Understanding Heavy-ion Fusion Cross Section Data Using Novel Artificial Intelligence Approaches

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Complete fusion reactions: a brief overview

Nucleus-nucleus collisions at low and intermediate energies are the ideal playground to explore the evolution of reaction mechanisms with the collision energy and to probe the interplay of nuclear structure and dynamics (including the occurrence of collective motions in hot rotating nuclei).
Complete fusion reactions: a brief overview

• Different, complementary, experimental methods can be effectively used to estimate the yield of evaporation residues (gamma-ray analysis, time-of-flight and magnetic spectrometers, charged particle detection with telescope arrays) → heavy-ion fusion cross section from the Coulomb barrier to the onset of multi-fragmentation →

Competition with incomplete fusion phenomena and isospin effects

→ higher probability of fusion-evaporation and fission-like processes for higher N/Z content in entrance channel.

→ Isospin effects on the competition between fusion-like processes and binary-like mechanisms.
→ Larger probability to produce heavy-residue for the systems with the largest neutron content.
→ Sensitivity to the density dependence of the symmetry energy term of the nuclear EoS using microscopic approaches.

→ Also recent results by INDRA-FAZIA support these findings!
Complete fusion reactions: a brief overview

Models for the description of fusion cross section between heavy-ions:

• **Microscopical approaches**: Time-Dependent Hartree–Fock (TDHF), Molecular dynamics;

• **Macroscopic models**: critical distance models, limitation to the compound nucleus model (empirical nuclear potentials from semi-classical considerations);

• **Empirical models**: starting from nuclear reaction theory and then optimizing to the experimental data.
Complete fusion reactions: a brief overview

Previous data-driven (phenomenological) approaches, see e.g. *Porto F and Sambataro S 1984 Nuov. Cim. 83* 339 → good description of data around the maxima of the cross section → few datasets in Region III (high energies) and Region I (close to the Coulomb barrier).
Complete fusion reactions: a brief overview

More recently → systematic study of Region III shows discrepancies for some of the systems → further investigation on both experiment and theory is required!

Fusion cross section in Region III → disagreement with the prediction of state-of-the-art for some collision systems such as:

- $^{28}\text{Si} + ^{12}\text{C}$
- $^{12}\text{C} + ^{27}\text{Al}$
- $^{48}\text{Ti} + ^{40}\text{Ca}$
- $^{16}\text{O} + ^{40}\text{Ca}$
- $^{14}\text{N} + ^{12}\text{C}$
- $^{14}\text{N} + ^{14}\text{N}$
- $^{14}\text{N} + ^{27}\text{Al}$
- $^{14}\text{N} + ^{52}\text{Cr}$
- $^{14}\text{N} + ^{58}\text{Ni}$

Approach, dataset, and modeling

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**Approach:** *supervised learning* using *symbolic regression* algorithms.

**Novelties:**
- Deriving mathematical expressions to describe the data → support to theories and models attempting to predict the fusion cross section between heavy-ions;
- Comprehensive analysis of large amount of nuclear data → universal model for the description of the entire dataset;
- Advanced feature selection → allows to inspect the dependence on several variables (including nuclear structure variables).

**Major challenges:**
- The amplitude of the cross section varies even by several orders of magnitude with the energy;
- Experimental errors associated to each individual data point differ by several orders of magnitude for each data point;
- Resulting models must have physical boundaries and extrapolation capabilities.
We used an extensive set of nuclear features linked to:

1) The nature of the collision partners;
2) The energy of the collision;
3) The structure of the collision partners;
4) The structure of the compound nucleus.
• Dataset used for model derivation → about 4500 experimental data points.
• Learning dataset: $Z_pZ_t < 250$ → light-to-medium mass nuclei.
• Testing dataset 1: $Z_pZ_t \geq 250$ → heavy systems (test the extrapolation towards heavy systems).
• Testing dataset 2: $Z_pZ_t < 250$ → some of the lighter systems.
The Brain Project

Brain Project – a neural-genetic tool for the formal modeling of data

Exploits a novel hybridization of genetic programming and artificial neural network → the task is that of symbolic regression. Genetic part → foresees the evolution of tree-like structures representing mathematical expressions → deals with the global search for the maximum of a suitable fitness function; Neural part → deals with the local search for the minimum of the error when the genetic part has identified a good maximum of the fitness function.

Genetic evolution of tree-like structures representing mathematical expressions

Artificial neural networks to optimize the constants (gradient descent technique)

Russo M 2016 Swarm Evo. Comput. 27 145
Russo M 2020 Soft Comput. 24 16885–16894
The Brain Project: genetic mechanism

**Brain Project**: the genetic part foresees the evolution of tree-like structures representing mathematical expressions to model the data. In these structures, a node is a mathematical function or operation, a constant or a variable. The number of nodes is used to evaluate the complexity of the model.

