

Diploma Thesis
Coulomb enhancement of correlated
 $\pi^+\pi^-$ pairs
DIRAC Experiment, CERN

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Spring 2000

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CM-P00080984

Thesis-2000-Schutz

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Abstract

The DIRAC Experiment measures the lifetime τ of a $\pi^+ - \pi^-$ bound state called $A_{2\pi}$ (Pionium) with an intended accuracy of 10%. This quantity enables to determine a combination of S-wave scattering lengths for $\pi - \pi$ scattering within 5%, which is theoretically calculated with Chiral Perturbation Theory (CHPT) to be around $3.25 \cdot 10^{-15}$ s but has not yet been experimentally verified. The measurement of τ will therefore provide a crucial test of the nonperturbative region of QCD. This diploma thesis stresses on the analysis of early data taken in 1999 and illustrates the basic plots on time difference and relative momenta distributions.

Acknowledgements

I would like to thank Prof. L. Tauscher for letting me write this diploma thesis in his group at CERN and for the many good ideas and advises he gave me. I also appreciated the help of Silvia, Panos, Sotiris and the two Daniels very much. Without them I would never have finished my thesis. The last few months were very exciting and interesting for me and I will keep them in good memory.

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Chapter 1

Introduction

While the high-energy region of strongly interacting hadrons is being described by elementary perturbation theory ($\alpha_s \ll 1$) this doesn't hold for the low-energy region ($\alpha_s \approx 1$), where nonperturbative QCD has to be used. At present, low energy $\pi - \pi$ scattering is still an unresolved problem in the context of QCD. However the use of Chiral Perturbation Theory (CHPT) allows to predict the S-wave $\pi - \pi$ scattering lengths within 5 % [1]. These predictions have not yet been experimentally tested at such a level of accuracy. The DIRAC experiment aims to measure the lifetime τ of an exotic atom $A_{2\pi}$ (Pionium) which is being formed by $\pi^+\pi^-$ in its ground state by coulomb interaction. The lifetime τ is related to the isoscalar a_0 and the isotensor a_2 S-wave scattering lengths: $1/\tau = C |a_0 - a_2|^2$. The value of τ predicted by CHPT is $3.25 \cdot 10^{-15}$ s. In order to measure the scattering lengths within 5% the lifetime τ has to be measured within 10% precision.

$A_{2\pi}$ (Pionium) is produced in proton-nucleus (e.g. Ti) interaction at 24 GeV/c (CERN Proton Synchrotron). It decays into $\pi^0\pi^0$ or gets excited and breaks up through ionisation in the target into $\pi^+\pi^-$. In the case of a breakup, characteristic pion pairs, called 'atomic pairs' will emerge with low relative momentum ($q \leq 3\text{MeV}/c$) — the variable q denotes relative momenta of the 2 particles, whereas p denotes the absolute momenta in the lab system — in their centre of mass system, a small opening angle ($\theta \leq 3$ mrad) and nearly identical energies in the lab system.

A magnetic double arm spectrometer with a resolution on relative pair momentum of $q \sim 1\text{ MeV}/c$ will determine the number of 'atomic pairs'. The number of 'atomic pairs' — and hence the number of $A_{2\pi}$ — is correlated precisely with the appearance of free pion pairs with low relative momentum. Free pion pairs result directly from the nucleus - target interaction and are just an arbitrary $\pi^+\pi^-$ pair. For a given target material and thickness the ratio between observed 'atomic pairs' and produced $A_{2\pi}$ depends on the lifetime

τ in a unique way. For the optimum target the observation of $\sim 10^4$ ‘atomic pairs’ allows to measure τ within the desired 10% precision. To evaluate the exact number of ‘atomic pairs’ at very low q values (this is the region, where the $A_{2\pi}$ is dominant) it is necessary to subtract a background contribution of coulomb-correlated pion pairs and free $\pi^+\pi^-$ pairs. This will be obtained by extrapolating the shape of the accidental pair q distribution recorded at the region $q > 3$ MeV/c into the desired very low relative momentum region $q \leq 2$ MeV/c.

Chapter 2

Theoretical description

2.1 Motivation

The standard model of elementary particles incorporates our understanding of the strong and the electroweak interaction. While the electroweak interaction is described by the GWS / QED theories the strong part uses the Quantum Chromo Dynamics (QCD) a nonabelian gauge theory as its description. The QCD leads to two distinct features, the asymptotic freedom in the case of large momentum transfers ($\alpha_s \ll 1$) and color confinement for low momentum transfers ($\alpha_s \approx 1$). While the QCD has been successfully tested for high momentum transfer, the use of Chiral Perturbation Theory (CHPT) for the low momentum transfer region has still not been tested experimentally very precisely. One of the aim of the DIRAC experiment is a precise test of CHPT for low q 's within 5%.

2.2 Chiral Perturbation Theory

The low energy $\pi-\pi$ scattering is analysed in terms of S-wave $\pi-\pi$ scattering lengths $a_{0,2}$. Within the framework of CHPT the difference $\Delta = a_0 - a_2$ is connected with the lifetime τ of pionium as follows:

$$\frac{1}{\tau} = C |a_0 - a_2|^2 \quad (2.1)$$

Gall et al.[2] have calculated the pionium lifetime in the ground state $\tau = 3.25 \cdot 10^{-15}$ s with an accuracy of about 3%. Equation (2.1) allows to get a relative error of the scattering lengths difference: $\frac{\Delta(a_0-a_2)}{(a_0-a_2)} \approx 5\%$, if DIRAC measures the lifetime with a $\frac{\Delta\tau}{\tau} \approx 10\%$ error[3].

2.3 Experimental method

$A_{2\pi}$ breaks up into $\pi^+\pi^-$ with characteristic features which help to tag them. In the proton – nucleus interaction also free π^+ and π^- are produced. Therefore a $\pi^+\pi^-$ pair resulting from free pions will be referred to as ‘free pairs’. In an abundant production of π^+ and π^- mesons the coulomb interaction can form atomic $\pi^+\pi^-$ bound states. $\pi^+\pi^-$ resulting from these bound states will be called ‘coulomb pair’. If the relative momentum within such a bound state is very small in the centre of mass system (cms) ($q \sim 1$ MeV/c) and if the pions are much closer together than the Bohr radius (387 fm), also strong interaction between the two pions will play an important role. This state will be called ‘pionium’ or $A_{2\pi}$. Pionium will either decay still within the target into $\pi^0\pi^0$ or get excited and breaks up due to electromagnetic interaction into $\pi^+\pi^-$. These $\pi^+\pi^-$ pairs will be referred to as ‘atomic pairs’. The $A_{2\pi}$ dissociation $\pi^+\pi^-$ will be detected in a magnetic double arm spectrometer and provides characteristic features such as low relative momentum ($q < 3$ MeV/c) of the two pions, equal energy in the lab system and a very small opening angle ($\theta \leq 3$ mrad).

2.3.1 Production and cross section of atomic pairs

Pionium originates mainly from short-lived sources (ρ, ω, Δ) which are produced in interactions of 24 GeV/c protons with target nuclei (mainly Ti). In ref. [4] an equation for the cross section of $A_{2\pi}$ has been derived:

$$\frac{d\sigma_{A_{2\pi}}^n}{d\vec{p}_{A_{2\pi}}} = R |\Psi_n(0)|^2 \frac{d\sigma_{2\pi}}{d\vec{p}_1 d\vec{p}_2} \quad (2.2)$$

with $\vec{p}_1 = \vec{p}_2 = \frac{1}{2}\vec{p}_{A_{2\pi}}$ being the momentum of the single pions after breakup and R being a known factor. $\Psi_n(0)$ is the atomic wave function at the origin. The cross section $\frac{d\sigma_{2\pi}}{d\vec{p}_1 d\vec{p}_2}$ will be measured by the DIRAC experiment.

2.3.2 Cross section of coulomb pairs

The production cross section of ‘coulomb pairs’ with pion momenta $\vec{p}_1$ and $\vec{p}_2$ can be written as:

$$\frac{d\sigma_c}{d\vec{p}_1 d\vec{p}_2} = A_c(\beta) \frac{d\sigma_{2\pi}}{d\vec{p}_1 d\vec{p}_2} \quad (2.3)$$

where the index c denotes ‘coulomb pairs’ and A_c is the Coulomb factor [5] which can be calculated very precisely. $\frac{d\sigma_c}{d\vec{p}_1 d\vec{p}_2}$ also includes the cross section of the ‘atomic pairs’ $\frac{d\sigma_{A_{2\pi}}^n}{d\vec{p}_{A_{2\pi}}}$ from Equation (2.2).

2.3.3 Cross section of free pairs

The production cross section of ‘free pairs’ — sometimes also called non-coulomb pairs or accidentals — is obviously:

$$\frac{d\sigma_a}{d\vec{p}_1 d\vec{p}_2} = \frac{d\sigma}{d\vec{p}_1 d\vec{p}_2} - \frac{d\sigma_c}{d\vec{p}_1 d\vec{p}_2} \quad (2.4)$$

where the index a is a reminder for accidentals and $\frac{d\sigma}{d\vec{p}_1 d\vec{p}_2}$ is the total cross section.

2.3.4 q dependence for atomic, coulomb and free pairs

Since ‘free pairs’ do not coulomb interact the q dependence of ‘free pairs’ differs greatly from the q distribution of ‘coulomb pairs’ or ‘atomic pairs’ at $q \leq 10$ MeV/c and can be used to extract the ‘atomic pairs’ from the background. The q dependence for atomic, coulomb and free pairs is shown in Figure 2.1 (figure is taken from the proposal [1]). In order to extract the

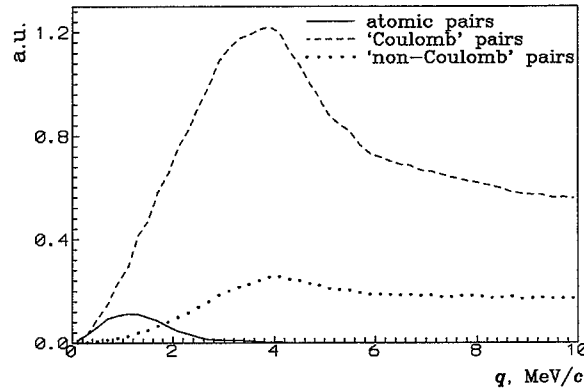


Figure 2.1: q dependence for atomic, coulomb and free pairs. The curves fall off for $q > 4$ MeV/c due to the cut on the transversal components of q : $q_x < 4$ MeV/c and $q_y < 3$ MeV/c.

signal — the ‘atomic pairs’ — the q distribution for $q > 3$ MeV/c — in this region are only ‘free pairs’ and ‘coulomb pairs’ — is used to extrapolate it into the very low q region ($q < 2$ MeV/c). By doing so the number of ‘free pairs’ and ‘coulomb pairs’ is known at low q ’s and the number of ‘atomic pairs’ can be extracted by subtracting the background from the data. Figure 2.1 shows how crucial it is to extrapolate the q distribution of the ‘free pairs’ and ‘coulomb pairs’ very precisely in order to find ‘atomic pairs’.

