Monte Carlo renormalization group minimal walking technicolor

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MCRG Minimal Walking Technicolor

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We present a Monte Carlo renormalisation group study of the SU(2) gauge theory with two Dirac fermions in the adjoint representation. Using the two-lattice matching technique we measure the running of the coupling and the anomalous mass dimension. We find slow running of the coupling, compatible with an infrared fixed point. Assuming this running is negligible we find a vanishing anomalous dimension, $\gamma = -0.03(13)$, however without this assumption our uncertainty in the running of the coupling leads to a much larger range of allowed values, $-0.6 \lesssim \gamma \lesssim 0.6$. We also attempt to measure the anomalous mass dimension using the stability matrix method. We discuss the systematic errors affecting the current analysis and possible improvements.

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I. INTRODUCTION

Technicolor theories with fermions in higher representations of the gauge group can potentially provide a dynamical electroweak symmetry breaking mechanism without conflicting with electroweak precision data. Minimal Walking Technicolor is an example of such a theory, a SU(2) gauge theory with two Dirac fermions in the adjoint representation [1, 2]. It is expected from perturbation theory to be in or near to the conformal window, although any new infrared fixed point (IRFP) is thought to occur at strong coupling and so nonperturbative results are necessary. Initial lattice simulations showed some evidence of walking dynamics and mapped out the phase diagram of the theory [3, 4]. Subsequent Schrödinger functional lattice simulations have indeed found that the gauge coupling runs very slowly [5–7], more slowly than the perturbative prediction. The more recent Schrödinger functional study [8] finds a change of sign in the discrete β function at strong coupling, indicative of an IRFP. A recent study using Creutz ratios to measure the running coupling found evidence for backwards running or absence of running at strong coupling [9]. If indeed the theory possesses an IRFP, then the anomalous mass dimension γ at the fixed point coupling will be a scheme independent quantity. One of the purposes of the present paper is to compute γ using Monte Carlo renormalisation group methods. In order to be phenomenologically viable (yield the correct quark masses while having an extended technicolor scale that is large enough to suppress flavour-changing neutral currents) the theory must have a large anomalous mass dimension ($\gamma \approx 1$) [10–12], and recent work suggests that $\gamma > 1$ is required [13].

A conjectured all-order beta function [14] predicts $\gamma = 11/24 \simeq 0.458$ for this model.[1] This value is also consistent with the perturbative result of $\gamma = 0.500$ in the $\overline{\text{MS}}$–scheme up to four loops [16, 17]. The anomalous mass dimension has been measured nonperturbatively in recent lattice studies [5, 8, 18, 19]. These give a variety of results: $0.05 < \gamma < 0.56$, $\gamma = 0.31 \pm 0.06$ and $\gamma = 0.51 \pm 0.16$.

In this work we measure the discrete β function and the anomalous mass dimension using the Monte Carlo Renormalisation Group (MCRG) two-lattice matching method. This technique has recently been used to investigate theories with many flavours of fermions in the fundamental representation [20, 21] of SU(3). One of our goals in this paper is to exhibit the systematic uncertainties in the MCRG approach. Indeed, we will find that the matching that is involved leads to significant errors, which we argue is due to being still some distance from the renormalised trajectory with the number of renormalisation group blocking steps that we are able to take. When the uncertainty in the matching of bare couplings is propagated through into the anomalous mass dimension analysis, a wide range of values is obtained. We also investigate using the stability matrix MCRG method [22], which in principle allows the determination of all the critical exponents of a system. For our simulations and measurements we use the HiRep [23] implementation of the Wilson plaquette gauge action with adjoint Wilson fermions and a rational hybrid Monte Carlo (RHMC) algorithm with two pseudofermions.

[1] This prediction supersedes the original all-order conjecture [15] of $\gamma = 3/4$ for this model.

