Manual for electroweak W^+W^+jj production in the POWHEG BOX

The VBF_Wp_Wp program is an implementation of the electroweak W^+W^+jj production cross section within the POWHEG BOX framework. It complements the Wp_Wp_j_j program, which provides the QCD-induced contributions to W^+W^+jj production in hadronic collisions.

This document describes the input parameters that are specific to the implementation of the EW channel. Note that the recommended settings are very similar to those for the QCD production mode. The parameters that are common to all POWHEG BOX implementations are given in the manual-BOX.pdf document, in the POWHEG-BOX/Docs directory.

If you use this program, please quote Refs. [1–3].

Running the program

Download the POWHEG BOX, following the instructions at the web site

http://powhegbox.mib.infn.it/

and go to

```
$ cd POWHEG-BOX/VBF_Wp_Wp
```

Running is most conveniently done in a separate directory, for instance do

```
$ mkdir testrun
```

The directory must contain the powheg.input file and, for parallel running, a pwgseeds.dat file (see manual-BOX.pdf and Manyseeds.pdf).

Before compiling make sure that:

- fastjet is installed and fastjet-config is in the path,
- lhapdf is installed and lhapdf-config is in the path,
- gfortran, ifort or g77 is in the path, and the appropriate libraries are in the environment variable LD_LIBRARY_PATH.

If LHAPDF or fastjet are not installed, the code can still be run using a dummy analysis routine and built-in PDFs, see the Makefile in VBF_Wp_Wp.

After compiling, enter the testrun directory:

```
$ cd testrun
```

When executing

```
$../pwhg_main
```

the program will ask you to

```
enter which seed
```

The program requires you to enter an index that specifies the line number in the `pwgseeds.dat` file where the seed of the random number generator to be used for the run is stored. All results generated by the run will be stored in files named `*-[index].*`. When running on parallel CPUs, make sure that each parallel run has a different index.

The program can be run in several steps. Each new step requires the completion of the previous step.

The timings given in the following refer to the program compiled with `gfortran` and run on a cluster with 2.7 GHz Opteron processors.

Step 1

Consists of a single run to generate the grid. At this point the user has to decide whether the weak bosons are to be generated on-shell (`zerowidth = 1`) or off-shell, distributed according to a Breit-Wigner distribution (`zerowidth = 0`). By default on-shell weak bosons are generated. The user can also select the decay modes of the weak bosons by assigning appropriate PDG code to the parameters `vdecaymodew1` and `vdecaymodew2` in `powheg.input`. Note that only leptonic decays are supported. The template analysis file `pwhg_analysis.f` needed in subsequent steps of the analysis is designed for the $e^+\nu_e\,\mu^+\nu_\mu$ mode.

We recommend to generate the grid with the option `fakevirt 1` in `powheg.input`. When using this option, the virtual contribution is replaced by a fake one proportional to the Born term. This speeds up the generation of the grid.

One needs at least 1000000 events and 10 iterations. Set the following tokens in the `powheg.input` file:

```
ncall1 1000000

itmx1 10

ncall2 0

fakevirt 1
```

Run the program via

```
$../pwhg_main
```

When prompted

```
enter which seed
```

enter 1 or any other valid seed number.

This step takes roughly 40 hours of CPU. By setting `ncall2 0` in the `powheg.input` file the program stops after the compilation of this step.

Step 2

Runs in parallel can be performed now. Comment out the `fakevirt` token from `powheg.input`.

The runs must be performed where the previously generated grid is.

The integration and upper bound for the generation of btilde can be performed with 50-100 runs with 5000-10000 calls each. Set for instance

```
ncall2 5000
```

```
itmx2 1
```

in `powheg.input`.

Folding numbers that are appropriate for runs at LHC energy are:

```
foldcsi 5 !  number of folds on csi integration
```

```
foldy 5 !  number of folds on y integration
```

```
foldphi 10 !  number of folds on phi integration
```

Time is about 3 hours of CPU for each run with `ncall2=5000`.

Setting

```
nubound 0
```

in `powheg.input` causes the program to stop after the completion of this step.

In order to run, for example, 100 processes in parallel do:

```
$../pwhg_main
```

When prompted

```
enter which seed
```

enter an index for each run (from 1 to 100). The `pwgseeds.dat` must contain at least 100 lines, each with a different seed.

Upon the completion of this step, for each parallel run a file `pwgNLO-*.top` is generated (where the * denotes the integer identifier of the run). These files contain the histograms defined in `pwhg_analysis.f` at NLO-QCD accuracy, if the variable `bornonly` is set to zero in `powheg.input`. Setting `bornonly` to 1 yields the respective LO results. In either case, the individual results of the parallel runs can be combined with the help of the `combineplots.f` file contained in the `testrun` directory. To this end, just compile the file by typing, e.g.,

```
$ gfortran combineplots.f
```

and run the resulting executable. The program will ask for the the number of `pwgNLO-*.top` files in the directory and the the number of calls per run which are set by `ncall2` in `powheg.input`. Finally, enter the integer identifier of the first file. The program will then generate the files `combinedNLO.top` and `combinedNLO-gnu.top` which contain the combined histograms in two

different formats (topdraw or gnuplot friendly).

Step 3

Also this step can be run in parallel. The number of processes can not be larger than the one used in the previous step. Setting

```
numevts 0
```

```
nubound 100000
```

takes roughly 2.5 hours per process.

The setting `numevts 0` causes the program to stop after completion of this step. The parallel execution of the program is performed as in the previous step.

Step 4

Set `numevts` to the number of events you want to generate per process, for example

```
numevts 5000
```

and run in parallel. The number of processes must not be larger than the one used in the previous step. Generating the specified number of events takes about 7 hours per process.

At this point, files of the form `pwgevents-[index].lhe` are present in the run directory.

Count the events:

```
$ grep '/event' pwgevents-*.lhe | wc
```

The events can be merged into a single event file by

```
cat pwgevents-*.lhe | grep -v '/LesHouchesEvents' > pwgevents.lhe
```

Analyzing the events

It is straightforward to feed the `*.lhe` events into a generic shower Monte Carlo program, within the analysis framework of each experiment. We also provide a sample analysis that computes several histograms and stores them in topdrawer output files.

Doing (from the `VBF_Wp_Wp` directory)

```
$ make lhef_analysis
```

```
$ cd testrun
```

```
../lhef_analysis
```

analyses the bare `POWHEG BOX` output, creating the topdrawer file `LHEF_analysis.top`. The targets `main-HERWIG-lhef` and `main-PYTHIA-lhef` are instead used to perform the analysis on events fully showered using `HERWIG` or `PYTHIA`. Various setting of the Monte Carlo can be modified by editing the files `setup-PYTHIA-lhef.f` and `setup-HERWIG-lhef.f` respectively.

References

[1] B. Jäger, C. Oleari, D. Zeppenfeld, *Next-to-leading order QCD corrections to W^+W^+jj and W^-W^-jj production via weak-boson fusion*, Phys. Rev. **D80** (2009) 034022. [arXiv:0907.0580 [hep-ph]].

[2] B. Jäger, G. Zanderighi, *NLO corrections to electroweak and QCD production of W^+W^+ plus two jets in the POWHEG BOX*, to appear.

[3] S. Alioli, P. Nason, C. Oleari and E. Re, *A general framework for implementing NLO calculations in shower Monte Carlo programs: the POWHEG BOX*, JHEP **1006** (2010) 043. [arXiv:1002.2581 [hep-ph]].