# Relval-Vp How To

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Relval-Vp is a python tool used to make comparisons of histograms directly from DQM...root files.

## Part 1 : how to use it

### *Remainders, definitions*

Validations are made to compare a new release (named as Release) with another (defined as Reference). Most of the computations are made into ROOT files which name is similar to :
DQM_V0001_R000000001__RelValQCD_Pt_80_120_13__CMSSW_7_4_1-
MCRUN2_74_V9_gensim71X-v1__DQMIO.root and except for new development there is no need to make those computations.

But, for most of the time, we still need to have a folder to work[1], so you can have something like :

cmsrel **RELEASE_TO_TEST**
cd RELEASE_TO_TEST/src

> We need to be in a release folder (/Release_Folder_Name/src) to make the « *cmsenv* ». It's necessary and if we don't have it, we don't have the libQT4 file access.

cmsenv git cms-addpkg Validation/RecoEgamma

this last cmd gives you the **RELEASE_TO_TEST/src/Validation/RecoEgamma/test** folder to work in.

Once the computations are done, the web pages can be stored locally into the test folder of the release or not (into the classical **afs folder** :
/afs/cern.ch/cms/Physics/egamma/www/validation/Electrons/Releases/**RELEASE_TO_TEST**).

To use the GUI tool, you need to go to https://github.com/archiron/Relval-Vp and load the main.py, ovalGui.py, fonctions.py, getChoice.py, getPublish.py and getEnv.py files, and put it into a folder.

### *Launching the GUI*

Next, with the command :
python NAME_OF_THE_PATH_TO_YOUR_PYTHON_FOLDER/main.py
such as :
python ~/lbin/Projet_Relval-Vp/main.py

Then you get the first window, divided into 3 parts, with several sub-parts. :



*Picture 1: General window*

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1    In a future version of this GUI, this need will be hidden.

**Upper part**

The upper part of the window have several sub parts :

on the right, you have the release you want to compare which is named **Release**. Just below you have the release to compare with the precedent. It's named **Reference**. By default it is the same as Release, but you can modify it.
You can even modify the release to test i.e. you can make a "cmsrel CMSSW_7_4_1" and make the comparison between CMSSW_8_0_1 and CMSSW_8_0_2.

On the left you have four parts :

### First part

The first named ***Calcul*** [2] let you choose the type of comparison you want to make. You can choose between FullSim, Piles Up and FastSim. Each of them had a default ***Data Set*** of samples which is dynamically modified by the selection. The default option is FullSim (named as **Full**) as presented on the picture 2 below.
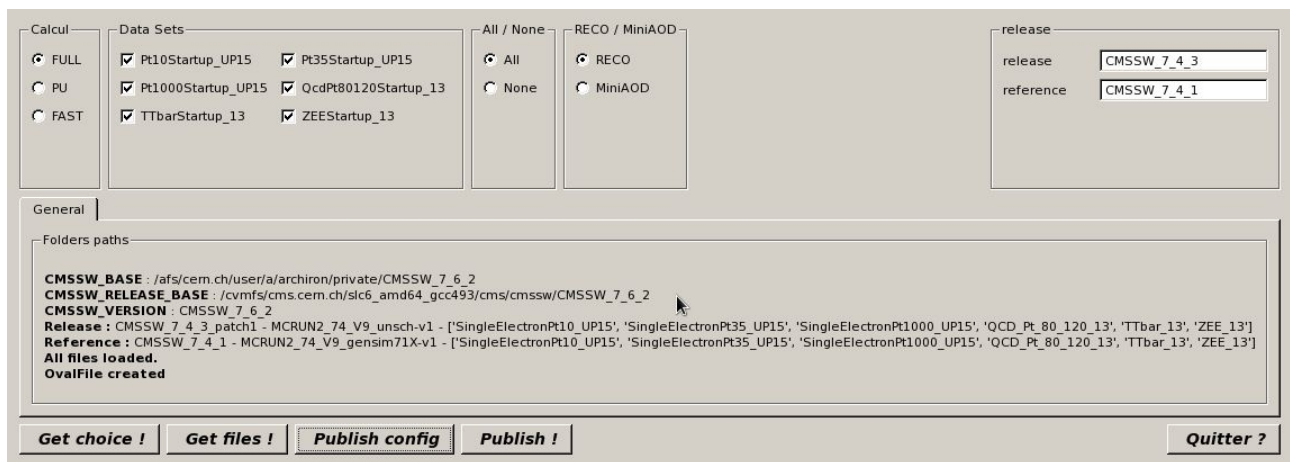