II. TWO-LATTICE MATCHING METHOD

Here, the renormalisation group (RG) is implemented by the real-space method of block transformations. Each blocking step changes the scale by a factor s; irrelevant couplings will flow towards the fixed point (FP), and relevant couplings will flow away from it. After a few steps the irrelevant couplings should die out, leaving the flow following the unique renormalised trajectory (RT). A crucial point is that the validity of the MCRG method relies on having taken enough blocking steps to end up on the RT. Spurious results will be obtained if this is not the case, and for this reason it is important to repeat studies on larger volumes in order to take more blocking steps. This aspect of MCRG also suggests exploring several blocking schemes, something that we do here, since they will approach the RT at different rates. Indeed, consistency between different blocking schemes is an indicator that the RT is being reached. It is also important that the flow begin in the basin of attraction of the Gaussian ultraviolet fixed point ($m = g = 0$), in order to extract continuum physics. This leads one to be suspicious of results for strong bare coupling.

Suppose we identify two sets of bare couplings which end up at the same point along the RT after n steps in one case and $n' = n-1$ steps in the second case. Then the lattice correlation lengths are related by $\hat{\xi} = s\hat{\xi}'$, where s is the blocking parameter. Since they correspond to the same point on the RT, the physical correlation lengths agree, $\xi' = \xi$, and hence the lattice spacings are related by $a' = sa$.

To identify such a pair of couplings, we need to show that the expectation values of all observables on these gauge configurations agree, modulo scaling violations. In the massless theory we only need to tune gauge couplings $\beta = 4/g^2$. (On the other hand if one tuned all of the couplings in a "perfect action" approach, the scaling violations would vanish and all observables would agree. In this paper we take the simpler approach of tuning the unimproved Wilson action, which will lead to larger uncertainties in our results.) Thus we will end up with a matched pair β, β'. The quantity

$$\Delta\beta = \beta - \beta' \equiv s_b(\beta; s) \tag{2.1}$$

is the discrete β function (step scaling function) for the bare gauge coupling. In the case with nonzero mass, one must also match the masses m, m'. (Because we use Wilson fermions, the masses must be measured; we use the standard partially-conserved axial current mass.) This will allow us to extract the anomalous mass dimension.

For the reasons alluded to above, we use three $s = 2$ RG blocking transforms, defined in Refs. [20, 21, 24]: ORIG, HYP and HYP2. In the limit of a large number of blocking steps, our results would be independent of the choice of blocking. Therefore, the use of three different blocking transforms allows us to check the systematic errors of the procedure and the distance from the RT. The HYP and HYP2 blocking transforms have also been empirically found to work better than the ORIG transform at strong coupling [21]. This is because optimization of the blocking forces the blocking parameter α to be larger than the stability limit $\alpha < 0.75$ for ORIG, at strong coupling. We have found the same problem in some of our analysis.

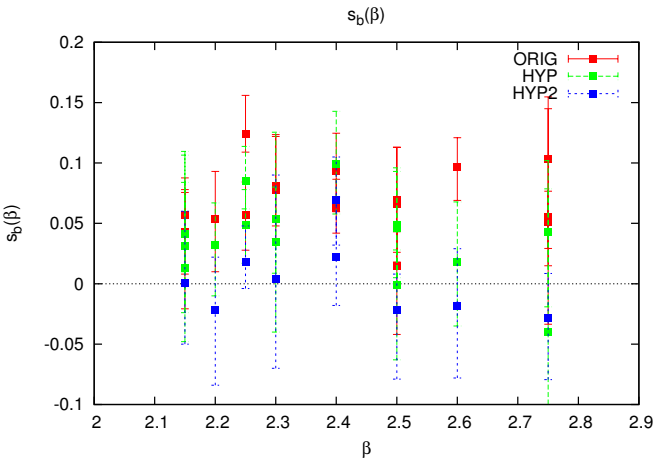

FIG. 1. Discrete β function obtained from 16^4 and 8^4 lattices, where the blocking parameter α is optimized between the same pair of lattices.

