The Revised Neural Atomic trigger

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This note presents the proposed revised neural network trigger for the DIRAC experiment and its performance. It uses the vertical SciFi information in coincidence with the ionization hodoscope combined with the two vertical hodoscopes to select pion pairs with low Q.

1.0 Introduction

This report describes a revised neural network trigger for the DIRAC experiment. It is called the Revised Neural Atomic trigger (RNA). The system is based on a similar event selection algorithm as the one used by DNA[1]. It is using however the vertical Scintillating Fibres (SciFi) as the main detector upstream the DIRAC's magnet. The choice of using the SciFi detector was based on its high granularity (240 fibre columns instead of 16 IH slabs), its relatively low noise and its distance from the magnet. In addition the response time of the scintillating fibres is comparable to that of the hodoscopes, hence an on-line trigger decision can be obtained in a similar delay as for DNA. It is expected that RNA will give a trigger decision about 100 ns after T1. As in DNA the SciFi information is combined with the two vertical hodoscopes downstream (VHL and VHR). The aim of this trigger is to select pion pairs with low relative momentum (Q) from background. RNA shall be evaluating events already selected by DIRAC trigger levels 0 and 1. As in our previous studies we have concentrated our efforts on selecting interesting pion pairs out of two-track events only. It is clear however that all types of background would have to be efficiently rejected.

It should also be pointed out that there are vertical and horizontal scintillating fibres and therefore one could envisage to use them all for a further upgrade of the system.

2.0 Data samples

For the present study T1-copl-pipi data taken during May 2000 were used. A sample of approximately 2 million events with 1 track per arm was produced. It was eventually sub-divided in two distinct classes needed for the neural network development phase. Events that satisfied the following criteria:

1. For a detailed description of the DNA trigger system see: 'The Neural Network First Level Trigger For The DIRAC Experiment', P. Kokkas et al., submitted to Nucl. Instr. and Meth. A.

- Q along x-direction less than 3 MeV/c
- Q along y-direction less than 10 MeV/c
- Q along z-direction less than 10 MeV/c
- Time difference between the two particles arriving in the VHs less than 1 ns

were defined as the ones to be selected (called GOOD in what follows). Events not satisfying all the above criteria were considered background (called BAD events in what follows) and the neural network had to be tuned to reject them. The GOOD data sample had approximately 20000 events, hence the BAD data sample was also made of a similar size.

Separate events were used for the training and evaluation phase of neural network development in order to obtain a realistic estimation of the system's acceptance. For the estimation of the rate reduction possible with RNA the original T1-copl-pipi data sample was used.

3.0 Data format and event selection

Given that there may be several hits in any of the detectors used by the RNA trigger, the same strategy as for DNA has been followed in order to have always similar patterns presented to the neural network (which has a fixed architecture). Each of the three detectors used (SciFi and VH) is treated in a well defined way.

Since there may many hits in the SciFi hit-map, RNA uses only the pair of hits which are closer together. These are the hits that most probably correspond to the two charged pions of a pionic atom and hence have to be further evaluated. In case there is only 1 hit it is considered that there are two charged particles passing through the same virtual slab. Therefore as the RNA NN requires two hits, the same hit is send to the NN twice. For each hit used, its position is transformed to a binary 8 bit number. Counting starts from 1 for convenience. These two binary numbers formed are always presented to the neural network in ascending order. If there are more than 5 hits the event is not considered for the neural network development phase and in real-time it is directly accepted.

The vertical hodoscopes may have 1 or 2 hits each. Hence RNA forms the 4 possible combinations with one hit in each hodoscope. Again for each pair of hits the position of each hit is transformed to a binary number. As the vertical hodoscopes have 18 slabs each, each position in a hodoscope is represented by a 5 bit binary number. Counting starts from 1 up to 18. Similarly as above if there are more hits in any VH again the event is not considered for the neural network development phase and in real-time it is directly accepted.