2.3.5 Pionium detection

$A_{2\pi}$ can be detected as $\pi^+\pi^-$ resulting from breakup by specific characteristics. $A_{2\pi}$ will either decay into $\pi^0\pi^0$ or break up into $\pi^+\pi^-$ still within the target due to coulomb interaction of $A_{2\pi}$ with target atoms. The $\pi^+\pi^-$ from breakup have characteristic kinematics, such as low relative momentum ($q < 3$ MeV/c) of the two oppositely charged pions, equal energy in the lab system and a very small opening angle ($\theta \leq 3$ mrad). They can therefore be detected and tagged in a double arm spectrometer, using a suitable tracking system.

2.3.6 Pionium lifetime measurement

The $A_{2\pi}$ -lifetime τ can be measured with two methods. Both methods use the breakup probability $P_{br}(A_{2\pi} \rightarrow \pi^+ + \pi^-)$ and the calculated function $P_{br}(\tau)$. The breakup probability P_{br} is defined by the dynamics of diatom interactions with the target matter and by its lifetime τ in the ground state. It is also a function of the target thickness and the atom momentum.

First method The first method uses the measured breakup probability P_{br} and the calculated dependence $P_{br}(\tau)$ to get τ assuming that the target thickness and atom momentum are fixed. Hence the measured $P_{br} = \frac{n_a}{N_a}$, where N_a is the number of produced and n_a the number of broken up pionium atoms, will give with $P_{br}(\tau)$ a final value for τ . The measurement of n_a is achieved by data analysis of the experimental $\pi^+\pi^-$ distribution. As mentioned earlier in subsection 2.3.4 the q distribution of the $\pi^+\pi^-$ in the region $q > 3$ MeV/c is fitted with a function obtained from experimental data and extrapolated into the very low q region $q < 2$ MeV/c. By subtracting the fitted function from the actual data in the very low q region, one will get the q distribution of the $\pi^+\pi^-$ resulting from $A_{2\pi}$ breakup and therefore the number of broken up atoms (n_a). N_a is strictly related to the number of free pairs with low q and is so determined. The exact method of extrapolation has been used in earlier experiments [6] and can be found in the proposal [1].

Second method The second method uses the different breakup probabilities P_{br} as a function of the target thickness. Thus by putting targets with different thickness in a row and observing the number of pairs, one can calculate τ .

Chapter 3

Experimental setup description

The experimental setup is designed to measure $\pi^+\pi^-$ pairs and to select 'atomic pairs' at low relative momentum with a resolution better than 1 MeV/c. After a calibration run at the end of 1998, DIRAC has been collecting data since summer 1999. An overview of the experimental setup can be seen in Figure 3.1 The experimental setup consists of various apparatus, which

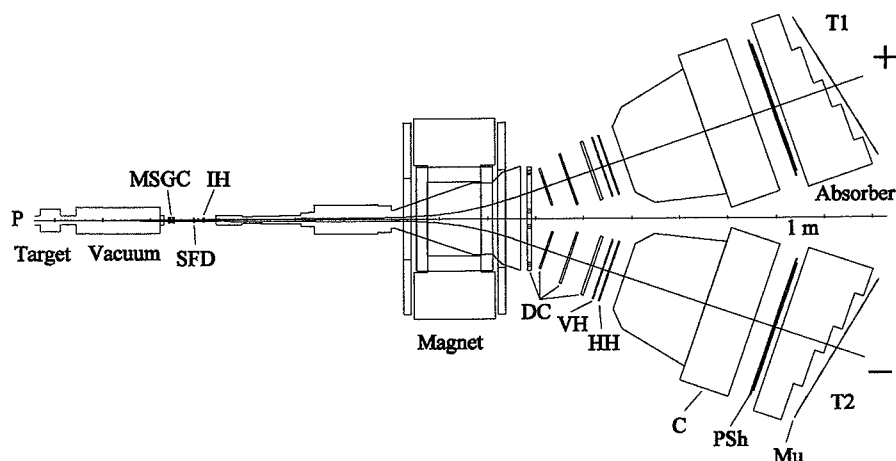


Figure 3.1: Experimental setup of the DIRAC experiment: P-proton beam, MSGC-microstrip gas chamber, SFD-scintillation fiber detector, IH-ionisation hodoscope, DC-drift chamber, VH-vertical hodoscope, HH-horizontal hodoscope, C-cherenkov detectors, PSh-preshower scintillation detector, Mu-muon counter.

will be described in the following section. In order to avoid most background in the detectors, the secondary particle channel is arranged at an angle of 3.5° with respect to the proton beam. The whole experimental setup has a relative pair momentum resolution of $q \leq 1 \text{ MeV}/c$.

3.1 Apparatus

Proton beam The experiment uses the extracted proton beam ZT1 in the east hall of CERN, which provides more than 10^{11} protons per 0.45 [s] long spill (slow PS extraction), at a momentum of 24 GeV/c.

Target While there are many possible target materials titanium (Ti) is the most suitable one. The advantages of titanium are a relatively large $A_{2\pi}$ production cross section and the number of needed $A_{2\pi}$'s in order to measure the lifetime τ within 10% is relatively small and constant for a wide range of τ 's. More information about different targets and their characteristics can be found in section 5.3, page 25 in the proposal [1]. During the first data taking period in 1999 also platinum (Pt) was used next to titanium (Ti).

MSGC The microstrip gas chamber (MSGC) just downstream of the target consists of 4 consecutive planes, each covering a sensitive area of $10 \times 10 \text{ cm}^2$ with a support thickness of $200 \mu\text{m}$. Each plane uses 512 channels. In order to be able to resolve multi-particle ambiguities, the detector planes are rotated at angles $0^\circ, 8^\circ, 82^\circ$ and 90° . The $90 \mu\text{m}$ wide chromium cathode strips are separated by $200 \mu\text{m}$. In between are the $10 \mu\text{m}$ anode strips. Figure 3.2 shows the geometry. This leads to a single hit space resolution of less than

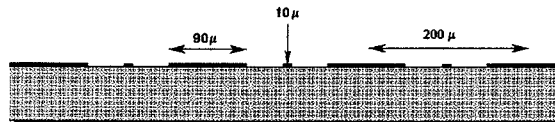


Figure 3.2: Geometry of the microstrip gas chamber (MSGC). The distance between cathode and anode is $50 \mu\text{m}$. This leads to a space resolution of $x \leq 50 \mu\text{m}$.

$50 \mu\text{m}$. The MSGC copes with two objectives in the detection of single points pertaining $\pi^+\pi^-$ track pairs: It has a high space resolution ($x \leq 50 \mu\text{m}$) and can operate in a very high rate environment ($\approx 10^7 \text{ Hz}$). It is mainly used for track reconstruction.

SFD The scintillation fiber detector (SFD) — sometimes also called SciFi — has 2 planes with 240 channels each. The fibre diameter is 0.5 mm. This leads to an effective thickness of 2.5 mm (5 layers $\times$ 0.5 mm) per plane. The dimensions of one plane are $\approx 10 \times 10 \text{ cm}^2$. The SFD is also being used for track reconstruction. The goal of the track reconstruction is to find out the opening angle of a $\pi^+\pi^-$ pair. The opening angle combined with the particle momenta leads directly to the relative momentum of the $\pi^+\pi^-$ pair. The SFD therefore has a good space resolution ($\approx 60\mu\text{m}$ for a single hit and $\approx 320\mu\text{m} \pm 60\mu\text{m}$ for a double hit) and can also operate at high rates. SciFi is used in trigger T2 see subsection 3.3.2.

IH The ionisation hodoscope IH or dE/dx consists of 2 planes with a geometry of $10 \times 10 \text{ cm}^2$ per plane. Each plane has 16 channels or strips. One strip has a width of 6 mm, a length of 10 cm and a thickness of 2 mm. dE/dx is used to measure the energy loss of incident particles. Since the $\pi^+\pi^-$ resulting from $A_{2\pi}$ breakup have small opening angle (see subsection 2.3.5) and therefore small relative distance, most pion pairs will be detected within the same strip (width of one strip is about equal to the upper limit of the average distance between to pions from $A_{2\pi}$. see [1], Figure 7.8 page 48.). Therefore the events of interest should be selected by the criterion of the double energy release in one single strip or in a pair of neighbour strips. The selection resulting from IH is used for level 2 trigger, see subsection 3.3.2.

Magnet The spectrometer magnet which is used has a bending power of 2.3 Tm. Downstream of the magnet the setup splits into two arms placed at $\pm 19^\circ$ relative to the central axis.

DC Each arm is equipped with 4 drift chambers (DC), the first one is common to both arms with 6 planes and 800 channels. Its geometry is $2160 \times 400 \text{ mm}^2$. DC(2) measures $800 \times 400 \text{ mm}^2$, has 2 planes and 120 channels. The third DC's dimensions are $1120 \times 400 \text{ mm}^2$ with 2 planes and 152 channels and DC(4) is $1280 \times 400 \text{ mm}^2$ with 4 planes and 336 channels. So the DC's 2 to 4 have altogether 8 planes and 608 channels per arm. The gas mixture of the DC's is Ar [49%] + $i\text{C}_4\text{H}_{10}$ [49.5%] + $\text{C}_2\text{H}_5\text{OH}$ [1%] + H_2O [0.5%]. The whole drift chamber system is used for track reconstruction of charged particles and has a space resolution of $x \leq 200\mu\text{m}$.

VH In each arm there is one vertical hodoscope (VH) plane with 18 channels and a geometry of $400 \times 1300 \text{ mm}^2$. The plane is subdivided in 18 slabs

($400 \times 72.3 \text{ mm}^2$) with a thickness of 20 mm. The used material is plastic. The vertical hodoscope together with the horizontal hodoscope (see next paragraph) is used to perform the fast coincidence between the two spectrometer arms for the first level trigger. The VH also helps to measure low q_t and q_x events which are used together with $d\epsilon/dx$ at the third level trigger T3 and neuronal trigger DNA (see subsection 3.3.3) to select and sort out multitrack events.

HH The horizontal hodoscope (HH) plane in each arm consists of 16 channels ($1300 \times 25 \text{ mm}^2$) with a thickness of 25 mm. This leads to a total aperture of $1300 \times 400 \text{ mm}^2$. The HH is made of plastic scintillators. It will also be used for particle selection. High time resolution as well as good space resolution will enable the HH in both arms to reject most accidental coincidence between the two arms. Due to low relative momentum of the $\pi^+\pi^-$ in cms, the π^+ in the left arm and the π^- in the right arm resulting from $A_{2\pi}$ breakup are expected to have roughly the same vertical position and will arrive there almost at the same time. So only events with up to ± 2 slabs for a hit in HH_1 relative to a hit in HH_2 are accepted as good events (coplanarity selection). The time difference between the two hits in arm 1 and arm 2 is very small ($\Delta t \leq 1 \text{ ns}$). The selection of such events is done at the first level trigger (see subsection 3.3.1).