III. DISCRETE β FUNCTION RESULTS

Here we measure $s_b(\beta, s)$. An IRFP would be indicated by a change of sign as the bare $\beta = 4/g^2$ is varied from weak to strong coupling. Since the mass is a relevant operator, while the coupling is expected to be at best nearly marginal, the mass has to be tuned to zero. We generated ~ 3000 configurations on 16^4 and 8^4 lattices for a range of β values, each run near the critical bare mass. We optimized the blocking parameter α such that n and $n-1$ blocking steps agree on the value of s_b. The resulting measurement of $s_b(\beta)$ is shown in Fig. 1. Errors result from the fact that different observables (plaquette, six-link loops and eight-link loops) give different matching pairs, and hence different estimates of s_b. This is interpreted as due to residing still some distance from the RT after the number of blocking steps that we are able to perform on these relatively small lattices. Our results include both the massless and small mass 16^4 runs; within errors, s_b shows no mass dependence for these small masses. The ORIG matching values of s_b are clearly positive throughout, the HYP values are lower, and the HYP2 values are consistent with zero within error bars. There is no clear crossover from positive to negative values of s_b for any of the blocking transforms. While the data are consistent with a fixed point, they are not sufficiently precise to distinguish slow running from a fixed point. This level of precision is nonetheless similar to that found in the Schrödinger functional studies.

We have also performed α optimization with volume matching, as described in [25], in order to demonstrate the effect of this alternative. This consists of matching 8^4 to 4^4 lattices with two and one blocking steps respectively to obtain $s_b = \Delta\beta_{8,4}$, as well as matching 16^4 to 8^4 lattices with three and two blocking steps respectively to obtain $s_b = \Delta\beta_{16,8}$. Then the blocking parameter α is optimized such that $\Delta\beta_{8,4} = \Delta\beta_{16,8}$. The purpose of this is to cancel finite volume corrections. Here we only present the modification that occurs when this approach is applied to the HYP blocking scheme, since our main interest is to see by how much this changes the picture. (We found that for ORIG blocking, the α that is obtained is above the stability bound, $\alpha > 0.75$, for all the β we have studied. Hence this type of blocking fails with this method of optimization for these sizes of lattices.) The results are shown in Fig. 2. It can be seen that this alternative method gives $s_b < 0$ for all but one value of β. Contrasting with Fig. 1, we see that there is a stronger signal for $s_b < 0$, but no region at which the discrete beta function clearly changes sign. It is unclear why one particular value of β has $s_b > 0$. One important point is that the error bars in Fig. 2 are similar to those in Fig. 1. Since the size of the error bars is determined by the mismatch in β' between different observables, what we see is that this alternative α optimization does not improve the matching. I.e., it does not reduce scaling violations, which is not surprising, since it was only designed to reduce finite size effects. We also remark that the single step of blocking that is performed on the 4^4 lattice is most likely insufficient to fall on the RT. For this reason, larger volumes will eventually be needed in order to obtain reliable results from this "volume matching" method. Thus the results shown here should only be taken as illustrative of the size of change that can result from this alternative α optimization.

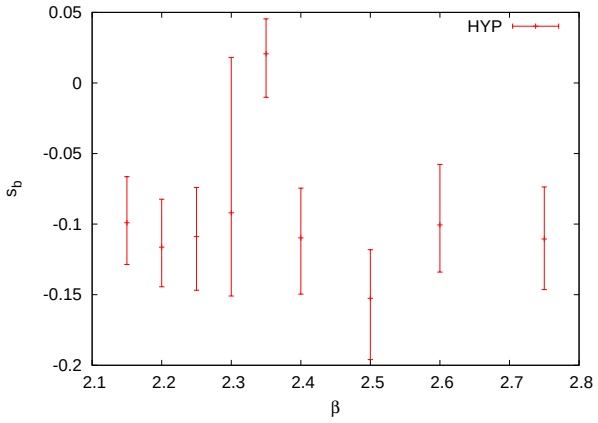

FIG. 2. Discrete beta function with volume matching α optimization, where different lattices are use in the comparison (16^4 to 8^4 versus 8^4 to 4^4).

IV. ANOMALOUS MASS DIMENSION RESULTS

Here we assume that an IRFP exists and attempt to extract what would in that case be a scheme independent quantity: the anomalous mass dimension at the FP of the RG flow. At an IRFP the gauge coupling is irrelevant, leaving the mass as the only relevant operator. We could therefore match the mass at arbitrary couplings, as long as we have sufficient RG steps for the gauge coupling to flow to its FP value. In practice we only have a small number of RG steps, and because the beta function is small, the coupling flows slowly towards its FP value. Nevertheless we begin by setting $\beta' = \beta$ and assume that the FP behavior will be approximated after the RG steps that we are able to take. Next we consider the impact of choosing $\beta' \neq \beta$ (i.e., within the uncertainty in s_b), and will find that this leads to a large systematic error for the anomalous mass dimension.

