

# Nucleus++: a new tool bridging Ame and NUBASE for advancing nuclear data analysis

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### Abstract

The newly developed software, *Nucleus*++, is an advanced tool for displaying basic nuclear physics properties from NUBASE and integrating comprehensive mass information for each nuclide from Atomic Mass Evaluation. Additionally, it allows users to compare experimental nuclear masses with predictions from different mass models. Building on the success and learning experiences of its predecessor, *Nucleus*, this enhanced tool introduces improved functionality and compatibility. With its user-friendly interface, *Nucleus*++ was designed as a valuable tool for scholars and practitioners in the field of nuclear science. This article offers an in-depth description of *Nucleus*++, highlighting its main features and anticipated impacts on nuclear science research.

Keywords  $Nucleus + + \cdot$  Nuclear physics properties  $\cdot$  NUBASE  $\cdot$  AME  $\cdot$  Nuclear science  $\cdot$  Software design

# 1 Introduction

Understanding nuclear properties is crucial for various scientific endeavors, ranging from fundamental nuclear physics research to practical applications in nuclear technology [1]. Therefore, in the field of nuclear science,

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accurate, comprehensive, and readily accessible data are essential. Existing web applications, such as *NuDat* [2], developed by the National Nuclear Data Center (NNDC) at the Brookhaven National Laboratory, and *Live Chart of Nuclides* [3], created by the Nuclear Data Section of the International Atomic Energy Agency (IAEA), are important platforms. These applications offer graphical interfaces to explore nuclear structures and decay data, provide invaluable support for nuclear research, and make crucial data available to the global research community.

However, web-based nuclear data services are inaccessible offline and are hampered by slow Internet speed. In such instances, offline software is more useful and has broader applicability than web-based services. We introduce *Nucleus*++, a cutting-edge software that overcomes these

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limitations and sets a new benchmark for efficiency and user convenience in nuclear science research.

*Nucleus*++ improves upon its predecessor, *Nucleus*, by incorporating feedback and lessons learned from its use in the scientific community. This new iteration enhances existing functionalities and introduces novel features that address the evolving needs of nuclear physicists. Moreover, *Nucleus*++ strongly emphasizes user experience. Its user-friendly interface allows easier navigation and faster data retrieval, thereby reducing the time spent on data collection.

This article comprehensively describes *Nucleus*++, highlighting its innovative features and the anticipated impact on nuclear science research. We explore its capabilities to demonstrate how *Nucleus*++ can revolutionize the manner in which nuclear data are accessed, analyzed, and utilized.

## 2 Importance of NUBASE and AME

The NUBASE evaluation [4] provides recommended values of nuclear physics properties for all known nuclides, such as masses, excitation energies, half-lives, decay modes, and branching ratios, for their ground and long-lived excited states. This comprehensive evaluation is critical for identifying the nuclear states involved in decay processes and mass measurements and supports theoretical modeling and experimental analysis in nuclear physics, astrophysics, and other applied nuclear fields.

While NUBASE compiles the evaluated nuclear physics properties, AME performs a critical survey of the evaluation of atomic masses based on nuclear reactions, decay, and mass-spectrometric measurements [5]. They derive the recommended mass values and their uncertainties using rigorous least-squares fit analysis. Moreover, in addition to providing mass values, AME traces the origin (lineage) of the data for each nuclide, connecting the current recommended values to the original measurements. This traceability highlights AME's commitment to transparency and accuracy and allows researchers to verify data integrity and understand the historical context of mass measurements. This depth of information is indispensable for advancing the domain of mass measurements.

## 3 Development and features

The first attempt to display nuclear physics properties on personal computers dates back to the 1990s [6]. The Windows-based software *Nucleus*, developed by one of us (G.A.), gained significant popularity within the nuclear physics community after its release [7]. It primarily aims to provide users with essential nuclear physics properties derived from the NUBASE database, thereby facilitating a comprehensive understanding of nuclear phenomena. *Nucleus* is widely used in experimental campaigns which require rapid consultation of all data concerning the nuclides of interest. However, its adaptation to diverse operating systems is essential, and accordingly, an Android version has been developed. Later, a web tool to display NUBASE was developed in collaboration with the IAEA [8]. Despite these advancements, the explicit connection to AME was missing, leaving users without a clear understanding of how a single mass value was determined from the underlying data in AME.

*Nucleus*++ builds upon the success of *Nucleus* by enhancing its capabilities and expanding its scope. A key advancement is the integration of the AME results with data from the NUBASE library, which provides users with unparalleled access to comprehensive information on nuclear properties and atomic masses through a unified interface. Moreover, the cross-platform compatibility of *Nucleus*++ provides access to users across various operating systems, including Windows, macOS, Android, and iOS. Below, we highlight the novel features and principal updates of *Nucleus*++.

