

Generalized Liquid Drop Model with Modified Asymmetry Energy Term

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Introduction

The original semi-empirical mass formula (SEMF) has been modified to overcome its inefficiency in reproducing theoretical binding energies for lower mass region, superheavy nuclei and along the drip lines. These modifications have been done either by improvising the five basic energy terms or by adding extra energy terms to the original formula.

In our previous work [1], we have observed that the main discrepancy between theoretical and experimental binding energies in the lower mass region ($A < 40$) is mainly because of asymmetry term. Samanta et.al [2] have extended this formula to improve the binding energies in lower mass region by modifying asymmetry and pairing energy terms along with two extra parameters added in these terms (denoted as SLDM). In this paper, as a first step, we have obtained the best parameters for SLDM by choosing latest Atomic Mass Evaluation(AME)-2020 data using our optimisation procedure [3] for minimising the mean absolute percentage error (MAPE).

Royer et.al [4] have added the microscopic dependent terms to original macroscopic terms of liquid drop model (LDM) resulting in generalized liquid drop model(GLDM). Recently, we have re-optimized the co-efficients of Royer's mass formula by choosing AME-2020 data and have obtained root mean squared error (RMSE) value of 0.65 [5].

In the present work, we have incorporated the assumptions of Samanta et.al for the asymmetry term into that of GLDM given by Royer. The energy co-efficients for the GLDM for-

mula and the one modified by us (denoted as MGLDM), are optimised and then discrepancy between theoretical and experimental binding energies for the overall data and for $A < 40$ regions have been calculated separately.

Methodolgy

The modified SEMF as suggested by Samanta et.al [2] is given in eqn 1.

$$B(A, Z) = a_v A - a_s A^{\frac{2}{3}} - a_c \frac{Z(Z-1)}{A^{\frac{1}{3}}} - a_a \frac{(A-2Z)^2}{[A(1 + e^{\frac{-A}{k}})]} + a_p \delta (1 - e^{\frac{-A}{c}}) A^{\frac{-1}{2}} \quad (1)$$

where δ is +1 for even(N)-even(Z) nuclei, -1 for odd-odd nuclei and 0 for odd A values. These modifications mainly affect the lower mass region. Similarly, one of the best possible mass formula using microscopic-macroscopic model, with minimum RMSE value, suggested by Royer et.al.[4] is given by

$$B(A, Z) = a_v (1 - k_v I^2) A - a_s (1 - k_s I^2) A^{\frac{2}{3}} - \frac{3}{5} \frac{e^2 Z^2}{R_0} + f_p \frac{Z^2}{A} - E_{shell} - E_{pair} - E_{wigner} \quad (2)$$

We have used the suggested correction in asymmetry energy term from eqn 1 into that of eqn 2. That is, the second term in GLDM has been included as follows:

$$a_v \left(1 - \frac{k_v I^2}{(1 + e^{\frac{-A}{k}})} \right) A \quad (3)$$

The theoretical shell effects (E_{shell}) obtained from Thomas Fermi (TF) model taken from [6] have been used. The pairing energy (E_{pair})

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TABLE I: Comparative analysis of MAPE and RMSE (in MeV) values of binding energies from different models for lower mass region and for total nuclei.

Models	A<40 ($N = 144$)		All Nuclei ($N = 2451$)	
	MAPE	RMSE	MAPE	RMSE
LDM	0.93	2.72	0.27	2.96
SLDM	0.86	2.27	0.27	2.91
GLDM	0.34	0.93	0.07	0.65
MGLDM	0.28	0.76	0.06	0.63

has also been calculated by following the expressions given for spherical nuclei in the same version of TF model. Wigner energy (E_{wigner}) has also been calculated by using the linear combination of two energy expression suggested by Royer [4].

A total number of 2451 nuclei satisfying the following two conditions [4] are considered in this study from the latest AME-2020 data.

- N and Z > 7
- The standard deviation in masses having value less than or equal to 150 keV

Results and Discussion

We have re-optimized the best macro-microscopic mass formula suggested by Royer with an extra modification in the asymmetry energy term as suggested by Samanta. So instead of seven parameters, we now have eight parameters in modified GLDM (MGLDM). The values of RMSE (in MeV) and MAPE between the theoretical and experimental binding energies using four different models for lower mass region and for total nuclei are shown in Table I. On comparing the results of LDM and SLDM, one can observe that there is an improvement in both MAPE and RMSE values on adding extra corrections in asymmetry and pairing energy terms for A < 40 region. The difference is not so evident in case of total number of nuclei. That is because, the total number of nuclei is $N = 2451$ as compared to number of nuclei in lower mass region, which is only $N = 144$, not even 10%. Also, as can be observed from SLDM formula,

it becomes equivalent to the original one as the mass number increases. Hence, the difference in MAPE or RMSE is not pronounced when all nuclei are considered.

On going from SLDM to GLDM, a significant decrease can be observed in both MAPE and RMSE values for both the data regions. Similar improvements can be seen on shifting from GLDM to MGLDM. A significant decrease in the values of RMSE for both lower mass region and for overall nuclei (as seen in the Table), shows that the extra correction in asymmetry term has certainly enhanced the ability of MGLDM to calculate theoretical binding energies. The binding energies obtained from this work are being applied in Cluster Formation Model (CFM) for determining alpha pre-formation probabilities [7].

References

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