

An ideal multifragmentation kinematics algorithm for nuclear physics, a binary reaction approach

F. FAVELA⁽¹⁾⁽⁶⁾, L. ACOSTA⁽⁶⁾⁽¹⁾, L. AUDITORE⁽¹⁾⁽⁴⁾, G. CARDELLA⁽¹⁾,
E. DE FILIPPO⁽¹⁾, S. DE LUCA⁽⁴⁾⁽¹⁾, B. GNOFFO⁽¹⁾⁽³⁾, G. LANZALONE⁽²⁾⁽⁵⁾,
C. MAIOLINO⁽²⁾, N. S. MARTORANA⁽²⁾⁽³⁾, A. PAGANO⁽¹⁾, E. V. PAGANO⁽²⁾,
M. PAPA⁽¹⁾, S. PIRRONE⁽¹⁾, G. POLITI⁽¹⁾⁽³⁾, L. QUATTROCCHI⁽¹⁾⁽⁴⁾, F. RIZZO⁽²⁾⁽³⁾,
P. RUSSOTTO⁽²⁾, A. TRIFIRÒ⁽⁴⁾⁽¹⁾ and M. TRIMARCHI⁽⁴⁾⁽¹⁾

⁽¹⁾ INFN Sezione di Catania - Catania, Italy

⁽²⁾ INFN LNS - Catania, Italy

⁽³⁾ Dipartimento di Fisica e Astronomia, Università di Catania - Catania, Italy

⁽⁴⁾ Dipartimento di Scienze MIFT, Università di Messina - Messina, Italy

⁽⁵⁾ Università Kore Enna - Enna, Italy

⁽⁶⁾ Instituto de Física, Universidad Nacional Autónoma de México - Apartado Postal 20-364,
México D. F. 01000, Mexico

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Summary. — A binary tree data structure is used to represent a nuclear multifragmentation, we constrict the tree in all but one of the leaf nodes. We use geometric arguments in the velocity space to graphically show how the tree can be solved by assigning velocity vectors in both the lab and CM systems at each of the nodes. An experimental comparison with a ternary reaction is also shown.

1. – Introduction

The approach is to study multifragmentation through a set of binary sequential reactions. Since different fragmentations may give the same final fragments we cannot describe the process adequately by simple variables and equations. We need a data structure to describe unambiguously a fragmentation and also a way to do kinematics on it. We will call this structure a binary reaction tree (BRT).

2. – Theory

Given the reaction times of any fragmentation ($< 10^{-18}$ sec), we can infer that macroscopically the fragmentation was punctual. This means essentially that the laboratory angles of the fragments and the angles of the laboratory velocity vectors are the same.

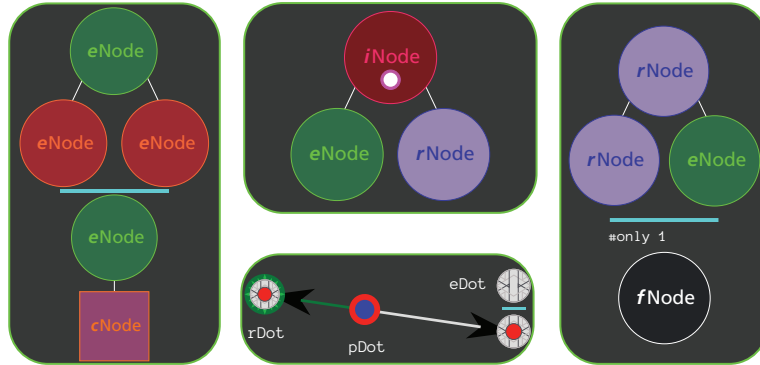


Fig. 1. – General representation of a BRT. It can be understood as a simple grammar.

We can therefore concentrate in getting the vectorial laboratory velocity solutions of the involved fragments.