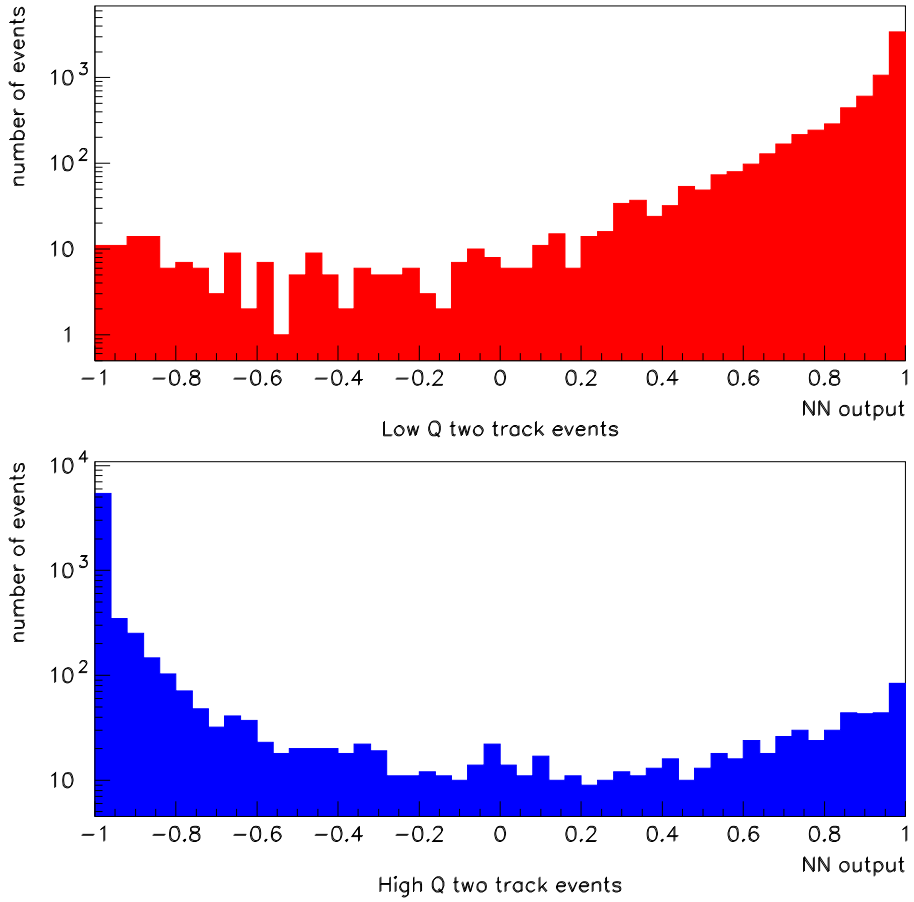
Each pair of VH positions together with the two virtual SciFi hits described above, are presented to an independent neural network unit. The total number of input bits per neural network is $2 \times 8 + 2 \times 5 = 26$. Given the number of possible combination of pairs of hits in the vertical hodoscopes, 4 separate neural network units are used which run all the same algorithm.

An event is eventually selected as good if any of the networks used with valid hits gives an answer above threshold. If there are not enough hits in the VH to form the maximum on the four possible pair combinations, only the networks that have a non-empty input pattern are considered for the event selection.

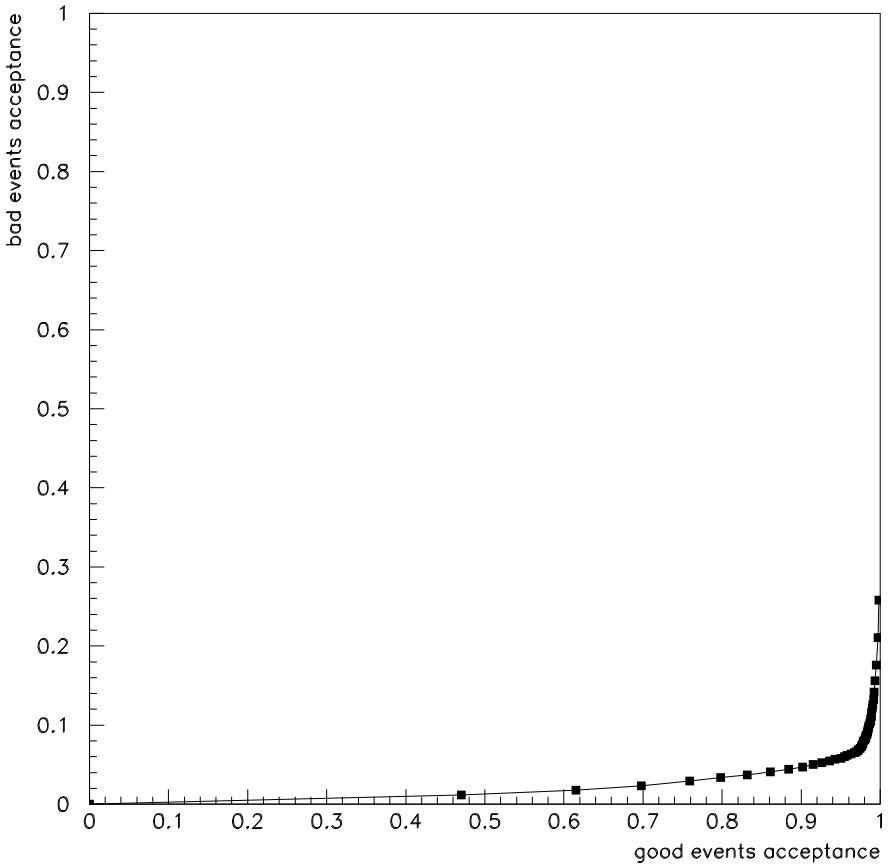
4.0 Neural Network training

As for DNA we have used a feed-forward neural network with a single hidden layer consisting of only two neurons. This architecture corresponds to the already existing hardware and hence on-line implementation is straight-forward. We have used a 'tanh' activation function (instead of the standard 'logistic' one). Hence the value of the output unit of the NN is in the range between -1 and 1. During the learning phase the NN was forced to answer 1 for good events and -1 for bad ones. For learning 10000 GOOD and 10000 BAD examples were used. After training for 800

epochs (an epoch being a weight update after the presentation of the full learning data set) the following distributions of the value of the output unit were obtained:



The neural network selection performance can be seen better in the following figure. as all events with an output value above a given threshold should be considered as good, the selection's efficiency for GOOD and BAD events is a function of the value of this threshold. The following plot shows the efficiency for GOOD events versus the one for BAD events for each value of the neural network threshold.