#### 3.1 Utility

*Nucleus*++ integrates the latest evaluations of nuclear properties from the NUBASE library (NUBASE2020) [9] along with the results from the Atomic Mass Evaluation (AME2020) [10, 11]. Presently, the software offers ten display options for nuclear properties: decay mode, half-life, precision, isomer number, spin, classification, binding energy per nucleon, mass excess, year of discovery, and theoretical model. Figure 1 shows a home screen displaying the adjusted mass precision, as reported in AME2020. This interface aims to elucidate the following:

- Precision: This option represents the adjusted precision of mass measurements as reported in AME2020. The precision of each nuclide is marked in a color-coded manner.
- *Driplines*: These are critical boundaries in nuclear physics that delineate the limits beyond which additional neutrons or protons cannot be bound by a nucleus. It enables direct comparisons with experimental data and highlights the differences in theoretical approaches.
- *Filtering*: This enables the clear identification of nuclides with precisions lower than 100 keV, as seen in Fig. 1b. By isolating these particular nuclides, the figure facilitates visualization and helps in identifying potential candidates that can be reached by current radioactive ion beam facilities.



**Fig. 1** (Color online) Visualization of adjusted mass precisions in AME2020. **a** Global view of precisions with one-proton and one-neutron driplines calculated based on the mass model FRDM12 [12]; **b** Same as **a** but displays nuclides with precisions lower than 100 keV

#### 3.2 New features

*Nucleus*++ is equipped with several key features to improve its functionality and extend its utility in nuclear physics research:

• Integration of mass models: The software now incorporates ten different mass models, enabling comprehensive comparisons with experimental values. Figure 2 shows



Fig. 2 (Color online) Comparison between experimental masses and predictions from the mass model HFB27 [13]

a comparison between experimental masses and predictions from the mass model HFB27 [13]. Predicted driplines ( $S_{2n}$ ,  $S_n$ ,  $S_{2p}$ , and  $S_p < 0$ ) calculated from up to four mass models can be displayed simultaneously, facilitating a direct comparison between model predictions and experimental data. Moreover, as the driplines can be shown alongside other properties of nuclides, changes in properties when they approach the driplines can be examined.

- *Classification*: A new classification feature based on the data connectivity in AME has been introduced. All masses are divided into *primary* and *secondary*, as shown in Fig. 3. The masses of *primary* and *secondary* nuclides are derived from least-square analysis and from a unique type of measurement, as defined in Ref. [10], respectively. This feature allows better insight into how mass evaluations are performed and propagated through different levels of connectivity.
- *Isomer counting: Nucleus++* has been improved to include a feature for cataloging the presence of isomers (with half-life longer than 100 ns) for each nuclide (see Fig. 4b), which enables researchers focus on nuclear isomerism.
- Software development framework: Nucleus++ is developed using C<sup>#</sup> and employs "Unity" [14], a popular cross-platform game engine and development platform. This choice of technology underscores the software's commitment to providing a robust, interactive, and userfriendly experience across various computing environments.



**Fig. 3** (Color online) Classification of masses in AME, where green and yellow represent *primary* and *secondary* masses, respectively. Red represents the nuclides whose masses are estimated from the extrapolation of the smoothness of the mass surface. The black square indicates the standard mass of <sup>12</sup>C

511 51 51 51 51 51 51 51 51 51 50 50 50 50 50 50 50 50 50 50 50 50 50	Sb 75 75 75 75 75 75 75 75 75 75 75 75 75 7	1 Sb 76   51 Sb 76   1 1 1 1   1 1 1 1   1 1 1 1 1   1 1 1 1 1 1   1 <th>1 0.01 0.02 0.</th> <th>51 Sb7 51 Sb7 51 Sb7 50 Sn7 50 Sn7</th> <th>51 Sb 79   1 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100</th> <th>1 0 80   51 80 80   All 1 80   All 1 1   130 0 0*   5 51 80   130 0* 0*   5 510 80   1 10 50   5 50 80*   5 50 80*   5 50 80*   5 50 80*   5 50 80*   5 50 80*   5 50 80*   5 100 80*   5 100 80*   5 100 80*   5 100 80*   5 100 80*</th>	1 0.01 0.02 0.	51 Sb7 51 Sb7 51 Sb7 50 Sn7 50 Sn7	51 Sb 79   1 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100   100 100 100	1 0 80   51 80 80   All 1 80   All 1 1   130 0 0*   5 51 80   130 0* 0*   5 510 80   1 10 50   5 50 80*   5 50 80*   5 50 80*   5 50 80*   5 50 80*   5 50 80*   5 50 80*   5 100 80*   5 100 80*   5 100 80*   5 100 80*   5 100 80*
(a) 127 Sn <sup>Z = 50</sup> Isomer: 4 🜌						
tate	Mass excess (	keV) Half-life	Excitation energy (keV)	Decay Mod	es Spin and	Parity
gs	-83470(9)	2.10(4) h		β-=1009	6 11/2-*	more
m	-83465(9)	4.13(3) m	5.07(6)	β-=1009	6 3/2+*	more
n	-81643(9)	4.52(15) us	1826.67(16)	IT=1009	6 19/2+	more
p	-81539(9)	1.26(15) us	1930.97(17)	IT=1009	6 (23/2+	) more
q	-80918(9)	250(30) ns	2552.4(10)	IT=1009	6 (27/2-)	more
(b)						



