Intrinsic limitations of inverse inference in the pairwise Ising spin glass

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Abstract. We analyze the limits inherent to the inverse reconstruction of a pairwise Ising spin glass based on susceptibility propagation. We establish the conditions under which the susceptibility propagation algorithm is able to reconstruct the characteristics of the network given first- and second-order local observables, evaluate eventual errors due to various types of noise in the originally observed data, and discuss the scaling of the problem with the number of degrees of freedom.
1. Introduction

The problem of inverse inference has been for a long time one of the main issues in neural networks analysis [1, 2, 3]. Given a number of stimuli, one measures the activity of some local components, such as spike trains of the neurons, to identify which connections between them, i.e. which synapses, are active, and, possibly, their strength [4, 5]. More recently the problem of inverse inference has manifested itself in other branches of biology. For example in structural biology the problem comes down to determine the probability distribution of amino acid strings by observing the way in which proteins naturally fold [6], or, in systems biology it consists in recovering structural details of protein-protein interactions from primary sequence information of gene regulatory networks [7, 8]. A solution to these types of problems usually comes about in the following way: one proposes a model capturing the characteristics of the network under study, and eventually develops methods to retrieve the structural characteristics, which can allow to disprove the underlying hypothesis depending on whether the findings are consistent with the observed behavior.

The pairwise Ising spin glass has been widely used as a starting point for analyzing the above problems. The fact that these problems have a number of common features has allowed to develop several algorithms addressing the corresponding inverse inference problem [9, 10, 11, 12]. However, as more accurate methods come along, new issues regarding the validation of the underlying hypothesis have been raised. For instance, it was pointed out in [13] that by only observing a subset of the nodes composing a neural network, reconstructing the original couplings according to a pairwise model does not necessarily lead to any added information as there exists a one-to-one relation between the couplings and the (normalized) second order correlation coefficient for a certain fraction of hidden variables onward. Thus, in this case one needs to consider higher order couplings. Moreover, binning spikes of the neurons, and accordingly representing their status by Ising-like variables, can oversimplify the actual observations. Similarly, determining the possible states in protein folding needs at least Potts-like variables. Note also that while for protein networks it is natural to assume a pairwise interaction model, in neural networks this is not necessarily the case and though in theory any network can always be transformed into one which contains only pairwise interactions [14], the practical way to go about this might not always be obvious.

In this paper, we do not address the interesting cases of the presence of hidden variables, of higher order interactions or of Potts-like variables. Rather, we question a more basic issue: given a situation where the pairwise Ising spin glass correctly describes the structure of the network under study, how much information can be gathered from an experimental input about the values of the couplings of the model? In other words, given all two-point correlations, or equivalently, given the susceptibilities, up to which point can we say something about the reconstructed couplings? Does this information allow us to reconstruct the original model or are there intrinsic uncertainties to this inverse inference problem? How does the quality of the reconstruction depend on the original
distribution of couplings or on the size of the system? The main question can be phrased as to what amount do the statistical errors that affect the measurements inhibit us to reconstruct the original model: if the original observations are incomplete or noisy, up to which point does it make sense to try and reconstruct the data? Ideally, one would like to answer the above questions from a theoretical viewpoint. Here, however, we start by numerically investigating several of the above problems by means of a message passing algorithm, first introduced in [10], which is currently among those delivering the best results [9]. We will use this algorithm to analyze the reconstruction of various types of networks given their first- and second-order local, possibly noisy, observables.

We want to analyze some basic features of the reconstruction process, by spotting some relevant weakness and by trying to focus on systematic trends that can be relevant in exploiting this approach and, consequently, in trying to devise improvements that could lead to better performances. We consider these result as a toolbox spelling and clarify a number of facts that can be useful for a better understanding of and improving this class of methods.

In Section 2 we introduce the message passing method, and define some relevant quantities. We describe in detail the iterative rules in presence of a memory term, that allows the convergence to a fixed point. In Section 3 we analyze the reconstruction procedure for different distribution of the couplings: we look at binary random couplings and at Gaussian couplings. In Section 4 we introduce synthetic random errors, by modifying randomly exact values for the susceptibility, and we try to understand how a larger incertitude affects the quality of the reconstruction of the couplings. We analyze both the case of an additive error and the one of a multiplicative error. In Section 5 we analyze data obtained by a Monte Carlo simulation, and we study the quality of the reconstruction as a function of the accuracy of the measurements. We draw our conclusions in Section 6.

