Violation of the Gell-man–Okubo Relation with Lattice QCD

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Motivation

Before QCD, with quarks and gluons, was proposed as the theory of strong interactions, Gell-man and other physicists used approximate SU(2) (known as isospin) and SU(3) flavor symmetry to describe interactions of hadrons [1]. While the SU(2) symmetry of isospin is a good symmetry of nature due to the similar masses of up and down quarks, SU(3) flavor symmetry is violated to the 20-30% level due to different mass of the strange quark. Under SU(3) flavor symmetry where the up, down, and strange quarks have identical mass, the light-quark mass matrix transforms as a singlet, and $M_N = M_\Sigma = M_\Lambda = M_\Xi$. However, under SU(2) symmetry but broken SU(3) symmetry, the light quark mass matrix changes to Figure 1. instead of being proportional to the identity.

Consequently, the Gell-Mann–Okubo (GMO) mass relation, T, shown in Eq. 1, becomes non-zero when SU(3) is broken. By using Lattice QCD to study the violation of the Gell-Mann–Okubo relation and its dependence on lattice spacing and pion mass, we hope to explore how well SU(3) Chiral Perturbation Theory describes the results.

Figure 1. The light mass matrix under SU(2) but not SU(3) symmetry

$$m_q = \begin{pmatrix} \bar{m} & 0 & 0 \\ 0 & \bar{m} & 0 \\ 0 & 0 & m_s \end{pmatrix}$$

The Gell-Mann-Okubo Mass Relation

$$T \equiv M_\Lambda + \frac{1}{3} M_\Sigma - \frac{2}{3} M_N - \frac{2}{3} M_\Xi \tag{1}$$

Lattice QCD

- In lattice quantum chromodynamics, time and space are discretized and Feynman's path integral formulation is used to calculate simulated amplitudes with the help of multidimensional integration and Monte Carlo methods.
- For this project, 39 ensembles of two point correlation functions with lattice spacings from 0.06 to 0.15 fm and pion masses from 130 to 400 MeV have been used, courtesy of CalLat/CoSMoN.
- The spectral decomposition of a typical two point function is given in Eq. 3. At large time it plateaus to 0.
- Using the two point functions of the baryons in the GMO relation, we can construct the GMO correlator (Eq. 4) which behaves as a regular two point function but with the GMO sum was its mass.
- Since each baryon correlator has excited states, we can factor out the ground state of the GMO correlator, giving Eq. 4
- To prepare the the data, each ensemble, consisting 1000 configurations of each baryon type with 64 or 96 timeslices each, was averaged with `gvar`

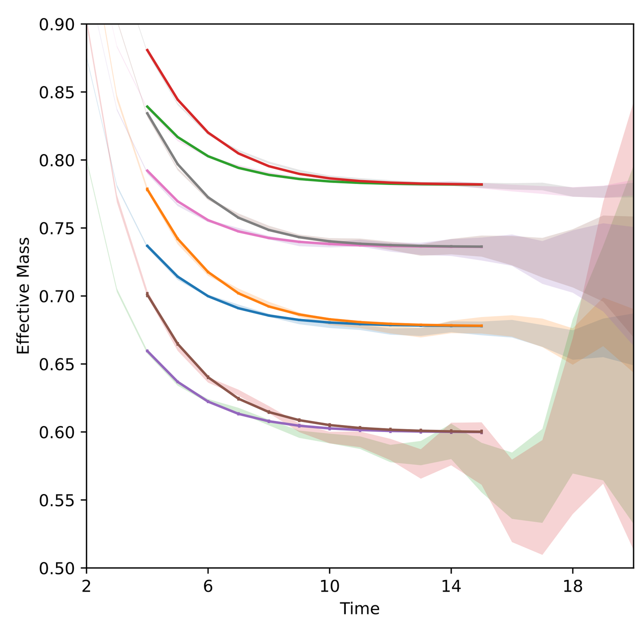
$$C_2(t) = \sum_i A_i e^{-E_i t} \tag{2}$$

