

LEAR Crystal Barrel Experiment, PS 197
Pi0 Reconstruction And Optional Fitting Software (PI0FND)
Ver. 2.0

P. Schmidt
I. Institut für Experimentalphysik
Universität Hamburg

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1 Introduction

This document describes the π^0 reconstruction software *PIOFND*. The routine package was written by John Tompkin and used at the *Crystal Ball Collaboration* under the name of *PHYSAC*. In the first step merged π^0 's (two photons resulting in one cluster) are searched by using the showermass of a cluster. Afterwards the other π^0 's are reconstructed by using the four-momentum of the two decay photons and their angular and energy resolution. In order to run the package the user has to call *PIINIT* once in routine *USINIT* where all necessary parameters are initialized with default values (see below). The user can extend the number of particles to be reconstructed up to ten different particles. In the current version *PIOFND* is able to handle 20 photons per event. This figure should not be exceeded. The values of the four-momentum as well as the values of resolution are taken from the Global-Tracking Bank *TTKS* where the main results are returned, such as the indices of the two π^0 decay photons (or the cluster id for merged π^0 's), the four-momentum vector of the π^0 , Φ and Θ of the π^0 and square-root of π^0 energy. **The errors are filled for a future version of the kinematic fitting package, which can fit π^0 's.** The index of the two decay photons is defined as

$$index = \gamma_1 \cdot 1000 + \gamma_2$$

The two photon indices are the *TTKS*-particle numbers. The flow of the software is shown in figure 1. Note that the global identification character for the π^0 reconstruction software is 'PI'.

Note:

This version requires at least BCTRAK 1.42. Major change since version 1.0: Before the π^0 reconstruction all clusters are searched for merged π^0 's and are not included in the following π^0 search (can be disabled by setting *QMRGPI* to *.FALSE.*). The *VETOPI* array is enlarged to dimension 70. Reconstruction is not possible for events with more than 70 particles in the global track bank. **If *QMRGPI* is true you need a *GTRACK* version greater 1.20/03 or you need some banks from *BCTRAK*. Watch out for error messages!** *PIOFND* cannot be called twice on the same event.

Note that for this package it is essential to have the errors of the measured variables. So it is not possible to do first a kinematic fit and then to use *PIOFND* because you don't have errors from the fit.

Please report any errors found in the software immediately to:

Gunter Folger (GUNTER@CERNVM)

Fritz-Herbert Heinsius (F31HEI@DHHDESY3)

2 For Urgent Usage

Call *PIINIT* in routine *USINIT*. In case you want to alter any values of parameters given in *PIINIT* (default values see *COMMON /PIUSER/*) do so after calling *PIINIT*. *PIOFND* has to be called in your own user routine. If you need more output informations than given in the *TTKS*-Bank use common blocks */PIUSER/* , */PIBEST/*. You will get a better review by reading the descriptions of subroutines *PIINIT*, *PIOFND*, */PIUSER/*. Note:

1. The optional kinematic fitting routine *PIFITS* is not sufficiently tested. Do not use it in this version!
2. If you exclude photons from reconstruction by using the *VETOPI(I)*-array, please reset *VE-TOPI(I)=.FALSE.* after *PIOFND*.(see example)

3. The default value of the variable CMAXPI for the first χ^2 -cut is 9 (corresponding to a 3σ value), the value of CONLPI 2.7% (CONLPI being the value for the confidence-level-cut and being the equivalent to a 3σ -value). If you want to change the cut value CMAXPI you should also change the value of CONLPI (the higher CMAXPI the lower CONLPI)
4. In case η 's should be reconstructed please set QETAPI=.TRUE. after calling PIINIT (default value =.FALSE.).
5. In case you don't wish to reconstruct merged π^0 's by using their showermass you should set QMRGPI=.FALSE. after calling PIINIT (default value =.TRUE.).