2. Susceptibility propagation and the inverse Ising spin glass

While message passing algorithms have been widely used to solve the direct inference problem where the characteristics of the underlying network are given and one wants to derive experimentally observable quantities [15], their adaptation to tackle the inverse problem is relatively recent. Here we consider the inverse Ising spin glass, which assumes that the basic constituent agents of the network interact only in a pairwise, symmetric way with the other agents. In other words, we assume the problem is described by the following partition function:

\[ Z = \sum_{\sigma} \exp \left[ -\frac{1}{T} \left( \sum_{i=1}^{N} h_i \sigma_i + \sum_{i<j} J_{ij} \sigma_i \sigma_j \right) \right], \] (1)

where the \( \sigma_i \) can take the values \( \pm 1 \), \( h_i \) are (potentially site dependent) magnetic fields, the couplings \( J_{ij} \) are quenched random variables that can have both a positive and a negative sign and are distributed under a probability function that we will discuss in
the following, and $T$ is a “temperature” governing the behavior of the system. We can now define the inverse Ising spin glass problem by considering as given (by a, potentially numerical, experiment) the local magnetizations and the susceptibilities, and by trying to compute the $N$ local fields $h_i$ and the $N(N - 1)/2$ couplings $J_{ij}$.

Mézard and Mora have recently introduced a message passing procedure, the so called susceptibility propagation [10], that is able, in appropriate conditions, to solve this problem. As for the direct problem, it is a distributed algorithm where messages are exchanged between any two pairs of nodes. In case of the inverse problem, the content of some of these messages concerns the probability distribution of the local field of a vertex, while other messages contain information about the distribution of the couplings between two vertices.

More specifically in the inverse problem one defines four types of messages, $h_{i\rightarrow j}$, $u_{i\rightarrow j}$, $v_{i\rightarrow j,k}$ and $g_{i\rightarrow j,k}$. The messages $h_{i\rightarrow j}$ and $u_{i\rightarrow j}$ are exchanged between couples of nodes, while the messages $v_{i\rightarrow j,k}$ and $g_{i\rightarrow j,k}$ are exchanged between triples of nodes. The susceptibility propagation algorithm starts by assigning a random value to each of these messages and setting all the “estimated couplings” $J_{ij}$ to zero. These quantities are updated iteratively according to the following rules (where the $m_i$ and the $\chi_{ij}$ are the “experimental” inputs):

\[ h_{i\rightarrow j} = \arctanh (m_i) - u_{i\rightarrow i} \]  

\[ g_{i\rightarrow j,k} = \frac{\delta_{i,k}}{T} + \sum_{l \in \partial i \setminus j} v_{l\rightarrow i,k} \]  

\[ \tanh \left( \frac{J_{ij}}{T} \right) = \varepsilon \left[ \frac{\tilde{C}_{ij} - \tanh (h_{i\rightarrow j}) \tanh (h_{j\rightarrow i})}{1 - C_{ij} \tanh (h_{i\rightarrow j}) \tanh (h_{j\rightarrow i})} \right] \]  

\[ + (1 - \varepsilon) \tanh \left( \frac{J_{ij}}{T} \right) \]  

\[ \tanh (u_{k\rightarrow i}) = \tanh \left( \frac{J_{ik}}{T} \right) \tanh (h_{k\rightarrow i}) \]  

\[ v_{l\rightarrow i,k} = g_{l\rightarrow i,k} \tanh \left( \frac{J_{il}}{T} \right) \frac{1 - \tanh^2 (h_{l\rightarrow i})}{1 - \tanh^2 (u_{l\rightarrow i})} , \]  

where

\[ \tilde{C}_{ij} \equiv \frac{\chi_{ij} - g_{i\rightarrow j,j}(1 - m_i^2)}{g_{j\rightarrow i,j}} + m_i m_j \].  

