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STUDY OF THERMAL EQUILIBRIUM IN HEAVY ION COLLISIONS VIA THE MA COINCIDENCE METHOD — TEST OF APPLICABILITY*

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The coincidence method of judging whether a system reached thermal equilibrium is shortly presented. It is used on the model data to test, whether it is applicable in the low-relativistic energy range. Also, the cuts corresponding to real detectors are introduced and their influence is briefly discussed.

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1. Introduction

The thermal models have been very successfully deployed in describing the results of heavy-ion collisions. These models assume that thermal equilibrium is reached during the collision and describe the spectra of reaction products using thermodynamical concepts of temperature and chemical potential, and have been used to describe single-particle spectra in the large range of beam energies.

On the other hand the question whether the thermal equilibrium has been indeed reached is not yet answered. One should bear in mind that the number of particles inside a nuclear system is relatively small (more then 20 orders of magnitude smaller then Avogadro's number), and the time of the collision is very short (about 10^{-22} s).

So far, the main test of the equilibration was the comparison of inclusive particle spectra and production cross-sections with the predictions of thermal models. There is, however, another method. It was proposed by Białas, Czyż and Wosiek [1], and is based on coincidence idea of Ma [2].

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In this work the applicability of coincidence method to the heavy-ion collisions in the energy range of SIS accelerator (projectile kinetic energy of around 1 A GeV) is investigated. An influence of the limitations imposed by the existing detector systems — limited phase space coverage, limited statistics, and limited detection capabilities — is also discussed.

2. The method

This is the brief outline of the arguments presented in [1]. It should be remembered, that those arguments are based on the assumption, that the system can be described by a microcanonical ensemble. This may be true if all the products are identified and registered, but may certainly be called into question if this is not the case.

One may define thermal equilibrium as a macrostate, that consists of the largest number of microstates (or configurations). Within this macrostate, there is equal probability of finding each configuration.

If the number of microstates within the macrostate is denoted by Γ, each microstate is equally probable, and p denotes the probability of finding any given microstate (configuration), p is equal to:

$$p = \frac{1}{\Gamma}\,.$$

Now, let us probe the equilibrated macrostate and measure N microstates constituting it. If p is small ($Np \ll 1$), then the probability of finding the same microstate twice is equal to p^2. So, the probability of finding identical microstates should be

$$P_i = \sum_{\text{all states}} (p^2) = \Gamma \times (p^2) = p = \frac{1}{\Gamma}\,.$$

If the number of participants and energy put into the system is constant and the thermodynamical equilibrium is assumed, one may treat every measured event as a configuration, probing the equilibrated macrostate. Thus the measured event represents a microstate. In addition one may estimate the probability P_i by noticing, that it is a probability, that two randomly selected events are identical (represent the same microstate).

So, if N configurations (events) are measured, and N_2 coincidences (pairs of identical events) are found, it may be concluded that

$$p = P_i = \frac{N_2}{\frac{1}{2}N(N-1)}\,,$$

and, therefore,

$$\Gamma = \frac{\frac{1}{2}N(N-1)}{N_2}\,.$$

Now, one is left with the question how to define "identical" events. One way to do it is to divide the phase-space into a lattice (with each cell having the volume σ), and "quantify" the events. In such a case, if the total phase-space volume occupied by the macrostate is denoted by Ω, one obtains:

$$\Gamma = \frac{\Omega}{\sigma},$$

and therefore

$$\log(\Omega) + \log\left(\frac{1}{\sigma}\right) = \log\left(\frac{1}{2}N(N-1)\right) + \log\left(\frac{1}{N_2}\right).$$

So, if the system is in equilibrium one may expect a linear dependence of $\log(N_2)$ on $\log(\sigma)$,

$$\log(N_2) = a\log(\sigma) + b\,.$$

One should bear in mind two limitations: for large σ the assumption of small p breaks down (the extreme case is when every particle falls within one giant cell), for small σ the number N_2 is dominated by statistical fluctuations, and for very small σ the quantum correlations may influence the results.

3. The application of the method

Current experiments in relativistic heavy-ion physics impose limitations on any method used to analyse the data. As a rule the phase-space coverage is pretty limited, only selected class of products is registered (for instance charged baryons), and the number of analysed events is also far from infinite. So a model comparison is necessary to check, whether those limitations permit the method to be used at all. As an approximate example the CDC detector [3], part of the FOPI spectrometer at SIS accelerator in GSI Darmstadt, was chosen.

"The data" were provided by the WIX code [4]. This is a relatively fast event maker that uses statistical principles and thermal equilibrium assumptions. It was used in a "single fireball" mode and was set to reproduce the super-central Ni + Ni collision at beam energy of 2 A GeV. Half of the available energy was put into collective mode (radial flow), the other half into thermal mode. Some 6×10^6 "events" were produced, this number being based on past FOPI experience (when 6–8×10^6 central events were registered during the run) and some technical limits imposed on the analysis.