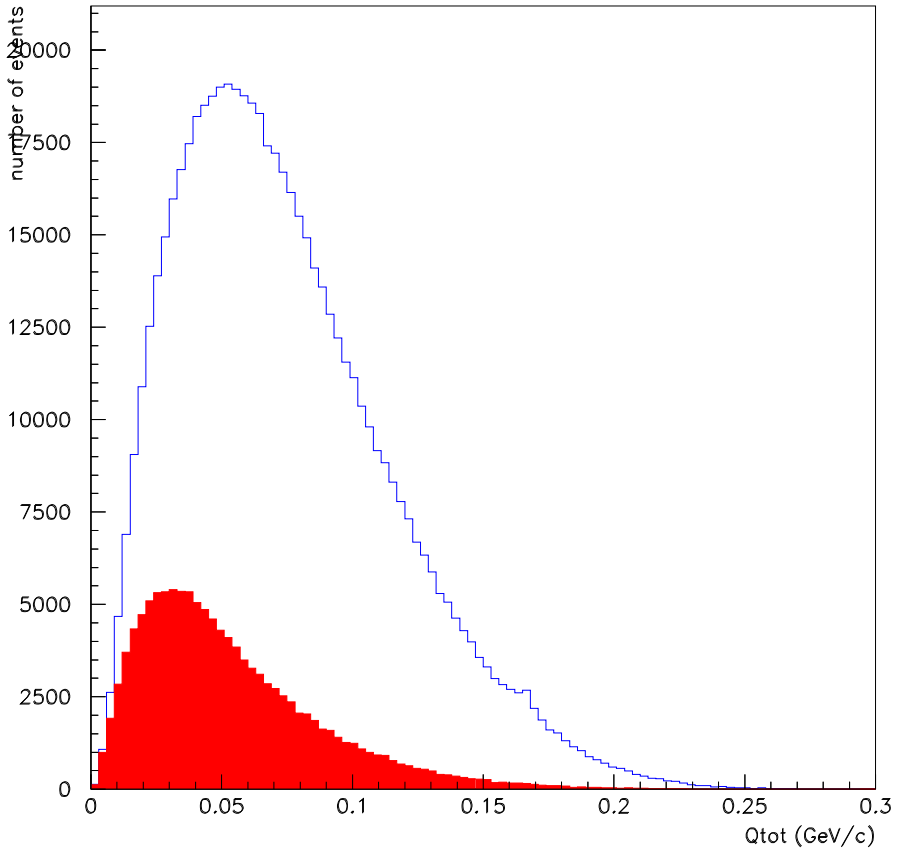
5.0 Selection performance

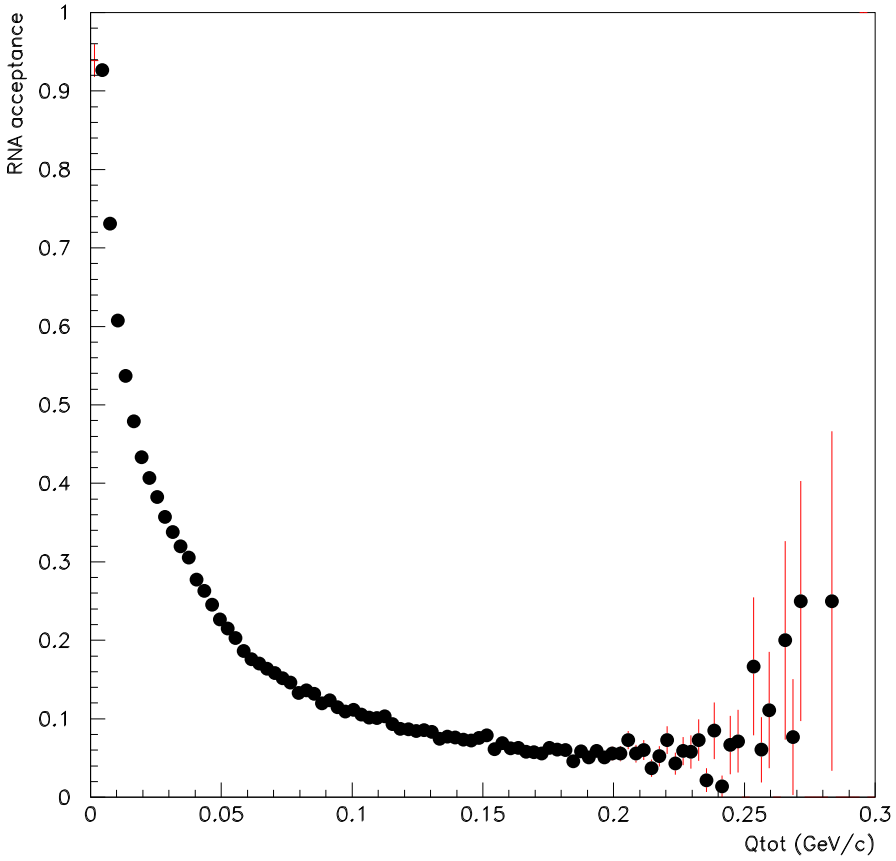
For a neural network threshold value of 0.0 (i.e. when selecting events if there is one out of the four networks with an output value greater than 0.0) the selection performance of the system is the following:

- acceptance of low Q two-track events: 97%,
- acceptance for T1-copl-pipi data: 24% (i.e. rate reduction of 4.2).

The last number was obtained using the original available T1-copl-pipi data sample.

