



# Kinematic approach for nuclei coalescence in transport models

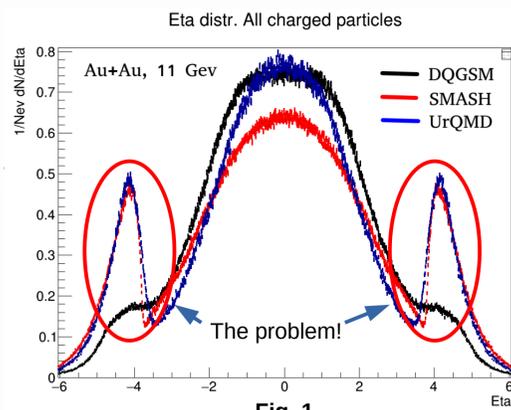
Vladislav Sandul, [vladislav2018@yandex.ru](mailto:vladislav2018@yandex.ru)



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## Motivation

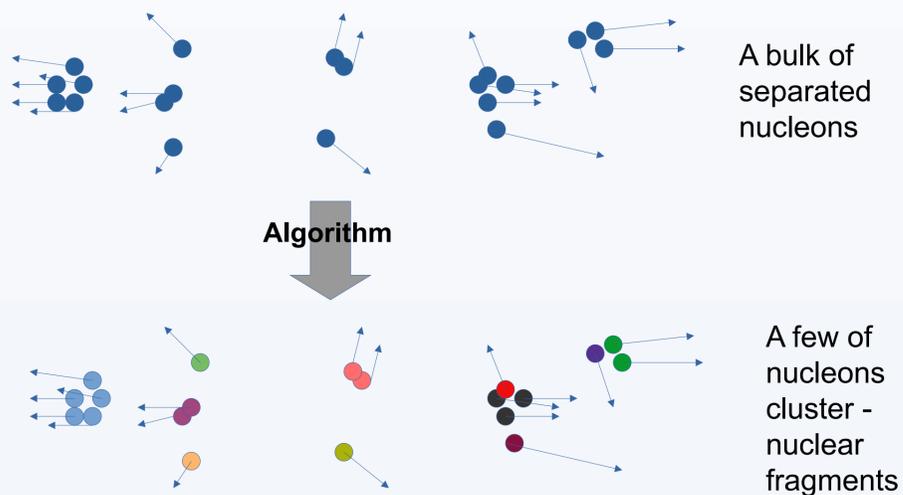
Transport approach [1,2] for nucleus-nucleus collisions description is widely used and underlies many popular Monte Carlo event generators, such as SMASH [3] and UrQMD [4]. Unfortunately, the mechanisms of nucleus fragmentation and coalescence are not taken into account by the transport approach based models. In final states, nucleus fragments (such as spectators or made by coalescence light nuclei) are presented as many individual protons and neutrons. It leads to significant overestimation of particle multiplicity in the regions of large pseudorapidity ( $|\eta| > 3.5$ ) (Fig. 1).



In the Fig. 1 you can see the charged particles pseudorapidity distributions comparison for DQGSM event generator (with built-in fragmentation mechanism) and transport-model based UrQMD and SMASH event generators. We can see the significant multiplicity overestimation with SMASH and UrQMD in high pseudorapidity regions in comparison with DQGSM.

## Main idea

To solve this problem, the kinematic approach for nuclei coalescence was developed. The main idea of the approach is to interpret a bulk of nearly spaced nucleons with close velocities as a single nucleus. Knowing the coordinates and velocities of nucleons in an event at some not too small moment in time (after chemical and kinematic freeze-out), we can determine their belonging to one or another fragment-cluster.



## Algorithm description

1. Every particle is described by structure that contains information about X, Y, Z coordinates of particle, Px, Py and Pz momentum components and about particle energy E.
2. Double looping through all pairs of particles we recalculate the coordinates of particles in the center of mass frame (taking into account Lorentz transformations). Further we compute the distance between particles of pair as  $r = \sqrt{(\Delta X)^2 + (\Delta Y)^2 + (\Delta Z)^2}$ . The result is then written into the distance matrix.
3. We apply one of the clustering algorithms: DBSCAN, Compound Component Labeling, Hierarchical clustering with single, complete, average or median linkage\*. It clusterizes particles into clusters by distances. For hierarchical clustering hclust-cpp package [5] was used.
4. Similarly, in each of the clusters by distance, we calculate the difference between the velocities for each pair of particles, fill in the distance matrix in the velocity space, reapply the clustering algorithm (another one can be used), and obtain the set of subclusters of the parent particle cluster
5. Finally we have to interpret each subcluster as a separate nuclear fragment and associate a PID, momentum, energy, coordinate, mass of cluster with this fragment.

\*Single linkage:  $D(A,B) = \min \{ d(a,b) : a \in A, b \in B \}$ .

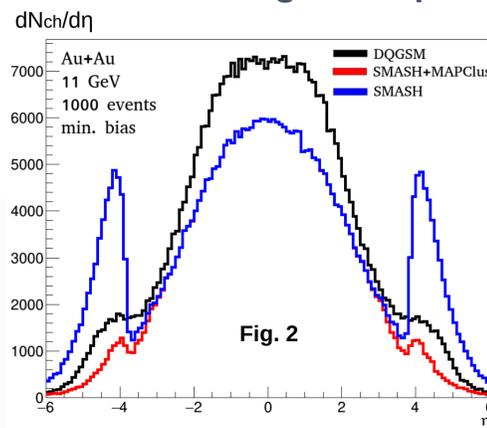
Complete linkage:  $D(A,B) = \max \{ d(a,b) : a \in A, b \in B \}$ .

