**Modifying a Classical PSHA job.ini File**Written by E. R. Abbott. Modified 12 August 2020.

Recommend editing files in Wordpad or an IDE, such as Spyder. The editor vi is automatically installed, so that can also be used if it is something you are comfortable with.

Always change.

Always evaluate/change if your analysis requires it.

Occasionally change.

Don’t touch this.

IMPORTANT NOTES:

* Between variable and value there always needs to be an equal sign
* Any unused variables need to have a # in front of them.
* The more you include in your input file (ie. the more you ask of your analysis, be it number of spectral periods, values of g per spectral period, number of probabilities of exceedance (poes) to solve for) the more it *could* slow down your analysis. This is ok, but something to be aware of.

|  |  |  |  |
| --- | --- | --- | --- |
| Category | Variable | Value | Meaning |
| [general] |  |  | General information about your hazard run. |
|  | description | Classical PSHA with NZ NSHM for Wellington | Description of the type of hazard you are running, with what source models, for where, etc. |
|  | calculation\_mode | classical | classical = classical PSHA etc. LIZZIE, ADD MORE |
|  | random\_seed | 23 | If you are running multiple sets, etc. setting the random seed allows you to reproduce your ‘randomised’ results. |
|  | concurrent\_tasks | 2 | This determines how many tasks you’re allowing your engine to run in parallel. This is related to the number of cores your engine can handle. Higher numbers of tasks *can* help your job move faster, but be careful you are not eating too far into your memory. Generally safe is 1 concurrent task per 2 cores available to your machine. |
| [geometry] |  |  |  |
|  | sites | 174.777 -41.289 | This is your individual site of interest. You can have multiple sites in this section: longitude latitude, longitude2 latitude 2, lon3 lat3) |
|  | #region | 166 -47.5, 179 -47.5, 179 -34, 166 -34 | If you want to run hazard for a specific region, this is your box. The points indicated here are the 4 corners. I don’t think they need to be in any order, but maybe just avoid jumping diagonally across your box, just in case. |
|  | #region\_grid\_spacing | 10.00 | The spacing of the grid across your region in km. |
|  | #sites\_csv | NSHM\_sites.csv | A csv site file for a region you are interested in the hazard for (ie. New Zealand). This file would be structured simply, with the longitude and latitude only of all grid points across your whole region.  NOTE: This file can be used in a run with a site model. The hazard will be calculated at the sites in this file, NOT the sites in the site model file. |
| [logic tree] |  |  |  |
|  | number\_of\_logic\_tree\_samples | 0 | 0 means that the program will do a “full path enumeration” of all logic tree branches (ie. it will calculate the result of each branch).  Any other number in this space will be the number of samples the program will take using a Monte Carlo approach. |
| [erf] |  |  |  |
|  | rupture\_mesh\_spacing | 0.2 | In km. Can change if you’re running into memory problems (ie. try 2.0 km) |
|  | width\_of\_mfd\_bin | 0.1 | Width of your magnitude-frequency bin. Don’t change for standard source model analyses. |
|  | area\_source\_discretization | 10.0 | The size of grid your area source is broken up into (km). Don’t change for standard source model analyses (we don’t have any area sources in our standard source models at this stage). |
| [site\_params] |  |  |  |
|  | #site\_model\_file | NSHM\_site\_model.xml | Only used if you are doing an analysis that requires a site model. Site model is an xml file representing different soil conditons, etc. across a variety of sites or a single regional site.  NOTE: this can be provided alone without specifying sites in the [geometry] section. If used with sites in [geometry], hazard will be calculated at the sites specified in that section. |
|  | reference\_vs30\_type | inferred | We generally do not want to change this. The other option is ‘measured’ but should be careful in using this as it changes the sigma on low probability events. |
|  | reference\_vs30\_value | 250.0 | Shear wave velocity at 30 m depth. Should be site-specific. |
|  | reference\_depth\_to\_2pt5km\_per\_sec | 5.0 | Depth to shear wave velocity of 2.5km/s. Given in km.  Please use the following equation to calculate a proxy for this value if you do not have one. |
|  | reference\_depth\_to\_1pt0km\_per\_sec | 100.0 | Depth to shear wave velocity of 1km/s. Given in metres.  Please use the following equation to calculate a proxy for this value if you do not have one. |
| [calculation] |  |  |  |
|  | source\_model\_logic\_tree\_file | source\_model\_logic\_tree.xml | This is the file that contains your source model logic tree. It must be in xml format. |
|  | gsim\_logic\_tree\_file | gmpe\_logic\_tree.xml | This is the name of the file that contains your GMPE logic tree. It must be in xml format. |
|  | investigation\_time | 50.0 | The probability of exceedance in [investigation\_time] number of years. (ie. 1 = annual; 50, years 100 years, etc.) |
|  | intensity\_measure\_types\_and\_levels | {"PGA": [0.01, 0.02, 0.04, 0.06, 0.08, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.2, 1.4, 1.6, 1.8, 2.0, 2.2, 2.4, 2.6, 2.8, 3.0, 3.5, 4, 4.5, 5.0], "SA(0.075)": [0.01, 0.02, 0.04, 0.06, 0.08, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.2, 1.4, 1.6, 1.8, 2.0, 2.2, 2.4, 2.6, 2.8, 3.0, 3.5, 4, 4.5, 5.0]…} | The spectral periods (ie. PGA, SA(0.075),… SA(1.0)…) and values of g for which you are interested in probabilities of exceedance.  Note that the values you can use vary from GMPE to GMPE (ie. the standard McVerry et al. 2006 GMPE will not compute beyond 3.0s and your analysis will fail if you try to exceed it). |
|  | truncation\_level | 3 | Sigma truncation. 3 is standard.  None: Means you are not truncating.  Zero: Means you are looking at the 50th percentile hazard |
|  | maximum\_distance | 400.0 | The distance from your source out to which sources are included in the analysis. Given in km. |
| [output] |  |  |  |
|  | export\_dir | ../output | Location of where you would like the output of this analysis to go relative to where this input file is located. |
|  | mean\_hazard\_curves | true | Do you want hazard curves? Yes = true. No = false  NOTE: This parameter is also important for automatic provision of individual logic tree branch results at the end of the calculation. If you select ‘false’ you will not get a ‘mean’ result, only the individual logic trees. |
|  | quantile\_hazard\_curves | 0.5 0.84 | What quantile hazard curves do you want? Given on a 0-1 scale. (ie. 50th-percentile is 0.5; 84th-percentile is 0.84)  You can have as many of these as you want; each new one is separated from the previous one by a single space.  You need to have these in order to get quantile uhs as well. |
|  | hazard\_maps | false | Do you want to produce a hazard map? Yes = true. No = false.  Note: this is probably not worthwhile unless you are running the hazard for a region. |
|  | uniform\_hazard\_spectra | true | Do you want uniform hazard spectra? Yes = true. No = false |
|  | poes | 0.28 0.095 0.0198 0.00499 | What probabilities of exceedance are you interested in? The probability is based off of your investigation time using the following equation:  poe = 1-e^(-investigation\_time \* 1/rate)  where rate is your return period of interest.  You can have as many of these as you want. Each new one is separated from the previous one by a single space. |