We generated $\sim$ 3000 configurations on 16^4 and 8^4 lattices, for a range of masses m and m' respectively, at each β. This allows for two versions of determining m' on the coarse lattice such that there is matching. In one case, matching is performed after blocking 3 and 2 times on the 16^4 and 8^4 lattices respectively. In the second case, matching is performed after blocking 2 and 1 times on the 16^4 and 8^4 lattices respectively. We optimize the blocking parameter α such that these two versions of matching agree on the matching m'.

Because the bare mass is additively renormalised we convert the bare masses to partially conserved axial current (PCAC) masses. We measure the PCAC mass, am, as a function of bare mass, am_0, for each β on the 16^4 lattices. We then use this to convert the bare masses on both 8^4 and 16^4 lattices to PCAC masses, as the measured PCAC masses on the 8^4 lattices suffer from finite volume effects. Our previous result [26] for the anomalous mass dimension used PCAC masses measured on the 8^4 lattices and hence contained a large finite volume effect, which has been removed in the present work.

The anomalous mass dimension appears in the RG equation for the mass

$$\frac{d(am)}{d\ln|\mu|} = -y_m am = -(1+\gamma)am. \tag{4.1}$$

where μ is the renormalisation scale. At an IRFP the anomalous mass dimension is a constant, so the expression can be integrated to give

$$\frac{a'm'}{am} = 2^{\gamma+1} \tag{4.2}$$

for a pair of matching masses $(am, a'm')$, from which a value for γ can be extracted.

We used four values of β, $\beta = 2.15, 2.25, 2.35, 2.50$. The matching PCAC mass pairs using the HYP blocking tranform are shown in Fig. 3. We also repeated the matching using ORIG and HYP2 blocking, with similar results. Different β values predict consistent values for the anomalous mass dimension, as shown in Fig. 3, which uses all the beta values and masses in the range $0.02 < am < 0.16$.

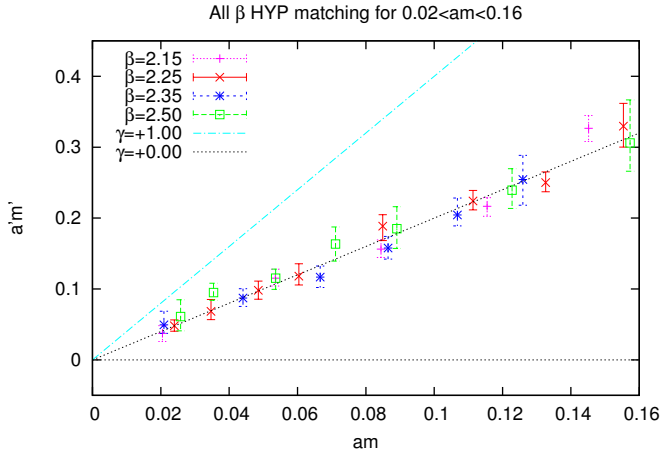

FIG. 3. HYP blocking, matching in mass using all $\beta' = \beta$ values in the mass range $0.02 < am < 0.16$.

A combined fit to all $\beta' = \beta$ results gives $\gamma = -0.03(13)$. However, we next must consider the effect of taking $\beta' \neq \beta$, since we expect some flow in the couplings under the RG transformations. For a given (β, am) there should be a unique matching set of couplings $(\beta', a'm')$. However, all of our observables are small Wilson loops, and as such are strongly correlated and have a very similar dependence on β' and $a'm'$. This means that we can in fact find a "matching" $a'm'$ for a range of values of β', which, given that we do not know the correct value of β' to use, significantly increases the error on our determination of γ. As an example, the matching mass pairs for $\beta = 2.25$ and various values of β' are shown in Fig. 4.

In Sec. III, while we find that $s_b = \beta - \beta'$ is compatible with zero, corresponding to setting $\beta = \beta'$, the error bars are relatively large, enclosing the region $-0.08 \lesssim \beta - \beta' \lesssim 0.16$. From Fig. 4 we see that for $\beta = 2.25$ this region is approximately bounded by $\beta' = 2.15$ and $\beta' = 2.35$, and encloses a large range of values for the anomalous mass dimension, $-0.6 \lesssim \gamma \lesssim 0.6$. This range is representative of the errors in the anomalous mass dimension due to the uncertainty in the correct value of β', and is the dominant source of systematic uncertainty in our results. In our conclusion, we identify steps that should be taken to reduce these uncertainties.