Example:

```

SUBROUTINE USER
+SEQ,PIUSER
+SEQ,PIBEST
etc.
*   reset the VETOPI array (only needed if set to .TRUE. in the last call)
    DO 10 I=1,70
        VETOPI(I)=.FALSE.
10  CONTINUE
    .
    .
*   in case certain photons(i) are excluded from reconstruction
    VETOPI(I)=.TRUE.
    .
    CALL PIOFND
    .
*   if IQ(LTTKS+2).EQ.2 then pi0/eta
    .
    END
SUBROUTINE USINIT
+SEQ,PIUSER
    CALL PIINIT
*   Change parameters of PIINIT here:
*   e.g. if you written output:
        NDMPPi=1
*   e.g. to change Pi zero mass
        FMASPI(1)=134.96**2
    .
    END

```

If you want to reconstruct η 's as well:

```

SUBROUTINE USINIT
+SEQ,PIUSER
    CALL PIINIT
*   Change default values of mass-flag etc.
*   default value of Eta mass = 2.689626E+05
        LISTPI(2)=2
        LTOTPI=2
        QETAPI=.TRUE.

```

.
. .
END

3 Description of Output-Banks

For more detailed description of the TTKS-Bank see *CB-Note 118*. Here are listed the output parameters which are stored in the TTKS-Bank. The contents of the bank are as shown and described below (as far as the π^0 's are concerned). π^0 with number N can be reached by looping

<i>Offset</i>	TYPE	<i>Quantity</i>
+1	INTEGER	<i>Number of particle</i>
+2	INTEGER	<i>= 2 if PIOFND reconstr. particle</i>
+3	INTEGER	<i>Part. id $\pi^0 = 7, \eta = 17$</i>
+4	INTEGER	<i>not filled</i>
+7	INTEGER	<i>....</i>
+8	INTEGER	<i>orig. vertex, not yet defined</i>
+9	INTEGER	<i>2 PED π^0: γ index = $\gamma_1 \cdot 1000 + \gamma_2$</i> <i>merged π^0: - cluster id (negativ)</i>
+10	<i>not filled</i>
+11	INTEGER	<i>merged π^0: see TTKS manual</i>
+12	INTEGER	<i>merged π^0: see TTKS manual</i>
+13	...	<i>...</i>
+14	REAL	<i>Momentum, P of π^0</i>
+15	REAL	<i>Energy of π^0</i>
+16	REAL	<i>Px of π^0</i>
+17	REAL	<i>Py of π^0</i>
+18	REAL	<i>Pz of π^0</i>
+..	...	<i>words 19 - 23 errors</i>
+..	...	<i>words 24 - 30 are not filled for π^0</i>
+31	REAL	<i>2 PED π^0: opening angle</i>
+35	REAL	<i>reconstructed π^0 mass</i> for GTRACK less 1.20/00 take IQ(-4)
+..	...	<i>words 36 - 42 are not filled for π^0</i>
+43	REAL	<i>Φ angle in XY plane for π^0</i>
+44	REAL	<i>Θ angle for π^0</i>
+45	REAL	<i>\sqrt{E} of π^0</i>
+..	...	<i>words 46 - 51 covariance matrix</i>

Table 1: Data in the **TTKS** sub-bank

through all particles and selecting those with particle identity = 7. (How to do it see CB-Note 118)

The number of particles in *word 1* is enlarged by the reconstructed π^0 's (also in **HTRK** bank word 3). *word 4* gives number of merged π^0 's, *word 5* gives number of 2 PED π^0 's. In *word 4* of the **HTRK** bank you find the PIOFND version number.

4 Common Blocks

4.1 Description of the PIOFND Common Blocks

All common blocks can be included with the patchy `+SEQ, name.` command. Only the PIUSER common block should be accessed from user routines.

