the first part of the number, the value `d` is replaced by the given dimension `dir` and the number is saved in `fwx[(v*dim+d)*2+fb]`.

The backward function works in a similar way, but `x_d` stays unchanged. Just `x_dir` is increased by 1 or stays unchanged according to `fb`. The number is put together in the same way as in the forward function, but leaving the parameter `x_d` unchanged, so that the function is looking at the back end of the bond. The number is saved in `bwx[(v*dim+d)*2+fb]`.

In the mixed percolation model, the additional input parameter `fb` is not needed anymore. The reason for this is the different structure of the lattice. Every bond has just two adjacent sites that have to be considered and every site has one adjacent bond in every direction, which is quite similar to site percolation when imagining the bonds as nearest neighbour sites. Those relations make it easy to determine a percolating cluster, since the bonds and the sites in between have to be occupied. Choosing the relations in this way makes sure, that just connections of bonds and sites are counted as clusters. The structure for the sorting of the points is the same as the sorting for bond percolation:

$$v = d \cdot \text{Vol} + x_0 + x_1L + x_2L^2 + \dots x_nL^n \quad (18)$$

The only difference lies in the parameter d , which now takes values between 0 and dim . This additional dimension takes care of the sites. Similar to the above models, the parameters are determined and saved. The `forward` and `backward` functions differentiate, whether the current point is a site or a bond.

The `forward` function for a site puts the number together in a similar way as for bond percolation. The bonds checked with the `forward` function belong to the same lattice point as the current site, the forward function just needs to select the correct bond. It changes no value x_n , but replaces d with dir . Starting from a bond, the `forward` function first increases x_d by 1, so the next lattice point to which the adjacent site belongs, can be reached. After this, the number is put together, but this time d gets replaced by dim , to choose the site. Again, the new number is saved in `fwx[(v*dim+d)*2+fb]`.

The `backward` function for a site first decreases x_{dir} by 1 to move to the lattice point of the chosen adjacent bond. When putting together the number, d is again replaced by dir . When the current point is a bond, the number is directly put together, just replacing d with dim , because the adjacent site belongs to the same lattice point as the current bond. Again, the number is saved in `bwx[(v*dim+d)*2+fb]`.

After the points are arranged in this way, the N-loop can be started.

4.3 Cluster analysis

Now the array `site[v]`, in which the information about the occupation of the points is saved, gets declared.

Whether a point is occupied is determined by random numbers. When $n_{\text{rand}} < p$, with n_{rand} a random number, the point counts as occupied and `site[n]` is set to 1.

For bond percolation and site percolation, there is only one occupation probability p , but in the case of mixed percolation there are two occupation probabilities, p_{bond} and p_{site} . In this case, relation (18) holds. Because the additional dimension saves the sites, the array `site[v]` is filled the following way:

$$v = 1 \text{ if } n_{\text{rand}} < p_{\text{bond}}; \quad d < \text{dim} \quad (19)$$

$$v = 1 \text{ if } n_{\text{rand}} < p_{\text{site}}; \quad d = \text{dim} \quad (20)$$

After `site[v]` is filled completely this way, the clusters are getting reconstructed.

Cluster reconstruction

For the cluster reconstruction, every cluster gets saved in the array `cluster[v]`. First, every component of the array is set to 0. After this, the recursive function for reconstructing the cluster gets called for every point of the cluster.

The `cluster_reconstruction` function is first determining, if the current point was visited before. This information is stored in the array `visited[v]`. When the point was visited before, the function returns. When the point was not visited, its corresponding component of `visited[v]` is set to `true`.

In the next step, the function determines, whether the current point is actually

occupied, if not, it returns. To get this information, the `cluster_reconstruction` uses the information of the `site[v]` array.

When the current point was not visited before and is occupied, its corresponding component of `cluster[v]` is set to `true`.

In the last step, the `cluster_reconstruction` is calling itself for all neighbours of the current point and is saving them in the same array `cluster[v]`, when they are occupied as well. For determining the neighbours, it uses the `fwx` and `bwx` arrays. It is calling itself for all points `fwx[v*dim+d]` and `bwx[v*dim+d]` with `d` varying from 0 to `dim-1`, or in the case of bond percolation for all points `fwx[(v*dim+d)*2+fb]` and `bwx[(v*dim+d)*2+fb]` varying over `d` and in addition switching `fb` between 0 and 1.

As soon as one cluster is reconstructed, it can be determined, whether it is percolating.

Determination of percolating clusters

To determine whether a cluster is percolating, two additional arrays `atLowerEdge[d]` and `atUpperEdge[d]`, with $0 \leq d < \text{dim}$, and two additional functions `isAtLowerEdge(v,d)` and `isAtUpperEdge(v,d)` are needed. The arrays are set to `false` first and than the two functions are called and if they return as `true`, the corresponding component of the arrays is set as `true` as well.

These functions work differently for every model as well.

Considering site percolation and the construction of the values for the points 16, the two functions simply calculate

$$x = \frac{v}{L^{\text{dir}}} \bmod L \quad (21)$$

`isAtUpperEdge(v,d)` then checks if `x==L-1` and `isAtLowerEdge(v,d)` checks if `x==0`. If one of these conditions is fulfilled, the component of the proper array is set to `true`.