What is of equal importance is the RNA acceptance as a function of Q, since this should be high and flat for low Q events. The next figure shows the total Q distribution of all the events analysed superimposed to the one of the events selected by RNA. The ratio of the two distributions is shown in the figure that follows.



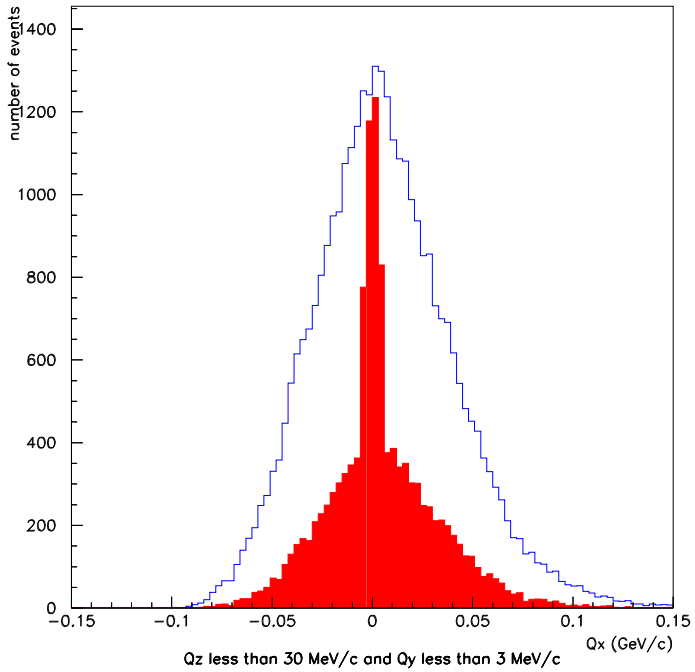


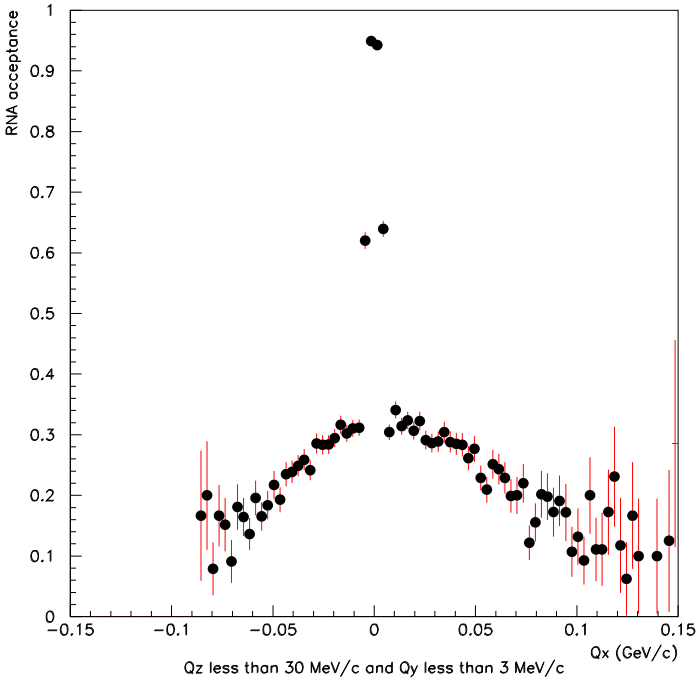
The next few figures show the spectra of all T1 events and the RNA superimposed as well as the RNA acceptance as a function of:

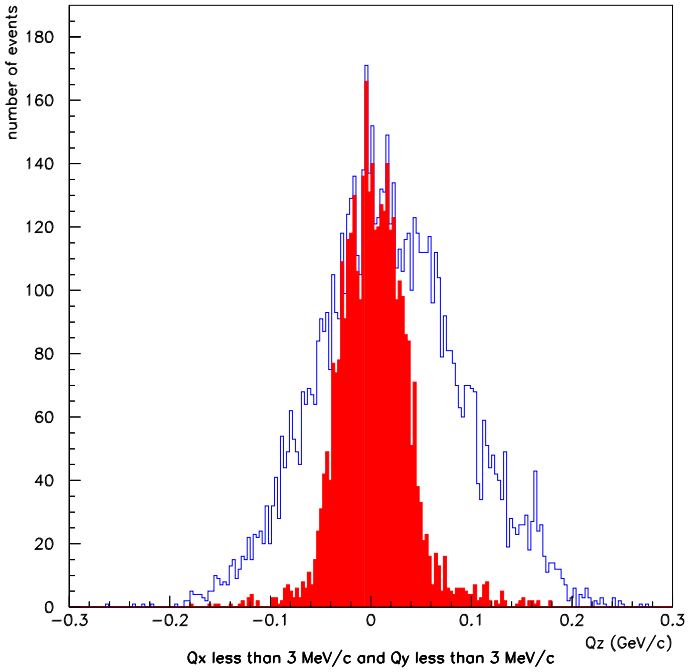
- Qx when Qz is less than 30 MeV/c and Qy less than 3 MeV/c
- Qz when Qx is less than 3 MeV/c and Qy less than 3 MeV/c
- Qtotal when Qz is less than 30 MeV/c and Qx is less than 3 MeV/c and Qy less than 3 MeV/c