4.2 PIUSER

In the /PIUSER/ common block are some changeable input and some output parameters stored:

```

    INTEGER MASSPI,NTOTPI,LISTPI,IPIOPI,LPIOPI,NDMPPI,
+       IVNTPI,IBSTPI,LTOTPI,NPIOPI,
+       IPIZPI,MFLAPI,METAPI,MPIOPI,IRETPI,IVERPI
    REAL   PAIRPI,CHITPI,FMASPI,CONLPI,CMAXPI,XMLTPI,RMINPI,RMAXPI
    LOGICAL VETOPI,QETAPI,QMRGPI
    COMMON /PIUSER/ PAIRPI(20,20,3), CHITPI(20,10),NTOTPI,IBSTPI,
+   FMASPI(10),MASSPI,LISTPI(10), LTOTPI,CONLPI,CMAXPI,
+   IVNTPI,XMLTPI,IPIOPI(2,50),LPIOPI(50),VETOPI(70),NDMPPI,NPIOPI,
+   IPIZPI(2,50),MFLAPI(50),
+   METAPI,MPIOPI,QETAPI,QMRGPI,IRETPI,RMINPI,RMAXPI,IVERPI

```

All figures in brackets () are default values. List of input parameters:

- FMASPI(K)-array stores in elements of K(≤ 10) the fit square-masses of the particles to be reconstructed. It is filled in PIINIT (fmaspi(1)=134.4**2, fmaspi(2)=551.6**2, fmaspi(3)=963.9**2)
- MASSPI is the number of fit masses in FMASPI (3)
- LISTPI(I) is the array which stores the flags for the fit-masses in FMASPI. I=1 means π^0 , I=2 η and I=3 η' . Is initialized in PIINIT (LISTPI(1)=1)
- LTOTPI is the number of particles to be reconstructed (1). Used by array LISTPI.
- CONLPI is the minimum confidence-level value which is required for each configuration in PICONF. CONLPI-value can be changed by User (0.0027)
- CMAXPI-value is the max χ^2 -value. PIFND requires that the $\chi_{\gamma\gamma}^2$ -value of each photon-photon pair is lower than CMAXPI. Can be changed by User in PIINIT (9.)
- XMLTPI is a dummy parameter which initializes the optional kinematic fit-routine PIFITS if XMLTPI > 0 (0)
- NDMPPI is a dummy parameter. NDMP ≥ 1 PIFND will give written output.(0)
- VETOPI(70) is a logical array. By setting VETOPI(I)=.TRUE. the user can sort out photons from the reconstruction process. This is done in PIMRGD. (.FALSE.)
- QMRGPI is a logical if PIMRGD should be called to search for merged π^0 's (.TRUE.)
- RMINPI is the lower bound for the showermass of merged π^0 's
- RMINPI is the upper bound for the showermass of merged π^0 's

These are the output parameters:

- PAIRPI(II,JJ,K) is an array which stores for all photon-photon pairs with index II,JJ in element of K the following informations:
 1. K=1 inv.mass of photon-photon pair
 2. K=2 mass-flag of the fit mass corresponding to inv. pair mass
 3. K=3 $\chi_{\gamma\gamma}^2$ -value of each pair

Note: the indices II,JJ of the photons are the PIFND internal indices.

- CHITPI(NSAVE,MAX)-array stores for each configuration NSAVE with number of pairs MAX the χ^2_{Σ} -value which is the sum of all $\chi^2_{\gamma\gamma}$ -values of each pair
- NTOTPI is the number of configurations
- IBSTPI help parameter to select configurations in PICONF
- IPI0PI(2,K) contains in elements (1,K) and (2,K) the indices of the two gammas that form the reconstructed particle No.K. Note the ordering condition: IPI0PI(1,K)<IPI0PI(2,K) Note: photon indices according to Global-Track Bank ordering
- LPI0PI(NG) contains in elements J the no.K of the reconstructed particle to which gamma no.J is assigned. NG is the number of all gammas in one event
- NPI0PI is the number of reconstructed not-merged π^0 's.
- MPI0PI is the number of reconstructed merged π^0 's.
- IPIZPI(2,K) contains in elements (1,K) and (2,K) the PI0FND internal photon indices of the two decay gammas from particle number K.