The Ma method was applied to this "data". Several analyses were performed: with all the reaction products taken into account, and then with only selected product categories. Following categories were used: charged products, free protons, and charged pions. In an additional analysis the angular cut was used in order to introduce the distortions related to limited coverage of momentum space by the detector. It corresponded to the angular range covered by the CDC detector.

The initial single-particle momentum "cell" size was set to $(4\,\mathrm{GeV}/c)^3$ (p_x, p_y, p_z between -2 and $2\,\mathrm{GeV}/c$), and in subsequent steps it was reduced by a factor of 2^3. The coincidence analysis was performed in the centre-of-mass system.

As discussed in [1], real events should be divided into classes according to the multiplicity of produced particles, and the method should applied to every multiplicity class separately. If all the particles are taken into account, the event multiplicity varies from 92 to 139 (with 6×10^6 events those boundaries roughly correspond to distances of $\pm 5\sigma$ from the mean), and the relative multiplicity spread rises with each cut applied. In this study there was no attempt to split the data into multiplicity classes.

4. Results

All the results are presented on the single figure. Full symbols denote result without angular cut, open symbols — with CDC angular cut. Stars denote all products, circles — charged products, squares — free protons and triangles — charged pions.

By examining this plot one can conclude, that with the "full data" the method does not produce any meaningful results (only one point). It may be due to the complexity of the data (many product types) and perhaps the statistics (6 million events) was insufficient. This is also the case if a wide class of products (like all charged particles) is taken into account.

If the class of analysed products is smaller (like unbound protons or charged pions) one may argue that the points seem to approximately follow a straight line. Given, however, that the results are on doubly logarithmic scale, it can also be argued, that this may be not a real effect.

Introducing momentum cuts that correspond to the existing detector, clearly distorts the results, but (in the case of protons up to 1 $(\mathrm{GeV}/c)^3$) perhaps not that much. The quality of straight-line fit seems to be quite similar as in the case of no momentum cut.

The "charged pions in CDC" are unusable for the coincidence analysis. It should be noted, that in this case the event multiplicity is relatively small, thus making multiplicity fluctuations large. The smaller-bin results are probably dominated by events with multiplicity zero and one.

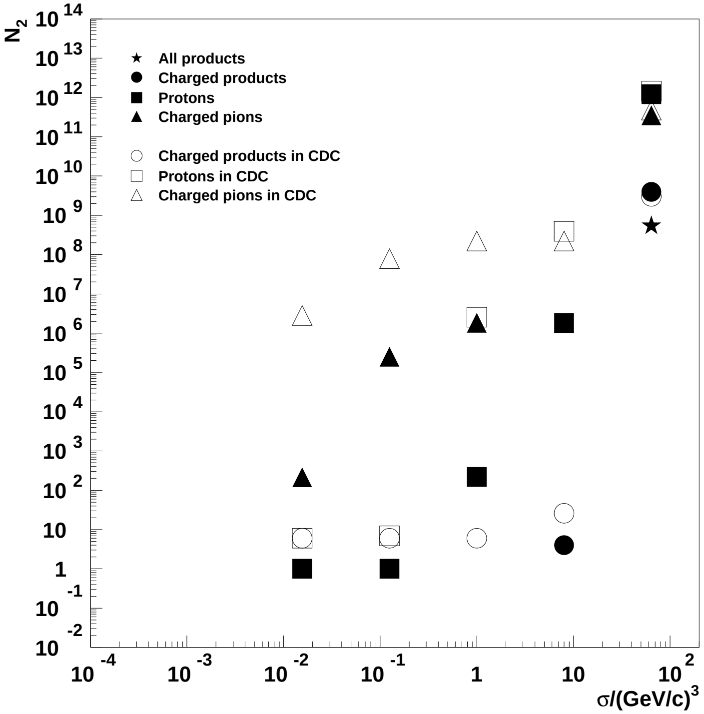

Fig. 1. Results of the coincidence analysis. Number of pairs of "identical" events is shown as a function of the size of "identity cell".

5. Conclusions and outlook

It appears, that the application of Ma method in the low-relativistic energy range is quite difficult. Large range of reaction products make coincidences very rare, and this effect, combined with limited statistics, makes identical events to disappear for any stricter identity criteria (any smaller size of "identity cell").

On the other hand, it seems to be possible to use the coincidence method in the ways not envisaged by its authors, namely for limited product class in perhaps limited phase space. One condition certainly has to be met — such products must be quite abundant, and the phase space limits must be wide, so that the results are not dominated by small multiplicity events. This way of proceeding has to be checked carefully, preferably both by model-testing and by theoretical considerations.

Short term tests may include comparing the results presented here with an analysis applied to the data produced by a slightly modified model. The currently used model includes some collective motion, so one may argue the results are not purely thermal. There is an analysis going on to check, whether the "turning off" those collectivities will produce better results.

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