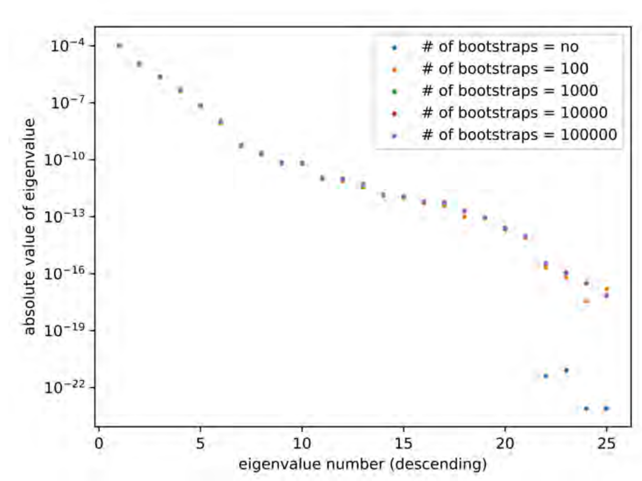
$$C_{GMO}(t) = \frac{C_\Lambda(t) C_\Sigma(t)^{1/3}}{C_N(t)^{2/3} C_\Xi(t)^{2/3}} \tag{3}$$

$$C_{GMO}(t) = A_{GMO} e^{-\Delta_{GMO} t} \frac{[1+\sum A_\Lambda e^{-\Delta_\Lambda t}][1+\sum A_\Sigma e^{-\Delta_\Sigma t}]^{1/3}}{[1+\sum A_N e^{-\Delta_N t}]^{2/3}[1+\sum A_\Xi e^{-\Delta_\Xi t}]^{2/3}} \tag{4}$$

Extracting the Mass Relation

- After being averaged, there are many ways to fit the data to obtain the value of T for each ensemble
- The number of fit states, the fit range, bootstrapping vs not bootstrapping, simultaneous vs individual fits, and choice of free fit parameters could all be varied
- The first strategy we tried was simultaneously fitting the baryons to two states and summing their masses to construct the GMO value (Figure 2).
- Next, we attempted to use the GMO correlator. One thing we noticed was that if we constructed the GMO correlator from regular `gvar` averaging, the eigenvalues of the covariance matrix of the baryon data and GMO correlator would have a large discontinuity by many orders of magnitude, corresponding to the GMO data (Figure 3).
- This eigenvalue behavior is undesirable because it means we would be underestimating the uncertainty of the GMO correlator. It can by remedied by bootstrap resampling the data and constructing the GMO correlator from the bootstrap means.
- Once the GMO correlator was fixed, we tried a two state fit to the correlator by itself, which gave results that were mostly consistent with the constructed GMO value. However, the uncertanties were still quite large.





Left: Figure 2. Simultaneous fit to all baryons for a = 0.15fm, m_π = 135MeV.
Right: Figure 3. A graph of the ordered eigenvalues of a covariance matrix

- After this, we moved on to simultaneous fitting of the GMO correlator and baryon correlators, using three strategies:
  - Constrained E_{GMO} and constrained A_{GMO}
  - Free E_{GMO} but constrained A_{GMO}
  - Free E_{GMO} and Free A_{GMO}

