**Manual**

**Introduction :** A python program to run TSA-IT on fMRI image(s)

**Installation:** Download the tsa-it.py file, and install/update python 3.8 in your system

**Usage**: Run the .py file in a command line/terminal using the command below. It supports the following optional/compulsory arguments.

$ python tsa-it.py [-h] [-f] -i Inputfile -o Outputfile [-m mask] [-w window] [-n] [-b] [-t trials\_file] [-x v1, v2, v3...] [--version]  
**Required arguments:**

-i <INPUT> [INPUT ...], --input <INPUT> [INPUT ...]  
   4D input files on which to compute TSA-IT. These can be of the following format type: NIfTI (. nii or.nii.gz), Analyze (.img), DICOM (.dcm), MINC (.mnc). Mask option is not mandatory if the file type is NIfTI, mandatory in all other cases.

-o <OUTPUT>, --output <OUTPUT>  
Output directory in which the results will be produced. It produces 6 (4D) files:  p-value (log10 and suitable signs), q-value (log10 and suitable signs), t-value (the t-value for the corresponding statistical test of change from the onset of the trial), z-values (t-values converted to z-values), mean difference from the baseline (percent signal change) and the standard deviation of the differences of the percent signal change from baseline.

-t or -x option (see below for their functionality)  
  
**Optional arguments:**

  -h, --help       Show this help message and exit

  -f, --file         Whether input is to be given as a file or not. If this option is given, then the -i <INPUT> is a file containing the names of input files and -t <trials.txt> is a file containing the list of EV files corresponding to the input files (-x option cannot be used in this case). These files contain multiple runs for the same subject and the trials in these need to be combined to produce the final inter-trial TSA output.

  -m <MASK>, --mask <MASK> NIfTI mask file (3D) for masking input data. If <MASK> is a number then input files are thresholded by that number to produce the mask.

  -w begin end, --window begin end  
The arguments begin and end can be integers or floating-point numbers. They are basically the time window (in seconds) from begin to end, relative to the start trials (begin can also be negative, which means that the window starts before the trial; end can also be negative or positive) for which to compute the ITS. The default window size is set to 25 seconds after the end of the task condition, which is the maximum duration for which hemodynamic response function can influence the BOLD signal)

  -n, --normal       Consider a null hypothesis of that the percentage signal change from the baseline is normally distributed with a mean of zero to calculate ITS probabilities (default).  
  -b, --binomial   Consider a null hypothesis of that the percentage signal change from the baseline is binomially distributed with a parameter p=0.5 (i.e., equal chance of the signal change random variable assuming a positive or negative value) to calculate ITS probabilities (default).

  -t <trials.txt>       Path to the location of the trials file (EV file). The file may be in a single column format (consisting of only the onset of the trial blocks) or three column formats (consisting of the onset, duration, and trial amplitude of the trial blocks) of FSL.

  -x v1, v2, ...          A list of volume numbers indicating the beginning of trials. Cannot be used with -t option.

  --version             Show program's version number and exit

**Output :** The 4D images of statistical test results (t-test, p values etc.) are generated in the output folder specified in the argument. The results can be viewed using any 4D image viewer eg. fsl.