The BRT structure can be described in a very generalized and compact way as in fig. 1. It has all but one of its leaf nodes constricted to reach at a certain angle in the laboratory frame. The constriction may be interpreted, for example, as the laboratory angles of the detectors or the observed angles inside a Time Projection Chamber. The prefixes are the first letters of *initial*, *ejectile*, *recoil*, *parent*, *constricted* and *final*. We can make the case that the initial node is actually a recoil node with a free laboratory solution. So we have basically 2 types of structures with their corresponding leaf conditions.

The main idea is to be able to solve locally each of the nodes and propagate the information between them such that we are able to assign a laboratory velocity vector to each of the nodes. From here on, we will assume that the BRT has already been solved in the CM system, that is every node has a CM velocity magnitude assigned. Due to the conservation of momentum, given any 2 sibling nodes, we know that their velocities will be pointing in opposite directions. An example of this is shown in fig. 2.

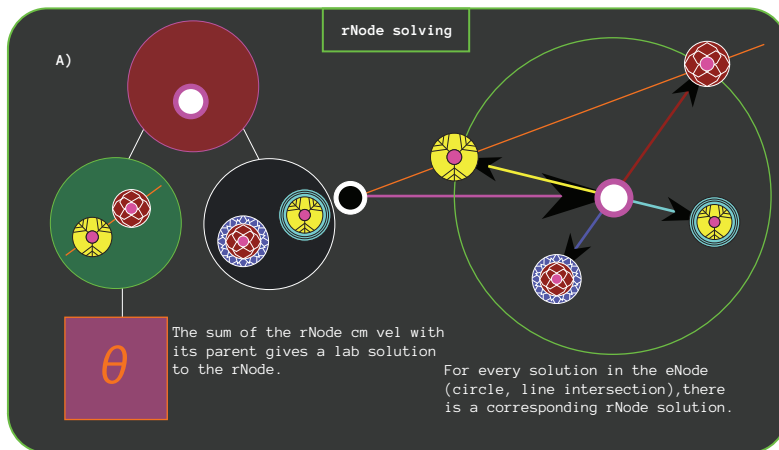


Fig. 2. – Example of 2 particles, constriction at $eNode$ depends only on $cNode$'s angle.

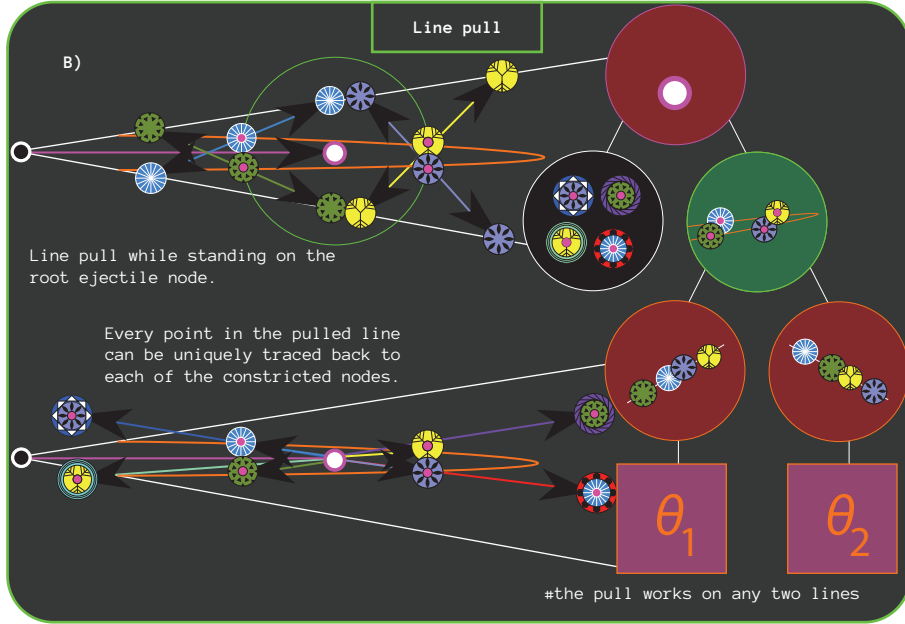


Fig. 3. – A 3 particle case, constriction at root $eNode$ depends also on the children's $|\vec{v}_{CM}|$ s.