*Picture 2: FullSim default option and data set*

You can also work with Piles Up (**PU** option) :



*Picture 3: Pile Up (PU) data set*

or with FastSim (**Fast** option) as shown on Picture 4. PU and Fast had only 2 samples to work with : TTbar and ZEE.
Note that as we see later, you can make PUpmx vs PU but you have to care about the **Reference**. It

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2    French word !

**MUST** be the same as the **Release**.



*Picture 4: Fast data set*

### Second part

The second part represents the **Data Sets** which can be individually selected (see Picture 2). We have 6 sets related to ElectronPt10, ElectronPt35, ElectronPt1000, Ttbar, ZEE and QCD. All are selected by default. By clicking on one item you can unselect it.

### Third part

The third part (**All/None**) presents the possiblity to check/uncheck all the samples (data sets) and only check those you want. It is very nice when you want only to make comparisons with one one sample. If you click on None, there will be no set selected. By clicking on All, you will have all selected.



*Picture 5: FullSim data set when None is selected.*

After you have choose None, you can click on one or two set and you will work only with them.

### Fourth part

The fourth part (**Reco/MiniAOD**) is here for miniAOD vs RECO comparison. Here, as for Pupmx vs PU you have to care about the **Reference**. It **MUST** be the same as the **Release**.

## Middle part

The middle part is here to recap where you work (3 first lines), which release and reference you are using (including data sets) and indications about files you are using. You cannot interact with this part.
One can see on previous pictures that we are working in the CMSSW_7_6_2 project/folders but we are working on CMSSW_7_4_3 and CMSSW_7_4_1 releases.

**Below part**

The last part have 5 buttons. The rightest (**Quit ?**) is as it is named to quit the GUI. For the 4 others, form left to right we have :

        Get choice ! : used to select the GlobalTag for computation of the histos,
        Get files ! : used to get the ROOT files after you have choosen the GlobalTag,
        Publish config : used to precise the configuration for publication of the web page,
        Publish ! : used to publish the web page.

When you have chosen which type of comparison you want (Full, PU or Fast), which samples you like and which reference you want to use, then you have to click on the leftest button called «**Get Choice !**».

This leads you to the next picture : the getChoice Window.