C The cherenkov counters (C) are gas cherenkov counters and are filled with 1 bar of N_2 . They have a aperture of $1500 \times 500 \text{ mm}^2$ which corresponds to an angular acceptance of $\pm 11^\circ$. Each cherenkov counter has 10 channels, is 3 meter long and is used to find out hits resulting from electrons. They can therefore also be used to calibrate the experimental setup with electrons. Since the cherenkov counters are the main detector to identify electrons in this setup, their efficiency is crucial to obtain a large electron rejection factor.

Psh If the cherenkov counters are not efficient enough to reject most of the electron, an additional preshower (Psh) is installed just after the cherenkov counters consisting of a Pb sheet of several radiation lengths followed by a plane of scintillation counters. The Psh's dimension is $2800 \times 750 \text{ mm}^2$. Each Psh has 8 channels or slabs with a geometry of $350 \times 750 \text{ mm}^2$ per slab. The slabs thickness are 10 mm for the outermost left and right counter and 25 mm for the other 6 counters. Since the Muon detectors are not implemented at the moment the Psh's are used also for Muon detection and are therefore used at the moment in trigger T0 and T1, see subsection 3.3.1 and 3.3.2.

Mu The muon counters (Mu) are scintillation counters placed just after the iron absorber to identify muons with 28 channels each. Each channel has a geometry of $120 \times 750 \text{ mm}^2$ and a thickness of 5mm. This leads to total dimensions of $3400 \times 750 \text{ mm}^2$. The muon counters will be in operation during the first run of 2000.

3.2 Rate estimates

The rates have been estimated using the LUND-model and GEANT simulations, assuming a Ti-target of $175 \mu\text{m}$ thickness. The number of inelastic interaction per proton is about 10^{-3} . Roughly 3% of all proton-interactions will lead to charged particles entering the magnet. The setup downstream of the magnet is expected to detect about 50% of them. Also including the background these number go up by a factor of two. this leads to roughly estimated rate of $4 \cdot 10^{-5}$ oppositely charged and detected pions. The number of $\pi^+\pi^-$ from $A_{2\pi}$ breakup accepted by the apparatus is $2.5 \cdot 10^{-9}$ per proton interaction. This will eventually lead with 10^{11} protons per spill to 250 detectable ‘atomic pairs’ per spill. These rates show that a powerful trigger system is required in order to achieve the necessary rate reductions.

3.3 Trigger

In order to achieve such a powerful rate reduction needed, there are 4 different triggers installed. While trigger 1, 2 and 3 simply compare measured values with given restrictions, the DNA-trigger — being a neuronal network — can enhance its selection by learning. More details about the exact mode of operation of DNA can be found in [7]. For the runs recorded in 1999 T2 was active all the time, T3 during the last two months and DNA during the last two weeks.

3.3.1 Level 1

Trigger T1 uses the detectors downstream of the magnet. It looks for coincidences in both arms with hits in VH, HH, Psh and no hits in C. This should eliminate most e^+e^- and $\mu^+\mu^-$ pairs and accidental hits in one arm. In addition it also checks for coplanarity (the difference of the slab numbers in HH_1 and HH_2 is ≤ 2). The resolution time of coincidence is chosen to be 20 ns in order to get enough accidental pion pairs to simulate the free pion pair distribution. T1 can be written as (x denotes hit, $\bar{x}$ no hit, $\cdot$ is AND, $\wedge$

is OR) :

$$T1 = (VH \cdot HH \cdot \bar{C} \cdot Psh)_1 \cdot (VH \cdot HH \cdot \bar{C} \cdot Psh)_2$$

3.3.2 Level 2

Trigger T2 works with the upstream detectors SciFi and de/dx. It selects particles with small relative distances (SciFi) of $x \leq 9$ mm or an energy loss (de/dx) corresponding to the expected energy loss of two pions (about 0.5 MeV per pion). Figure 7.9, page 50 in the proposal [1] demonstrates the energy loss distribution of the pions. To be accepted the two hits have to come from within one single or two adjacent strips of IH. T2 is initiated by a fast preliminary trigger

$$T0 = [(VH \cdot Psh)_1 \cdot (VH \cdot Psh)_2] \cdot IH$$

So

$$T2 = T0 \cdot (IH \wedge SciFi)$$

3.3.3 Level 3

T3 applies a cut to the relative momentum of a pair (q_x, q_l) by using the patterns of VH_1, VH_2 and IH. Since the $\pi^+\pi^-$ from $A_{2\pi}$ have almost equal momenta p in the lab system, their hits in VH_1 and VH_2 are correlated. Looking for allowed combination of VH hits with de/dx hits will generate the T3 selection. In the runs last year, T3 did not trigger at the beginning, but its decision were recorded. It began triggering in October 1999.

3.3.4 DNA

In addition to T3 the Basel group developed and installed a fast first level trigger bundled with a neuronal network (DNA), which was previously used for CPLEAR and is also in use for L3 [7]. The network is presented with the hit maps from the de/dx and VH in order to select interesting pion pairs. The exact mode of operation can be found in [7].

3.3.5 Trigger comparison and efficiency

Figure 3.3 shows the effect of T3 and DNA in comparison with T2. It is clearly visible that T3 and DNA select more events with smaller relative momenta ($q_{total} \leq 60$ MeV/c) and lesser events with bigger relative momenta ($q_{total} > 60$ MeV/c) as T2. The efficiency defined as number of events passing

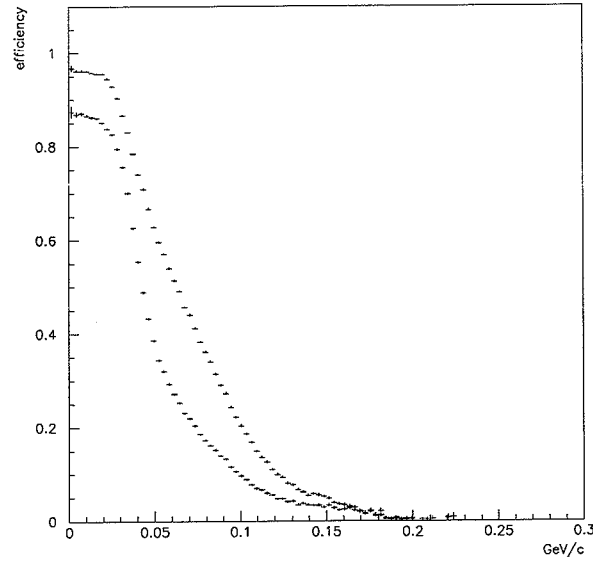


Figure 3.3: Trigger comparison: T3/T2 (black) and DNA/T2 (red) for total relative momentum q_{total} in GeV/c.

T3 or DNA compared to T2 is $96.9 \pm 0.7 \%$ for T3 and $87.5 \pm 1 \%$ for DNA for very small q_{total} events. For $q_{total} \geq 15$ MeV/c the efficiency decreases pretty fast. So most events with higher q_{total} are rejected. Using T3 and DNA would therefore increase the good events and decrease the accidentals compared to T2. The rejection factor¹ for T2 / T3 is 1.89 and for T2 / DNA it is 3.85.

¹Details about the calculation of the errors can be found in A.3

Chapter 4

Data analysis

This chapter describes my actual work for DIRAC. It is data analysis from the data taken in 1999. The triggers being used were T1 and T2, but T3 decision have been recorded and DNA can be simulated. It is therefore T2 data. As a target, Ni has been used. The sample consists of about 10^7 events. The aim of this data taking was calibration of individual detectors and tuning of the track reconstruction algorithm. But also characteristic features of important variables like δt or q were investigated and are presented hereafter.

4.1 Motivation

The motivation of my work is to find the desired fit function $f(x)$ which describes the coulomb enhancement for ‘coulomb pairs’ in the low q_{total} region with respect to accidentals. $f(x)$ can then be used to extrapolate the q distribution from high q values ($q \geq 3$ MeV/c) into the very low q region ($q \leq 2$ MeV/c).

4.2 Time difference

The time difference δt is defined as the time between a hit in the VH in arm 1 and VH in arm 2 and can be used for cuts to separate the ‘atomic pairs’ from background. There are two arms after the magnet (see figure 3.1), arm 1 has the negative particles, arm 2 the positive particles. A hit in a slab in VH_2 will open a time window of ± 20 ns in VH_1 . Figure 4.1 shows the time distributions of VH_1 and VH_2 relative to some arbitrary starting point. The mode ‘All events’ means that all events with at least one hit in each arm are considered. The ‘Goodpair’ mode selects from ‘All events’ only such events with one track in each arm. ‘Multiplicity 1 only’ additionally selects only

pairs with hit multiplicity 1 on VH_1 and VH_2 . A clear peak in arm 2 can

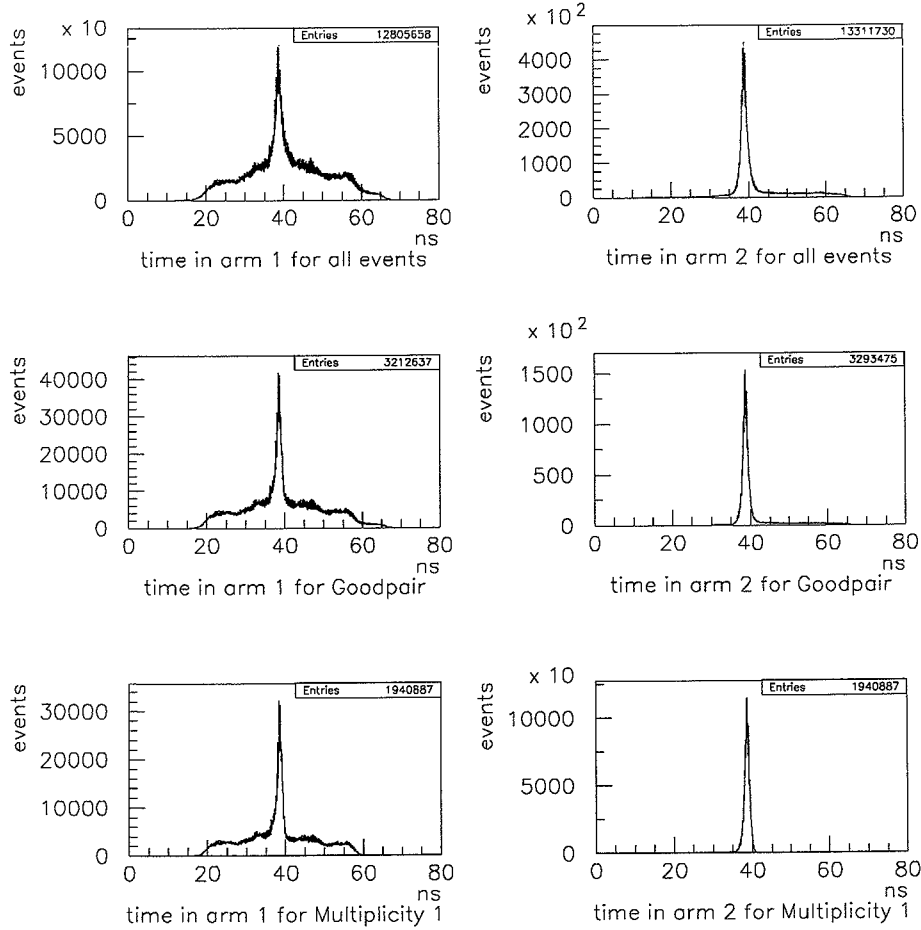


Figure 4.1: Absolute time of VH_1 and VH_2 for the three modes: 'All events', 'Goodpair' and 'Multiplicity 1 only'.