In case the user wants to reconstruct η 's here is the output parameter:

- METAPI is the number of reconstructed η 's
- IRETPI is the return code: -1: pi0fnd already called before on this event; 1=no TTKS bank; 2=too many particles in event; 3=too low number of PEDs; 4=more than 20 accepted PEDs; 5=PIRECO returned more pairs than possible.
- IVERPI PI0FND version number.

4.3 PIOPTI

In the /PIOPTI/ common block are some variables stored, which the program needs for the optional kinematical fitting.

```

REAL  GGOPPI,BOPTPI,COOPPI,COPTPI,XXOPPI,XOPTPI,GBOPPI,XTSTPI
COMMON /PIOPTI/ GGOPPI(6,6),BOPTPI(6),
+           COOPPI(6),COPTPI(6), XXOPPI(6),XOPTPI(6),
+           GBOPPI(6),XTSTPI(20,20)

```

- GGOPPI(I,J) contains in elements I,J the values of the energy and angular resolution of the two photons of each pair
- BOPTPI(I) contains in elements the derivatives for the calculation of the square mass resolution
- COOPPI(I) array which stores the differences between the original values of the energy and angle of each photon and the fitted values
- COPTPI(I) array which contains in elements of I the fitted values of the resolution
- XXOPPI(I),XOPTPI(I) arrays contain in elements of I the energy and Θ , Φ of each photon
- GBOPPI(i) help array in order to calculate the fitted resolution
- XTSTPI(IGAM,JGAM) contains in elements of IGAM,JGAM the $\cos\Theta$ of the angle between the two photons of each pair combination

4.4 PIBEST

In the /PIBEST/ common block are the values of the best reconstructed configurations stored.

```
REAL    PPAIPI,PMASPI,PCHUPI,XLEVPI
LOGICAL QGAMPI
INTEGER PFLGPI,JGAMPI,NPRMPI
COMMON /PIBEST/ PPAIPI(5,10),PMASPI(10),PFLGPI(10),PCHUPI(10),
+             JGAMPI(2,10),NPRMPI(10),XLEVPI,QGAMPI(20)
```

- PPAIPI(JJ,IP)-array contains for all reconstructed pairs with index IP the sum of each four-momentum component if $JJ \leq 4$. $JJ=4$ contains the total momentum of the reconstructed particle.
- PMASPI(IP) contains in elements IP the inv. mass of the reconstructed particle
- PCHUPI(IP) array where the $\chi^2_{\gamma\gamma}$ value of the reconstructed particle is stored
- XLEVPI variable which gives the confidence-level of the reconstructed pair
- QGAMPI logical parameter which helps to find best configuration
- PFLGPI(IP) stores the mass-flag of the fit mass to which the reconstructed particle is assigned
- JGAMPI(K,IP) contains the indices of the photons reconstructed as decay photons in the array of the best configuration
- NPRMPI(IPMF) array which is used to find the fit-mass which is to be assigned to the reconstructed particle

4.5 PIINPT

In the /PIINPT/ common block are the necessary input values stored

```
REAL    PGAMPI,BESTPI,MFLGPI,ERR4PI
INTEGER NGANPI,NCMBPI
COMMON /PIINPT/ PGAMPI(20,4),BESTPI(20,2),NGANPI,
+             NCMBPI(20,10,20),MFLGPI(20,20),ERR4PI(20,4)
```

- PGAMPI(NG,K) contains in elements of K the four momentum of each photon NG
- BESTPI(I,2) array which contains in BESTPI(I,1) the index of the configuration and in BESTPI(I,2) the χ^2 -sum value of this configuration
- MFLGPI(NCON,I) stores the mass-flag which is associated to each pair in configuration no.NCON
- ERR4PI(NG,J) contains in elements of J the values of the direction and energy resolution for each photon NG
- NGANPI is the number of gammas
- NCMBPI(NTOT,MAX,K[M]) is the array where the selected configurations are stored. Element $NTOT =$ index of configuration, $MAX =$ number of pairs in this configuration and $K =$ the $PI0FND$ -index of the photons belonging to a pair combination.