***Make your choice***
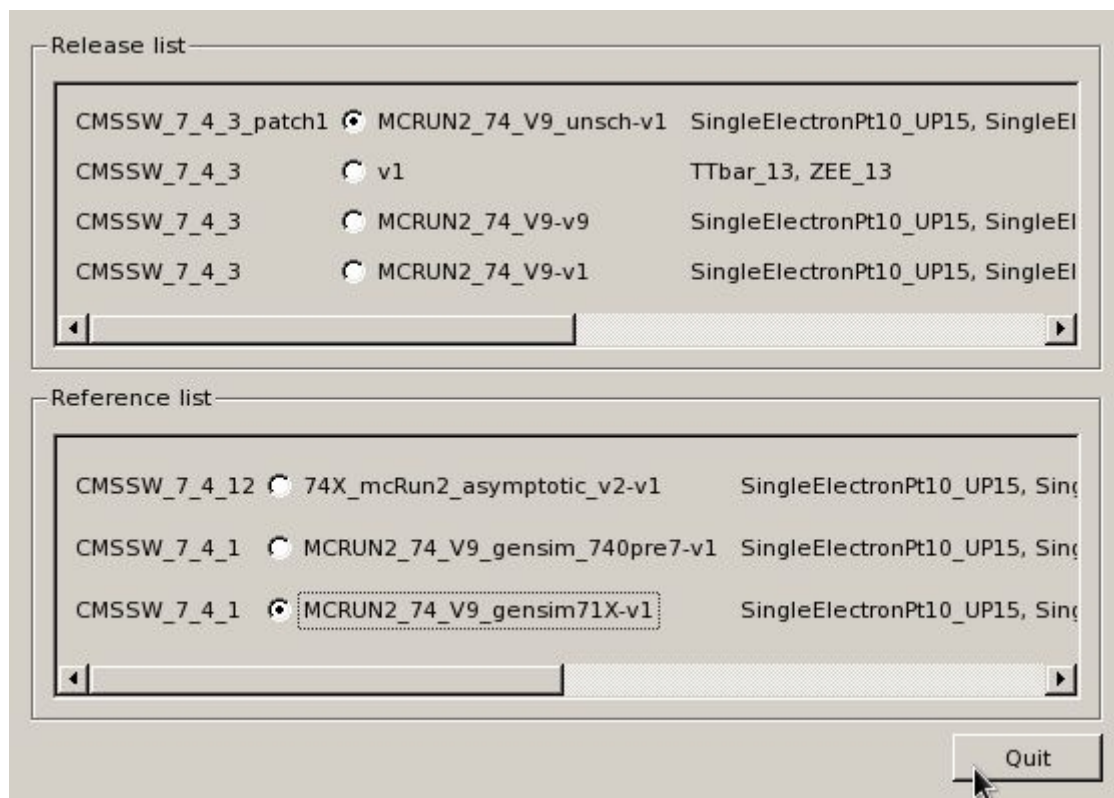


*Picture 6: getChoice window*

The upper part is referencing to the **Release** files you have to choose. The bottom part is referencing to the **Reference** files. Each line is written under the following form :
Release TAG GlobalTag Data sets
The Release TAG gives you all the releases that can be used, specially if there is patches. The GlobalTag gives you all versions that have been ran to get the ROOT files and Data sets gives you the samples which are valid for those TAGs.

You have to choose which release you want to compare as in Picture 3.

Please note that you have to select both Release and Reference. If not, when you close this window with the «**Quit**» button, you will cannot make the comparison.

Then, you select that you want and press Quit. So you go back to the general window.
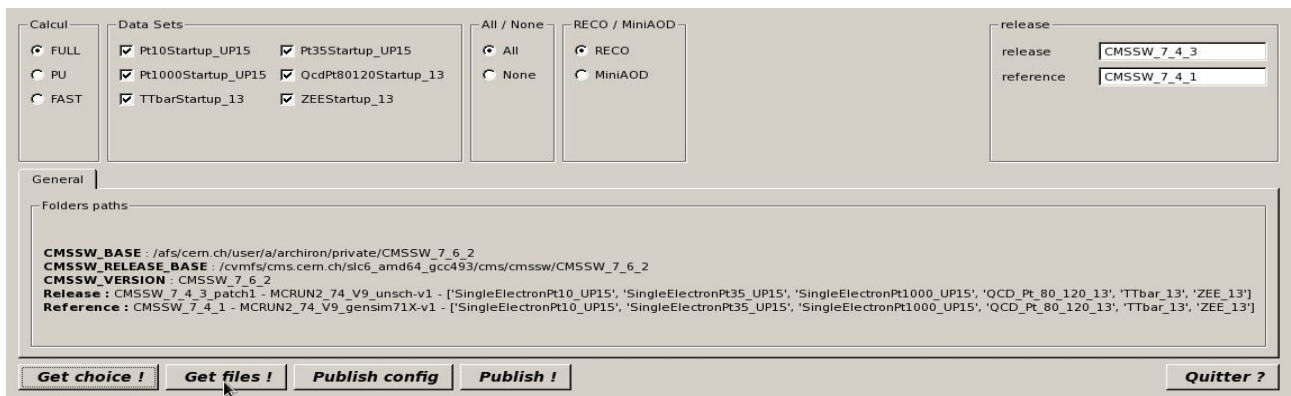
*Picture 7: back to the general window*

The «**Get files !**» button is not grayed no more. So by clicking on it you can load the files. One it's done, you get the «**All files loaded.**» and now you can click on the «**Publish config**» button.