For a detailed discussion of these equations (with $\varepsilon = 0$), see [16]. If this set of equations converges to a fixed point, the local fields are reconstructed as

\[ h_i = T \left( \arctanh (m_i) - \sum_{k \in \partial i} u_{k\rightarrow i} \right) . \]  

The couplings can be read directly from equation [15].

The additional external parameter [17] $\varepsilon \in ]0, 1[$ that we have introduced in the update rule [15] is a memory term: we keep, when computing the new value of a coupling,
part of the old value, and only modify the coupling partially. This is a possible way out to the fact that for $\varepsilon = 0$ the iteration typically fails since it ends up to propose an absolute value larger than one for updating $\tanh(J_{ij}/T)$. Clearly this slows down the convergence: in our scheme we had to use very small values of $\varepsilon$, but this eventually guaranteed that the susceptibility propagation algorithm was eventually leading in most part of the cases to a fixed point solution (as we discuss in the following section). We will discuss in some more detail the role of the “temperature” $T$ that appears in an explicit form in our iterative equations: if one thinks the local susceptibilities to be connected to spin-spin correlation functions according to the usual relation $\chi_{ij} = \beta_P \langle \sigma_i \sigma_j \rangle$ (where $\beta_P$ is the “physical” value of the inverse temperature) the parameter $T$ is naturally related to $\beta_P^{-1}$, but one has indeed some more freedom in tuning $T$.

In this note we will consider the case where all local fields are zero and we will focus on how to reconstruct the couplings when the local susceptibilities are given. One way to evaluate how close the reconstructed couplings are to the original ones is based on computing the Kullback-Leibler distance, which measures the weighted difference between the exact and the reconstructed distribution [5, 13]. An exact computation of the Kullback-Leibler distance involves a sum over all the states of the system, and can only be performed for rather small systems. We have used for our comparison a simpler indicator, that is appropriate for our goal: we consider the ratio of the average of the squared difference of the reconstructed couplings $J_{ij}^r$ and the original couplings $J_{ij}$, and the variance $\sigma$ of the distribution of the exact couplings,

$$\Delta = \frac{\sqrt{\left\langle \frac{\sum_{i<j}(J_{ij}^r - J_{ij})^2}{N(N-1)/2} \right\rangle}}{\sigma}. \tag{10}$$

In the following we always consider coupling distributions with zero mean and variance $\sigma = \tilde{J}/\sqrt{N}$, and we will set $\tilde{J} = 1$. In the case of fully connected graphs, i.e. the usual mean field theory of spin glasses (Sherrington-Kirkpatrick model), the spin glass phase sets in at $T_c = 1$ [18]. Using a different terminology [5, 9], one fixes the temperature (that disappears from the iteration scheme) $T \equiv 1$ and looks at $\tilde{J}^{-1/2}$, in which case the critical transition on the complete graph occurs at $\tilde{J} = 1$. Considering explicitly a “temperature” has the advantage that it provides direct connections to the (direct) studies of spin glasses in statistical mechanics, and it can allow to use the $T$ parameter to modify the iterative procedure. We have always averaged the quantity $\Delta$ defined in Eq. (10) over either a hundred (for small values of $N$) or twenty (for larger values $N$) different distributions of couplings (both in the case of binary couplings and in the case of Gaussian couplings). As we will describe in detail in the following we have analyzed both cases where the input to our inverse reconstruction procedure was based on exact values of the observables ($m$ and $\chi$) computed using an exact enumeration in small systems and cases where they were computed by Monte Carlo simulations (where the statistical accuracy of the time series was kept under control and is one of the relevant issues we have investigated).
3. The quality of the reconstruction as a function of temperature and of the coupling distribution

The first issue that we have analyzed is the quality of the reconstruction as a function of the temperature $T$ of the Ising spin glass and of the distribution of the couplings. We consider the two, somehow extreme cases, of binary couplings, where $J_{ij} = \pm 1$ with probability $\frac{1}{2}$, and of Gaussian couplings, where the $J$ have zero average and unitary variance. We obtain the susceptibilities that serve as input to the inverse reconstruction by exact enumeration. Thus, in this section we are dealing with inputs that are exact values (but for the finite precision of the input words, see later). All the results are sample averages, as described in the former section.