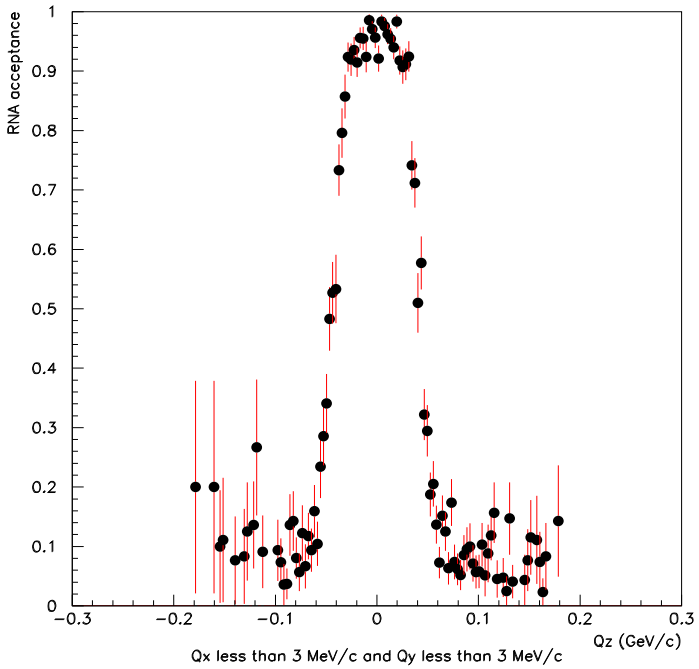
In each figure the blue plot corresponds to all the analysed events wit one track per arm, and the red filled plot to the subsample of the RNA selected events. The corresponding acceptance follows each momentum plot.

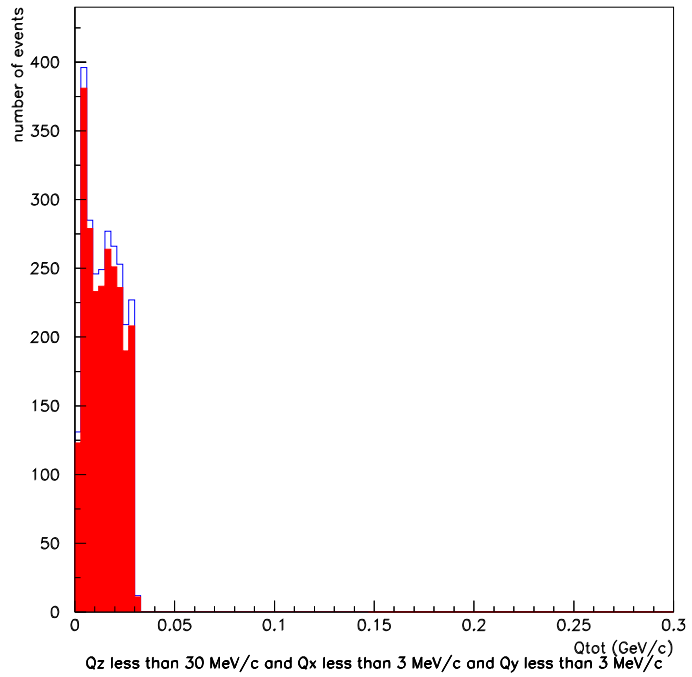
The last acceptance plot drawn shows the RNA acceptance for good low Q two track events. One can deduce from it that RNA the RNA acceptance for such events is flat and at the level of 97%.

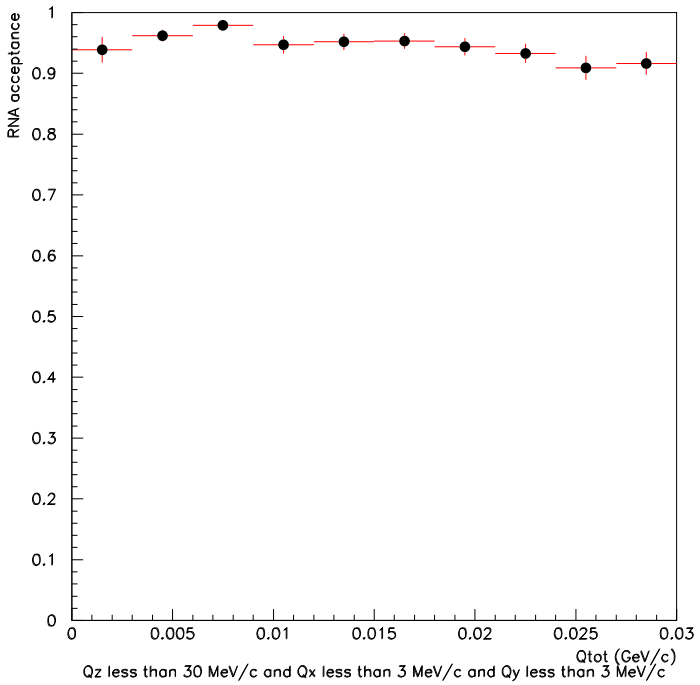

number of events
1400
1200
1000
800
600
400
200
0
−0.15
−0.1
−0.05
0
0.05
0.1
0.15
Qx (GeV/c)
Qz less than 30 MeV/c and Qy less than 3 MeV/c