**Be careful** : when you are working on a complete job () you can load up to 4 – 6 Go.

**Adjust the configuration**

This window gives you a summary of the used values. You can choose if you want to test something such like adding an histo on the web page (**dev** is the default option) or make a "standard" web page (by clicking on **std**).

You also have to choose if you want the web page stored on **local** (into the test folder of the release as defined on first page) or not (into the **dev**[3] or the **afs folder**[4] by clicking on **non local** which is the default option).
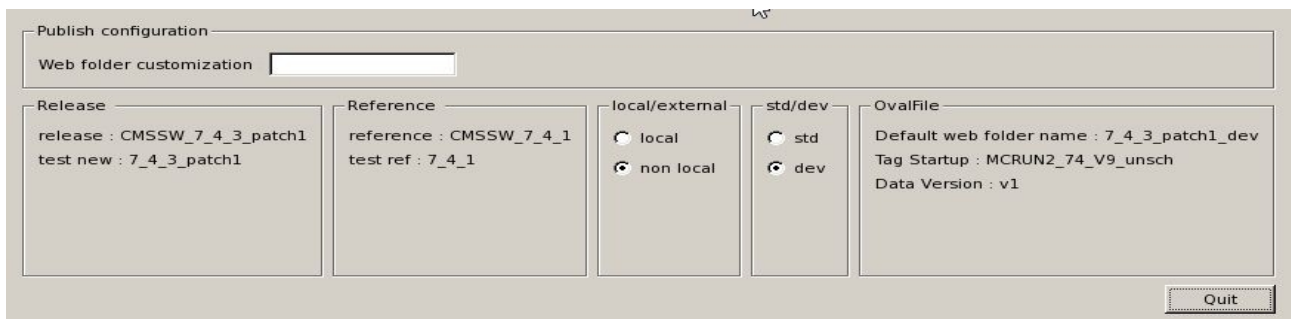


*Picture 8: getPublish window with dev and non local choice (default).*

The choice between **dev** and **std** options make the extension of the web page folder. We can see the difference on Picture8 (**dev**) and 9 (**std**).
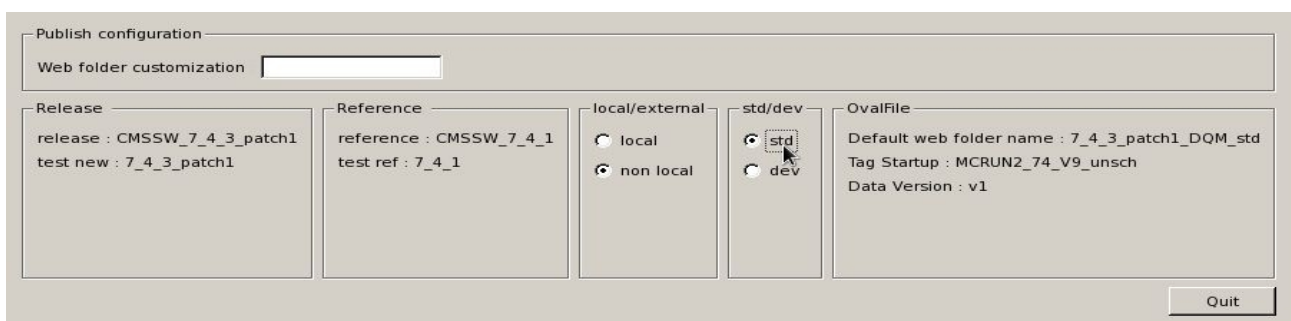


*Picture 9: getPublish window with standard (std) choice.*

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3    The **dev** folder is located on /afs/cern.ch/cms/Physics/egamma/www/validation/Electrons/Dev.
4    See the fisrt page.

If you want to make some personalization or work with Pupmx[5] you need to modify your folder name. The rule to do this is :

a – you make your selection (std vs dev),

b – you write into the blanck field (named Web folder customization) the modification to add.