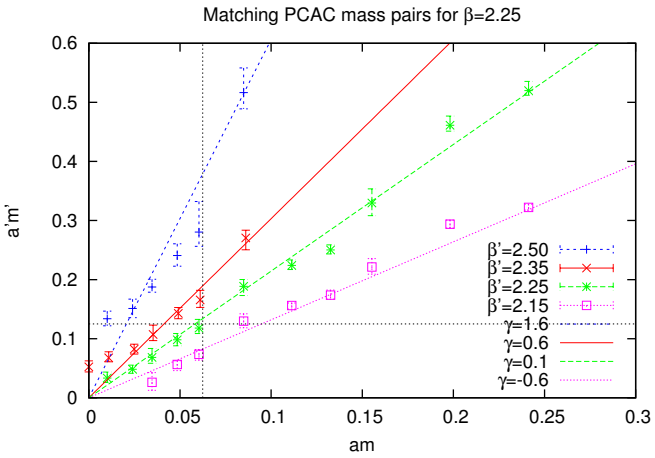

FIG. 4. Mass matching pairs at $\beta = 2.25$ for a range of β'. Varying β' can lead to very different results for γ. The dotted horizontal and vertical lines show $mL, m'L' = 1$.

V. STABILITY MATRIX METHOD

The two-lattice matching technique used in this work was first used to investigate quenched QCD [28–30], and more recently QCD with many flavours of fermions [20, 21]; it allows for a determination of the flow of the most relevant coupling in a system. The original MCRG method [22] in principle allows the extraction of all critical exponents of a system, both relevant and irrelevant.

A. Method

Consider a hamiltonian that can be written as a sum of couplings K_i and observables (operators) S_i, $H = \sum_i K_i S_i$, and an RG transform R_s of scale s such that

$$H^{(n+1)} = R_s H^{(n)} = \sum_i K_i^{(n+1)} S_i^{(n+1)}, \tag{5.1}$$

where $S_i^{(n+1)}$ is the same observable as $S_i^{(n)}$, only measured on the lattice blocked $n+1$ rather than n times. The fixed point of the RG transform is defined by the condition $H^* = R_s H^* = \sum_i K_i^* S_i^*$, and near this point the flow in the couplings can be expanded linearly to give

$$K_i^{(n+1)} - K_i^* = \sum_j T_{ij}^* (K_j^{(n)} - K_j^*), \tag{5.2}$$

where

$$T_{ij}^* = \left. \frac{\partial K_i^{(n+1)}}{\partial K_j^{(n)}} \right|_{H^*}. \tag{5.3}$$

The chain rule gives

$$\frac{\partial \langle S_i^{(n)} \rangle}{\partial K_j^{(n-1)}} = \sum_k \frac{\partial K_k^{(n)}}{\partial K_j^{(n-1)}} \frac{\partial \langle S_i^{(n)} \rangle}{\partial K_k^{(n)}} = \sum_k T_{kj} \frac{\partial \langle S_i^{(n)} \rangle}{\partial K_k^{(n)}} \tag{5.4}$$

from which T_{kj} can be constructed using the identities

$$\frac{\partial \langle S_i^{(n)} \rangle}{\partial K_j^{(n-1)}} = \langle S_i^{(n)} S_j^{(n-1)} \rangle - \langle S_i^{(n)} \rangle \langle S_j^{(n-1)} \rangle \equiv A_{ij}^{(n)} \quad (5.5)$$

$$\frac{\partial \langle S_i^{(n)} \rangle}{\partial K_j^{(n)}} = \langle S_i^{(n)} S_j^{(n)} \rangle - \langle S_i^{(n)} \rangle \langle S_j^{(n)} \rangle \equiv B_{ij}^{(n)} \quad (5.6)$$

The eigenvalues of the stability matrix T_{ij}^* give the critical exponents of the system [31], e.g. $\nu = \ln s / \ln \lambda_h$, where λ_h is the largest eigenvalue, and so in the case of MWTC $y_m = 1/\nu = \ln \lambda_h / \ln s$. From a single simulation close to the critical point, correlation functions of blocked observables are measured to construct the matrix T_{ij}, from which y_m and other exponents can be determined. The formulae for $A_{ij}^{(n)}$ and $B_{ij}^{(n)}$ require the computation of disconnected contributions, which generically lead to large statistical errors. However, since we are only extracting the largest eigenvalue in our analysis below, these errors are under control, as can be seen in our figures that follow.