4.6 PISAVE

```
INTEGER NPRIPI, IPRIPI
REAL PRVCPI
COMMON /PISAVE/ NPRIPI, IPRIPI(2,400), PRVCPI(6,400)
```

- NPRIPI is the number of photon-photon pairs with a $\chi_{\gamma\gamma}^2$ value which is less than CHIMAX
- IPRIPI(2,400) array stores the indices of the preselected photons ($\chi_{\gamma\gamma}^2 < \text{CHIMAX}$)
- PRVCPI(6,400) array stores the energy and Θ, Φ of the above mentioned preselected photons of each pair

4.7 PIBRAI

```
INTEGER IBRAPI, NGAMPI
COMMON /PIBRAI/ IBRAPI(20), NGAMPI
```

- IBRAPI(N) array which translates the PI0FND photon index back to photon index due to GLOBAL TRACK - bank
- NGAMPI the number of gammas

5 Subroutines

5.1 PIINIT

Common Blocks Used: PIUSER

This subroutine must be called by the user once in USINIT. PIINIT initializes values necessary for the reconstruction work. In here the number of particles MASSPI to be reconstructed and the "theoretical value" of the square mass of each particle in array FMASPI are evaluated. The theoretical value is taken from a fit mean value. Other important values are the minimum confidence-level CONLIM and the maximum value of the difference between theoretical and calculated invariant mass in units of the mass resolution CMAXPI. If the user doesn't want to use default values they can be altered after CALL PIINIT. For instance: With XMLTPI the user can use the kinematical fitting routine PIFITS by setting XMLTPI > 0. NDMPPI > 0 means PI0FND will give written output.

5.2 PI0FND

Common Blocks Used: CBLINK, CBSTOP, PIOPTI, PIUSER, PIBEST, PIINPT, PISAVE, PIBRAI

Subroutines Referenced: PIRECO, PIOUTP, PIMRGD, BCNCTP, BCNPTC

This routine called in the user's main routine is the frame routine for the reconstruction work. First PIMRGD is called to search for merged π^0 's (if QMRGPI is true). Afterwards PI0FND is taking the four-momentum vector and the corresponding values of the resolution from the TTKS bank. In the current version PI0FND can handle max. 20 photons. The main reconstruction work is done in PIRECO (former name PHYSAC) and PIOUTP. The results are stored again in the TTKS bank (see section *Description of Output Banks*). NPI0 being the number of π^0 's, IPI0 being the array which stores the indices of the photons of a π^0 decay. These two variables are stored in the /PIUSER/ common block. Note that there are two kinds of indices in use: the number of particles used by the TTKS-Bank and the PI0FND internal indices. The latter are "translated" back at the end of the routine by array IBRAPI. You can get a return code in variable IRETPI (see description of common /PIUSER/).

5.3 PIMRGD

Common Blocks Used: CBLINK,CBUNIT,PIUSER,PI2PI,BCFLAG

Subroutines Referenced: BITOPT, BCOSCL, BCVCOR, BCECOR, BCTTKS, MZPUSH, MZFORM, MZBOOK

This routine searches for merged π^0 's (i.e. two photons in one cluster). The found π^0 's are added to the global track bank. For the corresponding PEDs the array VETOPI is set to false. Note that you need BCTRAK output banks if the data is produced before GTRACK version 1.20/04. If the data to calculate the π^0 energy and direction is not available, the variable QMRGPI is set to false and this subroutine will not called again.

