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#### **ACCEPTED MANUSCRIPT**

# Comment on 'Analysis of decay chains of superheavy nuclei produced in the $^{249}\rm{Bk}$ + $^{48}\rm{Ca}$ and $^{243}\rm{Am}$ + $^{48}\rm{Ca}$ reactions'

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# Comment on "Analysis of decay chains of superheavy nuclei produced in the <sup>249</sup>Bk + <sup>48</sup>Ca and <sup>243</sup>Am + <sup>48</sup>Ca reactions"

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### Abstract.

Zlokazov and Utyonkov [J. Phys. G: Nucl. Part. Phys. 44, 075107 (2017)] question the validity of the methods and conclusions presented by Forsberg *et al.* [Nucl. Phys. A 953, 117 (2016)]. In this comment, we argue that the criticism is invalid.

The main point behind the statistical method published by Forsberg et al. [1] is that there is more information to access if entire  $\alpha$ -decay chains are considered, compared to when each decay step is considered separately. The method used in Ref. [1] applies to entire chains. Using this method, it is seen that the set of fourteen "short"  $\alpha$ -decay chains observed in the reaction <sup>48</sup>Ca+<sup>243</sup>Am are unlikely to have a common origin. This is not contradictory to the calculations by Zlokazov and Utyonkov [2], which show that if each decay step is considered separately there is no strong reason for questioning the congruence of the data set including both these fourteen short chains and decay chains assigned to start from the isotope <sup>293</sup>117. If the methods used by Zlokazov and Utyonkov were applied to the same data set as was considered in Ref. [1], the result would be that there is no strong reason to question the congruence of the fourteen short chains. This will be the conclusion of any method that uses each decay step separately, be it the method by K.-H. Schmidt [3], a  $\chi$ -square test or a Student's test. In fact, in Ref. [1] the Schmidt test [3] was applied to separate decay steps of the fourteen short chains, and the result from this test is that there is no strong reason to question their congruence. The non-congruence is seen only when entire decay chains are considered.

It is stated by Zlokazov and Utyonkov that the method described in Ref. [1] is doubtful, because in Fig. 4 in Ref. [1] it can be seen that "... none of the 14  $\rm FoM_1$  values, only one of the 14  $\rm FoM_2$  values, and one of the 10  $\rm FoM_3$  values fall within the suggested 90% interval of 0.181-0.255...". However, the confidence interval 0.181-0.255

is not meant to be used for individual  $FoM_{1,2,3}$  values or  $FoM_{geom}$  values, but for the "FoM" for the entire data set. The fact that almost all individual  $FoM_{1,2,3}$  values are outside the 90% confidence interval for the FoM value is irrelevant, and it does not make the method suggested in Ref. [1] doubtful.

Although it is in contradiction to how the proposed method should be used. Zlokazov and Utyonkov seem to argue that the confidence intervals for  $FoM_{1,2,3}$ ,  $FoM_{geom}$ , and FoM should be the same or at least similar. This will be discussed now. Zlokazov and Utyonkov argue that "... observation of decay chain with times which are close to one or another maximum should be much more probable than observation of chains with lower or larger times". It is indeed built into the method in Ref. [1] that the assigned  $FoM_{1,2,3}$  value is high if a measured lifetime is close to the average lifetime. This leads to the distribution of  $FoM_{1,2,3}$  values from single measurements being skewed to the extent that is it not meaningful to give an upper confidence limit: The highest  $FoM_{1,2,3}$  value is the most probable value (see Fig. 7.7 in Ref. [4]). Similarly, the distribution for  $FoM_{geom}$  for a single chain with two members is strongly skewed (see Fig. 6 in Ref. [1]) and an upper confidence limit is not given. However, as the chains get longer and/or averages are taken over a set of chains, the distributions for  $FoM_{geom}$  and FoM approach normal distributions. This is an inevitable consequence of the central limit theorem, as the  $FoM_{geom}$  and FoM are constructed as averages. The advance towards normal distributions explains why confidence intervals for  $FoM_{qeom}$  and FoMare necessarily different from those of  $FoM_{1,2,3}$ . The upper confidence limit for the FoM value expresses that it is unlikely for a data set to only contain chains with members that all have measured lifetimes that are close to the average lifetime. Such a data set is "too good" and it is unlikely that the lifetimes originate from a wide probability density function such as that from radioactive decay.

We would also like to clarify that g(t) is the probability density function for data from an exponential decay when the data are sorted in logarithmic-sized bins (see Ref. [3]). In the main part of Fig. 1 in Ref. [2] the function g(t) is plotted on a linear scale, which is perhaps misleading.

### Acknowledgments

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