This simply checks, if a site is on an edge of the lattice.

Looking at bond percolation and a sorting of points as in (17), the two functions first have to calculate `d=v/Vol` as an integer division and `vcor=v-d*Vol`. If `d==dir` holds, the functions also calculate (21), but with `vcor` instead of `v`. Also, they then check for `x==L-1` and `x==0` in the same way they do it with a site percolation model.

Here, the functions are determining if a bond lies on an edge, but only if the bond corresponds to the chosen dimension. If this is not the case, the current bond can not lie at the edge. For example when checking the dimension, that reaches from the left to the right, just for the bonds aligned from left to right it is checked, if they lie at the edges of the lattice in the given dimension.

In the case of mixed percolation and (18), the functions work nearly the same as for bond percolation. The only difference is in the `isAtLowerEdge(v,d)` function, where `x==0` should hold. Instead of calculating (21) when `d==dir`, it calculates (21) when `d==dim`.

The reason for this behaviour is, that every site is connected with a bond in every dimension. Therefore one half of the lattice has an edge of sites and the

opposite half has an edge of bonds. The `isAtLowerEdge(v,d)` therefore has to check, whether the current point is a site and only than calculate, if it lies on the side, that should be checked. If the current point is a bond, again it should be checked, whether it points in the right direction and if it lies at the side.

When it is determined for every edge if a point of the cluster lies there, it can be checked if the cluster percolates. For this, the program simply has to check if `atLowerEdge[d]` and `atUpperEdge[d]` are `true` for the same value of `d`.

If this is the case, a variable `percolationcount` is increased by 1 and the corresponding component of an array `isPercolating[N]` is set to 1.

When the `N`-loop is finished and it is determined for every system whether it percolates, it can be calculated how many percent of the systems did percolate:

$$\text{percolationper} = \frac{\text{percolationcount}}{N} \quad (22)$$

After this, the program calculates an error for this number with the method of standard deviation of the mean:

$$\text{error}_{\text{perc}} = \sqrt{\frac{1}{N \cdot (N - 1)} \sum_{n=0}^{N-1} (\text{isPercolating}[n] - \text{percolationper})^2} \quad (23)$$

In the last step, `pbond`, `psite`, `percolationper` and the error are written in a file.

4.4 Data analysis

To get the desired critical probabilities, this program has to be run for different `psite` and `pbond`. In this case, `psite` was set to different fixed values and `pbond` was varied, so $P(p)$ was obtained as $P(p_{\text{bond}})$. The value for `N` in two dimensions was `N=10000` and in three dimensions `N=1000`. It was also necessary to do this for different lattice sizes `L`, in two dimensions the chosen lattice sizes were `L=8,16,24` and in three dimensions `L=8,12,16`. The lattice sizes are small, because the cluster reconstruction is a recursive function, which makes it quite expensive, especially around the critical probability p_c .

The data, that was generated this way, has to be analysed to obtain $P(p_{\text{bond}})$ and with this, finally, p_c . This was done with a different program.

The critical probability p_c can be obtained by determining the intersection of the data lines for different lattice sizes. This can be done, because the slope differs for different lattice sizes, but because the critical probability p_c has to be the same for all lattice sizes, one can assume that the intersection of the data has to be the critical probability.

The program generated linear least square fits for $P(p_{\text{bond}})$ for every lattice size from the data. The parameters for a linear least square fit are calculated the following way, when assuming $f(x) = y = ax + b$:

$$a = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sum_{i=1}^n (x_i - \bar{x})^2} \quad (24)$$

$$b = \bar{y} - a\bar{x} \quad (25)$$

The next step is to calculate the intersections of the three lines. For this, the program saved every line in an array. The intersection is the point, on which the sign changes when calculating:

$$s = \text{linearfit}_m[x] - \text{linearfit}_n[x] \quad (26)$$

The critical probability follows then as:

$$p_c = \frac{1}{3}(p_{c1} + p_{c2} + p_{c3}) \quad (27)$$

with $p_{cx} = \frac{\text{linearfit}[\text{int}-1] - \text{linearfit}[\text{int}]}{2}$ and the assumption, that finite size effects are small in a percolation model.

The error for p_c is calculated the following way:

$$\text{error}_{p_c} = \sqrt{\frac{1}{3(3-1)}((p_{c1} - p)^2 + (p_{c2} - p)^2 + (p_{c3} - p)^2)} \quad (28)$$

It is not necessary to calculate an error with the jack knife method or similar methods, because all configurations are statistically independent, so there should be no autocorrelation.

The last step is to save p_{site} , p_c and the error in a file.