5.4 PIRECO

Call Arguments: NPIF

Common Blocks Used: PIUSER,PIOPTI,PIBEST,PIINPT,PISAVE,PIBRAI

Subroutines Referenced: PICOMB,PIFITS,PICONF,PISORT

In PIRECO the main reconstruction work is done. In a first step PIRECO calculates for all photon-photon pair combinations the square invariant mass, the corresponding theoretical square mass value (if more than one particle is chosen for reconstruction) and a χ^2 value being calculated from: $\chi_{\gamma\gamma}^2 = \frac{m_{th}^2 - m_{inv}^2}{\sigma_{\gamma\gamma}^2}$. $\sigma_{\gamma\gamma}$ is the value of the square mass resolution. Next PIRECO is choosing only those photon-photon pairs for further reconstruction, if $\chi_{\gamma\gamma}^2 \leq \chi_{max}^2$. In the next step PIRECO is forming groups of pairs under the condition that the involved photons are used only once for a pair combination. The routine then sums up the $\chi_{\gamma\gamma}^2$ values to a χ_{Σ}^2 sum which corresponds to a confidence-level. In the last cut PIRECO is forming configurations of these groups in case the confidence-level-value is higher than the given minimum value CONLIM and the number of pairs in this group is the highest possible one. The array of the configurations is NCMBPI. PIRECO offers a set of configurations (not more than 20) as a final result. These are sorted after the χ^2 -sum value in array BESTPI.

5.5 PICOMB

Call Arguments: IGAM,JGAM,*MASS2,*ERMM2,*MFLG,*MFIT,*CTHET,*CHISQ

Common Blocks Used: PIUSER,PIOPTI,PIBEST,PIINPT,PISAVE,PIBRAI

This routine is called by PIRECO and calculates for all photon-photon pair combinations (IGAM,JGAM being the indices of the two photons), the square inv.mass MASS2, the square mass resolution ERMM2 and the CHISQ value being the $\chi_{\gamma\gamma}^2$ -value mentioned above. MFIT is the "theoretical" mass value, corresponding to a mass flag MFLG. If more than one particle is chosen for reconstruction PICOMB is taking the MFIT,MFLGPI values which are closer to the calculated MASS2-value.

5.6 PIFITS

Call Arguments: XMP2,MIPZR2,II,JJ,CHIFIT

Common Blocks Used: PIUSER,PIOPTI,PIBEST,PIINPT,PISAVE,PIBRAI

Subroutines Referenced: PIERRS,PIMFIT,PISFIT

This routine is optional. PIFITS is a kinematical fitting routine which can be included by the user with setting XMULT > 0 in PIINIT. PIFITS returns the fitted square-mass value XMP2 and the fitted $\chi_{\gamma\gamma}^2$ -value CHIFIT for a given photon-photon pair with indices II,JJ and a given fit mass MIPZR2.

5.7 PIERRS

Call Arguments: II,JJ

Common Blocks Used: PIUSER,PIOPTI,PIBEST,PIINPT,PISAVE,PIBRAI

Subroutines Referenced:

This (optional) routine calculates, in case the user installes PIFITS, the error of the square-inv.mass together with the following other two routines PIMFIT,PISFIT. In array GGOPPI are stored the sigmas of the energy and angle of photon no. II and JJ.

5.8 PIMFIT

Call Arguments: X,XMS,XMFIT2,CON

Common Blocks Used:

Subroutines Referenced:

Routine calculates the square inv.mass XMS of each photon-photon pair and the difference CON between fit-mass XMFIT2 and XMS.

5.9 PISFIT

Call Arguments: X,B

Common Blocks Used:

Subroutines Referenced:

PISFIT calculates the necessary derivatives due to error progression.