In Fig. 1 we show a plot of the average error (10) of the reconstruction of the couplings as a function of the temperature for the two different distributions of the couplings and for different system sizes (in the main plot of the figure we used variables of 12 byte). With our normalization $T = 1$ is $T_c$, the critical temperature of the statistical model (the mean field, Sherrington-Kirkpatrick spin glass).

In a large temperature interval the quality of the reconstruction essentially only depends on the temperature $T$, and not on $N$, nor on the details of the distribution of the couplings: when increasing $T$ the quality improves. Close to $T_c$ the error becomes large. Still even for temperatures of the same order of magnitude as $T_c$ (at least down to $T = 2$, say) our procedure allows to get precise hints about the values of the individual couplings.

In the lower inset of the figure we enlarge the left part of the main plot, for temperatures in the range going from 2 up to 12. This demonstrates even more clearly that the error in the reconstruction does not depend much on the type of distribution we considered, nor on the size of the system. In other words, it is no problem for our algorithm to distinguish the two different cases where couplings can only take a few values (here two) and where they come from a continuous distribution: this can have some relevance when deciding how to analyze and interpret experimental data. Also $\Delta$ is an average of the systematic error of the reconstruction of one single coupling: this means that the algorithm is essentially more precise for increasing $N$, as is well known for MP-algorithms and was already observed in [10].

These facts have strong implications about the scope that the pairwise statistical model we are using can enjoy: there are situations, in other words, where we cannot gather any useful information by trying to determine the couplings $J_{ij}$. If all the correlation functions among the constituent agents of a system are known, and we know that they only interact in a pairwise manner, we are able to reconstruct each single coupling if the system is at a relatively high temperature, or if, in other words, the corresponding distributions of the couplings have large variance. The fact that for decreasing temperature the reconstruction becomes less precise, is most likely due to a lack of information on how to capture the complex structure of the solution space near and below the critical temperature $T_c = 1$. Unfortunately, all algorithms currently
Figure 1. The reconstruction error $\Delta$ as a function of $T$ for fully connected graphs with binary (full lines) or Gaussian distributed couplings (dotted lines): here variables occupy 12 bytes. We considered two different sizes of the graphs: $N = 10$ (+) and $N = 20$ (□). The $x$ and $y$ scales of the insets can be easily deduced from the main plot. The lower inset contains a detail of the same plot for $T \in [2, 12]$. The upper inset demonstrates the dependence of $\Delta(T)$ on the precision of the variables used in implementing the susceptibility propagation algorithm that allows reconstructing the binary distributed couplings. From top to bottom, we used 4, 8 and 12 byte variables, respectively.

available to tackle the inverse problem suffer this same symptom. In the present case of the susceptibility propagation algorithm the increasingly complex structure of the phase space also manifests itself as a non-convergent behavior of the algorithm. While for larger temperatures, the algorithm converges to a fixed point, as we approach the critical point, the average change in the messages (2)-(7) between two consecutive updates gradually converges to some increasing positive value until they, eventually, no longer converge. A better reconstruction of the couplings defeating this critical point could use additional information on the network, or a more advanced algorithm which take this extra complexity into account, such as the survey propagation algorithms [19].

Finally, Fig. 1 evidences another important feature, regarding the numerical precision needed for an accurate reconstruction. If the correlation functions or the susceptibilities have been obtained at high temperatures, and we are in the ideal case where at least in principle we know them exactly, the quality of the reconstruction will be essentially limited by the precision with which we represent them and that we use in implementing the iterative scheme. We analyze this phenomenon by finding the solution using variables of different sizes (respectively 4, 8 and 12 bytes) and we plot the results in the upper inset of Fig. 1. The situation is quite clear: selecting a level of precision $p$ sets a maximum temperature value $T^*(p)$ that would allow to improve the reconstruction. For $T > T^*(p)$ the information we gather is hidden by the insufficient precision $p$, and the reconstruction quality does not improve. All the results we will discuss in the following have been obtained with 12 bytes wide variables.
4. Synthetic noisy data

The susceptibilities (or the correlation functions) one obtains as the output of an experiment are far from exact. The error can either be due to the limitations of the experimental set-up, thus imposing some absolute error on the measured data, or to statistical fluctuations, that can originate from a number of different causes. In case the observables are averages of successive experiments, the two-point correlation functions are limited by some relative errors which can possibly be improved by performing more experiments. We will discuss here how these different types of error can affect the reconstructions of the couplings.