Average linkage:  $D(A,B) = \frac{1}{|A| \cdot |B|} \sum_{a \in A} \sum_{b \in B} d(a,b)$ .

Median linkage:  $D(A,B) = \|c_s - c_t\|$  where  $c_s$  and  $c_t$  are the centroids of clusters s and t, respectively.

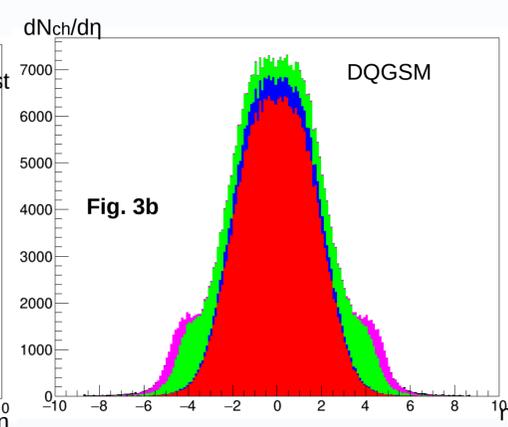
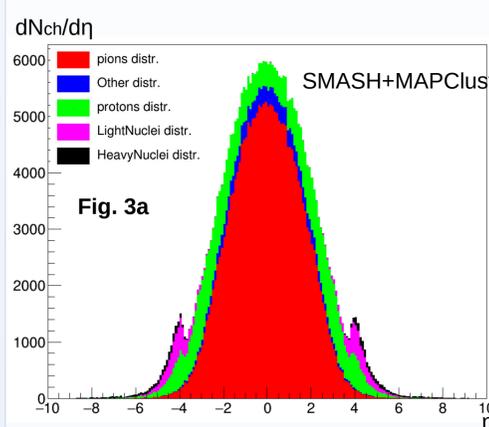
$D(A,B)$  is a distance between clusters A, B

## Algorithm performance results

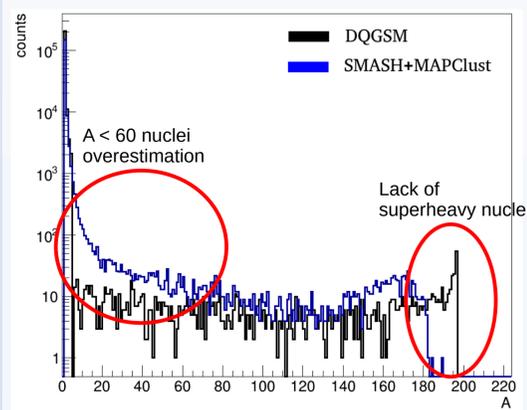


In the Fig. 2 the charged particles pseudorapidity distributions of DQGSM, SMASH and SMASH+MAPClust event generators are presented. It can be seen that the MAPClust usage allow us to decrease significantly the charged particles multiplicities in the region of high pseudorapidity down to the values, compatible to DQGSM results.

Used MAPClust parameters values:  
r\_max = 12; "Hclust\_Single"  
v\_max = 0.35; "Hclust\_Complete"



In the Fig. 3(a) and 3(b) structured pseudorapidity distributions for SMASH+MAPClust and DQGSM event generators respectively. We can see qualitative correspondence of the result of both generators – appearance of light nuclei ( $A < 5$ ) in the region of  $|\eta| > 3$ . Nevertheless, it seems like SMASH+MAPClust overestimates the number of heavy ( $A > 4$ ) nuclei. This can be caused by not very accurate parameters choice (such as r\_max and v\_max).



In the Fig. 4 the distribution of nuclear fragments for DQGSM and SMASH+MAPClust are presented. We can see the qualitative correspondence between the results. It can be noted, that SMASH+MAPClust overestimates the multiplicity of nuclei with atomic number  $A < 60$ , than it is in a good agreement with DQGSM in the interval  $60 > A > 180$ . Also we obtain the lack of superheavy nuclear fragments ( $A > 180$ ) in comparison with DQGSM. We hope to fix all this inconsistencies via more careful selection of parameters and clustering algorithms.

## Summary

We suggest MAPClust – the new kinematic approach for particle clusterization and nuclear fragments search in MC simulations of high energy nuclear collisions. Based on the idea of search of particle with close velocities and interpretation them as a nucleus, this algorithm was realized as C++ library [6], which can be implemented to the MC data.

The results show us that even such simple idea of nuclei recognition can provide us a good qualitative result in comparison with event generators, which have built-in fragmentation mechanism.

Nevertheless, there are some inconsistencies between the results of MAPClust appliance and generators with built-in fragmentation. We hope to reduce such inconsistencies by more accurate parameters and clustering algorithms selection in future.

## References

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3. J. Weil, V. Steinberg, J. Staudenmaier et al., Phys. Rev. C 94, no. 5., 054905 (2016).
4. S.A. Bass, M. Belkacem, M. Bleicher et al., Prog. Part. Nucl. Phys. 41, 225 (1998)
5. <https://github.com/cdalitz/hclust-cpp>
6. <https://github.com/vsandul/MAPClust>

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