be seen as expected. There are no tails for 'Multiplicity 1 only'. From the number of entries one can also see the rate reduction by applying 'Goodpair' ($\approx 4 : 1$) and 'Multiplicity 1 only' ($\approx 7 : 1$). Subtracting now one arm from the other will give δt :

$$\delta t = t_2 - t_1$$

In order to use a very clean sample the mode 'Multiplicity 1 only' will be used from now on. Figure 4.2 illustrates the time difference δt . A peak of correlated pion pairs can be seen around $\delta t \approx 0 \pm 1$ ns above a background from

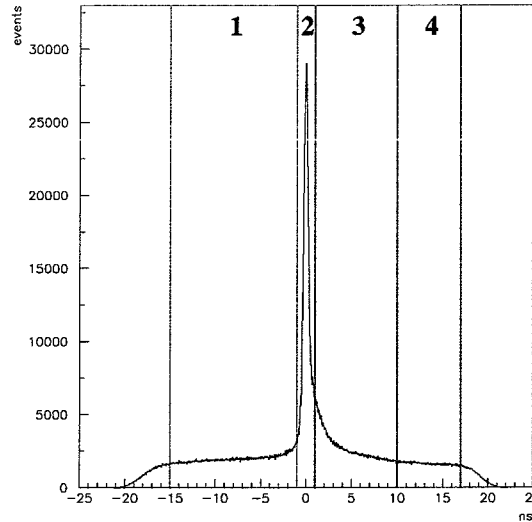


Figure 4.2: Time difference δt for mode ‘Multiplicity 1 only’ with 4 defined regions.

accidental hits. The width of the time difference resulting from correlated pair events yields the time resolution of the vertical hodoscope ($\delta t \approx 0.5$ ns). The asymmetry on the right end of the peak results from protons. Most of these protons come directly from the beam. A small percentage also results from Λ decay: $\Lambda \rightarrow p + \pi^-$. More details about the Λ 's can be found in section 4.4. The discrimination between $\pi^+\pi^-$ and $p\pi^-$ can be done by applying a cut on $p < 4.0$ GeV/c. This can be seen in figure 4.3 where the momentum in the lab system is plotted against the time difference δt for particles in arm 2. The structure on the right side of the histogram 4.3 results from protons and can be explained as follows: for low energy ($1.3 \leq p_{lab} \leq 3$ GeV/c) the proton mass ($0.93827 \text{ GeV}/c^2 \pm 0.28 \cdot 10^{-6} \text{ GeV}/c^2$ [8]) is the dominant factor in the $p\pi^-$ total energy. Hence the protons are slow and will arrive later at VH_2 than the π^- at VH_1 . At higher energies ($p_{lab} > 4$ GeV/c) the proton mass doesn't have such an influence on the total energy. Therefore the protons and π^- have about equal velocities and the time difference should be small. Figure 4.2 also defines a ‘natural’ way to select time difference regions. As a convention, I give the regions numbers: for $(-15 < \delta t < -1)$ region 1 – accidentals left, for $(-1 < \delta t < 1)$ region 2 – correlated pairs, for $(1 < \delta t < 10)$ region 3 – protons, and for $(10 < \delta t < 17)$ region 4 – accidentals right.

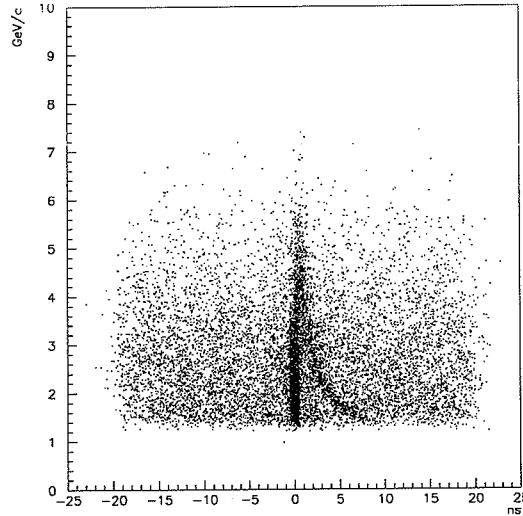


Figure 4.3: Momentum of positive particles in the lab system as a function of time difference δt in mode ‘Multiplicity 1’.

4.3 q distributions for the four time difference regions

This section explains the exact definition of the different $\vec{q}$ values and investigates their intrinsic characteristic. The definitions of the different $\vec{q}$ values is somehow arbitrary. The q variable denotes the relative momentum of one pair from one event on a predefined axis. These pairs will be mostly $\pi^+\pi^-$. But also $p\pi^-$ is possible. The direction of the beam is defined to be the z -axis. Its q value is named q_{long} . The q_x direction is the second axis together with q_{long} , which span up the plane parallel to the earth surface. Figure 3.1 is a schematic representation of the experiment in the $q_{long} - q_x$ plane. q_y is perpendicular to this plane, it points “towards the sky”. q_{trans} is defined as:

$$q_{trans} = \sqrt{q_x^2 + q_y^2}$$

q_{total} finally is the total length of the $\vec{q}$ vector:

$$q_{total} = \sqrt{q_x^2 + q_y^2 + q_{long}^2}$$

The q distributions q_x , q_y , q_{long} , q_{trans} and q_{total} of the four regions defined in the previous section 4.2 have characteristic graphs which will be discussed

in the following. In order not to get protons into region 2 (see figure 4.3) a momentum cut of $p < 4.0$ GeV/c is applied to all data. Only data with ‘Multiplicity 1’ is used. Also the histograms for T2, T3 and DNA result from the same amount of processed events. The histograms can therefore be compared and the trigger efficiency for T3 and DNA can be seen. Graphs from all three trigger decisions are shown hereafter.

4.3.1 q_x distribution

Looking at the q_x distributions for the four δt regions for T2, T3 and DNA (figure 4.4) reveals an enhancement for small q_x values ($-10 \text{ MeV/c} < q_x < 10 \text{ MeV/c}$). This enhancement comes from SciFi, which selects only events with $x \leq 9$ mm. This leads to a higher acceptance of events with smaller relative momentum. The enhancement in region 2 is not only from SciFi but also from the coulomb enhancement due to ‘coulomb’ and ‘atomic’ pairs for low q_x values. DNA emphasises this enhancement better than T3. Looking at the ratios between region 2 / region 1 for all three triggers should reveal the coulomb enhancement. T2, T3 and DNA data look similar but their

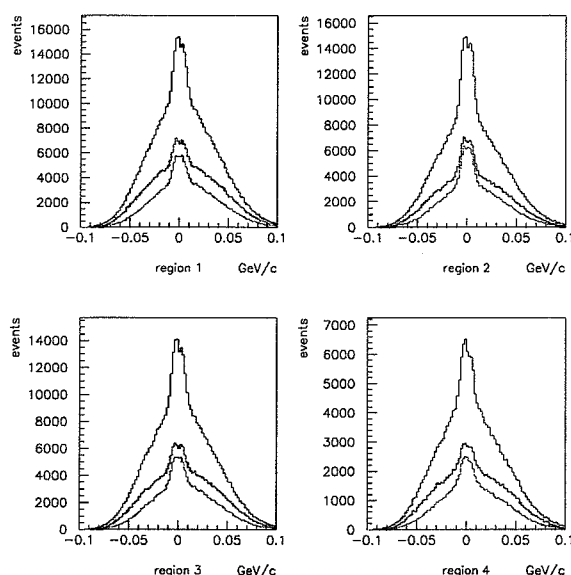


Figure 4.4: q_x distribution for the regions 1-4 with momentum cut $p < 4.0$ GeV/c for T2(black), T3(red) and DNA(green).

ratios with respect to region 1 differ slightly. Region 1 — the left accidentals — is used as the reference region. The other regions (2 to 4) are therefore

divided by region 1 after normalisation¹. Figures 4.5, 4.6 and 4.7 are the ratios relative to region 1 for T2, T3 and DNA data. The first histograms

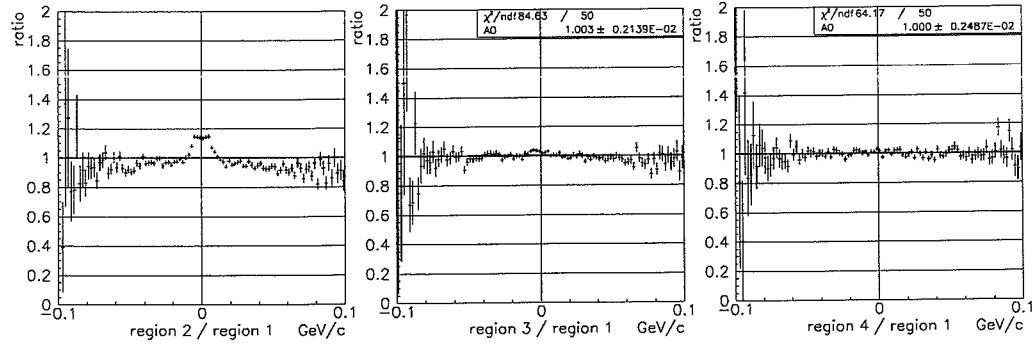


Figure 4.5: q_x ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T2.

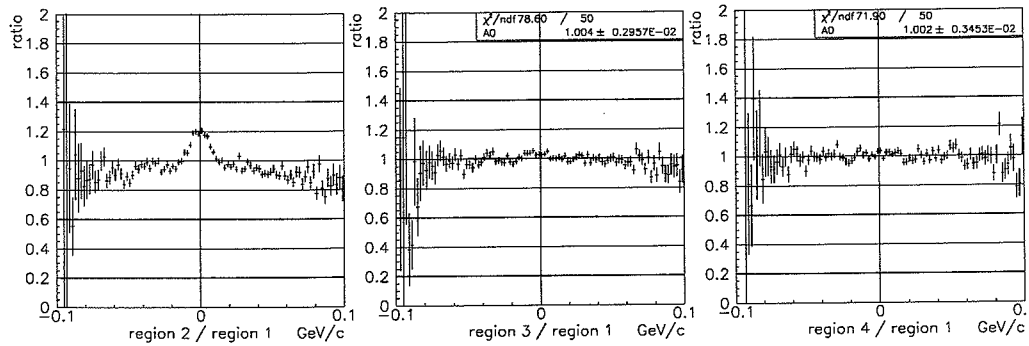


Figure 4.6: q_x ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T3.

in figures 4.5, 4.6 and 4.7 demonstrate neatly the coulomb enhancement due to correlated ‘coulomb’ and ‘atomic’ pairs. These pairs have smaller relative momenta and therefore an enhancement for low q values is expected (see subsection 2.3.4). Histograms 2 and 3 are perfectly flat. No enhancement at all can therefore be found in region 3 and region 4. This implies that for q_x also region 4 could be used as a reference and also that the protons in region 3 don’t influence the q_x greatly. The comparison of the coulomb enhancement of T2, T3 and DNA reveals as well a better trigger efficiency for T3 and DNA for small q_x .