The case of an error that is on average constant in magnitude (independently from the size of the observable we are considering) and the one where its ratio to the signal is constant in magnitude are indeed very different. In the case of an error that is constant on average small correlations functions will not give any significant amount of information: if, for example, for a model endowed with a Euclidean distance $d$ we expect an exponential decay with $d$, only the first, larger contributions, will be of use in our reconstruction, while the smaller ones will be completely hidden by the noise.

We start again from exact values of the susceptibility that we compute by exact enumeration, summing all the contributions of the $2^N$ spin configurations. We simulate the presence of an absolute error by including an additive noise term to the exact observables: the susceptibilities $\chi_{ij}^A$ used for reconstruction are given here by the exact susceptibilities $\chi_{ij}$ with the addition of a noise term $r_\eta$, uniformly drawn from the interval $[-\eta, +\eta]$, with $\eta > 0$: $\chi_{ij}^A = \chi_{ij} + r_\eta$, $\forall ij$.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure2.png}
\caption{$\Delta$ as a function of $T$. Here the susceptibilities used as input for the reconstruction of the couplings are only approximate due to an additive noise. From bottom to top: $\eta = 10^{-8}, 10^{-7}, 10^{-6}, 10^{-5}$ for $N = 10$ (+) and $N = 20$ (□).}
\end{figure}

We show our results for the reconstructed couplings in Fig. 2. We show the values obtained for different choices of $\eta$. The effect of this random noise is irrelevant for the low $T$ range where the reconstruction is possible, but becomes large when $T$ increases. The
larger is $\eta$, the smaller is the $T$ range where the reconstruction becomes unreliable. In presence of this kind of noise the quality of the reconstruction worsens when $T$ increases: this can be an interesting observation when trying to optimize a reconstruction scheme of experimental data. It is interesting to note that the error on the reconstructed coupling is several orders of magnitude larger than the additive error on the susceptibilities. This is due to the fact that the order of magnitude of the susceptibilities is large at small temperatures, and much smaller at high temperatures. Therefore, especially at high temperatures, additive noise terms are very damaging.

In Fig. 3 we show the effect of a multiplicative noise term on the susceptibilities. More precisely, these reconstructed couplings are computed starting from the approximated susceptibilities $\chi_{ij}^M$, which were obtained from the original susceptibilities by multiplying them by a factor $r_\epsilon$, which was drawn uniformly from the interval $[1-\epsilon, 1+\epsilon]$, with $\epsilon > 0$: $\chi'_{ij} = r_\epsilon \chi_{ij}, \forall ij$.

![Figure 3. $\Delta$ as a function of $T$. Here the susceptibilities used as input to the reconstruction scheme are only approximate due to the presence of a multiplicative noise. From bottom to top: $\epsilon = 10^{-8}, 10^{-7}, 10^{-6}, 10^{-5}, 10^{-4}, 10^{-3}$ for $N = 10$ (+) and $N = 20$ (□).](image)

Again, the error on the observables influences severely the reconstruction of the couplings at higher temperatures. Here there is a clearer threshold effect than in the former case, and there is a clear dependence of the “breaking point” $T^*(\eta)$ over $\eta$. The situation is very similar to the one that we have discussed in the previous section, where we were using “short” variables with a finite, small width (down to four bytes).

5. Monte Carlo noisy data

A Monte Carlo numerical experiment is one of the best proxy for a real experiment. One gets sets of data that are asymptotically distributed according to a certain probability function. These data are affected by statistical errors, as it would happen in an experiment. We analyze here how the reconstruction works when starting from Monte...
Carlo data obtained under variable accuracy requirements: this is an issue of paramount
interest, since we need to know if a given real experiment, with a given level of accuracy,
will give information that can lead to a useful coupling reconstruction.