RNA acceptance
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
−0.15
−0.1
−0.05
0
0.05
0.1
0.15
Qx (GeV/c)
Qz less than 30 MeV/c and Qy less than 3 MeV/c


number of events
180
160
140
120
100
80
60
40
20
0
−0.3
−0.2
−0.1
0
0.1
0.2
0.3
Qz (GeV/c)
Qx less than 3 MeV/c and Qy less than 3 MeV/c

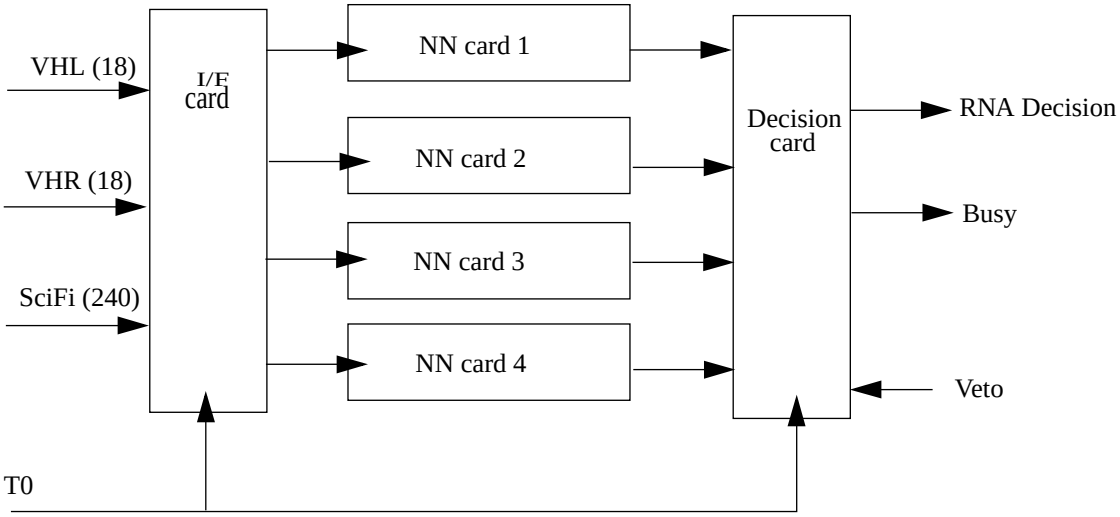

RNA acceptance
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
−0.3
−0.2
−0.1
0
0.1
0.2
0.3
Qz (GeV/c)
Qx less than 3 MeV/c and Qy less than 3 MeV/c


number of events
400
350
300
250
200
150
100
50
0
0
0.05
0.1
0.15
0.2
0.25
0.3
Qtot (GeV/c)
Qz less than 30 MeV/c and Qx less than 3 MeV/c and Qy less than 3 MeV/c


RNA acceptance
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
0.005
0.01
0.015
0.02
0.025
0.03
Qtot (GeV/c)
Qz less than 30 MeV/c and Qx less than 3 MeV/c and Qy less than 3 MeV/c

6.0 Hardare Implementation

The hardware implementation of the RNA system is a natural extension of the DNA system hardware. The following drawing gives a schematic overview:



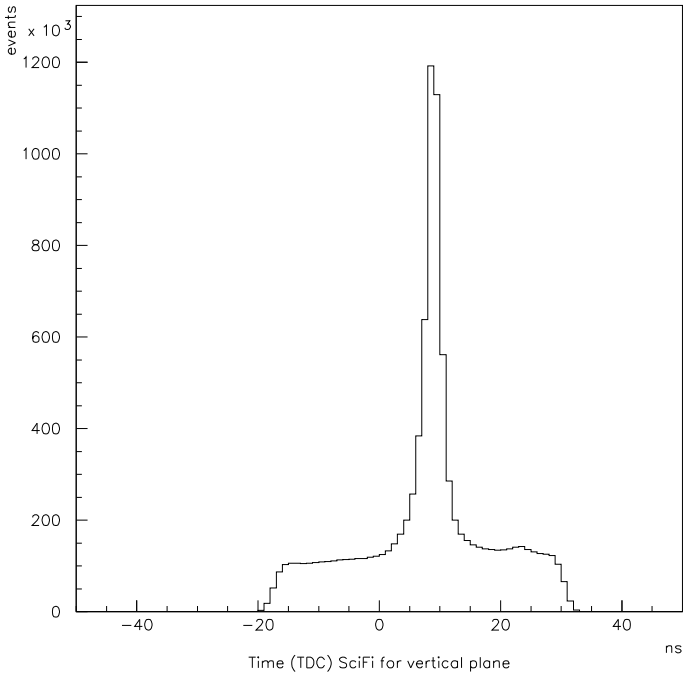
The inputs to the RNA trigger system are:

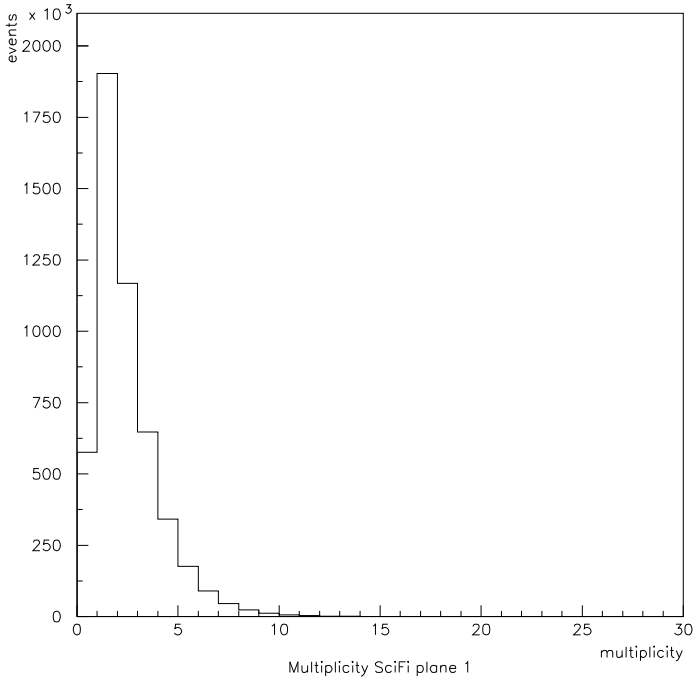
- T0 is the same initial trigger signal as in DNA, used to initiate the event processing.
- 18 Left Vertical Hodoscope signals (VHL) and 18 Right Hodoscope signals. They are identical to the ones used for the DNA system. The timing of these signals is well established in the DNA operation (the delay lines used there with a maximum delay of 100 ns are perfectly adequate).
- 240 SciFi signals. They are in differential ECL form. Since these signals some in various times (see plot in what follows) one can either format them to an appropriate pulse width (about 60ns) or use a monoflop per input signal which shall be active in a given time window. The time relation between these SciFi signals and T0 has still to be determined. From these signals the pair of hits with the smallest distance has to be established and formatted as defined earlier. A maximum number of hits should also be implemented, in a way to accept all events with a number of hits about that.
- In addition a Veto signal should be foreseen in case the RNA system has to be temporarily disabled (in case for example an event is being read out).

RNA should provide the ‘typical’ signals to the outside world:

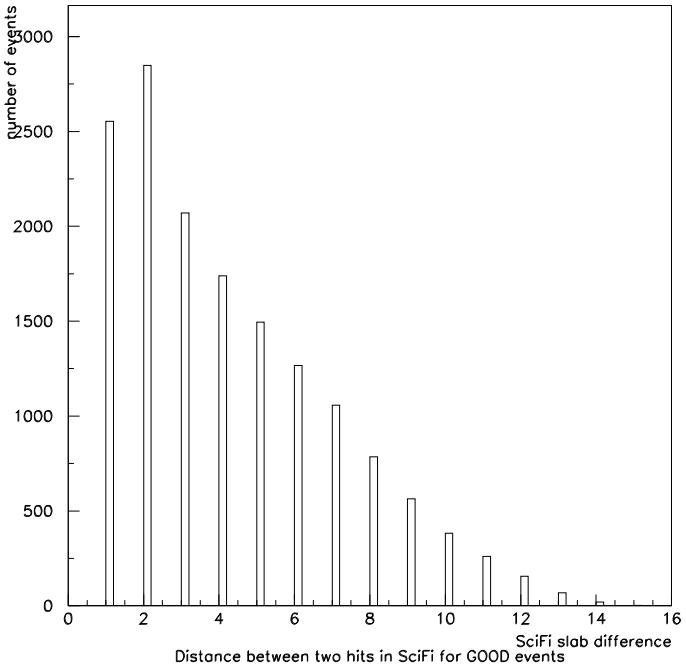
- a RNA decision (in two forms: as a decision level and as a pulse obtained by the coincidence between this level and a delayed T0).
- A Busy signal which is on when the system is evaluating an event.

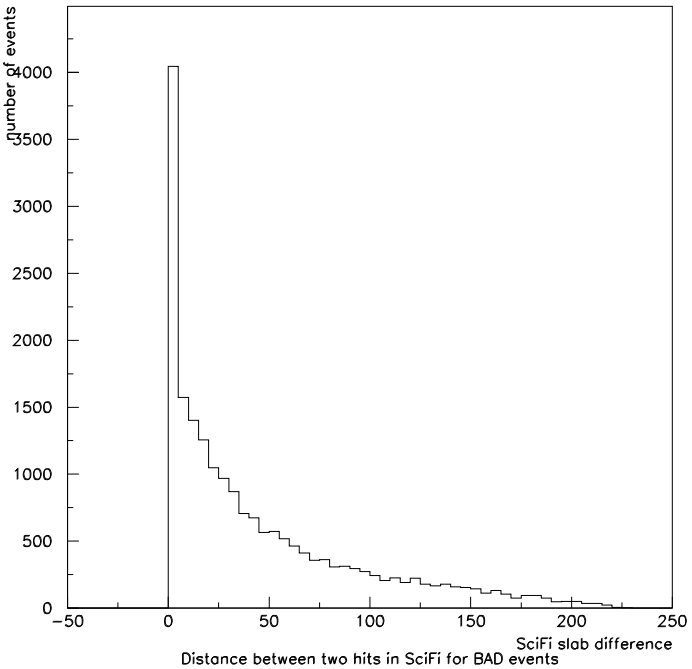
For a complete picture of the kind of input signals used for RNA the following plots maybe useful. The first two show two distributions for what are called minimum bias events, which are the ones that mostly resemble real-time data. The first plot shows the distribution of the arrival time of the SciFi signals, and the second one the SciFi hit multiplicity.


events
x 10 3
1200
1000
800
600
400
200
0
−40
−20
0
20
40
ns
Time (TDC) SciFi for vertical plane


events
x 10 3
2000
1750
1500
1250
1000
750
500
250
0
0
5
10
15
20
25
30
multiplicity
Multiplicity SciFi plane 1

The next two plots show the distance (in number of SciFi slabs) between the two hits used for the RNA event decision. One plots shows the distribution for good events and an other for bad ones. They may be useful for a reasonable algorithm to find the two best hits to be used for the RNA NN cards.