5 Results

5.1 The phase boundary

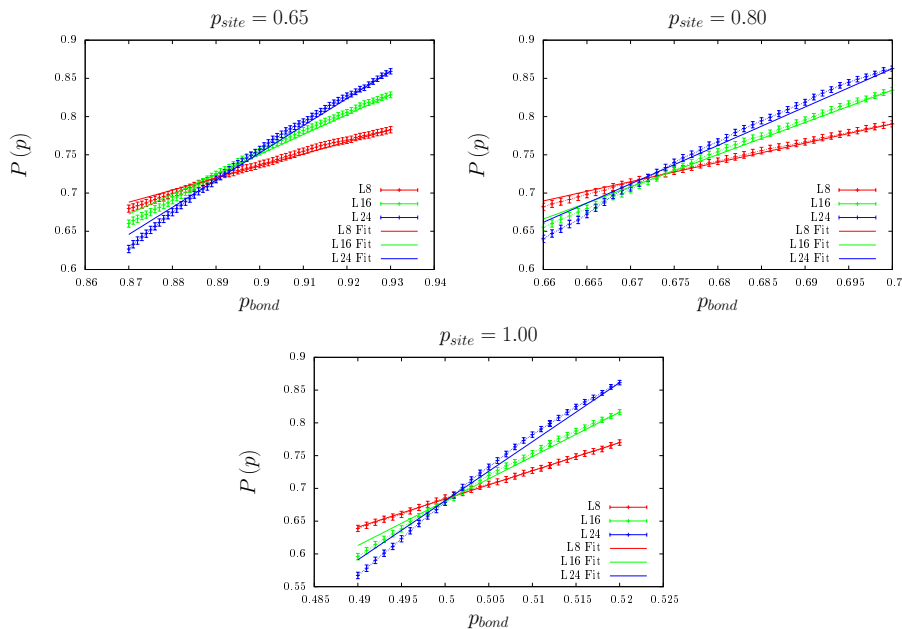


Figure 7: Zoom into the critical region for two dimensions and the corresponding linear fits

For the mixed percolation model, figure 7 and figure 8 show a zoom into the critical region and the corresponding linear fits. Figure 7 shows the plots for three different values of p_{site} for two dimensions and figure 8 shows the plots for five different values of p_{site} for three dimensions.

The linear fits are describing the data close to the critical probability p_c quite well, just for few statistical series they are lying outside of the error bars. For two dimensions, this occurs more frequently than in three dimensions, because some of the data points are not close enough to the critical probability p_c to use a linear fit. The different intersections are getting closer to each other with increasing p_{site} , the error bars however have similar values and have for two dimensions a range from approximately $\Delta P(p) \sim 0.0035$ to $\Delta P(p) \sim 0.005$ and for three dimensions a range from approximately $\Delta P(p) \sim 0.010$ to $\Delta P(p) \sim 0.016$. The reason for this difference are the different N-loop-counts for two and three dimensions. In two dimensions the statistics are ten times better, which minimises the errors.

The line of the biggest lattice size L has, as expected, the steepest slope. This effect occurs, because for a second order phase transition, the slope becomes infinite in the thermodynamic limit $L \rightarrow \infty$, which weakens for finite lattices. The different deviations of the intersections from each other could relate to the different occupations of the lattice. When p_{site} is big, nearly all sites are occupied. From this it follows, that nearly every percolating bond-cluster is also