So here we do not start from exact data, but from data obtained by a usual
Monte Carlo simulation, with a local, accept-reject Metropolis updating scheme, and
we use our inverse algorithm to get the couplings from these data. We first lead the
system to equilibrium (and discard data obtained during this thermalization phase of
the simulation), and eventually collect data for a number of Monte Carlo steps. We show
in Fig. 4 the error $\Delta$ on the reconstruction of the couplings, given the values $\chi_{ij}^{MC}$ of the
susceptibilities, obtained by sampling the solution space with a Monte Carlo Markov
Chain.

![Figure 4](image)

**Figure 4.** The error $\Delta$ as a function of $T$ for fully connected graphs of size $N = 16$ ($\circ$)
and $N = 128$ ($\bigcirc$), with binary couplings. The different curves represent reconstructions
starting from the exact susceptibilities for the $N = 16$ system (continuous line), and
starting from approximations of the susceptibilities generated from $10^4$, $10^5$, $10^6$, $10^7$
and $10^8$ MC data (from top to bottom) for $N = 16$, and $10^5$, $10^6$ and $10^7$ MC data
(from top to bottom) for $N = 128$.

Given a fixed number of Monte Carlo measurements the error on the susceptibilities
increases with the temperature, resulting in a less precise reconstruction of the couplings.
However, by increasing the duration of the experiments, i.e. increasing the number of
independent observations, the relative error can be drastically reduced as can be seen
from Fig. 4. The pattern is, as one would have expected, very similar to the one
of a statistical error of constant average size. Indeed, this is exactly what happens
here, where we estimate all correlation functions by adding numbers of order one (the
individual values of the correlations, that can be $\pm 1$). For each level of the error the
reconstruction works as if correlations were exact up to a given $T$ value, beyond which
its accuracy does not increase anymore with $T$, but, on the contrary, it starts decreasing
with $T$.

We also analyzed the low-temperature limit down to which the couplings can
be reconstructed starting from approximated two-point correlations. While the exact correlations in general allow to reconstruct the couplings down to a temperature as low as $T = 1.7$, no solution could be found, for example, starting from susceptibilities obtained from only $10^4$ independent MC data at this same temperature: the susceptibility propagation algorithm can be additionally limited by an inaccurate original data set.

We have also tried to understand how the performance of the susceptibility propagation algorithm varies when we increase the number of elements of the system. In the Monte Carlo case we have studied the two cases $N = 16$ and $N = 128$, where the second system is eight times larger than the first one: we show both sets of data in Fig. 4.

Larger size systems require more experiments to get a reconstruction of the same quality as for the smaller systems: the $N = 128$ curves overlap with $N = 16$ curves obtained with ten times less statistics. After assuming this rescaling our data clearly show that the reconstruction procedure also works very well even when we heavily increase the volume of the system. Let us look carefully at “low” values of $T$. For example, when starting from observables with a good precision, at $T = 2$ the $N = 128$ reconstruction clearly improves in quality with respect to those for $N = 16$ (the same phenomenon can already be observed, on a smaller scale, in Fig. 1 when comparing $N = 10$ and $N = 20$). Reconstruction on large systems sizes is possible and reliable even if the “temperature” of the system is not so far from criticality, which certainly is good and useful news.

6. Conclusions

We have analyzed a number of features of the inverse Ising spin glass problem, by using the susceptibility propagation algorithm, first introduced in [10]. In a very large temperature window, this algorithm is able to reconstruct the individual couplings and, consequently, their overall distributions with a remarkable precision. If the system is “at high temperature” (or, in other, maybe more physical terms), if the (zero average) disorder does not fluctuate too much, the quality of the reconstruction is basically only limited by the precision under which the experimental input is known, and by the precision used when implementing the susceptibility propagation algorithm.

For smaller temperatures approaching the critical temperature, or equivalently, for distributions of the couplings characterized by a large variance, the reconstruction is less accurate and eventually the algorithm fails to find any solutions to the problem. This is due to the fact that it does not take the possibility of multiple states into account, which is exactly what happens in the spin-glass phase.

All algorithms currently available suffer this same problem. However, the message passing algorithm used in this paper could possibly be improved by using the probability distributions of the observables as basic working ingredients, rather than the observables themselves to obtain a type of survey propagation algorithm for which the exchanged messages do not contain information on the couplings, but rather on the probability distribution of each individual coupling. Furthermore, the nature of the susceptibility propagation algorithm suggests it could be easily adapted to include the case of Potts-
like variables allowing to treat problems in structural biology [8].