Note that the concentric circles (“dots”) are a visual aid to represent velocity vectors, in the node notation, from the inner part to the outer. If there are 3 regions then the inner two regions represent the sibling ejectile dot. This is an important piece of information that will be propagated through the BRT. If we are able to assign at least one of these dots to each of the nodes, then we say that we have solved (at least partially) the BRT.

We call a line pull, an operation that brings the laboratory constrictions to a root ejectile node. It is in essence a construction of geometric places, an example of this is shown in fig. 3; note that the operation is invertible and that the lines might break in the pulling operation leading to multiple lines.

For propagating the solutions down the tree, we notice that on the root ejectile node we can visualize the CM constrictions as a set of velocity sphere surfaces each centered

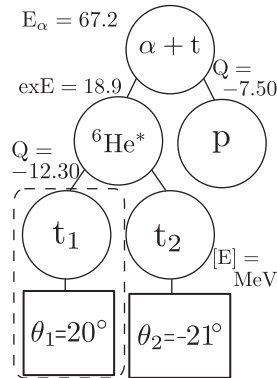


Fig. 4. – BRT corresponding to a reaction in [1].

TABLE I. – Calculated energies (in MeV) for the BRT shown in fig. 4, $Q = -19.81$ MeV. The values that are indicated in the plot in fig. 5 are highlighted in bold.

p angle (deg)	p	t_1	t_2	sum $- Q$	error	% error
-29.44	8.70	9.95	28.81	67.28	0.08	0.11
-38.55	3.91	13.38	30.16	67.28	0.08	0.11
23.32	10.81	28.04	8.60	67.27	0.07	0.10
36.76	2.08	30.45	14.91	67.26	0.06	0.09

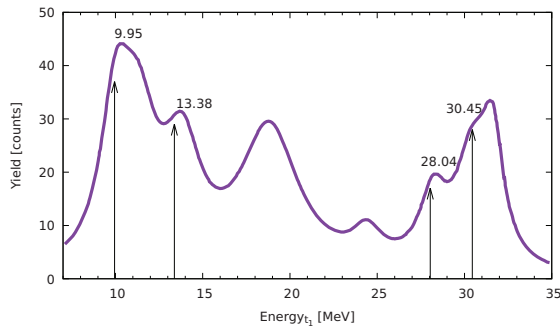


Fig. 5. – Adapted from fig. 4 of [1].

at each of the solutions of the parent node. The set of dots that satisfy the CM and lab constrictions at the same time (intersections between lines and sphere surfaces) are potential solutions (some fragmentation paths might lead to a dead end).

In the ideal case, direct fragmentations can always be expressed as a sequential fragmentation between 2 sets of particles. This leads to a base set of solutions independent of a particular grouping and extra solutions that are grouping dependent.

Algorithm:

0) If we are at the f Node we have finished. 1) Pull the lines in the e Node. 2) For every dot in the current node: a) do intersections in the e Node; b) get the dots in the r Node. c) Propagate the solutions down the ejectile branch. 3) Descend to the child r Node. 4) Repeat from 0).

It is important to point out that we are ignoring deliberately the potential. This can redistribute the energy and momentum between the fragments.

3. – Results

We confronted the technique with a ternary reaction taken from [1], fig. 4 shows a BRT of their studied reaction (with a slight difference in excitation). Using a rudimentary implementation of the algorithm [2] we get the laboratory energies given in table I.

Part of the spectra shown in fig. 5, can be explained with the help of table I.

4. – Conclusions

The BRT allows to unambiguously keep track of the properties of each of the participating particles (within its nodes) in a given fragmentation while simplifying the kinematical problem, reducing the solutions to a simple vectorial velocity sum.

As it was shown in table I and fig. 5 spectroscopic analysis can be done with 3 particles. A potential use of the algorithm for more particle systems might be to create kinematical software filters.

The implementation [2] is still under development but it provides promising results.

REFERENCES

- [1] POVOROZNYK O., *Phys. Rev. C*, **85** (2012) 064330.
- [2] FAVELA F., <https://github.com/ffavela/multifrag-test>.