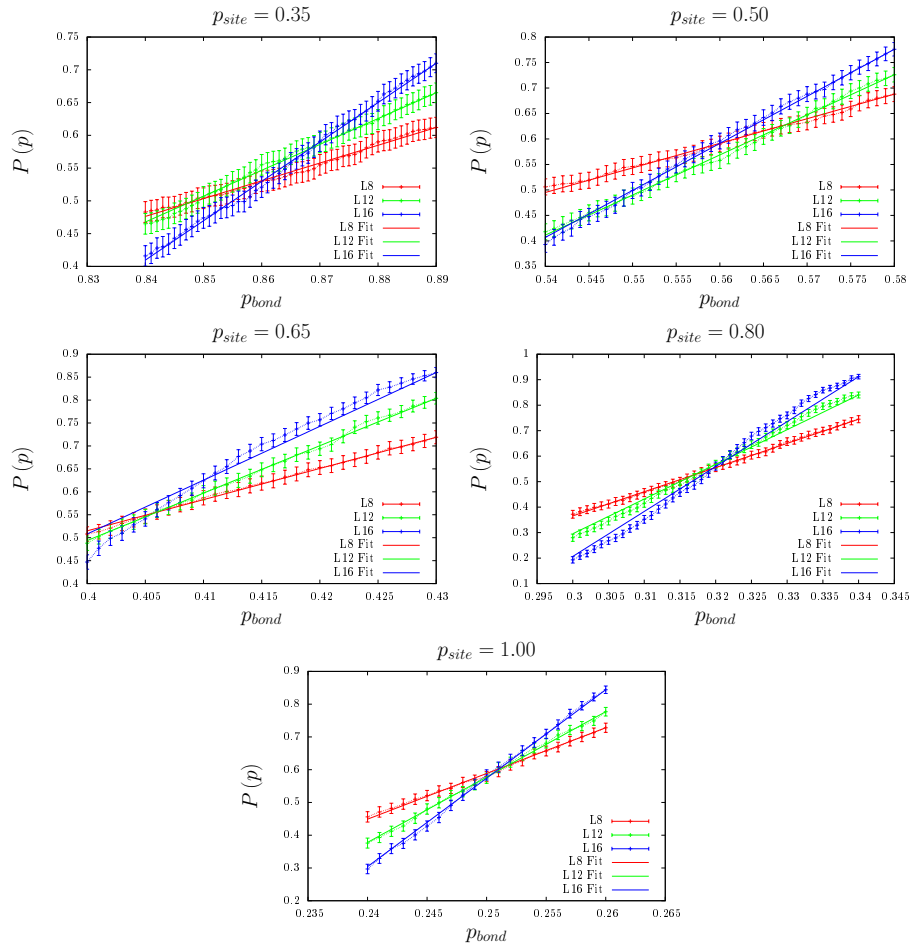


Figure 8: Zoom into the critical region for three dimensions and the corresponding linear fits

p_c in 2 dimensions

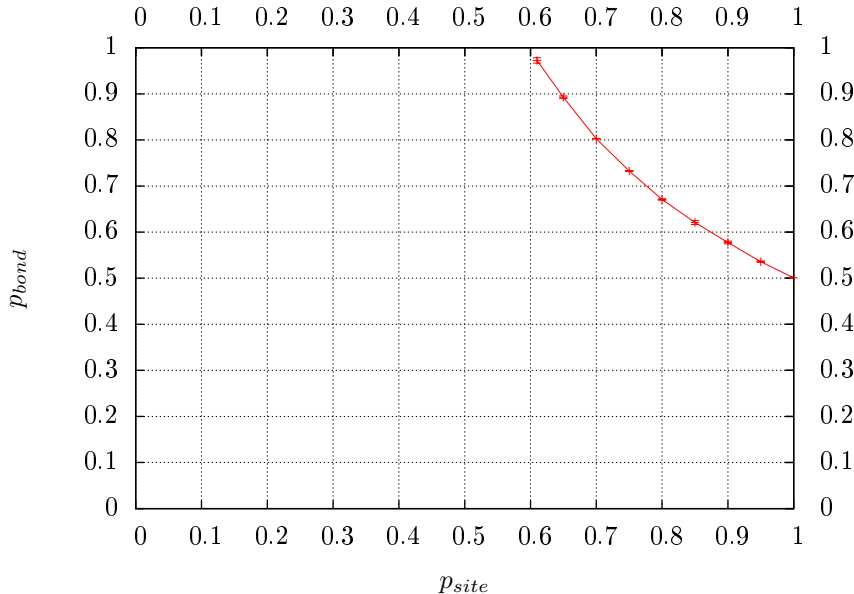


Figure 9: Phase boundary of the mixed percolation model in two dimensions

a percolating mixed-cluster. When p_{site} is small, not every percolating bond-cluster can refer to a percolating mixed-cluster, because the sites in between have to be occupied as well. This effect could possibly have a slightly different weight for different lattice sizes which causes the divergence of the intersections.

As soon as the program determined all intersections, the phase boundary can be identified. Figure 9 and figure 10 show the phase boundaries for two dimensions and three dimensions.

The phase boundaries seem quite similar, the biggest difference are the much smaller values for the critical probability in three dimensions compared to two dimensions. This effect is known from pure bond percolation and pure site percolation and occurs, because there are more possibilities to connect two points in three dimensions than there are in two dimensions.

The phase boundaries are both very smooth and the error bars are small, which can be seen in figure 9 and in figure 10. Just in three dimensions at an occupation probability $p_{site} \sim 0.7$ the phase boundary has a small irregularity. It could be possible, that this irregularity could smooth out, when the statistics is higher.

For the case $p_{site} = 1$ one obtains pure bond percolation. The computed critical probability is close to the literature value. For two dimensions, the computed value is $p_c = 0.501 \pm 0.002$, with a literature value $p_c = 0.5$. In three dimensions, the computed value is $p_c = 0.253 \pm 0.0000002$ and the literature value $p_c = 0.2488$. The value for two dimensions lies within the error margins, for three dimensions, the value is a little bit off the literature value. The error margins for three dimensions are so small, because the three individual intersections