If we are sufficiently close to a fixed point, then the largest eigenvalue of T should stay constant as the number of blocking steps is varied, and also as the number of observables used to construct T is varied. This method requires a larger lattice and higher statistics than the two-lattice method, but potentially allows more information to be extracted, in addition to being a useful consistency check of the two-lattice method results.

B. Pure SU(2) Gauge Results

In this case the stability matrix approach is used to study behavior in the vicinity of the ultraviolet fixed point, $\beta \to \infty$. One does not expect any relevant couplings, and so the largest eigenvalue will correspond the gauge coupling, with critical exponent of approximately zero. Hence the eigenvalue that we expect to extract is unity.

We have seven blocked observables and four blocking steps on the 32^4 lattices that we have simulated in this case. This means that we can vary the number of observables, and hence the size of the stability matrix T, from 1 to 7. We can calculate T after 1/2, 2/3 and 3/4 blocking steps, for any choice of our blocking parameter α. Unlike in the two-lattice method there is no cancellation of finite size effects, so these are likely to be large.

Using more than four observables (i.e. including 8-link loops) tends to give a complex largest eigenvalue of T, so we only use 1 to 4 observables to construct T. Fig. 5 shows the largest eigenvalue after 1/2, 2/3 and 3/4 blocking steps, as a function of α using ORIG blocking, on a 32^4 lattice at $\beta = 3.0$. At each blocking step T is constructed using 1 to 4 observables, and the spread of eigenvalues for the same blocking level is used as a measure of the systematic uncertainty. This is combined with the statistical uncertainty, obtained from 100 bootstrap replicas, to give the overall uncertainty represented by the error bars.

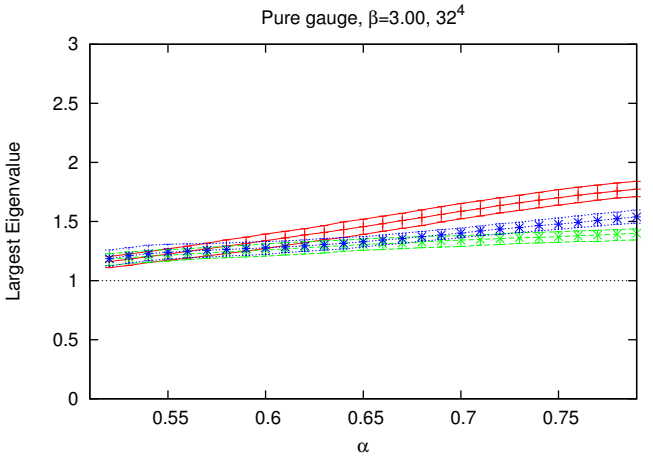

FIG. 5. The largest eigenvalue of the stability matrix T as a function of α, after 1/2 (solid, red on-line), 2/3 (dashed, green on-line) and 3/4 (dotted, blue on-line) ORIG blocking steps on a 32^4 pure gauge lattice at $\beta = 3.0$. Error bars indicate combined systematic and statistical uncertainties.

In general the results seem sensible: the variation with α is reduced as the number of blocking steps is increased. For small α, the eigenvalues are independent of the number of blocking steps, within the spread of eigenvalues that one obtains by varying the number of observables. The eigenvalues are consistent with a marginal eigenvalue of 1, corresponding to the expected logarithmic flow of the coupling in "pure-glue" Yang-Mills.