**Fig.4** (Color online) Visualization of nuclear physics properties. **a** Interface displaying the properties of nuclides around <sup>127</sup>Sn. **b** Nuclear properties of <sup>127</sup>Sn for the ground and isomeric states in order of excitation energy

**Fig. 5** (Color online) Examples illustrating the new feature of mass lineage in *Nucleus*++. **a** Detailed mass evaluation results of the *primary* nuclide  $^{127}$ Sn and the derived quantities; **b** Same as (**a**) but for the *secondary* nuclide  $^{159}$ Hf

#### 3.3 Enhanced integration with AME

*Nucleus*++ offers a significant advancement in the integration of the AME results, providing researchers with more detailed and accessible information than ever before. Figure 4a shows the nuclear properties of  $^{127}$ Sn in its surrounding region for the ground state and the first two isomeric states in the order of excitation energy. This information is beneficial for online experiments, which require the rapid identification of long-lived isomeric states. By interacting with the displayed information, users can obtain detailed information regarding  $^{127}$ Sn, as shown in Fig. 4b, which displays the properties of all the long-lived isomeric states.

#### 3.4 Mass lineage

In *Nucleus*, data integration from AME was limited to mass-excess values. In contrast, *Nucleus*++ significantly extends its scope by incorporating a broader range of the AME results. Figure 5a reveals the "*Mass lineage*" of <sup>127</sup>Sn and the derived quantities for separation and decay energies. <sup>127</sup>Sn is the *primary* nuclide (corresponding to the green symbols in Fig. 3), and its mass is determined from four measurements: the Penning-trap mass measurement [15] and three beta-decay end-point energy measurements [16,

17]. The Penning-trap result contributes 68.12% to its mass determination, while the decay measurements account for the rest. The "*Mass lineage*" features the first attempt to display detailed information related to each mass determination and helps in quantifying the reliability and significance of each measurement.

Often, the new mass data disagree; therefore, probable reasons must be examined, such as the favorable production of a given nuclide in an excited state (rather than its ground state) or the "pandemonium effect" observed in decay-energy measurements [18]. This discrepancy analysis is crucial for ensuring the reliability of the mass data and understanding the underlying causes of differences.

For *secondary* nuclides (corresponding to the yellow symbols in Fig. 3), an additional label called "*mass degree*" is appended. This reflects the distance along the chains connecting them to the network of *primary* nuclides and allows better understanding of the potential error propagation from nuclides with lower mass degrees (see Sect. 4.2 in Ref. [10]). As shown in Fig. 5b, <sup>159</sup>Hf has a mass degree of 4 and is connected to <sup>155</sup>Yb by  $\alpha$ decay from several experiments. Furthermore, the mass uncertainty of <sup>159</sup>Hf primarily originates from the mass uncertainty of <sup>155</sup>Yb because the evaluated uncertainty of 17 keV is significantly larger than those of  $\alpha$ -decay measurements. The integration of AME is the most important feature of *Nucleus*++, which allows better understanding of the methods used to determine the mass of each nuclide, and enables researchers trace the original experimental results that contributed to the final mass values.

To enhance research efficiency, *Nucleus*++ includes interactive hyperlinks to references. Users who click on these references are directed to the NNDC website [19], where they can directly access the originally published articles.

# 4 Summary and impact of Nucleus++ on nuclear physics research

We introduce *Nucleus*++, a considerable advancement over its predecessor *Nucleus*, which is designed to meet the evolving demands of nuclear physics research. *Nucleus*++ bridges the AME and NUBASE libraries and serves as a robust tool that significantly enhances data visualization, accessibility, and analysis capabilities and facilitates comparison with theoretical models. The key enhancements and impacts include the following.

- *Improved search efficiency*: The software's user-friendly interface and advanced functionalities enable rapid access to and analysis of nuclear data, meeting users' needs for speed and efficiency.
- Enhanced transparency to mass data: The integration with the evaluation results from AME allows users to trace the mass measurements contributing to a given nuclide, which enhances the reliability and depth of mass analysis. This transparency is critical for validating experimental results and understanding discrepancies in nuclear data.

*Nucleus*++ is an indispensable tool in the pursuit of a deeper understanding and new discoveries in nuclear science. In future, we will incorporate information on the excited states of known nuclides (spin, parity, and half-life). These nuclear spectroscopic data are expected to be of great reference value in the interdisciplinary fields of nuclear structure, reactions, and astrophysics. *Nucleus*++ will assist researchers by readily providing the latest nuclear science information during discussions, facilitating on-the-go discussions and contemplation. The software can be freely downloaded from the AMDC website [20].

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Author contributions All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by Wen-Jia Huang, Meng Wang, Jin-Yang Shi, Georges Audi, Filip Kondev, Sarah Naimi. The first draft of the manuscript was written by Wen-Jia Huang and Meng Wang and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

**Data availability** The data that support the findings of this study are openly available in Science Data Bank at https://cstr.cn/31253.11. sciencedb.j00186.00327 and https://www.doi.org/10.57760/sciencedb.j00186.00327.

#### Declarations

**Conflict of interest** The authors declare that they have no conflict of interest.

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