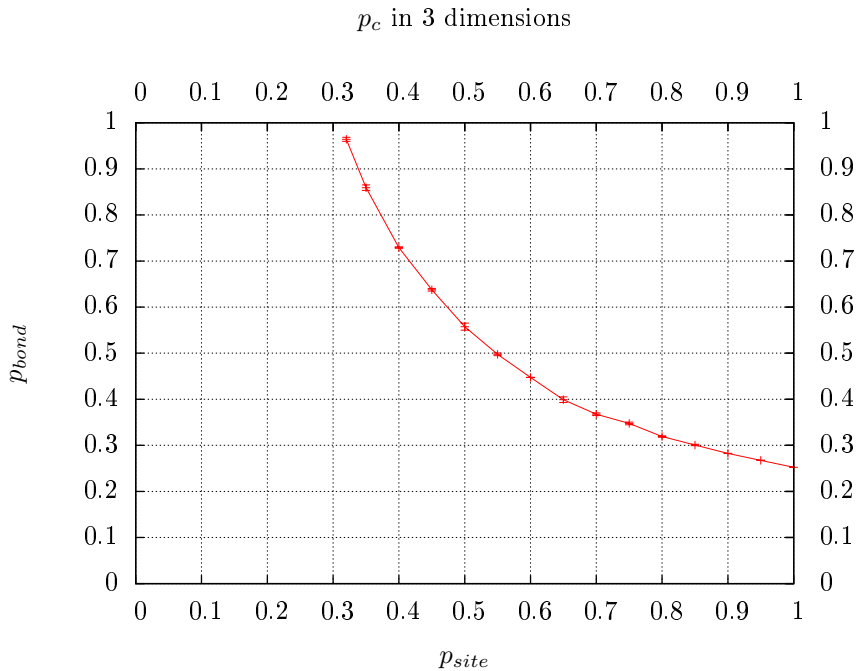


Figure 10: Phase boundary of the mixed percolation model in three dimensions

lie very close together. The difference of the value to the literature value could be caused by a small statistic and finite size effects, probably even the lattice sizes are too close to each other.

A pure site percolation could not be reached, because p_{site} was chosen first and it is not possible to then reach an exact value of 1 for p_{bond} . The reason for this are the intersections. They vary from each other and to get a value of 1, the intersections must lie all exactly at 1, because it is not possible to compute $P(p_{bond})$ for values larger than 1. Since the intersections are varying for the different lattice sizes, the mean value is always $p_{bond} < 1$. Still, when roughly estimating a value for $p_{bond} = 1$ by taking a look on the graphics 9 and 10, one can assume, that the values for p_{site} would lie close to the literature values $p_c = 0.592746$ for two dimensions and $p_c = 0.3116$ for three dimensions

Most of the irregularities should occur because of finite size effects, which occur because the used lattice sizes were probably too small.

Getting a bigger lattice sizes was not possible, because the computation were done on an ordinary laptop on which the run-time of the program with a better statistics or bigger lattice sizes would have been exceedingly long.

5.2 Cluster analysis

This part should give a short insight in the cluster analysis. This cluster analysis is carried out on a two dimensional site percolation model. It is important to take into account, that the percolating cluster and clusters with size 1 are

included in this analysis.

To get the data, the size of the clusters and the number of the clusters were saved for every system.

Number of clusters

Figure 11 shows a distribution of the number of clusters per system for different occupation probabilities for a two dimensional site percolation model. The graphic can be divided in two parts, the distributions for an occupation probability $p \gtrsim 0.6$ and the distributions for an occupation probability $p \lesssim 0.6$. Those limits are quite interesting, because the critical probability p_c takes the value $p_c = 0.592746$ for site percolation. This means, that the distributions are changing fast when the critical probability p_c is reached.

For the part where $p \lesssim 0.6$, the distributions are looking quite similar, even for $p = 0.6$, although the shape starts being compressed and is a lot more shifted towards the y-axis. The distributions are rather flat and smudged out and look nearly the same, just the absolute number of clusters per system varies approximately between 150 and 350 clusters per system. The distribution, which has the most clusters per system, is the one for $p = 0.3$. That something like this happens is expected. The distributions for smaller p do not contain a lot of occupied sites, so even when all occupied sites build single-point clusters, it is not possible to have significantly more than $p \cdot L^2$ clusters. When p increases, more sites are occupied but they also get closer to each other and build bigger clusters, so there are less clusters, but the clusters get bigger.

For $p \gtrsim 0.6$, the distributions become more peak-like, for $p = 1$ the distribution actually is a peak with 1 cluster per system, because all sites are occupied, which leads to one big cluster. For smaller occupation probabilities, this peak is smearing out. In those systems, there is still one main cluster, which spans over the whole system, but there are little spaces in between, where smaller clusters can build. The smaller the occupation probability p gets, there more free spaces are carved in to the big cluster, which leads to more smaller clusters, which can exist in the empty spaces of the lattice.

Cluster sizes

Figure 12, figure 13 and figure 14 are showing the distributions of the sizes of clusters for different occupation probabilities p . Figure 12 shows all cluster sizes plotted logarithmic, figure 13 shows the sector for small cluster sizes and 14 for big cluster sizes.

In figure 12 there are five main peaks, one for cluster sizes smaller than 500 and the other ones for cluster sizes bigger than 1000. Both sections are described in more detail in the figures 13 and 14.

In figure 13, the distributions have the same shape, a huge peak at size 1 which is quickly decreasing afterwards, only the absolute number of clusters is varying. The highest number of clusters is reached for $p = 0.2$, which could be expected. When p gets much smaller, there are nearly no sites occupied at all, so they can not contribute to the peak at size 1. When the occupation probabilities p get bigger, there are less small clusters, because the occupied sites located closer to each other, so they form bigger clusters.