C. MWTC Results

Here the mass is a relevant direction and will control the largest eigenvalue of the stability matrix. Since this is all we extract, our measurements will give an indication of $y_m = \ln \lambda_h / \ln 2$. For MWTC we have 16^4 lattices, so we are able to construct T after 1/2 and 2/3 blocking steps; again, finite size effects are likely to be large. Fig. 6 shows the largest eigenvalue of T after 1/2 and 2/3 ORIG blocking steps for $\beta = 2.25$, $am \simeq 0.2$. Between 1 and 7 observables are used to construct T, and the spread of the largest eigenvalue at a given blocking level is small, showing little dependence on the number of observables used. Again, this systematic uncertainty has been combined with statistical errors (computed with 100 bootstrap replicas) to give the error bars shown in the figure. On the other hand there is a large difference between the two blocking steps, which suggests that we are not close to a fixed point. Larger lattices and more blocking steps are required. Incidentally, this gives an indication that more blocking steps will be required for the two-lattice method as well.

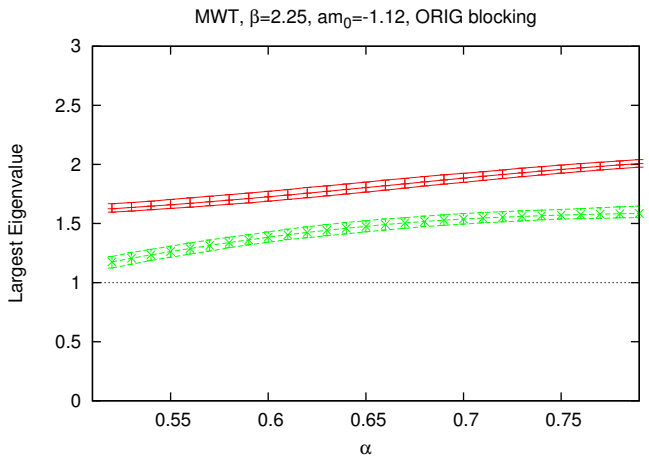

FIG. 6. The largest eigenvalue of the stability matrix T as a function of α, after 1/2 (solid, red on-line) and 2/3 (dashed, green on-line) ORIG blocking steps on a 16^4 lattice for MWTC, at $\beta = 2.25$, $am \simeq 0.2$. The error bars combine the systematic and statistical uncertainties.

This is representative of the situtation for all of our runs: the picture is qualitatively the same for virtually all of our values of β and m, and for all three RG blocking transforms.

VI. CONCLUSION

We find a small anomalous mass dimension and at most a slow running of the coupling. Our results are in fact consistent with the existence of an IRFP. There are large uncertainties in our results, which we interpret as being due to scaling violations.

While the MCRG method is potentially a promising technique for studying theories with an IRFP, our analysis indicates that it is currently limited by several sources of systematic error. Perhaps the single largest factor contributing to this error is the relatively small lattices that have been used in this study; this limits the number of blocking steps that can be taken. Because we seem to be far from the RT, and the putative IRFP as well, extraction of an exponent like γ is problematic.

Adding more matching observables, in particular fermionic ones such as meson correlation functions, will give a more stringent set of constraints on matching (β', m') and (β, m). Improved actions and observables would help to reduce scaling violations and hence systematic errors in matching. We are currently pursuing these improvements to the present analysis.

A final issue that should be mentioned is that it is possible to be in the wrong basin of attraction. If the bare coupling is too strong, the physics may be determined by an ultraviolet fixed point other than the Gaussian one. There is no simple criterion for deciding whether one is in the wrong basin of attraction. Scaling violations are certainly not an indicator, since they will also vanish in the vicinity of another ultraviolet fixed point, where there is an alternative continuum limit defined. Modifying the lattice action may help, but a careful study of the flow of couplings needs to be performed in order to reliably address this potential problem. Regardless of whether it is useful for phenomenology, MWTC is a good testing ground for approaches that propose to investigate this crucial issue.