¹see appendix A.2 and A.4 for correct normalisation and error calculation

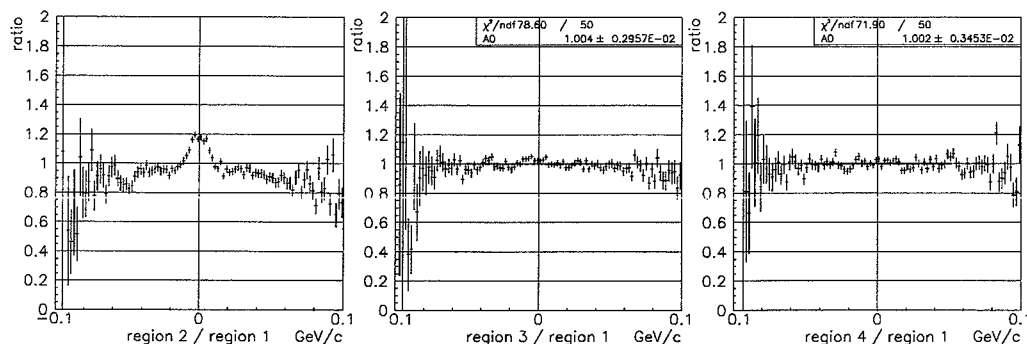


Figure 4.7: q_x ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for DNA.

4.3.2 q_y distribution

The four q_y regions in figure 4.8 look pretty much the same for all triggers and all regions. This implies that T2, T3 and DNA are insensitive to q_y . Most q_y values lie within 20 MeV/c around zero. So only in this section is good statistics available. The asymmetric part on the right half of the peak results from a mistake in the off-line track reconstruction and should be corrected in newer version of the track reconstruction algorithm. Hence it is completely artificial. Looking at the ratios (figures 4.9, 4.10 and 4.11) for the good statistics section reveals no big differences between the regions 1 to 4. For regions 3 and 4 the drop off starts at ± 18 MeV/c while for region 2 it starts at -15 MeV/c on the left side and $+12$ MeV/c on the right side. Therefore region 2 seems to have less events for $q_y \leq -15$ and $q_y \geq 12$ MeV/c.

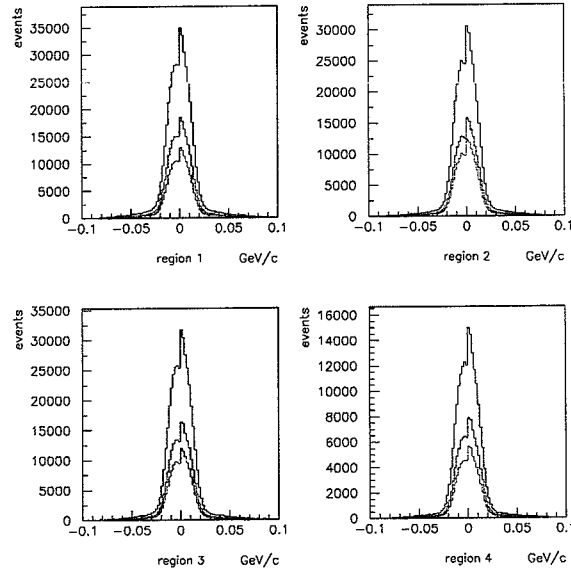


Figure 4.8: q_y distribution in GeV/c for the regions 1-4 with momentum cut $p < 4.0$ GeV/c for T2(black), T3(red) and DNA(green).

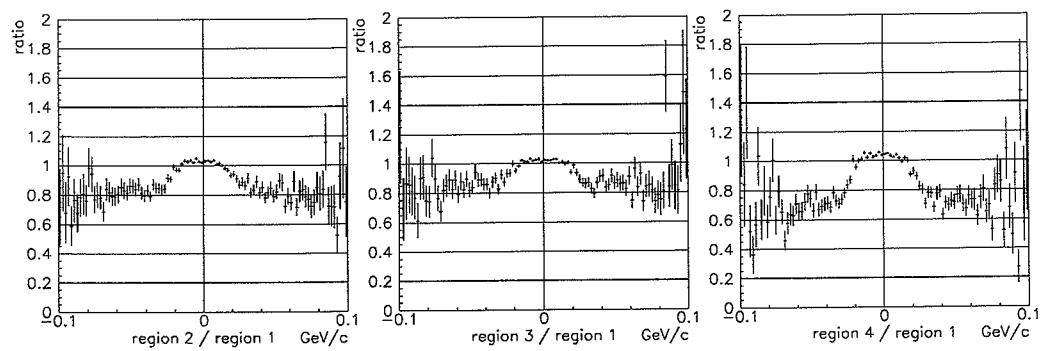


Figure 4.9: q_y ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T2.

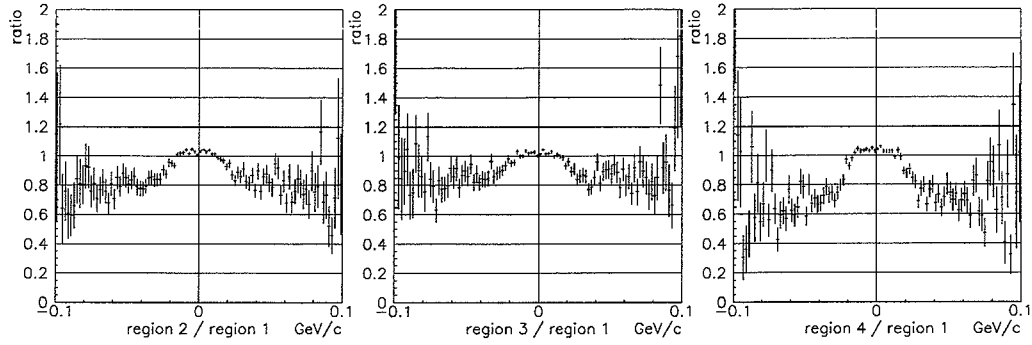


Figure 4.10: q_y ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T3.

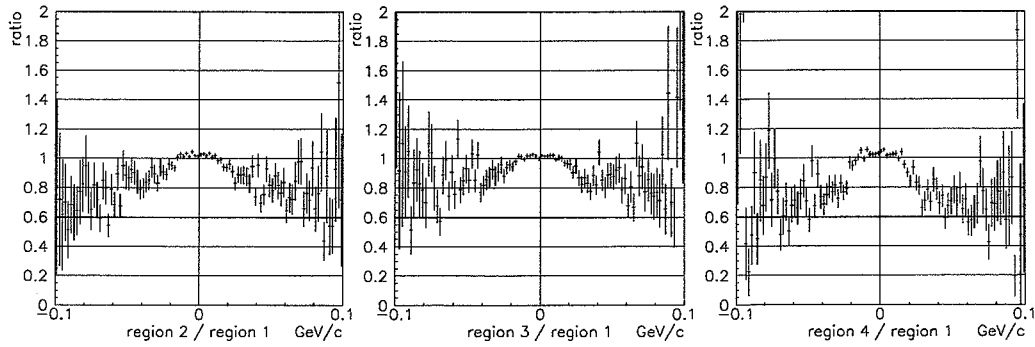


Figure 4.11: q_y ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for DNA.

4.3.3 q_{trans} distribution

The ratios resulting from divisions of the histograms in figure 4.12 for q_{trans} can be seen in the figures 4.16, 4.13, 4.14 and 4.15. Unlike the previous q

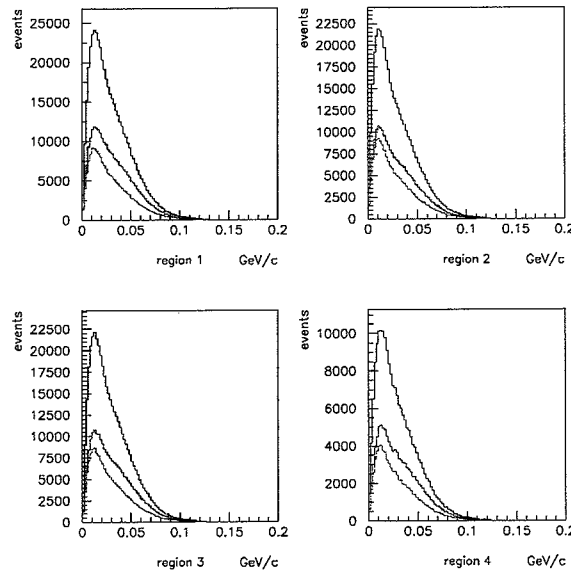


Figure 4.12: q_{trans} distribution in GeV/c for the regions 1-4 with momentum cut $p < 4.0$ GeV/c for T2(black), T3(red) and DNA(green).

distributions for q_{trans} region 1 and 4 are not identical anymore. A clear slope can be found for each trigger. Therefore region 1 was subdivided into 2 new regions: 1a (from $\delta t = -15$ ns to -10 ns) and 1b (from $\delta t = -10$ ns to -1 ns).

The ratio of 1a/1b is presented in histogram 4.16. It is perfectly flat and indicates that region 1 is slope independent. As a consequence only region 1 can be used as a reference. Region 4 shouldn't be used for ratio plots and had been left away for all q 's. Region 2 has more events with small q_{trans} up to $q_{trans} \leq 20$ MeV/c. T3 selects most small q_{trans} events, DNA and T2 a little less. See figure 4.17 for the trigger behaviour for small q_{trans} of T2, T3 and DNA.

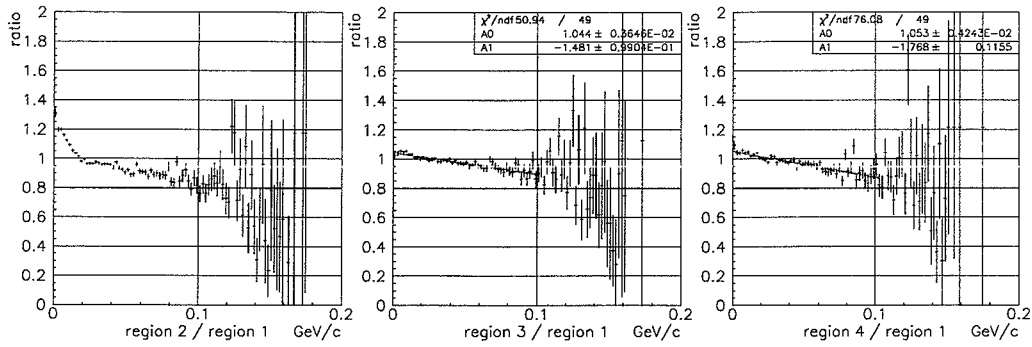


Figure 4.13: q_{trans} ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T2.