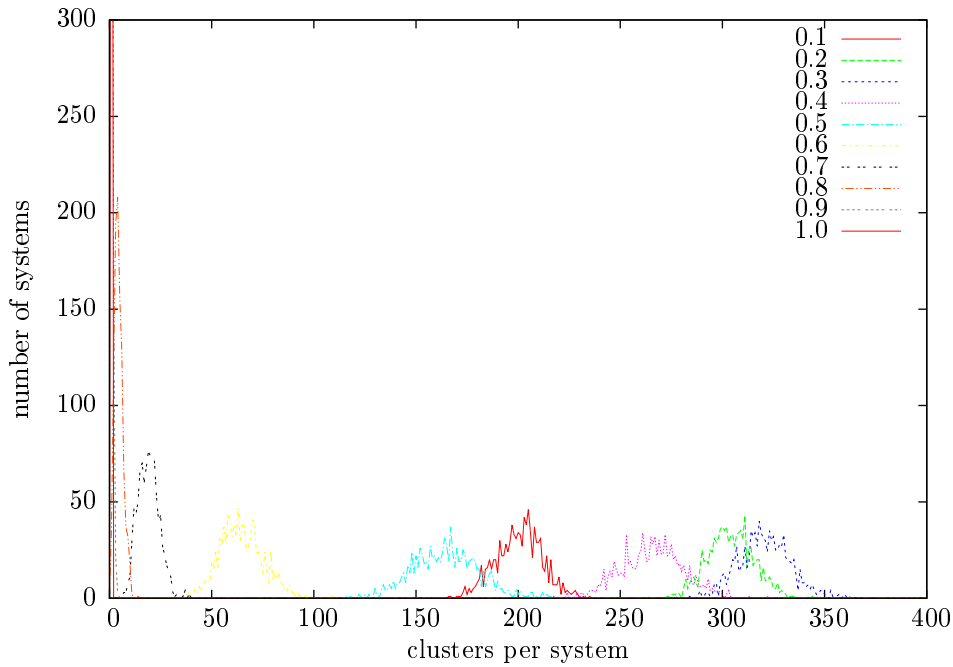


Figure 11: Distribution of the number of clusters in one system for different occupation probabilities for a two dimensional site percolation on a $L=50$ lattice with $N=1000$

Figure 13 itself is not a complete description of the distribution of cluster sizes, because for bigger occupation probabilities p the clusters get bigger, but they rarely have the same size, so the distribution gets smeared out heavily. Figure 14 shows a different part of the distributions. Here again, the critical probability p_c can be identified just from looking at the distributions. The first distribution forming a small peak is the one for $p = 0.6$, which is almost exactly the critical probability p_c . This peak is still smeared out heavily, but the bigger the occupation probability gets, the smaller the peak gets. For $p = 1$ we should see a sharp peak at just one cluster size, but it was excluded from this graphic, because this would have led to a higher number of clusters again, whereby the other peaks would not have been visible again. Those peaks form approximately at $size_{cluster} = p \cdot L^2$, because at these high occupation probabilities there exists one big cluster and a few clusters, that are a lot smaller and only have contributions in figure 13. For occupation probabilities smaller than p_c those peaks do not exist, because there is no big enough cluster to dominate the system and the few bigger clusters are very different in size, so the distribution is smeared out very heavily.

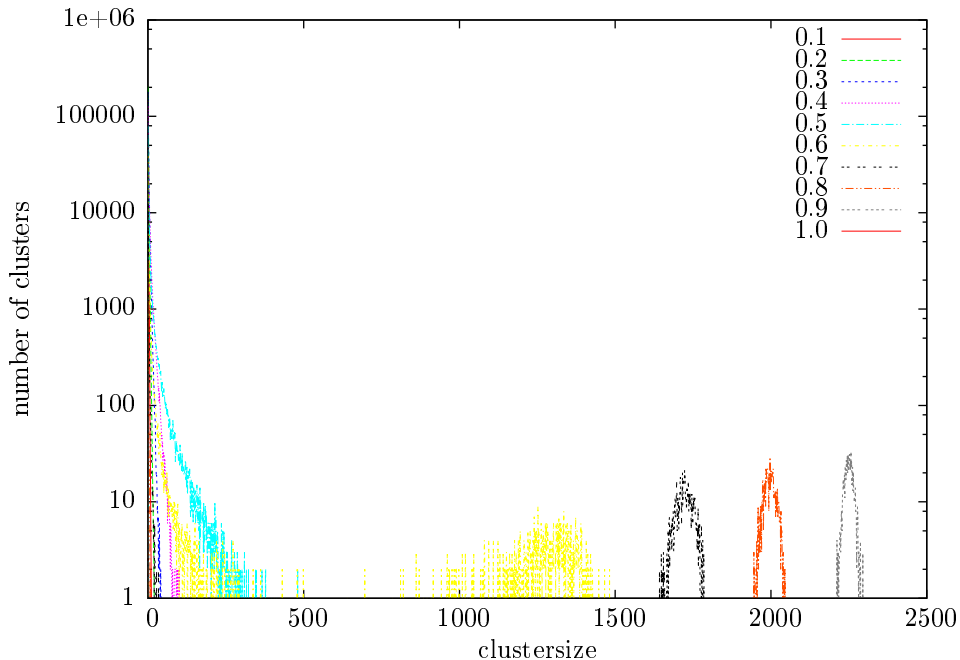


Figure 12: Distribution of the sizes of clusters for different occupation probabilities for a two dimensional site percolation on a $L=50$ lattice with $N=1000$ in a logarithmic plot

5.3 Principal result

It has to be kept in mind, that the phase boundary of the percolation model corresponds to a second order phase transition everywhere. The actual interest is however the point of the transition between a second order phase transition and a first order phase transition. This can not be achieved while just considering the second order phase transition of the mesonic percolation, as it was done previously. Therefore one has to consider a second type of model, which is the baryonic percolation. The baryonic percolation is a pure site percolation.