See on Picture 10 for example.
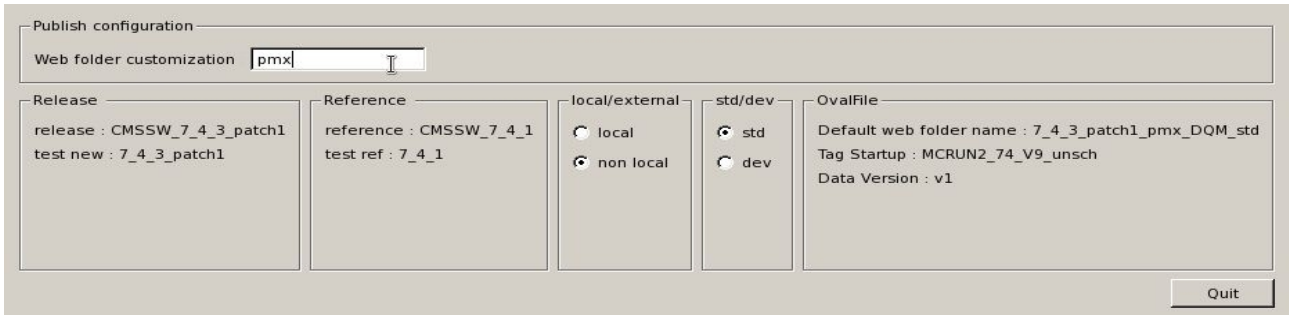


*Picture 10: getPublish window with pmx customization.*
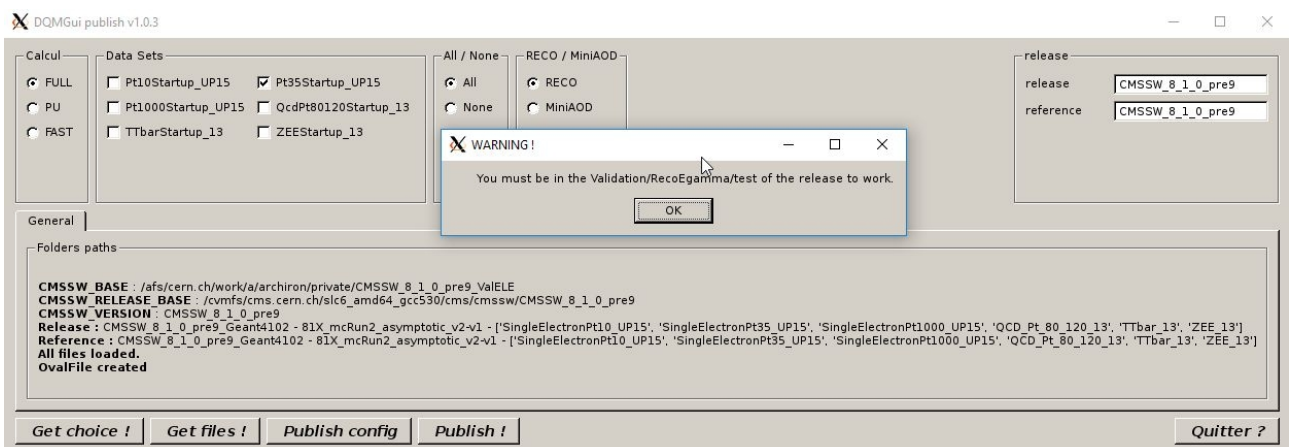
Once you have chosen your parameters, click on **Quit**.

### Publish !

On the general window, into the central part we have a new line : **OvalFile created**. This imply we can do the web pages.



*Picture 11: back to the general window (the return !)*

So Click on **Publish!** And see. If you are not in the correct path (the test folder defined on first page),



*Picture 12: error message if you are not in the correct path.*

5    In case of pmx, if you don't take care, the PU pmx web page is written on "classical" PU web page.

you will get an error message such as in Picture 12 above.

If all the parameters are OK, when it's done the line Publish done is written at the bottom of the central part (Picture 13).



*Picture 13: Final view of the general window : publish done.*