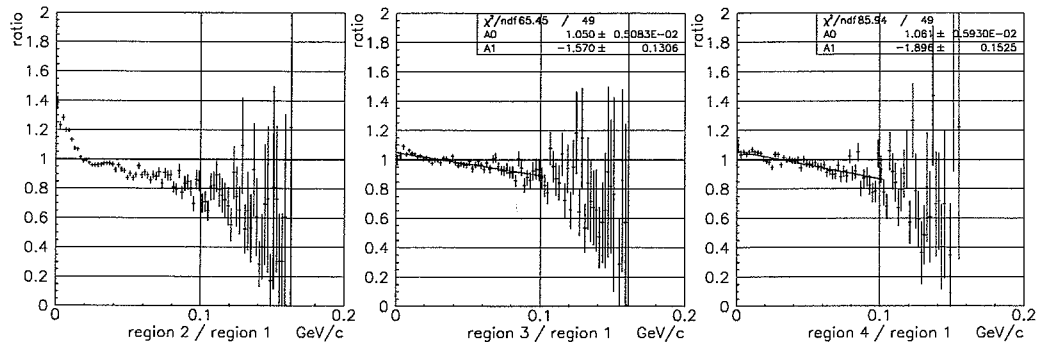


Figure 4.14: q_{trans} ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T3.

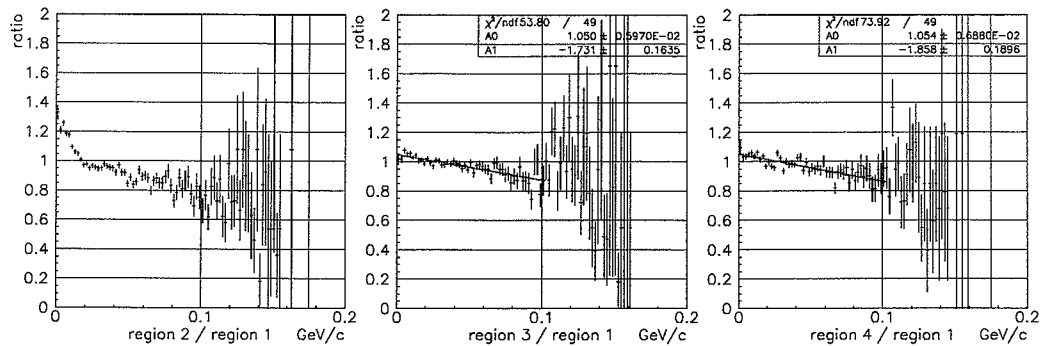


Figure 4.15: q_{trans} ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for DNA.

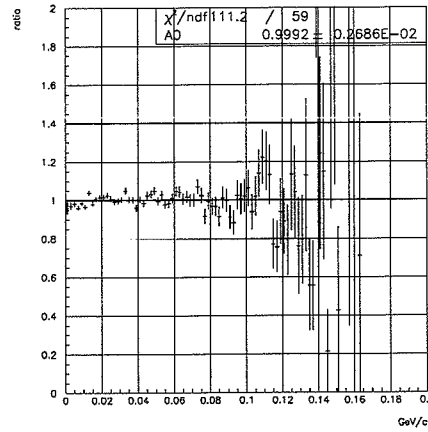


Figure 4.16: q_{trans} ratio in GeV/c for region 1a / region 1b with momentum cut $p < 4.0$ GeV/c for T2.

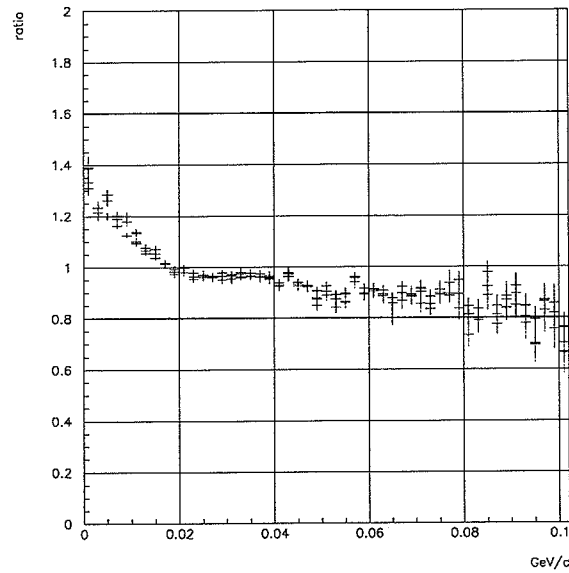


Figure 4.17: q_{trans} ratios in GeV/c for the region 2 / region 1 with momentum cut $p < 4.0$ GeV/c for T2(black), T3(red) and DNA(green).

4.3.4 q_{long} distribution

Figure 4.18 shows the effect of the triggers on q_{long} . The difference in the T2, T3 or DNA distributions is due to trigger selection. T3 and DNA cut off events with $q_{long} > 150$ MeV/c (T3) and $q_{long} > 125$ MeV/c (DNA). The enhancement region lies between $(-30 \text{ MeV/c} < q_{long} < 30 \text{ MeV/c})$ for region 2. The ratios in figures 4.19, 4.20 and 4.21 resulting from division of

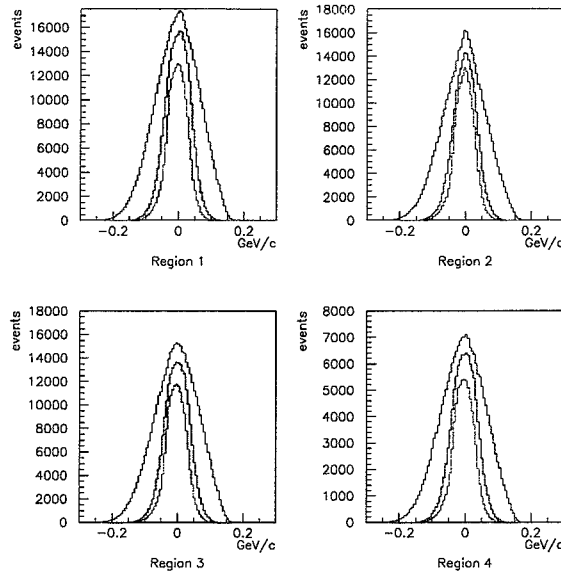


Figure 4.18: q_{long} distribution in GeV/c for the regions 1-4 with momentum cut $p < 4.0$ GeV/c for T2(black), T3(red) and DNA(green).

histograms in figure 4.18 reveal an interesting aspects: The signal region has a clear enhancement in low q_{long} values. Also for q_{long} the ratios between the regions 3 and 4 / region 1 are flat. This indicates that the regions 1, 3 and 4 are very similar with respect to q_{long} . A good impression of the coulomb enhancement in region 2 is given in figure 4.22. Here Region 2 (black) and region 1 (red) are normalised in the same histogram. The enhancement lies around $q_{long} \approx 0 \pm 15$ MeV/c and has up to 40% more events for the signal region. The cut on $q_{trans} \leq 4.0$ MeV/c has been applied to increase the fraction of low relative momentum pairs.

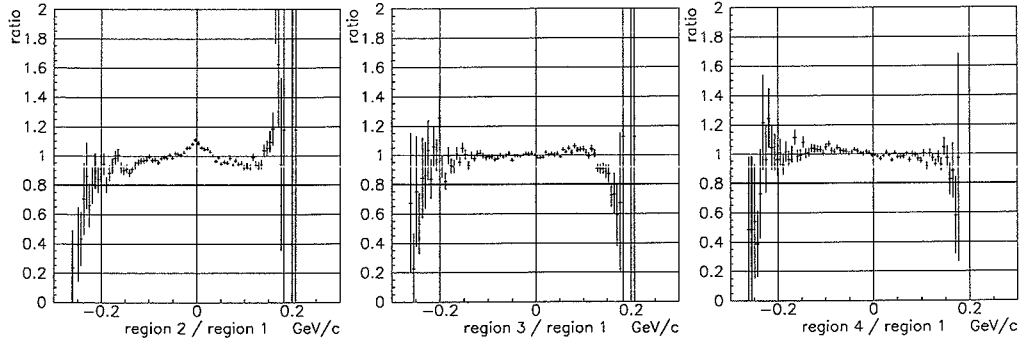


Figure 4.19: q_{long} ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T2.

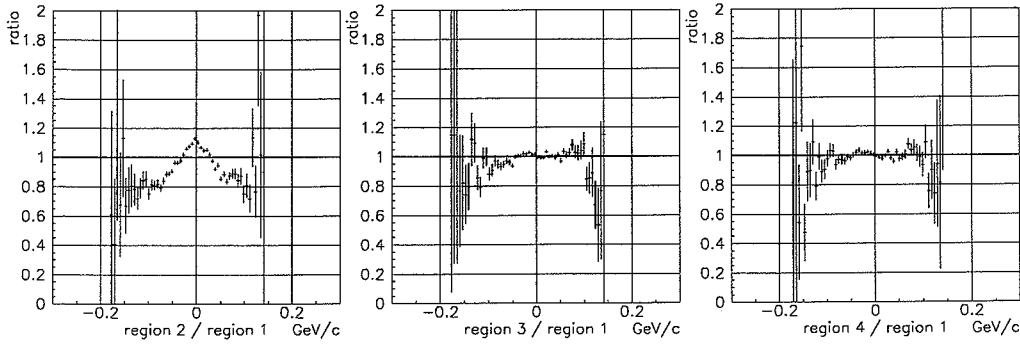


Figure 4.20: q_{long} ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T3.

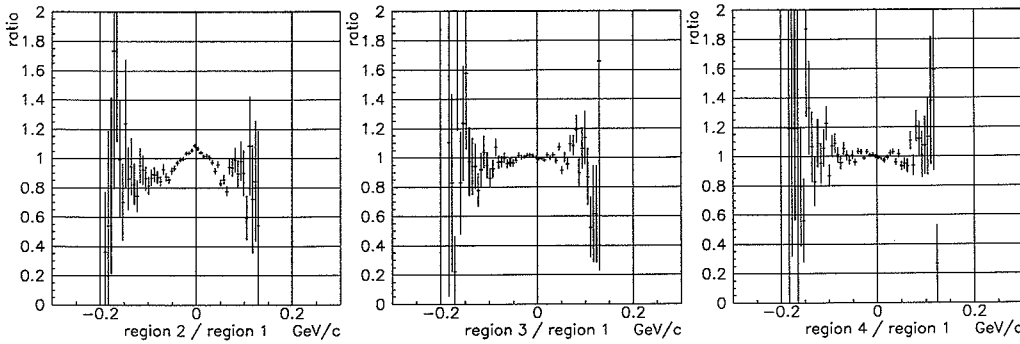


Figure 4.21: q_{long} ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for DNA.