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[1] F. Sannino and K. Tuominen, Phys. Rev. D **71**, 051901 (2005) [arXiv:hep-ph/0405209].
[2] M. A. Luty and T. Okui, JHEP **0609**, 070 (2006) [arXiv:hep-ph/0409274].
[3] S. Catterall and F. Sannino, Phys. Rev. D **76**, 034504 (2007) [arXiv:0705.1664 [hep-lat]].
[4] S. Catterall, J. Giedt, F. Sannino and J. Schneible, JHEP **0811**, 009 (2008) [arXiv:0807.0792 [hep-lat]].
[5] F. Bursa, L. Del Debbio, L. Keegan, C. Pica and T. Pickup, Phys. Rev. D **81**, 014505 (2010) [arXiv:0910.4535 [hep-ph]].
[6] L. Del Debbio, B. Lucini, A. Patella, C. Pica and A. Rago, Phys. Rev. D **80**, 074507 (2009) [arXiv:0907.3896 [hep-lat]].
[7] A. J. Hietanen, K. Rummukainen and K. Tuominen, Phys. Rev. D **80**, 094504 (2009) [arXiv:0904.0864 [hep-lat]].
[8] T. DeGrand, Y. Shamir and B. Svetitsky, Phys. Rev. D **83**, 074507 (2011) [arXiv:1102.2843 [hep-lat]].
[9] J. Giedt and E. Weinberg, Phys. Rev. D **84** (2011) 074501 [arXiv:1105.0607 [hep-lat]].
[10] B. Holdom, Phys. Rev. D **24**, 1441 (1981).
[11] K. Yamawaki, M. Bando and K. i. Matumoto, Phys. Rev. Lett. **56**, 1335 (1986).
[12] T. W. Appelquist, D. Karabali and L. C. R. Wijewardhana, Phys. Rev. Lett. **57**, 957 (1986).
[13] R. S. Chivukula and E. H. Simmons, Phys. Rev. D **82**, 033014 (2010) [arXiv:1005.5727 [hep-lat]].
[14] C. Pica and F. Sannino, Phys. Rev. D **83**, 116001 (2011) [arXiv:1011.3832 [hep-ph]].
[15] T. A. Ryttov and F. Sannino, Phys. Rev. D **78**, 065001 (2008) [arXiv:0711.3745 [hep-th]].
[16] T. A. Ryttov and R. Shrock, Phys. Rev. D **83**, 056011 (2011) [arXiv:1011.4542 [hep-ph]].

[17] C. Pica and F. Sannino, Phys. Rev. D **83**, 035013 (2011) [arXiv:1011.5917 [hep-ph]].
[18] L. Del Debbio, B. Lucini, A. Patella, C. Pica and A. Rago, Phys. Rev. D **82**, 014510 (2010) [arXiv:1004.3206 [hep-lat]].
[19] J. Giedt and E. Weinberg, arXiv:1201.6262 [hep-lat].
[20] A. Hasenfratz, Phys. Rev. D **80**, 034505 (2009) [arXiv:0907.0919 [hep-lat]].
[21] A. Hasenfratz, Phys. Rev. D **82**, 014506 (2010) [arXiv:1004.1004 [hep-lat]].
[22] R. H. Swendsen, Phys. Rev. Lett. **42**, 859 (1979).
[23] L. Del Debbio, A. Patella and C. Pica, Phys. Rev. D **81**, 094503 (2010) [arXiv:0805.2058 [hep-lat]].
[24] A. Hasenfratz and F. Knechtli, Phys. Rev. D **64**, 034504 (2001) [arXiv:hep-lat/0103029].
[25] A. Hasenfratz, arXiv:1106.5293 [hep-lat].
[26] S. Catterall, L. Del Debbio, J. Giedt and L. Keegan, PoS **LATTICE2010**, 057 (2010) [arXiv:1010.5909 [hep-ph]].
[27] L. Del Debbio and R. Zwicky, Phys. Rev. D **82**, 014502 (2010) [arXiv:1005.2371 [hep-ph]].
[28] A. Hasenfratz, P. Hasenfratz, U. M. Heller and F. Karsch, Phys. Lett. B **143**, 193 (1984).
[29] K. C. Bowler *et al.*, Nucl. Phys. B **257**, 155 (1985).
[30] A. Hasenfratz, P. Hasenfratz, U. M. Heller and F. Karsch, Phys. Lett. B **140**, 76 (1984).
[31] K. G. Wilson and J. B. Kogut, Phys. Rept. **12**, 75 (1974).
[32] H. S. Fukano and F. Sannino, Phys. Rev. D **82**, 035021 (2010) [arXiv:1005.3340 [hep-ph]].
[33] M. Albanese *et al.* [APE Collaboration], Phys. Lett. B **192**, 163 (1987).