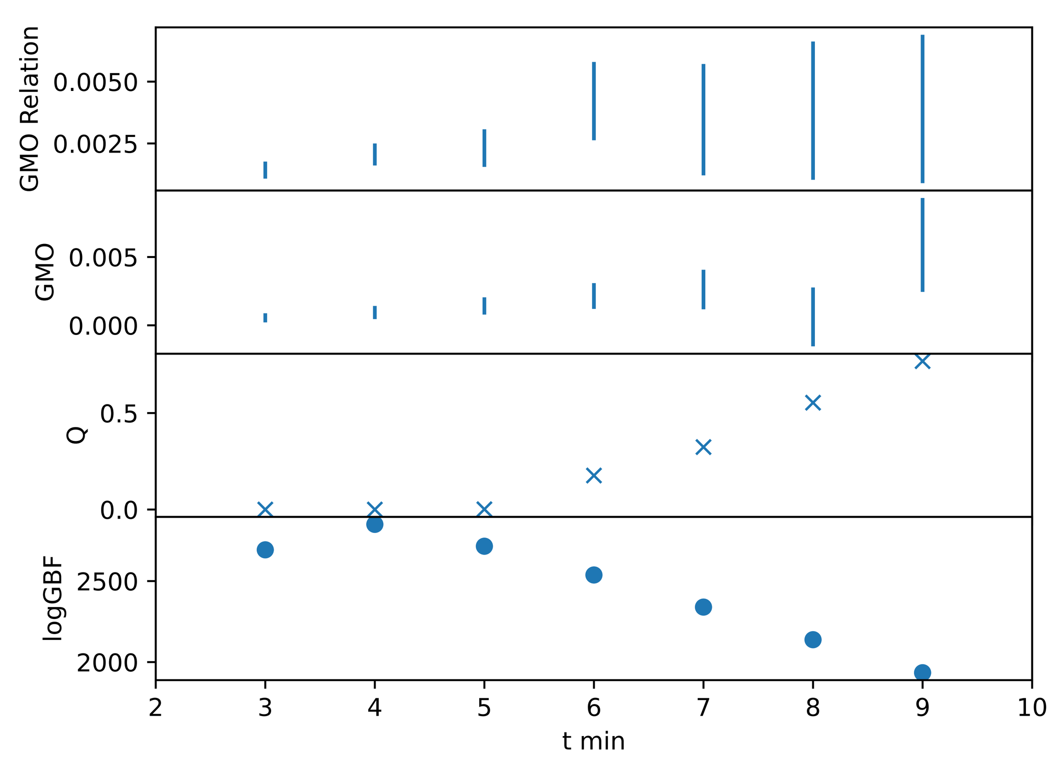


Figure 4: Various fit parameters for fit strategy 3 when the minimum of the fit range is varied. An ensemble with lattice spacing 0.15fm and m_π = 135MeV was used.

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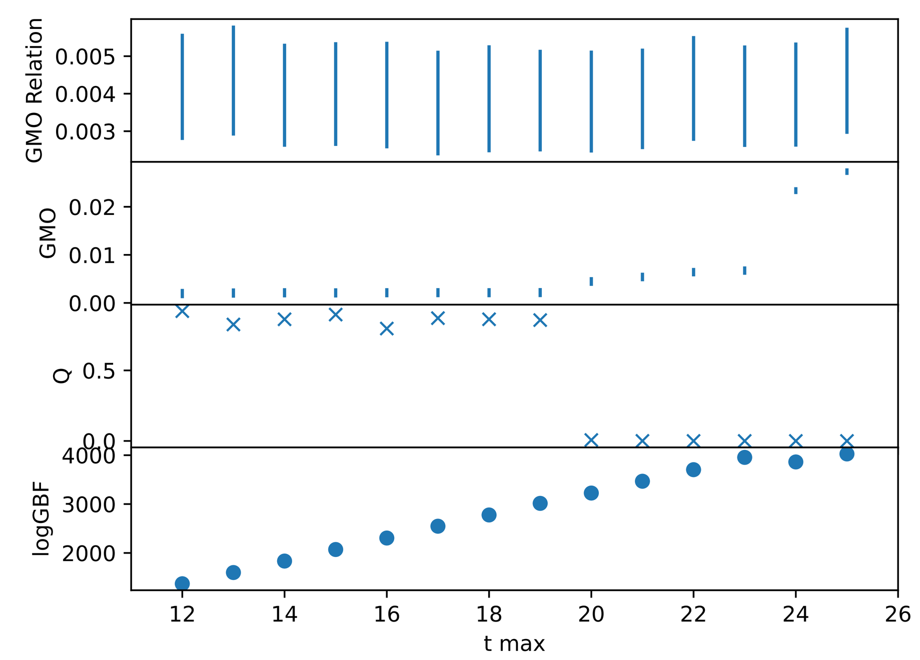

Figure 5: Fit parameters for fit strategy 3 when the maximum of the fit range is varied. Same ensemble as Figure 4.

Outlook

The GMO mass relation project was put on hold recently after a closer look at the ensembles with physical pion mass revealed that the current data would not be good enough to produced the required accuracy or precision. However, a project involving fits to pion, kaon, and omega correlation functions for the purpose of scale setting has been happening in parallel with the GMO project, and the results of that will be applicable to any efforts that use the same ensembles. Since the scale setting project is already underway, our focus has been redirected to fitting the same correlation function for the purpose of hyperon spectrum analysis, with plans to investigate the nucleon mass and nucleon-pion sigma term once that is complete.

References

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The computations were performed with LaLiBe, linked against Chroma with QUDA solvers and HDF5 for I/O. They were efficiently managed with METAQ and EspressoDB. The numerical analysis utilized gvar and lsqfit.