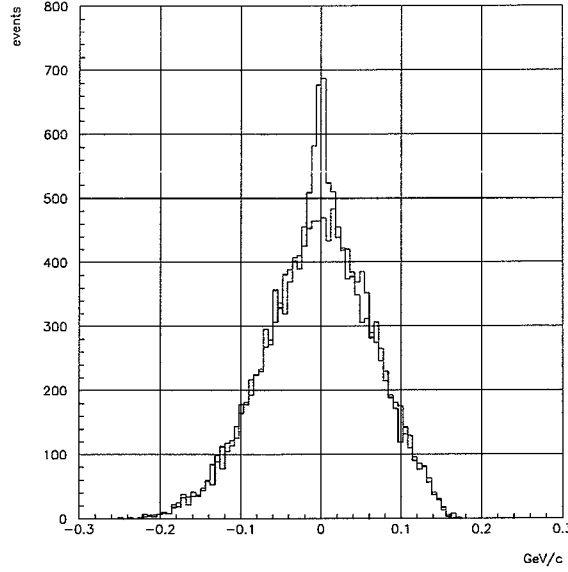


Figure 4.22: q_{long} distribution in GeV/c for $q_{trans} \leq 4.0$ MeV/c and $p < 4.0$ GeV/c. Region 1(red) and region 2(black).

4.3.5 q_{total} distribution

Figure 4.23 shows the q_{total} distributions for the four regions for T2, T3 and DNA. The trigger efficiency for low q_{total} is close to 1 while it drops sharply for higher q_{total} values as desired. The detailed comparison can be found in subsection 3.3.5. The ratios relative to region 1 are shown in figures 4.24, 4.25 and 4.26. In the first histograms of these figures a clear enhancement for small $q_{total} < 30$ MeV/c due to coulomb correlation of ‘coulomb’ and ‘atomic’ pairs is visible for all three triggers. The enhancement resulting from ‘atomic pairs’ is only existent in the region $q_{total} \leq 3$ MeV/c as indicated in figure 2.1. The total enhancement can be fitted with an arbitrary fit function. A good fit with 3 parameters can be achieved with the function:

$$f(x) = p_1 + p_2 \cdot e^{\frac{x}{p_3}} \quad (4.1)$$

where p_1 , p_2 and p_3 are fit parameters. Figure 4.27 illustrates a good fit for the coulomb enhancement for q_{total} . The function is fitted for the interval ($0 \text{ MeV/c} < q_{total} < 150 \text{ MeV/c}$). If the lower limit is taken to be 3 MeV/c, the fit doesn’t change at all. The fit parameters for the three triggers are shown in table 4.1.

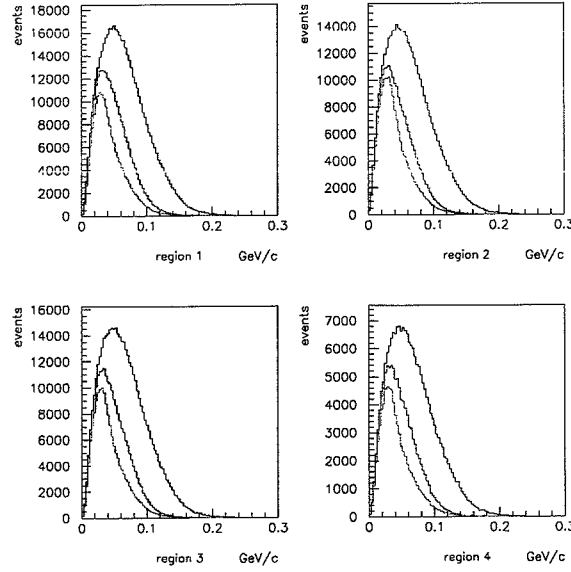


Figure 4.23: q_{total} distribution in GeV/c for the region 1-4 with momentum cut $p < 4.0$ GeV/c for T2(black), T3(red) and DNA(green).

Fit parameters

	T2	T3	DNA
p_1	$0.946 \pm 0.34 \cdot 10^{-2}$	$0.838 \pm 0.86 \cdot 10^{-2}$	$0.848 \pm 0.11 \cdot 10^{-1}$
p_2	$0.668 \pm 0.39 \cdot 10^{-1}$	$0.757 \pm 0.27 \cdot 10^{-1}$	$0.637 \pm 0.31 \cdot 10^{-1}$
p_3	$-0.0168 \pm 9.87 \cdot 10^{-4}$	$-0.0241 \pm 1.49 \cdot 10^{-3}$	$-0.0229 \pm 2.08 \cdot 10^{-3}$
χ^2	102.3/47	117.2/47	106.7/47

Table 4.1: Fit parameters for the fit function 4.1 for the three triggers T2, T3 and DNA.

The exact parametrisation is needed for the extrapolation of q_{total} into the very low q region, see also subsection 2.3.4. It will help to extract the 'atomic pairs' above background. Since the 'atomic pairs' occur only in the very low $q_{total} \leq 3$ MeV/c region (see figure 2.1) fitting the $\pi^+\pi^-$ q distribution for $q_{total} \geq 3$ MeV/c will include 'free pairs' and 'coulomb pairs' in the fit but no 'atomic pairs'. Thus the extrapolation of the approximation function to the region $q_{total} \leq 3$ MeV/c yields the number of 'atomic pairs' in the relative momentum interval.

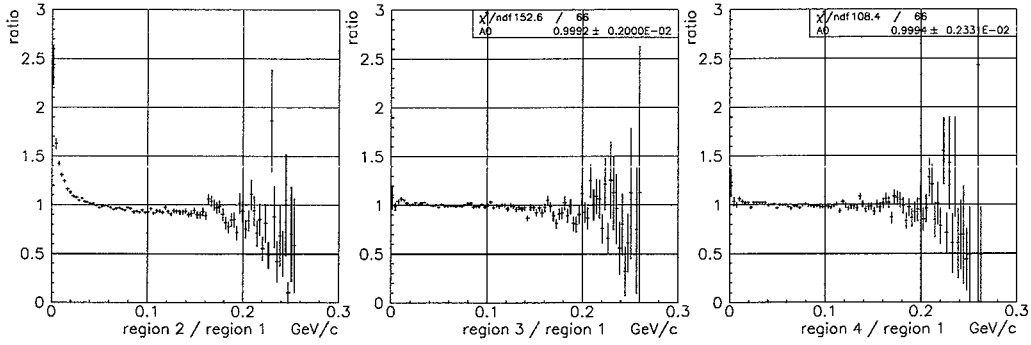


Figure 4.24: q_{total} ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T2.

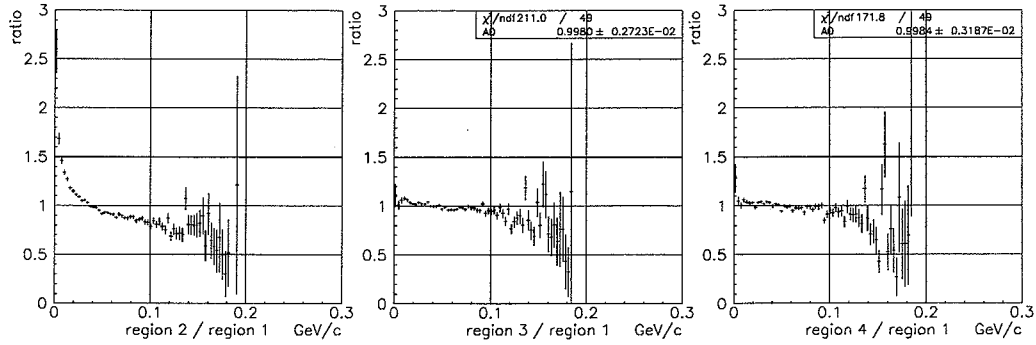


Figure 4.25: q_{total} ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for T3.

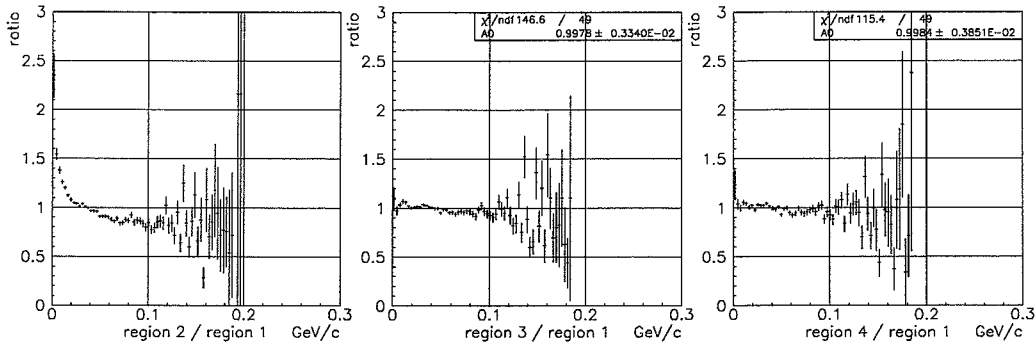


Figure 4.26: q_{total} ratios in GeV/c for the region 2-4 with region 1 with momentum cut $p < 4.0$ GeV/c for DNA.

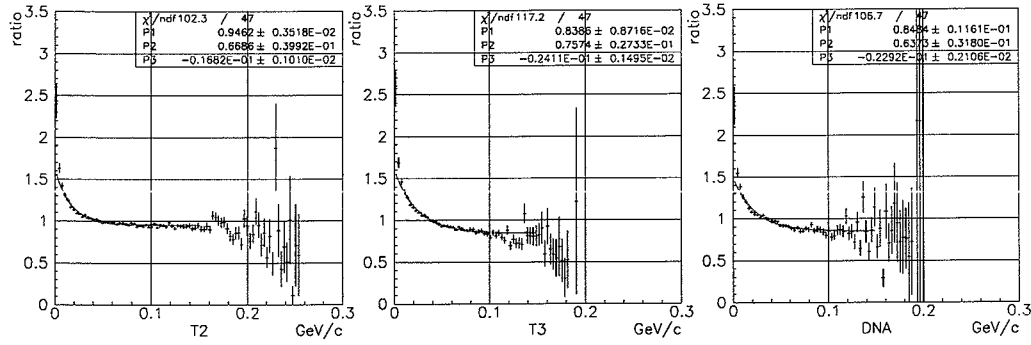


Figure 4.27: q_{total} ratios in GeV/c for region 2 / region 1 with momentum cut $p < 4.0$ GeV/c for T2, T3 and DNA. Fit function see equation 4.1.