To understand the baryonic percolation and the difference to the mesonic percolation, one has to take a closer look on the baryon density. The baryon density depends on the chemical potential, so that for $\mu = 0$ the baryon density is $n_B = 0$ and for $\mu \rightarrow \infty$ the baryon density is $n_B = 1$. For baryons, a critical chemical potential μ_{crit} exists. It defines the point, at which the energy is big enough to produce a baryon. This means, that the baryon density is $n_B = 0$ for $\mu < \mu_{crit}$. For a chemical potential $\mu > \mu_{crit}$, the baryon density jumps to $n_B = 1$. This means, that the baryon density actually is an order parameter of the first order nuclear phase transition.

When baryonic clusters develop, the mesons cannot take part in meson hoppings across the lattice, so no bond percolation is then possible. This means, that the chiral condensate is not diverging, so the chiral symmetry is restored, because the baryonic clusters hinder the formation of meson clusters, hence the meson

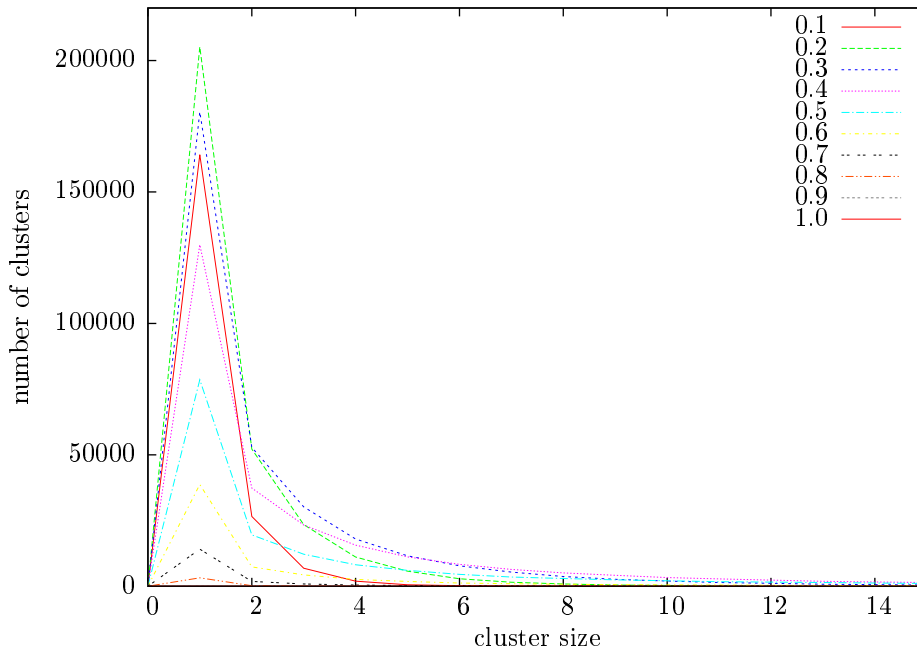


Figure 13: Distribution of the sizes of clusters for different occupation probabilities for a two dimensional site percolation on a $L=50$ lattice with $N=1000$ at small sizes

correlation length will not diverge.

The phase transition for the mesonic percolation is a curve in the μ_B - T -plane, because it depends on two criteria, the number of holes and the number of spatial meson hoppings. The phase transition of baryonic percolation is a perpendicular line to the μ_B -axis, because it just depends on the number of baryons n_B .

Therefore, the phase transition of mesonic percolation gets split in two qualitatively different phase transition, one where the baryons are building walls and one where they are not. The section of the percolating phase, where the baryons already percolate can exist, because it lies in the section, where the baryonic percolation is possible, but the percolation of the holes is possible as well. This means, that even though the baryonic walls prohibit spatial meson hoppings across the whole lattice in most cases, there are cases, where the spatial meson hoppings can cross the whole lattice. This is possible, because in this part of the percolating phase, the probability for spatial meson hoppings is a lot bigger than it would be needed to just build a percolating bond-cluster.

For the order of the phase transition this means, that if the nuclear transition is first order, also the chiral transition is first order. When the baryonic clusters do not percolate any more at higher temperatures, the chiral transition turns second order.

From this follows, that the intersection of both phase transition yields the tricritical point.