5.10 PICONF

Call Arguments: ICHI,CHI,MAX

Common Blocks Used: PIUSER,PIOPTI,PIBEST,PIINPT,PISAVE,PIBRAI

Subroutines Referenced: PICHEK

Routine PICONF is forming so-called configurations under the limiting condition that photons are used only once for a pair combination. In order to do so PICONF takes only those photon-photon pairs stored in ICHI if $\chi_{\gamma\gamma}^2 < \chi_{max}^2$. For each configuration PICONF a χ -sum value is calculated which corresponds to a confidence-level value. PICONF then requires a minimum confidence-level CONLIM for each configuration *and* a maximum number MAX of photon-photon pairs . All configurations surviving this cut are stored in array NCMBPI. PICONF can handle up to 20 configurations. If there are more than 20 PICHEK is called.

5.11 PICHEK

Call Arguments: II,CHINEW,NSAVE

Common Blocks Used: PIUSER,PIOPTI,PIBEST,PIINPT,PISAVE,PIBRAI

Subroutines Referenced:

This routine is called by PICONF in case there are more than 20 configurations. PICHEK then sorts out those configurations with the lowest confidence-level (CL) value and returns the 20 configurations with the highest CL-value.

5.12 PISORT

Call Arguments: NPIF

Common Blocks Used: PIUSER,PIOPTI,PIBEST,PIINPT,PISAVE,PIBRAI

Subroutines Referenced:

PISORT is the last routine in the PIRECO package. The configurations stored in array NCMBPI are sorted due to their confidence-level value. The sorted configurations with the number of pairs NPIF are stored in array BESTPI.

5.13 PIOUSP

Call Arguments: NPAIR,QETA

Common Blocks Used: PIUSER,PIOPTI,PIBEST,PIINPT,PISAVE,PIBRAI

Subroutines Referenced:

This routine is called by PIOUSP after the main reconstruction work is done by PIRECO. Because the photon-photon pairs are referred to in PIRECO by their indices the information of the best configuration PIRECO has reconstructed is decoded in this routine. NPAIR gives the number of reconstructed photon-photon pairs. QETAPI is a logical variable which helps to find the best configuration. It is set .FALSE. if there is only one particle to be reconstructed. The photon-photon pairs are identified as the particles the user wanted to be reconstructed.

6 List of Functions

6.1 PICONL

Function PICONL calculates the confidence-level for a given χ^2 -sum value.

6.2 PIERRA

Called Arguments: PGAMPI,ERR4PI,II,JJ

Function PIERRA calculates for a given four-momentum vector PGAMPI and its corresponding values of resolution ERR4PI the $\sigma_{\cos\theta}$ of the angle Θ between two photons of each photon-photon pair. The formula for $\sigma_{\cos(\Theta)}$:

$$\sigma_{\cos(\Theta)} = (D_1^2 \cdot \sigma_{\Theta_1}(E_1) + D_2^2 \cdot \sigma_{\Theta_2}(E_2) + D_3^2 \cdot (\sigma_{\Phi_1}(E_1)^2 + \sigma_{\Phi_2}(E_1)^2)^{1/2}$$

The elements D_1 , D_2 and D_3 being the derivatives according to error progression:

$$D_1 = \frac{x_1x_2 + y_1y_2}{\sin(\Theta_1)} \cdot z_1 - \sin(\Theta_1) \cdot z_2$$

$$D_2 = \frac{x_1x_2 + y_1y_2}{\sin(\Theta_2)} \cdot z_2 - \sin(\Theta_2) \cdot z_1$$

$$D_3 = x_1y_2 - x_2y_1$$

6.3 PIERRE

Function PIERRE calculates the $\sigma_{E\gamma}$ of each photon. Needed in PIFITS, otherwise not in use.

6.4 PIMASS,PIPTOT

Called Arguments: IGAM,JGAM,PIPTOT,PSUM

Common Blocks Used: PIUSER,PIOPTI,PIBEST,PIINPT,PISAVE,PIBRAI

Function PIMASS calculates the square inv. mass for a photon-photon pair IGAM,JGAM. PSUM is an array filled with the sum of the components of each photon momentum vector, PIPTOT is the value of the total momentum of this pair. Both functions are needed in PIOUSP.