While the overall reconstruction of the pairwise model is quite precise in case the original data set is accurate, the results can deteriorate fast if data are affected by a statistical error. The number of experiments that have to be used to obtain the average two-point correlations needs to be increasingly large for increasing sample size. Also, at large temperatures, where the values of the susceptibilities are small, this error on the reconstruction of the couplings becomes more pronounced. For the same reason, an absolute error on the two-point correlations is increasingly damaging at higher temperatures.

All together we feel that our conclusion lead to an optimistic scenario. Even in presence of a large statistical or systematic ignorance the reconstruction is possible and can be effective. Large samples still allow for a good reconstruction quality, under the condition that the statistical inaccuracy that affects the data is lowered down to a reasonable level.

Acknowledgments

We thank Thierry Mora for describing us the use of the $\varepsilon$ term in this context. We acknowledge interesting conversations with Federico Ricci-Tersenghi.

References

[1] Schneidman E, Berry MJ, Segev R and Bialek W, “Weak pairwise correlations imply strongly correlated network states in a neural population”, Nature 440, 04701 (2006).
[2] Broderick T, Dudk M, Tkacik G, Schapireb RE and Bialek W, “Faster solutions of the inverse pairwise Ising problem”, preprint arXiv:0712.2437 (2007).
[3] Neri I and Bollé D, “The Cavity Approach to Parallel Dynamics of Ising Spins on a Graph”, preprint arXiv:0905.3260 (2009).
[4] Amit D, “Modeling brain function: the world of attractor neural networks” (Cambridge University Press, Cambridge, UK 1989).
[5] Kappen HJ and Rodriguez FB, “Efficient learning in Boltzmann machines using linear response theory”, Neural Computation 10, 1137 (1998).
[6] Socolich M, Lockless SW, Russ WP, Lee H, Gardner KH and Ranganathan R, “Evolutionary information for specifying a protein fold”, Nature 437, 03991 (2005).
[7] Szallasi Z, “Genetic network analysis in light of massively parallel biological data acquisition”, Pacific Symposium on Biocomputing 4, 5 (1999).
[8] Weigt M, White RA, Szurmant H, Hoch JA and Hwa T, “Identification of direct residue contacts in protein-protein interaction by message passing”, PNAS 106, 67 (2009).
[9] Sessak V and Monasson R, “Small-correlation expansions for the inverse Ising problem”, J. Phys. A: Math. Theor. 42, 055001 (2009).
[10] Mézard M and Mora T, “Constraint satisfaction problems and neural networks: a statistical physics perspective”, (2008)
[11] Roudi Y, Tyrcha J and Hertz J, “Ising model for neural data: model quality and approximate methods for extracting functional connectivity”, Phys. Rev. E 79, 051915 (2009).
[12] Roudi Y, Aurell E and Hertz J, “Statistical physics of pairwise probability models”, (2009)
[13] Roudi Y, Nirenberg S and Latham PE, “Pairwise maximum entropy models for studying large
biological systems: when they can work and when they can’t”, *PLoS Comput. Biol.* **5**, e1000380 (2009).

[14] Yedidia JS, Freeman WT and Weiss Y, “Understanding belief propagation and its generalizations” in *Exploring artificial intelligence in the new millennium* (Morgan Kaufmann Publishers Inc. 2003), 239–269.

[15] Mézard M and Parisi G, “The Bethe lattice spin glass revisited”, *Eur. Phys. J.* B **20**, 217 (2001).

[16] Mora T, “Géométrie et Inférence dans l’optimisation et en théorie de l’information.”, *PhD thesis* (2007).

[17] Mézard M and Mora T, private communication (2008).

[18] Sherrington D and Kirkpatrick S, “Solvable Model of a Spin-Glass”, *Phys. Rev. Lett.* **35**, 1792 (1975).

[19] Mézard M, Parisi G and Zecchina R, “Analytic and Algorithmic Solution of Random Satisfiability Problems”, *Science* **297**, 812 (2002); Mézard M and Zecchina R, “The random K-satisfiability problem: from an analytic solution to an efficient algorithm”, *Phys. Rev. E* **66**, 056126 (2002).