4.3.6 Slopes in q distributions

As seen in subsection 4.3.3 region 1 and region 4 are not identical. This is surprising because both regions should be pure accidentals and therefore be equal. A closer look indicates that the problem lies within region 4 (see for example figure 4.16). Region 1 has therefore been used as a reference in all plots. It is also important to cut away the tails ($\delta t \leq -15$ ns and $\delta t \geq 17$ ns.) because they also produce slopes. This can be seen in figure 4.28. For the left tail the time difference region ($-25 < \delta t < -15$) has been used.

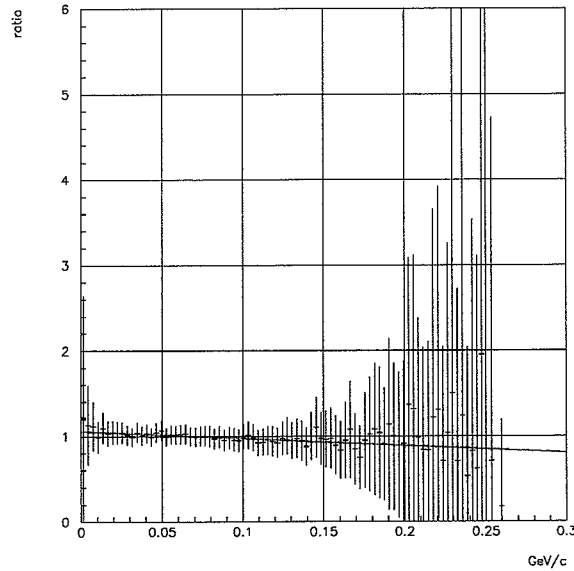


Figure 4.28: q_{total} ratio for left tail / region 1.

4.4 Λ peak

The proton – nucleus interaction in the target also produces Λ 's which decay: $\Lambda \rightarrow p + \pi^-$. This decay can be used to calibrate the apparatus. Figure 4.29 shows the invariant mass of $p\pi^-$. The protons were restricted to momenta larger than 3 GeV/c. A clear peak can be seen at 1115.64 ± 0.02083 MeV/c² with $\sigma = 0.801 \pm 0.0099$ MeV/c². The mass of Λ is 1115.683 ± 0.006 MeV/c² [8]. This demonstrates that the calibration of the apparatus is very accurate.

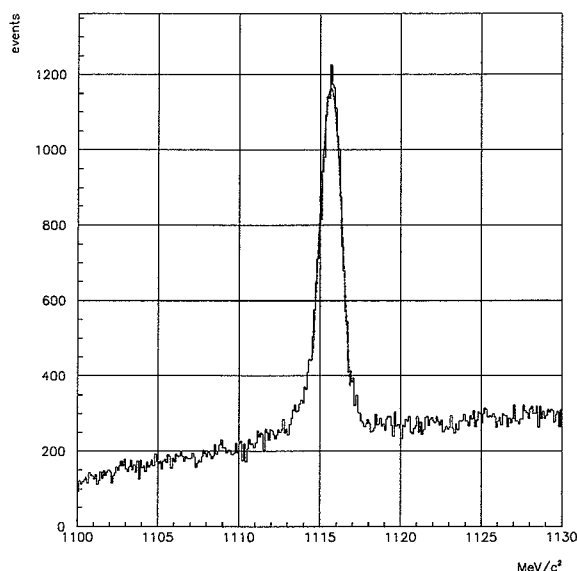


Figure 4.29: $p\pi^-$ invariant mass in MeV/c² with momentum restriction of $p_{proton} > 3$ GeV/c.

The data used to extract this peak was taken with a special Λ trigger. Figure 4.30 illustrates the total momenta distributions for the protons and π^- from within the Λ peak (1114 MeV/c² $< m_\Lambda < 1117$ MeV/c²). The protons have momenta around 5 GeV/c while the momenta of the corresponding π^- are distributed around 1.5 GeV/c. The relative time difference between the protons and pions is very small. So most Λ events are from region 2. The target material used was platinum (Pt).

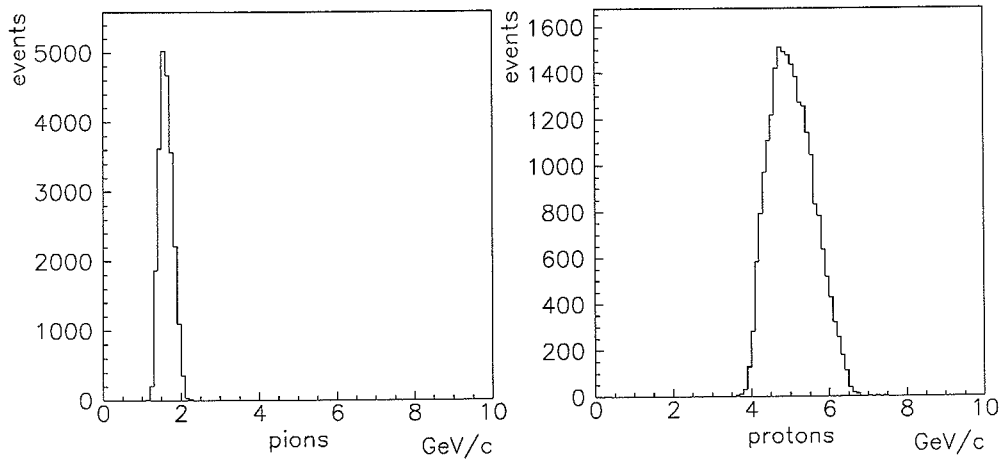


Figure 4.30: p_{lab} for the π^- and protons from within the Λ peak.

Chapter 5

Conclusion

The DIRAC setup is ready and since summer 1999 data is being taken. A first look at the data indicates a good performance of the apparatus and the triggers. DNA seems to work very good. Its trigger selection for good events is better than T3. The expected coulomb enhancement is clearly visible for q_x , q_{trans} , q_{long} and q_{total} . A first fit for the coulomb enhancement for $q_{total} < 150$ MeV/c was found and looks reasonable. The slopes in the q distribution are not fully understood. They can be avoided by taking the left accidentals as a reference. Therefore the right accidentals region for $\delta t \geq 10$ ns is not needed and the time window could be shifted by at least 10 ns: A hit in VH_2 would then open a time window on VH_1 of (-30 ns to +10 ns). The next run will start in may 2000 through October 2000 and will increase the statistics by many factors. This should result in a first significant sign from the 'atomic pairs'.

Appendix A

Statistics

Statistics plays a very important role for data analysis. All measured data is distributed around an expectation value with errors and standard deviations and therefore dealing with data always includes dealing with statistics. Also important is the law of error propagation if two or more distributions are mathematically connected together.

A.1 Mean value and error of distributions

Every distribution has its expectation value

$$\mu = \int x f(x) dx \quad (\text{A.1})$$

and variance

$$\sigma^2 = V(x) = E(x - \mu)^2 = \int (x - \mu)^2 f(x) dx \quad (\text{A.2})$$

$f(x)$ is the density function p.d.f. σ is the standard deviation or the error. Let's $F_1(x)$ be such a distribution. If $F_1(x)$ is used in a function, i.e. $y(F_1(x))$, then the mean value and the variance of $y(F_1(x))$ are given approximately (under the assumption that $(x_i - \mu_i)$ are small):

$$E[y(F_1(x))] \simeq y(\mu) \quad (\text{A.3})$$

$$V[y(F_1(x))] \simeq \sum_{i=1}^n \left(\frac{\delta y}{\delta x_i} \right)^2 \Big|_{x=\mu} V(x) \quad (\text{A.4})$$

where $V(x)$ is the variance of $F_1(x)$ Equation A.4 is known as the *law of error propagation*. It can be used if $F_1(x)$ and $F_2(x)$ are independent of each other.

A.2 Error propagation

By dividing two histograms the error of the resulting histogram has to be calculated with error propagation. To make differences between two q distribution visible, it is convenient to divide the two histograms after normalisation (see below). In order to calculate the resulting error, error propagation (see equation A.4) has to be used. Therefore, the error of $G(X) = \frac{F_1(X)}{F_2(X)}$ — where $F_1(X)$ is the distribution 1, $F_2(x)$ is the distribution 2 — can be calculated [9]:

$$\delta G(X)^2 = \left[\frac{dG(X)}{dF_1(X)} \right]^2 [\delta F_1(X)]^2 + \left[\frac{dG(X)}{dF_2(X)} \right]^2 [\delta F_2(X)]^2 \quad (\text{A.5})$$

$$\Rightarrow \delta G(X)^2 = \frac{1}{F_2(X)^4} \left[F_2(X)^2 [\delta F_1(X)]^2 + F_1(X)^2 [\delta F_2(X)]^2 \right] \quad (\text{A.6})$$

A.3 Calculation of efficiency and its error

If the two distributions are somehow connected this has to be taken in account. Let's suppose that $F_1(x)$ is the distribution of a variable x whereas $F_2(x)$ is the distribution of the same variable x but after applying an algorithm (a trigger for example). So the two distributions are connected: If N is the number of events of $F_1(x)$ and N_a is the number of events of $F_2(x)$ (these are the events which were accepted by the algorithm) then the number of rejected events by the algorithm is obviously $N_r = N - N_a$. The process of applying an algorithm is itself of binomial nature because either an event is accepted by the algorithm or it is not. If one is interested in the relative number of successful trials $\frac{r}{n}$ (r denotes the number of successful trials and n the total number of trials) then the mean and variance are given by:

$$E\left(\frac{r}{n}\right) = \frac{1}{n} E(r) = p \quad (\text{A.7})$$

$$V\left(\frac{r}{n}\right) = \left(\frac{1}{n}\right)^2 V(r) = \frac{p(1-p)}{n} \quad (\text{A.8})$$

p is the probability that a success occurs. In the case of applying a trigger, p becomes the efficiency ϵ of the trigger. So the error of applying a trigger can be calculated as follows [9]:

$$\sigma(\epsilon) = \sqrt{\frac{\epsilon(1-\epsilon)}{N}} \quad (\text{A.9})$$

A.4 Normalisation of histograms

For normalisation of one histogram with another histogram the first histogram is multiplied with the number of events from histogram 2 and is divided by its own number of events. A correct .kumac file for PAW can be found in the following section.

A.5 Histogram division: kumac file for PAW

```
macro 2histosdiv [1] [2] [3]
  vec/cr hist1(100)
  vec/cr hist2(100)
  vec/cr thist(100)
  vec/cr scaled(100)
  vec/cr scerror(100)
  vec/cr divi(100)
  vec/cr divier(100)
  h/get_vect/contents [1] hist1
  h/get_vect/contents [2] hist2
  sigma thist =sumv (hist2)/sumv(hist1)
  vec/oper/vscale hist1 thist(100) scaled
  sigma scerror=sqrt(hist1)*thist(100)
  vec/oper/vdivide scaled hist2 divi
  sigma divier = sqrt(hist2**(-4)*(hist2**2*scerror**2 + hist1**2*hist2))
  hi/cre/1DHISTO [3] 'normalised' 100 0.0 0.3 0.
  h/put_vect/contents [3] divi
  h/put_vect/errors [3] divier
  return
```

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