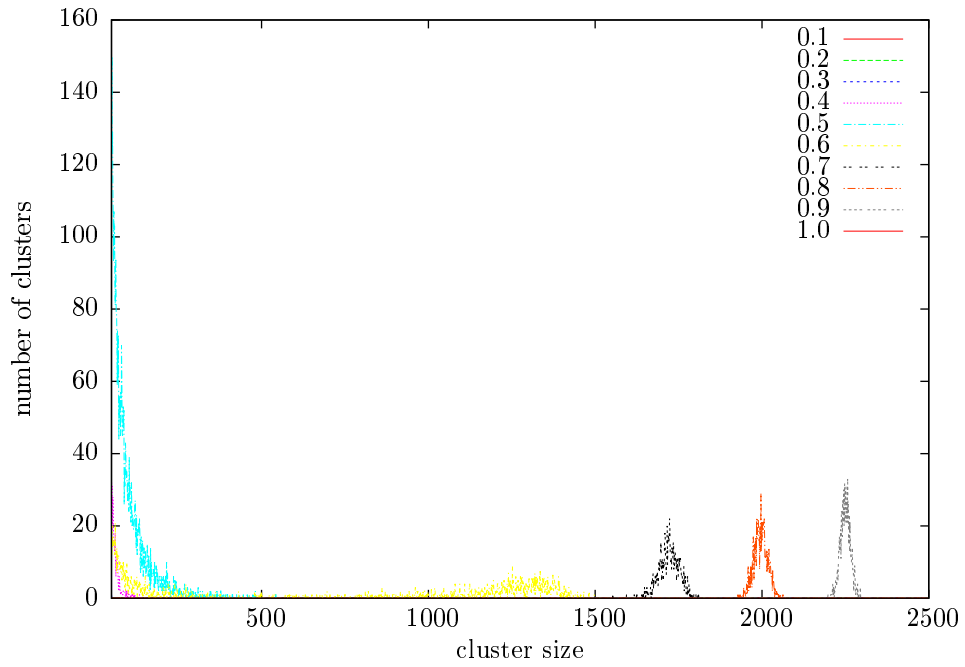


Figure 14: Distribution of the sizes of clusters for different occupation probabilities for a two dimensional site percolation on a $L=50$ lattice with $N=1000$ at larger sizes

Figure 15 shows a schematic, unscaled example in which the baryonic percolation is put together with the mesonic percolation in three dimensions. As well, the connection between the phase boundaries is just represented proportionally.

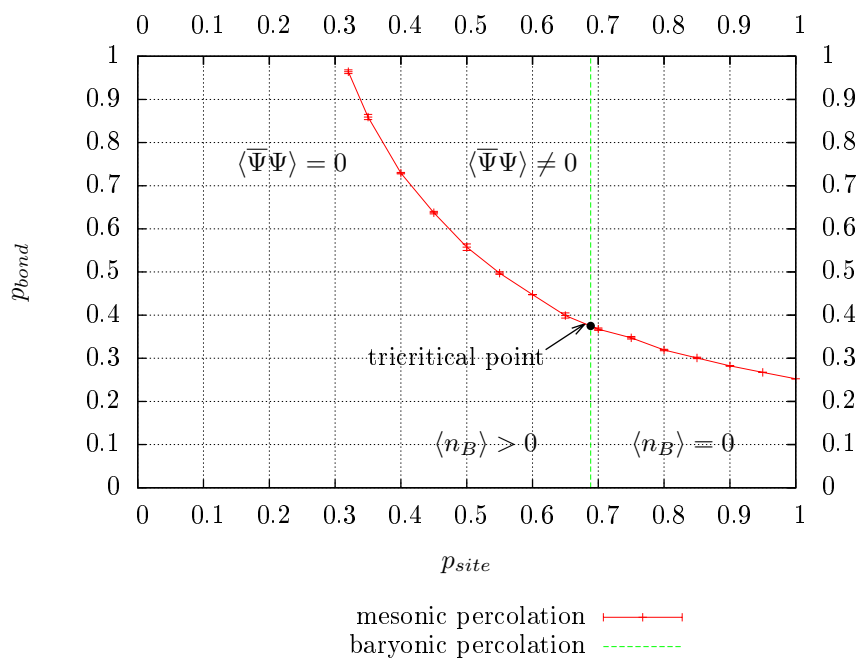


Figure 15: Schematic, unscaled example for the determination of the tricritical point

6 Summary

The main part of this thesis was to establish a connection between percolation models and strong coupling lattice QCD. The first step was to develop a mixed percolation model, where sites and bonds are both considered with different occupation probabilities. From this, a connection between the two remaining degrees of freedom in the strong coupling limit, the mesons and the baryons, and the bonds and sites of the percolation model had to be drawn. This yielded two different phase transitions, a phase transition depending on the spatial meson hoppings and a phase transition depending on the baryonic clusters, as discussed in the previous chapter.

To obtain the tricritical point out of the two phase transitions, the percolation model still has to be scaled properly. This means, that the proper connection between the probabilities p_{site} and p_{bond} and the baryonic chemical potential μ_B and the temperature T has to be obtained in order to find a meaningful value for the tricritical point. To obtain these relations, it is necessary to perform a cluster analysis in the strong coupling ensemble. This will then provide a mapping of the $(T - \mu)$ -plane to the $p_{bond} - p_{site}$ -plane.

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