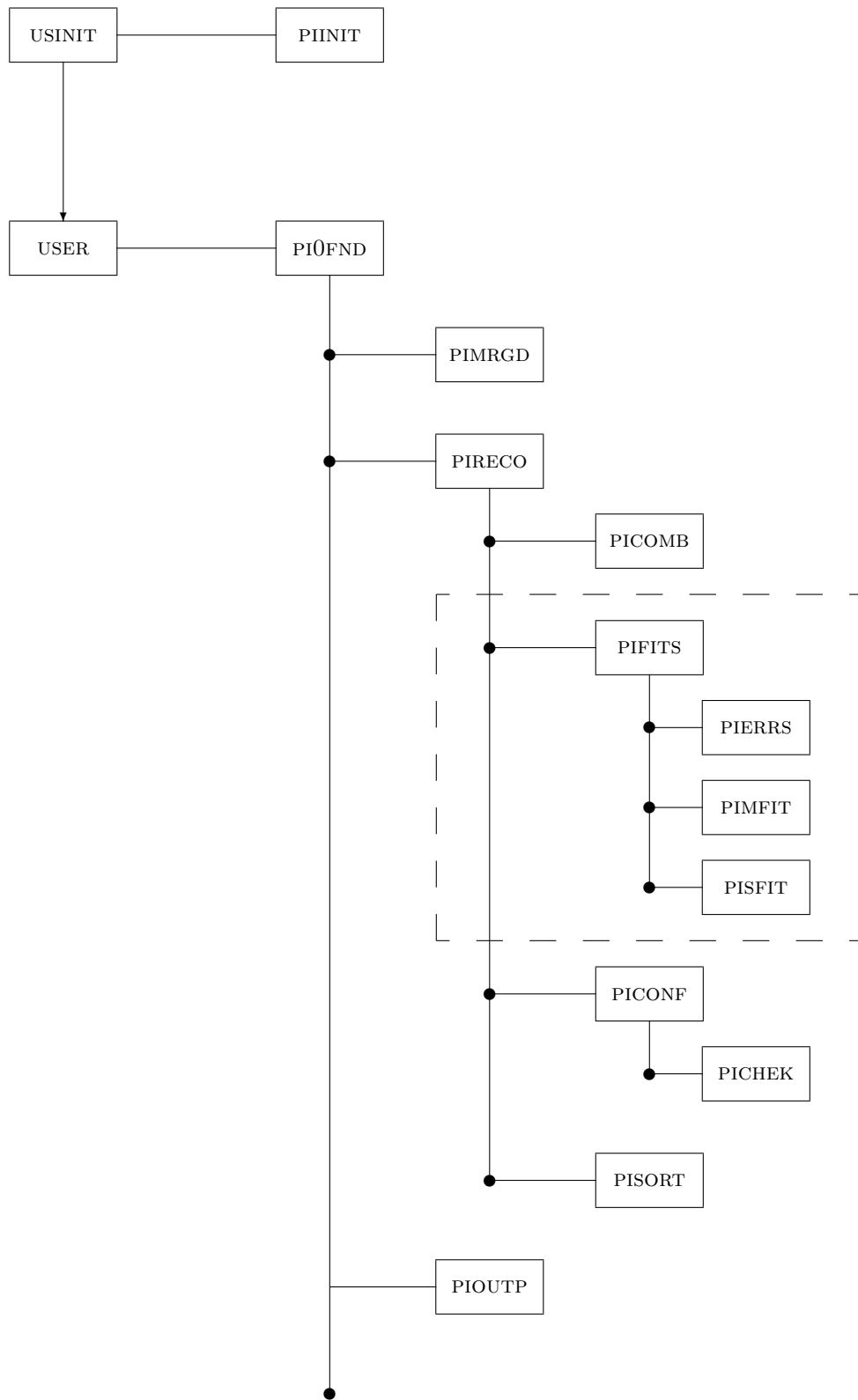


Figure 1: Flow Chart of the Software