

Table of Contents

Electron Identification using Likelihood.....	1
Introduction.....	1
Configuration.....	1
Setup of the code.....	2
Tags in 20X.....	2
Tags in 17X.....	2
Tags in 16X.....	2
Tags in 131HLT6 (obsolete!).....	2
Run with CRAB.....	2
Test the likelihood.....	3

Electron Identification using Likelihood

Complete: 

Introduction

The following variables are currently used to discriminate between real and fake electrons in the likelihood:

- Energy of closest BasicCluster to track impact point at ECAL / outermost track momentum
- DeltaEta between SuperCluster position and track direction at vertex extrapolated to ECAL assuming no radiation
- DeltaPhi between SuperCluster position and track direction at vertex
- Ratio of energy in HCAL behind SuperCluster to SuperCluster energy
- Cluster shape variables:
 - ◆ Energy in 3x3 crystals / energy in 5x5 crystals
 - ◆ SigmaEtaEta cluster shape covariance

Specialized pdfs are for:

- ECAL barrel, ECAL endcap
- electron $p_T < 15\text{GeV}$ / $>15\text{GeV}$
- electron classes (only for signal). Two possibilities are allowed:
 - ◆ split by "fullclass": golden, bigbrem, narrow, showering
 - ◆ split by "class": non-showering (golden+bigbrem+narrow all together weighted by their fractions), showering

Species: only two species are currently considered:

- **Electrons:** pdfs taken from pure di-electron sample, particle gun
- **Jets:** QCD samples, pdfs are the weighted sum of pdf's for di-jets from different p_T bins from enriched samples. The weight is the product of the L1 filter efficiency and the cross section.

Configuration

Configuration can be done changing the .cfi file:

- EgammaAnalysis/ElectronIDESSources/data/likelihoodESetup.cfi

In the default configuration, signal species (electrons) pdf's are split by "fullclass" and background species is not split. For the signal species, the possibilities are:

- split by "fullclass". The configuration is:

```
string signalWeightSplitting = "fullclass"  
bool splitSignalPdfs = true
```

- split by "class":

```
string signalWeightSplitting = "class"  
bool splitSignalPdfs = true
```

- do not split at all:

```
string signalWeightSplitting = "fullclass"
```

```
bool splitSignalPdfs = false
```

In principle also for background the same procedure is available. Due to the low MC statistics available in the Bigbrem/Narrow classes, right now only the unsplit pdf's are available in the DB. Configuration is:

- do not split at all:

```
string backgroundWeightSplitting = "fullclass"
bool splitBackgroundPdfs = false
```

Setup of the code

Tags in 20X

no extra tags needed! all is in the release.

Tags in 17X

```
cvsv co -r V00-00-07-02    EgammaAnalysis/ElectronIDAlgos
cvsv co -r V00-00-04      EgammaAnalysis/ElectronIDProducers
cvsv co -r V00-00-03-01  EgammaAnalysis/ElectronIDESSources
cvsv co -r V00-01-01     CondCore/EgammaPlugins
cvsv co -r V00-02-00     CondFormats/EgammaObjects
```

Tags in 16X

```
cvsv co -r V00-00-07-02    EgammaAnalysis/ElectronIDAlgos
cvsv co -r V00-00-04      EgammaAnalysis/ElectronIDProducers
cvsv co -r V00-00-03-01  EgammaAnalysis/ElectronIDESSources
cvsv co -r V00-01-01     CondCore/EgammaPlugins
cvsv co -r V02-06-02     CondFormats/DataRecord
cvsv co -r V00-02-00     CondFormats/EgammaObjects
cvsv co -r V00-01-03     CondFormats/PhysicsToolsObjects
```

Tags in 131HLT6 (obsolete!)

```
cvsv co -r V00-00-04      EgammaAnalysis/ElectronIDAlgos
cvsv co -r V00-00-01     EgammaAnalysis/ElectronIDESSources
cvsv co -r V00-05-00     DataFormats/EgammaReco
cvsv co -r V00-01-00     CondCore/EgammaPlugins
cvsv co -r V00-01-10     CondFormats/BTauObjects
cvsv co -r V02-06-02     CondFormats/DataRecord
cvsv co -r V00-01-00     CondFormats/EgammaObjects
cvsv co -r V00-03-04     RecoEcal/EgammaClusterAlgos
cvsv co -r V00-05-07     RecoEcal/EgammaClusterProducers
cvsv co -r V00-03-00     RecoEcal/EgammaCoreTools
cvsv co -r shr-8aug07    PhysicsTools/StatPatternRecognition
```

Run with CRAB

Since the SQLite DB file is not yet distributed on sites, it has to be exported in the CRAB InputSandBox. To do it, change, in EgammAnalysis/ElectronIDESSources/data/likelihoodPdfsDB.cfi:

- in CMSSW_16X:

```
replace CondDBCommon.connect = "sqlite_file:electronIdLikelihoodTkIsolated.db"
replace CondDBCommon.catalog = "file:electronIdLikelihoodTkIsolatedCRAB.xml"
```

and, in the CRAB cfg file:

```
## files to be put in InputSandBox, full path or in the current directory
## (wildcard * are allowed): comma separated list
additional_input_files = /afs/cern.ch/user/e/emanuele/public/4Likelihood/PDFsSQLite/CMSSW_1_6_8/e
/afs/cern.ch/user/e/emanuele/public/4Likelihood/PDFsSQLite/CMSSW_1_6_8/electronIdLikelihoodTkIsol
```

- in CMSSW_20X

this is temporary, until the files are exported on all the sites.

```
replace CondDBCommon.connect = "sqlite_file:electronIdLikelihoodTkIsolated.db"
```

and, in the CRAB cfg file:

```
## files to be put in InputSandBox, full path or in the current directory
## (wildcard * are allowed): comma separated list
additional_input_files = /afs/cern.ch/user/e/emanuele/public/4Likelihood/PDFsSQLite/CMSSW_2_0_X/e
```

Test the likelihood

Examples of analyzers can be found here:

- CMSSW_1_6_X:

```
> cvs co -d emanuele/EgammaTools UserCode/emanuele/EgammaTools
> scramv1 b
> cmsRun emanuele/EgammaTools/test/testElectronIDWithLH.cfg
```

- CMSSW_2_0_X:

```
> cvs co -r edm-22Apr08 -d emanuele/EgammaTools UserCode/emanuele/EgammaTools
> scramv1 b
> cmsRun emanuele/EgammaTools/test/testElectronIDWithLH.cfg
```

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-- EmanueleDiMarco - 12 March 2010

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