The Brain Project: genetic mechanism

1. A set of possible solutions to the optimization problem, encoded according to a predefined scheme, is generated (often randomly). Each of such solutions is called individual. A set of individuals forms a population.

2. A numerical value, called fitness, is associated to each individual. The fitness quantifies how much a given solution is suitable to the problem to solve. Generally speaking, the higher the fitness associated to an individual the more promising is the individual itself. This is a crucial quantity for the success of the optimization procedure.

3. Until a predefined convergence criterion is reached, the following steps are iterated:
   (a) Some individuals are selected (parents) to be used as a starting point for the generation of new individuals (offsprings).
   (b) Offsprings are obtained through a suitable mechanism of parents encoding recombination (crossover). In this phase, the chromosomes of the parents, i.e. their encoding, are suitably combined to generate new individuals. A valid crossover should produce individuals whose genetic code is, to some extent, similar to that of the parents. Crossover is usually followed by a random variation, with low probability, of some portions of the derived encoding. Such a process is called mutation and has a crucial importance as it allows to introduce missing genetic code and to keep genetic diversity in the population. The fitness is finally calculated for all newly obtained individuals.
   (c) Some offsprings live sufficiently long to replace other pre-existing individuals.
The Brain Project: fitness function

**Fitness function** is the function to maximize suitably contains the prediction error and a term related to the complexity of the model and/or feature costs.

\[
\begin{align*}
  f_{\text{fit}} &= 100.0 \cdot \frac{f_e u(f_e) + \alpha f_n u(f_n)}{1 + \alpha} \\
  f_e &= \frac{e_{\text{max}} - e}{e_{\text{max}}} \\
  e &= 100 \sqrt{\frac{\sum_{o=1}^{N_o} \sum_{p=1}^{N_p} (w_{\text{pat}_p,w_{\text{out}_o}}(y_{o_p}^{\text{d}} - y_{o_p}^{\text{op}}))^2}{N_o N_p_{\text{eq}}}} \\
  f_n &= \frac{n_{\text{max}} - n}{n_{\text{max}} - 1}
\end{align*}
\]

to tune the desired trade-off between accuracy and complexity

related to the accuracy of the model

related to the complexity of the model
Results

\[ f_{fit} = f_{fit} \cdot e^{\frac{n_{tgt} - n}{n_{tgt}}} \] required to reach a predefined, target, number of nodes. Brain Project usually tries to optimize the error with a given number of nodes \( \rightarrow \) interesting to more easily tune the complexity of the desired model.

\[ \sigma_{f_{fit}^{(10)}}(E_{cm}) = 1103 \cdot \exp\left[-\left(1.387 - 0.468 \cdot \frac{Z_2 \cdot Z_4}{E_{cm}}\right)^2\right] \]

\[ \sigma_{f_{fit}^{(15)}}(E_{cm}) = 1116 \cdot \exp\left[-\sinh^2\left(-1.359 + \text{erf}\left(\frac{S_{tn}}{E_{cm}}\right) + 0.061 \cdot \frac{A_1 \cdot A_3}{E_{cm}}\right)\right] \]
Comparison with other models

Our model slightly overestimates data in region 0;

Regions I-III → good overall description of data;

The positions of maxima are well reproduced, for lighter systems the maximum is predicted at slightly lower energies;

Nearly-symmetric systems → variances in agreement with surface friction model and slightly larger than those obtained with the proximity model.
Other applications...

Other decay channels $\rightarrow (n,p)$, and $(n,\alpha)$ reactions

$\rightarrow$ The feature selection can help to inspect shell effects in the reaction cross sections... Difficult with traditional analysis methods!
Some Conclusions...

• Artificial Intelligence approaches based on hybridization of genetic programming and artificial neural networks are promising to help the description and understanding of large datasets of nuclear variables;

• One of the key aspects of these methods is the advanced feature selection, implemented via a programming simulation of the natural selection \(\rightarrow\) help to probe the existence of correlations between variables;

• The present application focused on modeling an unprecedentedly large dataset of heavy-ion fusion cross section data and a broad body of nuclear variables;

• The newly developed models are capable to describe the entire systematics with a few variables, which are found to contain the whole informative content of a larger set of variables;

• These methods are readily applicable to numerous datasets in the nuclear domain!
Thank you for your attention!

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Recently published results.

→ An interesting by-product of this study → refined dataset to investigate fusion cross section even with traditional methods → a new Sum-of-Difference (SoD) approach to unveil structure and shell effects on over-barrier fusion.