# **ValidationsTools**

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this repository get all the validations tools such as Kolmogorov-Smirnov (KS Tools) or AutoEncoders Tools (AE).

## Launching the installation:

- git clone https://github.com/archiron/ValidationsTools ValidationsTools
- cd ValidationsTools

then launch: . installValidationsTools.sh

This install the library (ChiLib), the release file env (cmsrel \$Release \$Release) and copy the ZEE\_Flow/CCA or ZEE\_Flow/LLR files (depending of the site you are working on - the CC or the LLR site) onto the \$Release/src/Kolmogorov folder.

\$Release is the release you want working with.

## **Launching the ROOT files creation:**

From the top of the Tools (i.e. ValidationsTools), then launch:

. createROOTFiles.sh

This script launch the creation of the ROOT files, using the step[1-4].py scripts.

You can use own but they have to be similar to the existing ones (see 4).

later create a link to an explanation of the common files used for the ROOT files creation (CommonFiles/path...).

#### Reducing size:

When ALL ROOT files are created, launch (always from the top folder):

. reduceROOTSize.sh

this will reduce the size of the ROOT files (typically from 150/200 Mo to 1.5/2 Mo), keeping the name of the file.

#### **Extracting values:**

When all the ROOT files are created and reduced, we need to creates 1 file per histo with all the histo values for each ROOT file.

It is the first job of the extractValues[\_init].sh scripts.

It can be launched with: . extractValues\_init.sh

and create into the RESULTFOLDER (see 4) a lot of text files. All ROOT files are read, and then for each histo, the values of the histo curve is stored into an array, ROOT file after ROOT file. Once we have all the ROOT files read, the array is stored into a text file dedicated to this histo.

#### **ANNEXE**

## **Annexe: ROOT scripts to modify**

Here we are talking about the step[1-4].py scripts.

## **Annexe: paths definitions**

RESULTFOLDER: path where you want your created ROOT files are located. It also contain the txt files for each histo.