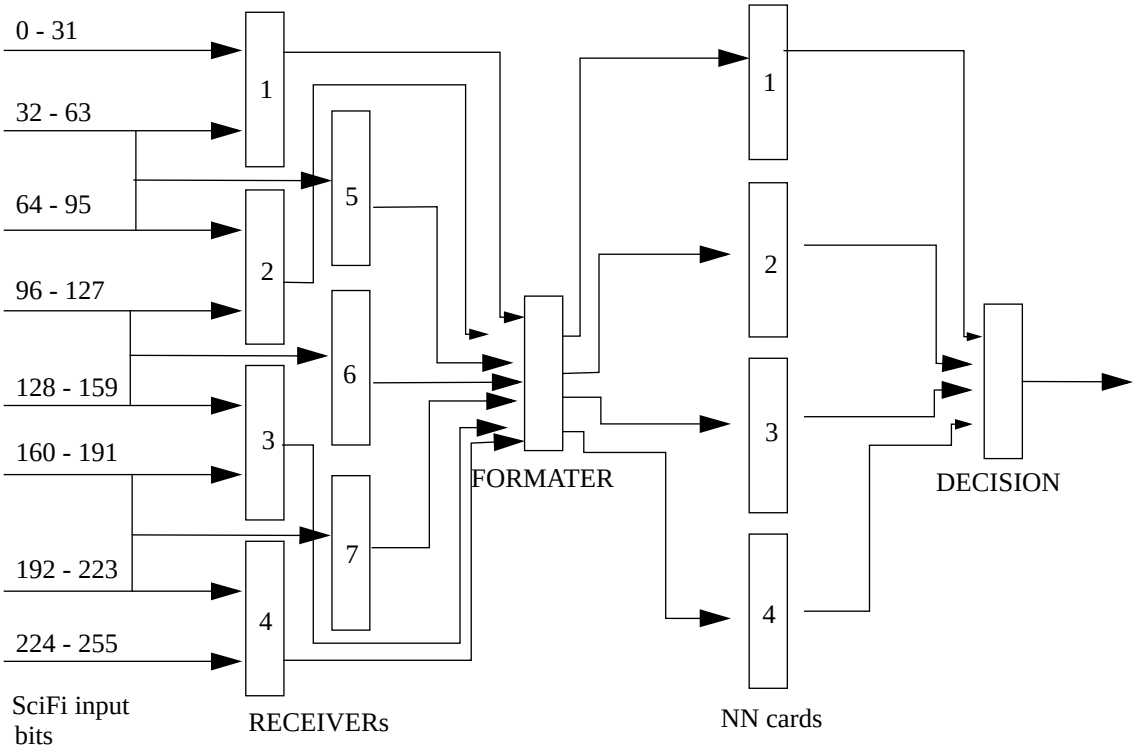




The main difficulty with the RNA hardware system is the design of the SciFi interface card. Special effort is needed to design an interface with 240 inputs. In addition all of them have to be combined to locate the pair of hits with the smallest distance. this combination should preferably be executed in a few parallel steps for decision time optimization. If the input SciFi hit-map has to be splitted in several parts, each part connected to an individual card the problem of accidentally splitting adjacent hits to different cards has to be addressed. One way around it is a partial overlap of the input receptive fields of the individual cards. As seen in the previous plot good events have a distance between the two SciFi hits of a few (up to 16) fibres. Hence a minimum overlap should be 16 input bits.

The following block-diagram is a proposal of an implementation of the RNA SciFi interface. It comprises of 7 identical RECEIVER cards which accept 64 SciFi signals each, and a FORMATER card that combines their output and provides the input to the NN cards. The RECEIVER cards have an overlap of 32 input bits with adjacent cards. This value is well above the one required hence without performance degradation. In addition in this way all RECEIVER cards are identical. However each card has to have an individual ‘address’ so that the FORMATER card can properly transform the data to the NN cards. In principle each RECEIVER card can find in its input field the two closest hits and transfer their location to the FORMATER. The FORMATER should then establish the global closest pair of hits (by comparing the hit distances of the pairs it has received) and transfer the relevant hits to the NN card. As the NN cards need the absolute position of each of the two hits used, the RECEIVER cards should somehow have an individual address transmitted to the FORMATER so that information about absolute hit position gets propagated.

The FORMATER card can also accommodate the decision part of the RNA system (in an equivalent way as it is done for the DNA trigger).



7.0 Conclusions

Based on similar algorithms and methods as already used for DNA, RNA is proven to be both more efficient for interesting two pion events and more selective towards background. With an efficiency of 97% and an expected rate reduction of 4.2 it an effectively replace DNA in the DIRAC trigger system. This conclusion is only verified by the acceptances as a function of several variables as proven in the last section of this report. Based on existing Basel hardware RNA can be implemented pretty soon and increase the quality of events available for off-line analysis.